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Phylogenetic relationships and the evolutionary history of *Tillandsia*, a species-rich genus of Bromeliaceae

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Abstract

Understanding the drivers and constraints of species formation is at the heart of evolutionary research. The processes that give rise to new species often involve colonization of novel ecological niches and the evolution of novel traits, achieved through an intricate interplay of environment, phenotype and genotype. Modern high-throughput sequencing enables to resolve phylogenomic relationships and to investigate the genomic footprints of evolutionary history. However, research on these topics in recent rapid radiations poses unique challenges: a brief diversification period in adjacent habitats increases the probability of incomplete lineage sorting and introgression among closely related taxa, confounding phylogenetic signal and complicating phylogenomic inference. This thesis focuses on the evolutionary history of the highly diverse and rapidly radiating genus Tillandsia (family Bromeliaceae). This genus is the largest and most diverse within the family and presents a variety of ecological adaptations to various habitats, mostly epiphytic and saxicolous. The first main chapter reports the design and efficacy of a target capture bait set specific for Bromeliaceae, devised to address evolutionary questions at both micro- and macro-evolutionary scales. The set targets 1,776 single- and multi-copy genes, including some putatively associated with key innovation traits. Using a wide sampling of members across the family with a particular focus on Tillandsia, the taxon-specific bait set was compared to a universal bait set, the Angiosperms353 kit. The comparison considered the kits' performance for both phylogenomics and population genetics, with the expectation that the taxon-specific kit will obtain higher information content and provide increased utility in rapidly radiating clades, compared with the universal kit. Despite retrieving higher information content in the taxonspecific kit, we found that the universal kit performed comparatively well for phylogenomics inference. However, the taxon-specific kit is preferable for detailed investigations, such as estimation of gene tree incongruence and population genomics analyses. The second main chapter explores phylogenomic relationships among 32 species in the clade Tillandsia, focusing on rapidly-radiating central-American taxa from subgenus Tillandsia. Using wholegenome resequencing data, we inferred relationships among species and explored the evolutionary history of the clade using tree-based and network-based approaches. We found a lack of monophyly and deviations from a tree-like structure, coupled with rampant gene tree discordance. In contrast to classical hypotheses, the uncovered pervasive hybridization along

the phylogeny suggests that the expansion of the subgenus from South into Central America proceeded in several migration waves, followed by episodes of diversification and gene flow. Focusing on hybridization, Patterson's D (ABBA-BABA) and related statistics were used to describe the rates and timing of introgression events. Finally, we discussed the possible contribution of interspecific gene flow to adaptive trait shifts. In summary, the thesis generates novel insights into the evolutionary processes that contribute to a Neotropical rapid radiation and offers future prospects for research in Bromeliaceae at large and specifically in *Tillandsia*.

Zusammenfassung

Das Verständnis der Triebkräfte und Zwänge der Artenbildung steht im Mittelpunkt der Evolutionsforschung. Die Prozesse, die zur Entstehung neuer Arten führen, beinhalten oft die Besiedlung neuartiger ökologischer Nischen und das Auftreten neuartiger Merkmale, die durch ein kompliziertes Zusammenspiel von Umwelt, Phänotyp und Genotyp erreicht werden. Die moderne Hochdurchsatzsequenzierung (HTS) ermöglicht es, phylogenomische Beziehungen zu klären und den genomischen Fußabdruck der Evolutionsgeschichte zu untersuchen. Die Erforschung dieser Themen bei den jüngsten schnellen Ausbreitungen stellt jedoch eine besondere Herausforderung dar: Eine kurze Diversifizierungsphase erhöht die Wahrscheinlichkeit einer unvollständigen Sortierung der Abstammungslinien und der Introgression zwischen eng verwandten Taxa und verwirrt gleichzeitig die phylogenomischen Signale, was die Schlussfolgerungen erschwert. Diese Arbeit konzentriert sich auf die Evolutionsgeschichte der äußerst vielfältigen und sich schnell ausbreitenden Gattung *Tillandsia* (Familie Bromeliaceae). Diese Gattung ist die größte und vielfältigste innerhalb der Familie und weist eine Vielzahl ökologischer Anpassungen an verschiedene Lebensräume auf, die meist epiphytisch und felsbewohnend sind.

Das erste Hauptkapitel beschreibt das Design und die Wirksamkeit eines Target-Capture-Bait-Sets für Bromeliaceae, das speziell entwickelt wurde, um evolutionäre Fragen sowohl auf mikro- als auch auf makro-evolutionärer Ebene zu beantworten. Das Set zielt auf 1.776 Single-Copy- und Multi-Copy-Gene in allen Bromeliaceae ab, darunter auch Gene, die vermutlich mit wichtigen innovativen Merkmalen in Verbindung stehen. Anhand einer breiten Stichprobe von Mitgliedern der Familie mit Schwerpunkt auf Tillandsia wurde das taxonspezifische Bait-Set mit einem universellen Bait-Set, dem Angiosperms353-Kit, verglichen. Bei dem Vergleich wurde die Leistung der Kits sowohl für die Phylogenomik als auch für die Populationsgenetik berücksichtigt, wobei die Erwartung bestand, dass das taxonspezifische Kit im Vergleich zum universellen Kit einen höheren Informationsgehalt und einen größeren Nutzen vor allem für die Forschung auf Populationsebene in sich schnell ausbreitenden Kladen bieten würde. Trotz des höheren Informationsgehalts des taxonspezifischen Kits zeigte das universelle Kit eine vergleichsweise gute Leistung bei phylogenomischen Schlussfolgerungen. Für detaillierte Untersuchungen, wie z. B. die Abschätzung der Genbauminkongruenz und populationsgenomische Analysen, ist das taxonspezifische Kit jedoch vorzuziehen.

Im zweiten Hauptkapitel werden die phylogenomischen Beziehungen zwischen 32 Arten der Gattung Tillandsia untersucht, wobei der Schwerpunkt auf der mittelamerikanischen Untergattung Tillandsia liegt. Unter Verwendung von Ganzgenom-Resequenzierungsdaten haben wir die Beziehungen zwischen den Arten abgeleitet und die Evolutionsgeschichte der Gattung mit Hilfe eines baumbasierten Ansatzes untersucht. Wir stellten fest, dass es keine Monophylie und keine baumähnliche Struktur gibt, und dass der Genbaum sehr uneinheitlich ist. Im Gegensatz zu klassischen Hypothesen deutet die aufgedeckte weit verbreitete Hybridisierung entlang der Phylogenie darauf hin, dass die Ausbreitung der Untergattung nach Mittelamerika in mehreren Migrationswellen erfolgte, gefolgt von Episoden der Diversifizierung und des Genflusses. Mit Blick auf die Hybridisierung wurden Pattersons D (ABBA-BABA), verwandte Statistiken und ein modellbasiertes phylogenetisches Netzwerk verwendet, um die Raten und den Zeitpunkt von Introgressionsereignissen zu beschreiben. Schließlich wurde der mögliche Beitrag des intraspezifischen Genflusses zu adaptiven Merkmalsverschiebungen diskutiert. Zusammenfassend lässt sich sagen, dass diese Arbeit neue Erkenntnisse über die evolutionären Prozesse liefert, die zu einer raschen neotropischen Radiation beitragen, und Zukunftsperspektiven für die Forschung an Bromeliaceae im Allgemeinen und an Tillandsia im Besonderen bietet.

Introduction

The genetics of rapid evolutionary radiations

Biodiversity has transformed from an idiosyncratic research topic of highly specialised scholars to an issue at the center of social, economic and political discourses (Escobar, 1998; Gowdy, 1997; Shih et al., 2020; Watermeyer et al., 2021). The aspiration to understand the mechanisms that promote speciation dates back to biologists of the evolutionary synthesis and remains pivotal to evolutionary biology (Brown, 2014; Dobzhansky, 1937; Lewin et al., 2018; Mayr, 1999; Pennisi, 2005; Terborgh, 2015). 'What drives biological diversity?' is a question of multifaceted, interdisciplinary nature: diversity differs among taxonomic groups and geographical regions and is determined by a complex interplay of past events, ecological heterogeneity, phenotypic features and genetic makeup (Brown, 2014; Hillebrand, 2004; Linder, 2008; Rabosky, 2009).

Rapid evolutionary radiations, defined as the generation of a large number of species over a short time, give researchers the opportunity to link inherent traits and extrinsic environmental processes. Much attention has been given to rapid radiations, which are so pervasive among the Tree of Life some suggest they generated most of the extant biodiversity (Givnish, 2015; Linder, 2008; Rabosky, 2009; Rundell & Price, 2009; Wiens, 2017). Within the flourishing investigation of rapid radiations several taxa had been thoroughly studied, like the African cichlid fishes (Brawand et al., 2014; Malinsky et al., 2015; Wagner et al., 2012), Heliconius butterflies (Merrill et al., 2015; Van Belleghem et al., 2021) and Anolis lizards (Losos, 2009; Losos, 1994; Stroud & Losos, 2020). Comparable, albeit more limited research focused on plant groups, for example the New World genus Lupinus (Contreras-Ortiz et al., 2018; Drummond et al., 2012), the Neotropical family Bromeliaceae (Givnish et al., 2014; Palma-Silva & Fay, 2020), American live oaks (Cavender-Bares et al., 2015; Eaton et al., 2015) and New Caledonian persimmons (Paun et al., 2016; Samuel et al., 2019). These investigations of plant radiations already provided examples to the mechanisms of diversification and yet much remains unexplored (de La Harpe et al., 2017; Linder, 2008; Suarez-Gonzalez et al., 2018).

When a rapid increase in speciation rates is driven by the adaptation of organisms to new ecological contexts, the process is termed adaptive radiation. Modern definitions of adaptive radiations developed and gained controversy, but all generally focus on an increase in ecological diversity (Glor, 2010; Schenk, 2021; Schluter, 2000). Schluter (2000) posed four criteria for the diagnosis of adaptive radiations: common ancestry, phenotypeenvironmental correlation, trait utility and rapid speciation. The first and fourth criteria were more deeply studied and fewer studies attempted to present functional evidence of a trait utility and to identify significant correlation between phenotype and environment (Losos & Miles, 2002; Schenk, 2021). Arguably, studies that focus on the tempo of diversification may be overlooking the ecological aspects of adaptive radiation (Givnish, 2015; Schenk, 2021).

In order to describe the evolution of radiations through time, Naciri & Linder (2020) offered a model focused on population genetic structure and trait genetic architecture:

- Initially, a taxonomic lineage disperses into a novel adaptive zone which is usually a new geographic area. This stage may be driven by prior acquisition of traits that allow that lineage to prosper or avoid stress in the novel habitat (Klak et al., 2004). Evolutionary biologists often accompany this with the assumption of relaxed biotic competition either competitors for the same niche have not yet arrived or antagonists like herbivores or diseases are absent. These hypotheses are termed the ecological release and the enemy release hypothesis, respectively (Hughes et al., 2015; Yoder et al., 2010).
- In the next two steps, the new lineage undergoes (1) geographical or (2) ecological expansion or both. Range expansion happens rapidly and is assumed to be associated with the appearance of novel adaptive traits, especially in the case of adaptive radiations. These adaptations are termed 'key innovations', defined as traits that allow a lineage to utilize novel niches (Stroud & Losos, 2016). Populations across the new geographical range experience differing rates and types of selection, population bottleneck, isolation by distance (IBD) or by environment (IBE; Prunier et al., 2017; Sexton et al., 2014).
- As a consequence, populations that adapted sufficiently survive while others perish. The remaining populations may speciate by achieving reproductive isolation or retain genetic connectivity (Lexer et al., 2005; Linck & Battey, 2019; Nei et al., 1983; Nosil, 2008).

The conditions that favour rapid diversification have been rigorously explored in the last few decades with the quick progression of new sequencing technologies. Molecular biologists studying rapid radiations usually address several challenges: (1) recognizing the evolutionary processes that drive or limit divergence; (2) exploring the balance between selection and neutral processes and (3) addressing the 'radiation paradox': How can lineages that expand from small genetic pools develop, in a short amount of time, enough genetic variation to create abundant phenotypic diversity? (Brawand et al., 2014; Gillespie, 2016; Hidalgo et al., 2017; Naciri & Linder, 2020; Pease et al., 2016). Since genomic processes occur across both deep and shallow timescales, addressing questions on the genomic basis of radiations requires connecting two conceptual worlds: macro-evolutionary approaches based on phylogenetics and micro-evolutionary approaches based on population genetics (de La Harpe et al., 2017).

Numerous, mutually-inclusive processes were found to facilitate genetic differentiation in rapid radiations, especially after long-distance dispersal. The roles of standing ancestral variation and hybridization were at the focus of research in the last decades. Both processes are virtually universal in rapid radiations (Novikova et al., 2016; Wu et al., 2018). The persistence of ancestral allelic polymorphism during radiation (incomplete lineage sorting, henceforth ILS) contributes to genetic variability during phases of selection and stochastic allele fixation. Additionally, ample evidence suggests that hybridization and gene flow increase genetic variability by exchange of genetic composition between incipient species. The introduction of alleles upon which selection has already acted is expected to enable diversification through adaptive introgression (Abbott et al., 2013; Meier et al., 2017; Pease et al., 2016; Suarez-Gonzalez et al., 2018). Both whole genome and gene duplications contribute to adaptation by offering genetic variability for selection and the latter may lead to genome structural shifts (Barrier et al., 1999; Couvreur et al., 2010; Soltis & Soltis, 1999). Transposable elements may create genomic changes that generate variability (e.g., Chuong et al., 2015). In cichlid fishes, TE activity was found to alter gene expression during periods of relaxed selection (Brawand et al., 2014; Choudhury & Parisod, 2017). Finally, Epigenetic changes are thought to allow populations to extend the suitable range of habitats, providing more time for other genetic processes to occur. It's been further suggested that epigenetic changes may generate heritable phenotypic variation (Ashapkin et al., 2016; Flatscher et al., 2012; Paun et al., 2007).

Phylogenomics of rapid radiations

Evolutionary research requires a fundamental understanding of the relationships between studied taxa. Molecular studies joined the field of taxonomy for the task of identifying and delimiting species, applying approaches that investigate the diversity between DNA sequences to infer the level of divergence between taxa. The power to infer the past from contemporary data depends on the type of data obtained, the study system and the properties of the analytical models (Delsuc et al., 2005; Hebert et al., 2003; Philippe et al., 2011). Molecular phylogenies were usually based on sequencing a few highly conserved markers like organellar DNA sequences, microsatellite markers and Sanger-sequenced nuclear genes or genome regions. These remain popular due to the moderate cost efficiencies, the ease of designing the necessary PCR primers and of detecting polymorphism (Barbara et al., 2007; de La Harpe et al., 2017; Schlotteröer et al., 1991; D. X. Zhang & Hewitt, 2003). A single genomic region is then used to infer a gene tree which can be, but often is not an estimate of the 'true tree' describing species relationships (Huson & Bryant, 2006). Conserved markers, however, often provide insufficient variation to resolve relationships among closely related taxa. This is especially true for studies of rapidly radiating lineages and incipient species that have recently diverged (Escudero et al., 2020; Straub et al., 2012; Urantowka et al., 2017).

In the last decades, increased accessibility to next-generation sequencing (NGS) transformed phylogenomic approaches and analytical tools advanced accordingly. As molecular biologists now utilize large amounts of multi-locus genomic data, they achieve unprecedented resolution of the relationships between clades across the tree of life (Davey et al., 2011; Escudero et al., 2020; Philippe et al., 2011). Reviewing the current wealth of NGS methods is beyond the scope of this introduction, but generally, the methods can be divided between whole-genome sequencing and reduced representation approaches (e.g., RNA sequencing, target capture and restriction site associated DNA sequencing (RAD-Seq); Baird et al., 2008; de La Harpe et al., 2017; Puritz et al., 2014; Weitemier et al., 2014; Zimmer & Wen, 2013).

A vast volume of data did not, however, immediately clarify the phylogenies of 'difficult lineages'. First, an increase in the amount of data is coupled with multiplication of technical biases and limitations: random noise, misspecified model parameters, substitutional saturation and errors in data assembly or filtering are a few examples (Kandziora et al., 2022;

Morales-Briones et al., 2021; Philippe et al., 2011). More importantly, extensive genomic data showcases the boundless complexity of evolutionary genomic processes: modern phylogenomic data-sets are sequenced from one or a few individuals per species and alignments of individual loci are used to estimate gene trees. Since recombination decouples genomic regions, the result is a collection of thousands of tree topologies, each representing a different part in the history of a lineage (Hibbins et al., 2020; Kandziora et al., 2022; Wu et al., 2018). Gene tree discordance between the different topologies is unexceptional and indeed is considered quintessential in rapid radiations. An array of successive speciation events result in low sequence variation and increase the probability of ILS, hybridization, and gene duplication and loss, reducing phylogenetic signal and leading to high gene tree discordance (Huson & Bryant, 2006; Maddison, 1997). Some phylogenomic studies approach gene tree discordance as a technical challenge, while others exploit the information it conveys about evolutionary processes (Morales-Briones et al., 2021; Philippe et al., 2011).

The advent of phylogenomics proceeded with novel methods of data-processing and phylogenetic inference from large data-sets. A common approach to the analysis of multiple gene sequences per species is concatenation of sequences and subsequent analysis of the matrix as a single 'supergene' (Degnan & Rosenberg, 2009; Gadagkar et al., 2005). Concatenation often results in well-supported phylogenies, however it assumes that all sequences evolved according to one evolutionary tree and may lead to inference of the wrong species tree, especially in the presence of ILS (Degnan & Rosenberg, 2009; Edwards et al., 2007; Kubatko & Degnan, 2007). In contrast, the multi-species coalescence (MSC) addresses phylogenetic reconstruction in the presence of ILS and is considered more robust in several contexts (Edwards et al., 2016; Liu et al., 2015). Furthermore, inference employing the MSC can model gene tree incongruence with methods like BEAST and ASTRAL (Degnan & Rosenberg, 2009; Jiang et al., 2020; Mirarab et al., 2014). The MSC however obtains a nonreticulated species tree which does not account for hybridization and introgression, two relatively common evolutionary processes (but see network extensions: Wen et al., 2016; C. Zhang et al., 2018). In contrast, a few methods can account for ILS and simultaneously infer hybridization explicitly, among them the D-statistic and related statistics (Box 1; Malinsky et al., 2015; Martin & Jiggins, 2017; Patterson et al., 2012), and model-based construction of phylogenetic networks. The latter represents a new frontier in reconstructing evolutionary histories, yet remains computationally challenging and thus only feasible for small data-sets

(Wen et al., 2018; Yu & Nakhleh, 2015). Ultimately, the field of molecular evolution is experiencing more than a mere methodological shift, but rather a philosophical and conceptual one. As evidence accumulates for both data structures and lineages whose history contradicts a simple bifurcating species tree, the predominant use of bifurcating trees to describe diversification is being challenged (Ellstrand, 2014; Mallet et al., 2016; Novikova et al., 2016; Oaks et al., 2022).

Box 1. D-statistics and variations used in the second chapter of this work.

1. **Patterson's D** (ABBA-BABA) – Illustrated in figure 1, a simple test for introgression, robust to the presence of ILS. It exploits asymmetries in the frequencies of nonconcordant gene trees in a three-population tree ordered (((P1,P2,),P3),O), where the outgroup O carries the ancestral allele A and the derived allele is denoted as B. Allele frequencies are used to calculate the D-statistic, with values ranging between -1 and 1, indicating an excess of shared derived alleles between P1 and P3 at one end of the range, and between P2 and P3 in the positive range (Patterson et al., 2012; Green et al., 2010).

2. D_G – a test for consistency of clade assignment. $D_G(A,G_1;G_2,O)$ is calculated for all possible combinations of individuals, where G_1 and G_2 are assigned to the same clade and A is assigned to a different clade. The results indicate whether individuals assigned to the same clade always share more derived alleles with each-other than with any individual from another clade (Malinsky et al., 2018).

3. \mathbf{D}_{\min} – indicates taxon relationships that deviate from a tree structure. Calculating the minimum value of D across all possible arrangements of a trio (((P1,P2,),P3),O), it provides a 'lower bound' estimate of the amount of gene flow within each trio. A positive score signifies the sharing of derived alleles between the species in the trio is inconsistent with a tree structure (Malinsky et al., 2018, 2021).

4. f_4 -ratio – known as admixture fraction f, a method for estimating ancestry proportions. The statistics measure correlations in allele frequencies among sets of four populations. Observed values reflect degrees of shared ancestry based on the difference in allele frequencies at biallelic loci, providing a measure for the proportion of the genome involved in admixture. The f4-ratio is a variation informative of admixture between 4 populations P1, P2, P3 and O (Green et al., 2010; Lipson, 2020).

5. $f_b(C)$ – also named *f*-branch, a statistics that disentangles correlated f_4 -ratio results and assigns gene flow signal to specific, possibly internal, branches on a phylogeny. Using all *f*-scores on a given tree, $f_b(C)$ captures excess allele sharing involving branches, including internal ones. By utilizing multiple *f*4-ratio calculations, it provides additional information about the timing of introgression events (Malinsky ey al., 2018, 2021).

6. f_{dM} developed to test for introgression in genomic windows, assesses whether the admixture signal is confined to specific loci. As a modification of the f_d statistic, it can quantify shared variation between P3 and P2 (positive values) or between P3 and P1 (negative values). The calculation of f_{dM} further depends on the frequency of the derived allele in P1 and P2 (Malinksy et al., 2015; 2021).



Figure 1. Sharing of derived alleles is informative of gene tree topologies. Above: ABBA sites are those in which P2 and P3 share a derived allele (star), while P1 features the ancestral allele. Under a null hypothesis of only ILS, the frequencies of ABBA and BABA patterns are expected to be equal. Below: Introgression between P2 and P3 will lead to increased frequency of ABBA patterns and positive values of D (see Box 1; adapted from Malinsky et al., 2021).

Study group

The present thesis is dedicated to the plant genus *Tillandsia* (family Bromeliaceae). The taxon was chosen for its impressively high phenotypic diversity, young crown age and unique characteristics. Furthermore, this study complemented larger group efforts to develop molecular resources for studying *Tillandsia*, envisioning it as an emerging model group for studying Neotropical radiations.

Bromeliaceae, a Neotropical radiation of flowering plants, was described by Benzing (2000) as a family that "exemplifies botanical radiation in the extreme" due to its remarkable diversity. This conspicuous monocot angiosperm family of >3,000 species is characterized by unique appearance, with distinctive leaf rosettes that often impound rainwater in central tanks (phytotelmata; figure 2). With high abundance in tropical regions and exquisite beauty, bromeliads fascinated botanists and amateurs for centuries and are still rigorously described, delimited and studied today (Benzing, 2000; Mez, 1904; Picado-Twight, 1913; Schimper, 1888; Tietze, 1906). Bromeliaceae thus constitutes an excellent research system for studying the drivers and constraints of adaptive radiations, especially the evolution of Neotropical biota (Givnish et al., 2011; Palma-Silva & Fay, 2020). According to fossil-calibrated phylogenies, the family originated in the Guayana Shield c. 100 Mya and most of the extant taxa in the family expanded beyond their ancestral distribution, quickly diversifying over a short period of 10-15 Mya. Occurring from northern Patagonia to southeastern USA with a single species in West Africa, bromeliads occupy a range of habitats, from moist mountainous rainforests to dry, rocky sites. Their diversification is associated with orogenic changes, the most notable of which is the uplift of the Andes, and with acquisition of 'key innovations', functional traits that allowed them to prosper in diverse adaptive zones (Givnish et al., 2007, 2011; Schulte et al., 2009).

Bromeliad phenotypic adaptations evolved multiple times and in a correlated and contingent manner, creating adaptive syndromes. The association of spatial and temporal patterns in bromeliads allows researchers to hypothesize and test for reciprocity between ecology, habit and rates of diversification (Crayn et al., 2015; Givnish et al., 2014; Schulte et al., 2009). I will further focus on epiphytism which is highly prevalent in *Tillandsia* as in the family altogether: bromeliad epiphytism is associated with humid tropical montane habitats and both are associated with a tank habit, as heavy nutrient-rich rain and detritus derived

from host plants accumulate within the tank. Moreover, the tank hosts a diversity of arthropods and other small animal species and microbes, providing the plants with nutrients through indirect carnivory¹. Epiphytism is further associated with "entangling seeds" that ensure attachment to tall tree branches (Benzing, 2008; Gentry & Dodson, 1987; Givnish et al., 1984, 2014; Romero et al., 2010). Inversely, in dry, terrestrial sites, epiphytism is rather associated with adaptations to prolonged periods of drought. The most commonly observed adaptations are the evolution of CAM photosynthesis, leaf succulence and a dense cover of water-and-nutrient-absorptive trichomes, all which reduce transpiration and provide longer periods of carbon uptake in xeric environments (Benzing, 2008; Givnish et al., 2014; Koch et al., 2020; Mez, 1904). The correlated occurrence of these phenotypes produce the 'atmospheric' epiphytic habit, one which is especially common in *Tillandsia* (see below). Notably, CAM evolution is also common in terrestrial bromeliads and at low elevations (Benzing & Renfrow, 1974; Koch et al., 2020). Finally, bromeliads repeatedly developed ornithophilous pollination syndromes which in turn are associated with fertile, humid habitats (Kessler et al., 2020; Krömer et al., 2006). Numerous adaptations favour high rates of diversification: as epiphytism provides a range of micro-niches over a dynamic habitat, entangled seeds offer greater dispersal ability and hummingbird pollination increases diversification, possibly through pollination specialization, limitation of pollen transfer and differential speciation rates mediated through phenology and animal behavior (Gentry & Dodson, 1987; Givnish et al., 2014; Kessler et al., 2020; Krömer et al., 2006).

Bromeliad phylogenetic classification is dynamic and new species and genera are periodically described. Regardless, phylogenetic studies consistently recognize eight subfamilies, out of which Tillandsioideae is the largest with <1,400 species. Diversification in this family is estimated to be associated with the uplift of the Andes (Barfuss et al., 2016; Givnish et al., 2007). Subject to ongoing taxonomic revisions, 6-9 genera are recognized in the subfamily and *Tillandsia* is the most diverse and species-rich with approximately 600 species of predominantly epiphytic plants (Barfuss et al., 2016; Till, 2000).

Archaeological evidence suggests that *Tillandsia* were of great cultural importance before their description by European scientists: *T. usneoides* ('Spanish moss') was found in

¹ And the bromeliad research community with stories of the miscellaneous bites and stings they accumulated during fieldwork.

pottery-making societies of the Archaic period in North America and was used for fruit wrapping and pillow filling (Gilmore, 2015; Pierce, 2000). *Tillandsia* was used ritually as decoration and depicted on pottery in religious contexts - probably as early as the Aztec culture - and its ceremonial use continues to this day (Arslanian et al., 1986; Bye Jr, 1979; Gilmore, 2015; Pierce, 2000). The economic and medical uses of *Tillandsia* are historically documented and extend into the 20th century, from the use of leaf decoction to control diabetes and as a contraceptive agent, to modern Brazilian and US farmers using *Tillandsia* as cattle feed (Delaporte et al., 2004; Keller et al., 1981). The family and genus are both of current horticultural interest. Meanwhile, conservation concerns increase due to unsustainable harvesting practices (Estrella-Parra et al., 2019; Hietz, 2005; Wolf & Konings, 2001). Research in this genus therefore holds cultural relevance and importance for conservation.

Several morphological characters were historically employed for generic classification of the taxon (Gardner, 1986; Mez, 1904). Most noteworthy is the work of Gardner (1982) who used flower morphological characters to circumscribe Tillandsia into five taxonomic groups (see also: Gardner, 1986). Revisions of Tillandsia classification continued as its taxonomy developed amid the age of genomics. Past phylogenetic work on Tillandsia was based on a few conserved plastid and nuclear markers and often lacked subgeneric resolution. The taxon's low genetic divergence was early suggested to be representative of an exceptionally young radiation (<5Mya; Barfuss et al., 2005). Barfuss et al. (2016) constructed a sub-family multi-locus phylogeny using four plastid loci, the nuclear DNA gene PHYC and re-evaluated morphology. While they ident'fied subgeneric clades within Tillandsia, species relationships were generally poorly supported. Other studies continued to achieve sub-generic resolution and meanwhile encountered taxonomic issues like fuzzy clade and species boundaries (Chew et al., 2010; Pinzón et al., 2016). Recently, Granados Mendoza et al. (2017) expanded the sampling of Barfuss et al. (2016) to cover ca. 30% of the known species' diversity in Tillandsia. Their work confirmed two monophyletic Tillandsia clades, characterized by a distinct geographic distribution: a clade containing species from subgenus Tillandsia, distributed in North and Central America (clade K), and a South and Central American clade containing species from subgenera Aerobia, Anoplophytum, Diaphoranthema and Phytarrhiza (clade Q). They estimated that clade K diversified in North- and Central America, whereas within the second most migratory events occurred from the Andes to the Brazilian shield.

Tillandsia generally present the a similar range of phenotypic diversity as that found in the entire family, with great variation in life habits, photosynthetic pathways, pollination syndromes, and presence or absence of absorptive trichomes, among other presumably adaptive traits (Barfuss et al., 2005; Crayn et al., 2015; Givnish et al., 2014; Till, 2000). The combination of traits most commonly result in one of two phenotypes: the "green" Tillandsia are adapted to cool, moist habitats, exhibiting predominantly C3 photosynthesis, a pronounced tank habit, low trichome density and no pronounced leaf succulence. The socalled "grey" Tillandsia are recognized by adaptations to xeric environments with a strong tendency for CAM photosynthesis, dense leaf trichome cover and pronounced leaf succulence (figure 2; Benzing, 2000; de La Harpe et al., 2020). While instances of intermediate or 'mixed' phenotypes are ubiquitous in the genus, the high rates of correlated diversification and the multiple shifts between phenotypic states suggests that *Tillandsia* had undergone adaptive radiation. Little is known about the evolutionary processes and genomic basis of shifts in these adaptive traits: the ancestor of *Tillandsia* is thought to have been mesic and most likely exhibited C3 photosynthesis. Photosynthetic shifts were found to be correlated with changes in rates of gene duplication and loss (de La Harpe et al., 2020). As chromosome numbers are overall stable within the genus, trait shifts most likely did not involve radical genome rearrangements (de La Harpe et al., 2020; Till, 2000; but see Clara Groot Crego et al., in preparation).



Figure 2. Examples of *Tillandsia* species with varying photosynthetic syndromes. **A**, *T*. *leiboldiana* and **B**, *T. complanata*, are predominantly C3 species with a typical tank habit. **C**, *T. caput-medusae* and **D**, *T. ionantha*, predominantly CAM species (Crayn et al., 2015; de La Harpe et al., 2020). [photographs: A, *Tillandsia leiboldiana* in the Botanischer Garten, Berlin-Dahlem by Krzysztof Ziarnek used under CC BY-NC-SA 4.0. B, Ecuador, Tungurahua, Quebrada Chamanapamba, Rio Ulba by Alexey Yakovlev under CC BY-SA 2.0. C, *Tillandsia caput-medusae* by KENPEI under CC BY-SA 3.0. D, Botanical specimen in the Lyman Plant House, Smith College, Northampton, Massachusetts, USA by Daderot under public domain (CC0 1.0).

Research objectives

This thesis is aimed at exploring the evolutionary history of *Tillandsia* and the genomic processes that accompanied diversification. To that end, we made use of two NGS techniques, target capture sequencing and whole-genome resequencing. In addition, the advantages and limitations of both methods are highlighted in the context of phylogenomics of recent, rapid radiations.

(1) **Chapter 1** examines the potential of target capture sequencing in evolutionary studies in Bromeliaceae with a focus on *Tillandsia*. The chapter describes the design of a taxon-specific bait set for Bromeliaceae and a comparison to a universal bait set for all flowering plants. We sought to bridge the methodological gap between micro- and macro-evolutionary approaches and evaluated the sets' performance in both contexts. Using a family-wide sampling of 72 Bromaliaceae samples, including five species of *Tillandsia* subgenus *Tillandsia*, we performed phylogenomic inference and explored population structure and demographic processes in *Tillandsia*. Our aims were to generate a toolkit for the bromeliad research community, to add knowledge on the utility of target capture in studying rapid radiations, and to present a road-map for the possible use of a single data-set in addressing both macro- and micro- evolutionary questions.

(2) **Chapter 2** employs a tree-based approach to study the evolutionary history of *Tillandsia*. We used whole-genome re-sequencing of 65 individuals representing 32 species, with a focus on clade K of Mexican *Tillandsia* and additional sampling of South American *Tillandsia*. The chapter describes phylogenetic inference and exploration of *Tillandsia* evolutionary history employing a tree-based approach, D-statistics and a network approach. The relationships between the sampled species were inferred using a concatenation-based and a species tree methods, obtaining phylogenies that contradicted previous phylogenetic work on *Tillandsia*. We proceeded to assess the extent of variation in tree topologies along the genomes and deviations from a tree structure. We finally characterized patterns of hybridization between and within different clades, and constructed a species network to understand the evolutionary history of this highly diverse clade. This chapter illuminates the history of *Tillandsia* and provides a case study of exploring genomic processes in a recent and rapid radiation.

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Chapter 1

Taxon-specific or universal? Using target capture to study the evolutionary history of rapid radiations

Gil Yardeni¹, Juan Viruel^{2,} Margot Paris³, Jaqueline Hess^{1,4}, Clara Groot Crego^{1,5}, Marylaure de La Harpe¹, Norma Rivera¹, Michael H. J. Barfuss¹, Walter Till¹, Valeria Guzmán-Jacob⁶, Thorsten Krömer⁷, Christian Lexer¹, Ovidiu Paun¹, Thibault Leroy¹

¹Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria
²Royal Botanic Gardens, Kew, Richmond, UK
³Unit of Ecology & Evolution, Department of Biology, University of Fribourg, Fribourg, Switzerland
⁴Department of Soil Ecology, Helmholtz Centre for Environmental Research, UFZ, Halle (Saale), Germany
⁵Vienna Graduate School of Population Genetics, Vienna, Austria
⁶Biodiversity, Macroecology and Biogeography, University of Goettingen, Göttingen, Germany
⁷Centro de Investigaciones Tropicales, Universidad Veracruzana, Xalapa, Mexico

Christian Lexer, Ovidiu Paun, and Thibault Leroy shared last authorship.

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RESOURCE ARTICLE

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Taxon-specific or universal? Using target capture to study the evolutionary history of rapid radiations

Gil Yardeni¹ | Juan Viruel² | Margot Paris³ | Jaqueline Hess^{1,4} | Clara Groot Crego^{1,5} | Marylaure de La Harpe¹ | Norma Rivera¹ | Michael H. J. Barfuss¹ | Walter Till¹ | Valeria Guzmán-Jacob⁶ | Thorsten Krömer⁷ | Christian Lexer¹ | Ovidiu Paun¹ | Thibault Leroy¹

¹Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria

²Royal Botanic Gardens, Kew, Richmond, UK

³Unit of Ecology & Evolution, Department of Biology, University of Fribourg, Fribourg, Switzerland

⁴Department of Soil Ecology, Helmholtz Centre for Environmental Research, UFZ, Halle (Saale), Germany

⁵Vienna Graduate School of Population Genetics, Vienna, Austria

⁶Biodiversity, Macroecology and Biogeography, University of Goettingen, Göttingen, Germany

⁷Centro de Investigaciones Tropicales, Universidad Veracruzana, Xalapa, Mexico

Correspondence

Gil Yardeni, Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, A-1030 Vienna, Austria. Email: gil.c.yardeni@gmail.com

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Abstract

Target capture has emerged as an important tool for phylogenetics and population genetics in nonmodel taxa. Whereas developing taxon-specific capture probes requires sustained efforts, available universal kits may have a lower power to reconstruct relationships at shallow phylogenetic scales and within rapidly radiating clades. We present here a newly developed target capture set for Bromeliaceae, a large and ecologically diverse plant family with highly variable diversification rates. The set targets 1776 coding regions, including genes putatively involved in key innovations, with the aim to empower testing of a wide range of evolutionary hypotheses. We compare the relative power of this taxon-specific set, Bromeliad1776, to the universal Angiosperms353 kit. The taxon-specific set results in higher enrichment success across the entire family; however, the overall performance of both kits to reconstruct phylogenetic trees is relatively comparable, highlighting the vast potential of universal kits for resolving evolutionary relationships. For more detailed phylogenetic or population genetic analyses, for example the exploration of gene tree concordance, nucleotide diversity or population structure, the taxon-specific capture set presents clear benefits. We discuss the potential lessons that this comparative study provides for future phylogenetic and population genetic investigations, in particular for the study of evolutionary radiations.

KEYWORDS

Bromeliaceae, phylogenomics, plant radiation, population structure, target capture, *Tillandsia* La captura selectiva de secuencias de ADN ha surgido como una herramienta importante para la filogenética y la genética de poblaciones en taxones no-modelo. Mientras que el desarrollo de sondas de captura específicas para cada taxón requiere un esfuerzo sostenido, las colecciones de sondas universales disponibles pueden tener una potencia disminuida para la reconstrucción de relaciones filogenéticas poco

Christian Lexer, Ovidiu Paun, and Thibault Leroy shared last authorship.

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profundas o de radiaciones rápidas. Presentamos aquí un conjunto de sondas para la captura selectiva desarrollado recientemente para Bromeliaceae, una familia de plantas extensa, ecológicamente diversa y con tasas de diversificación muy variables. El conjunto de sondas se centra en 1776 regiones de codificación, incluyendo genes supuestamente implicados en rasgos de innovación clave, con el objetivo de potenciar la comprobación de una amplia gama de hipótesis evolutivas. Comparamos la potencia relativa de este conjunto de sondas diseñado para un taxón específico, Bromeliad1776, con la colección universal Angiosperms353. El conjunto específico da lugar a un mayor éxito de captura en toda la familia. Sin embargo, el rendimiento global de ambos kits para reconstruir árboles filogenéticos es relativamente comparable, lo que pone de manifiesto el gran potencial de los kits universales para resolver las relaciones evolutivas. Para análisis filogenéticos o de genética de poblaciones más detallados, como por ejemplo la exploración de la congruencia de los árboles de genes, la diversidad de nucleótidos o la estructura de la población, el conjunto de captura específico para Bromeliaceae presenta claras ventajas. Discutimos las lecciones potenciales que este estudio comparativo proporciona para futuras investigaciones filogenéticas y de genética de poblaciones, en particular para el estudio de las radiaciones evolutivas.

1 | INTRODUCTION

Targeted sequencing approaches have emerged as a promising tool for studying evolutionary relationships in nonmodel taxa, enabling researchers to retrieve large data sets while requiring few genomic resources (Bossert & Danforth, 2018; Escudero et al., 2020; McDonnell et al., 2021; Soto-Gomez et al., 2019). Using custom baits, the method largely retrieves the same loci across a wide taxonomic scale, obtains comparable and mergeable data sets and may be combined with genome-skimming (Lemmon & Lemmon, 2013; Weitemier et al., 2014). Pre-existing knowledge of the targeted loci further provides opportunities to address specific questions on both deep and shallow timescales (Hale et al., 2020; Lemmon et al., 2012). Finally, the method does not necessarily require a reference genome, is highly cost-effective and, with the ability to sequence herbarium samples, reduces the need for extensive sampling campaigns (Blaimer et al., 2016; Hale et al., 2020; Weitemier et al., 2014). Target capture has been successfully applied to resolve phylogenies in diverse groups, from arthropods such as bees (Xylocopa, Blaimer et al., 2016; Apidae, Bossert et al., 2019) and Araneae (Hexathelidae, Hedin et al., 2018) to mammals (Cetacea, McGowen et al., 2020), and in numerous plant groups (Heuchera, Folk et al., 2015; Gesneriaceae, Ogutcen et al., 2021; Zingiberales, Sass et al., 2016 to name a few). The method's utility for studies at microevolutionary scales has been to date marginally explored, but several studies have pointed to the ability to analyse genomic diversity and estimate population genomic parameters (Choquet et al., 2019; Christmas et al., 2017; Derrien & Ramos-Onsins, 2020; de La Harpe et al., 2019; Sanderson et al., 2020). Nonetheless, the development of probes for target enrichment may pose several challenges: first, the need to identify regions conserved enough to ensure recovery, yet polymorphic

enough to provide ample information (Soto-Gomez et al., 2019; Villaverde et al., 2018). Second, probe design requires detecting regions without pervasive copy number polymorphism (Kadlec et al., 2017; Lemmon et al., 2012), a particular challenge for angiosperms and other groups, where duplication events are ubiquitous (Van de Peer et al., 2017).

In contrast, universal kits offer an attractive alternative that require reduced efforts to establish, and provide comparable data sets across wider ranges of taxa (Johnson et al., 2019; Kadlec et al., 2017). Such kits were designed to retrieve single-copy markers, for example, in the broad scope of amphibians (Hime et al., 2021), anthozoans (Quattrini et al., 2018), vertebrates (Lemmon et al., 2012) or angiosperms (Johnson et al., 2019). In the latter example, the Angiosperms353 kit is designed to target 353 single-copy genes across angiosperms. So far the kit has been employed successfully in resolving phylogenies, including but not limited to Nepenthes (Murphy et al., 2020), Schefflera (Shee et al., 2020) and the rapid radiations of Burmeistera (Bagley et al., 2020) and Veronica (Thomas et al., 2021), establishing the kit as an eminent tool in macroevolutionary research. Its utility at microevolutionary levels is yet to be fully realized, although several works have established its suitability to deliver informative signals at a lower taxonomic level (Beck et al., 2021) and in acquiring population genomics parameters (Slimp et al., 2021). The use of highly conserved markers in a universal kit may, however, limit resolution power. Generally, taxon-specific baits are expected to deliver a higher information content and hence more accurate results (Kadlec et al., 2017), as enrichment success is known to drop with the level of divergence between sequences used for probe design and the targeted taxa (Liu et al., 2019). However, one study comparing the power of the universal Angiosperms353 kit and a taxon-specific kit to resolve phylogenomic relationship in

Cyperaceae reported surprisingly similar performance (Larridon et al., 2020) and similar findings were reported in Malinae (Ufimov et al., 2021) and in Ochnaceae (Shah et al., 2021). It remains to be established whether these findings apply to other taxa and other evolutionary scales, including at population level, where ample genomic variability is required to resolve intraspecific relationships and investigate patterns of genetic differentiation.

Until recently, the technology available to investigate evolutionary questions in rapidly evolving groups featuring high net diversification rates has presented major obstacles, in particular for nonmodel groups. Decreasing costs of sequencing coupled with an ever-growing plethora of bioinformatic tools for data processing and downstream analysis has led to an increase in the use of methods like whole-genome sequencing, RNA sequencing and restriction-site associated DNA sequencing (RAD-Seq) in lieu of traditional methods employing few conserved markers (de La Harpe et al., 2017; McKain et al., 2018; Weitemier et al., 2014; Zimmer & Wen, 2013). Whole-genome sequencing however remains costly, posing barriers for research targeting large numbers of samples, organisms with large genomes and nonmodel organisms for which the availability of high-quality genomic resources is often limited (Hollingsworth et al., 2016; Supple & Shapiro, 2018). While RAD-seg is an affordable alternative and widely used in population genetics, the resulting data sets may fall short when screened for homologous sequences across distantly related lineages (but see, e.g., Heckenhauer et al., 2018). Additionally, RAD-seg is less feasible when using degraded DNA from herbarium samples, and the use of short and inconsistently represented loci across phylogenetic sampling may result in low information content and difficulties in assessing paralogy (Jones & Good. 2016; Lemmon & Lemmon. 2013; McKain et al., 2018).

Rapid evolutionary radiations are key stages in the evolutionary history across the Tree of Life and highly recurrent, hence an essential part of biodiversity research (Gavrilets & Losos, 2009; Givnish et al., 2014; Hughes et al., 2015; Soltis et al., 2019; Soltis & Soltis, 2004). Fast evolving groups provide potent opportunities to investigate important questions in evolutionary biology, such as the interplay between ecological and evolutionary processes in shaping biodiversity. A few notable study systems are the cichlid fish (McGee et al., 2020; Salzburger, 2018), *Heliconius* butterflies (Dasmahapatra et al., 2012; Moest et al., 2020), *Anolis* lizards (McGlothlin et al., 2018; Stroud & Losos, 2020), Darwin's finches (Lamichhaney et al., 2015; Zink & Vázquez-Miranda, 2019), white-eyes birds (Moyle et al., 2009) and New World lupins (Nevado et al., 2016). Nevertheless, much remains unknown about the genomic basis underlying species diversification outside these intensively studied systems.

Research of rapidly diversifying lineages presents several challenges. First, a brief diversification period typically leads to imperfect reproductive barriers and incomplete lineage sorting, reflected in significant gene tree discordance and ambiguous relationships (Degnan & Rosenberg, 2009; Lamichhaney et al., 2015; Pease et al., 2016; Straub et al., 2014). In addition, understanding 'speciation through time' poses a methodological challenge and requires connecting two conceptual worlds: macroevolutionary investigations, MOLECULAR ECOLOGY WILEY-

concerned with spatial and ecological patterns over deeper timescales, and microevolutionary approaches, providing insight into the processes acting during population divergence and speciation (Bragg et al., 2016; de La Harpe et al., 2017). Resolving phylogenomic relationships and disentangling the contribution of different genomic processes through time typically require large-scale genomic data sets and thorough taxon sampling efforts (Lemmon & Lemmon, 2013; Linder, 2008; Straub et al., 2012).

Here, we present Bromeliad1776, a new bait set for targeted sequencing, designed to address a wide range of evolutionary hypotheses in Bromeliaceae: from producing robust phylogenies to studying the interplay of genomic processes during speciation and the genetic basis of trait shifts, such as photosynthetic and pollination syndrome. This highly diverse Neotropical radiation provides an excellent research system for studying the drivers and constraints of rapid adaptive radiation (Benzing, 2000; Givnish et al., 2011; Loiseau et al., 2021; Mota et al., 2020; Palma-Silva & Fay, 2020; Wöhrmann et al., 2020). Bromeliaceae as a whole is considered an adaptive radiation (Benzing, 2000; Givnish et al., 2011) and contains several rapidly radiating lineages, most notably within Bromelioideae (Aguirre-Santoro et al., 2020) and Tillandsioideae (Loiseau et al., 2021). It is a species-rich and charismatic monocot family, consisting of over 3000 species, including crops in the genus Ananas and other economically important species (Luther, 2008). Members of the family are characterized by a distinctive leaf rosette that often impounds rainwater in central tanks (phytotelmata). A diversity of arthropods and other animal species and microbes reside in bromeliad tanks, in some cases even leading to protocarnivory and other forms of nutrient acquisition (Givnish et al., 1984; Leroy et al., 2016). Bromeliads present a diversity of repeatedly evolving adaptive traits, which allowed them to occupy versatile habitats and ecological niches (Benzing, 2000). CAM photosynthesis, water-absorbing trichomes, formation of tank habit, extensive rates of epiphytism and a diversity of pollination syndromes are some of the adaptations correlated with high rates of diversification within the family (Benzing, 2000; Crayn et al., 2004; Givnish et al., 2014; Kessler et al., 2020; Quezada & Gianoli, 2011).

To assess the utility of the Bromeliad1776 kit, we performed a comparison between our taxon-specific kit and the universal Angiosperms353 kit using several methods across different evolutionary timescales. We present Bromeliad1776 in the light of methodological considerations on bait design, data handling, analyses and other practical considerations.

2 | MATERIALS AND METHODS

2.1 | Custom bait design

Whole-genome sequences and gene models from *Ananas comosus* v.3 (Ming et al., 2015) were used to design a bait set aiming to target (i) single-copy protein coding genes distributed across the whole genome, (ii) genes previously described as associated with key

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innovation traits in Bromeliaceae (see below), (iii) markers previously used for phylogenomic inference in Bromeliaceae and (iv) genes orthologous to those in the Angiosperms353 bait set. The 1776 selected genes are detailed in Table S1.

Genes in subset i were selected based on genetic diversity parameters calculated using whole-genome sequence and RNAseq data previously published by de La Harpe et al. (2020); data publicly available online at SRA Bioproject (PRJNA649109) with the POPGE-NOME R package v.2.1.6 (Pfeifer et al., 2014). Genomic regions were retained in this category if they shared at least 70% identity between A. comosus and T. sphaerocephala, and if they had nucleotide diversity (π) values not exceeding the 90% quantile of the (π) distribution across genes for four Tillandsia species (Tillandsia australis, Tillandsia fasciculata, Tillandsia floribunda and T. sphaerocephala; data and analysis performed by de La Harpe et al. (2020)). We further excluded genes with a total exonic size smaller than 1100 bp, or individual exons smaller than 120 bp. Next, copy number variation was calculated based on clustering of A. comosus and Tillandsia transcriptome assemblies to generate three copy number categories—'single copy', 'low copy' (i.e. less than five copies) and 'high copy' (i.e. five or more copies). We included only single-copy genes in the design for bait subset *i*. Finally, we excluded genes that were located in genomic regions outside those assigned to linkage groups in the A. comosus reference (Ming et al., 2015). A total of 1243 genes were identified for this part.

The bait subset of genes associated with key innovative traits in Bromeliaceae (subset *ii* above) included (1) genes putatively under positive selection along branches relevant to C3/CAM shifts (de La Harpe et al., 2020), (2) genes that exhibit differential gene expression between CAM and C3 *Tillandsia* species (de La Harpe et al., 2020) and (3) genes putatively associated with photosynthetic and developmental functions, or with flavonoid and anthocyanin biosynthesis, according to the literature (e.g. Goolsby et al., 2018; Ming et al., 2015; Palma-Silva et al., 2016; Wai et al., 2017). *Ananas comosus* genes with the highest match scores (calculated as lowest E-score in BLASTP, Madden (2003)) against the sequences of genes from the literature were added to the bait set (see Table S2 for details). A total of 1612 genes underpinning innovative traits were included in the bait design, regardless of criteria used for subset *i* for size, similarity and duplication rate.

Markers previously used for phylogenomic inference in Bromeliaceae (subset *iii*) were obtained from the literature, spanning 13 genes (e.g. Barfuss et al., 2016; Machado et al., 2020; Schulte et al., 2009, see TS2 for full list). Genes orthologous to those in the Angiosperms353 bait set (Johnson et al., 2019) were identified using the orthologous gene models from A. *comosus* based on gene annotations (Ming et al., 2015) or using BLASTP (Madden, 2003), totalling 281 genes.

Finally, we used a draft genome of *T. fasciculata* (Jaqueline Hess, personal communication) to exclude from all candidates genes that exhibited multiple BLASTN hits, if they have not been previously described as duplicated within the genus (de La Harpe et al., 2020). Specifically, we excluded genes that matched another genomic

sequence of at least 100 bp with high similarity score (>80%) and low E-value ($<10^{-5}$). In an additional round of filtering performed by the manufacturer of the final bait set, Arbor Biosciences (Ann Arbor, MI, USA), multicopy genes with sequences that are more than 95% identical were collapsed into a single sequence and baits with more than 70% GC content or containing at least 25% repeated sequences were excluded. In addition, targets including exons smaller than 80 bp were completed with regions flanking the exons according to the A. comosus reference genome. The final kit included 1776 genes: 801 genes in subset i, 681 genes associated with key innovative traits, 13 genes representing phylogenetic markers and 281 genes orthologous to the Angiosperms353 set. Probes were designed with 57,445 80-mer baits tiling across targets in 2× coverage, targeting approximately 2.3 Mbp. The kit is subsequently referred to as the Bromeliad1776 bait set. Further specifications can be found in Tables S1 and S2 and in the github repository: https://github.com/ givany/Bromeliad1776/tree/main/MS 2021 scripts.

2.2 | Plant material collection

We sampled a total of 70/72 Bromeliaceae samples (for Angiosperms353 and for Bromeliad1776, accordingly; Table S3), including 56 accessions from the Tillandsioideae subfamily and 16 representing the other subfamilies, except Navioideae. The divergence time between Tillandsioideae and subfamily Bromelioideae to which *A. comosus* belongs is estimated at 15 Mya (according to Givnish et al., 2014). Within Tillandsioideae, we sampled 38/40 individuals from five species of the *Tillandsia* subgenus *Tillandsia* ('clade K' in Barfuss et al., 2016; Sampling in Mexican populations illustrated in Figure S1).

2.3 | Library preparation & enrichment

DNA extractions were performed using a modified CTAB protocol (Doyle & Doyle, 1987), purified using Nucleospin[®] gDNA cleanup kit from Macherey-Nagel (Hudlow et al., 2011) following the supplier's instructions with a twofold elution step and finally quantified with Qubit[®] 3.0 Fluorometer (Life Technologies).

For each sample, 200 ng DNA was sheared using Bioruptor[®] Pico sonication device (Diagenode) aiming for an average insert size of 350 bp, dried in a speed vacuum Eppendorf concentrator 5301 (Eppendorf) and eluted in 30 L ddH2O. Genomic libraries were prepared using the NEBNext[®] Ultra TM II DNA Library Prep Kit for Illumina[®] (New England Biolabs) using reagents at half volumes following Hale et al. (2020) and using 11 PCR cycles, increased up to 13 cycled for libraries with low genomic output. Samples were double-indexed with NEBNext[®] Multiplex Oligos for Illumina[®] (New England Biolabs). Fragment sizes were inspected with Agilent Bioanalyzer (Agilent Technologies), and concentrations were measured with Qubit[®] 3.0 Fluorometer. Subpools of 11–14 equimolar genomic libraries were prepared using phylogenetic proximity and We used the Angiosperms353 and the Bromeliad1776 bait sets from Arbor Biosciences to enrich each subpool of genomic libraries independently with a single hybridization reaction of myBaits[®] target capture kits from Arbor Biosciences, following Hale et al. (2020). Average fragment size and DNA yield were estimated for each subpool using Agilent Bioanalyzer and Qubit[®] 3.0 Fluorometer. Subpools were then pooled in equimolar conditions and sequenced at Vienna BioCenter Core Facilities on Illumina[®] NextSeqTM 550 (2 × 150 bp, Illumina). Sequencing was conducted independently for either bait kit.

2.4 | Data processing

The raw sequence data in BAM format were demultiplexed using DEML v.1.1.3 (Renaud et al., 2015) and SAMTOOLS VIEW v.1.7 (Li et al., 2009), converted to fastq using BAMTOOLS v.2.4.0 (Barnett et al., 2011) and quality checked using FASTQC v.0.11.7 (Andrews, 2010). Reads were then trimmed for adapter content and quality using TRIMGALORE v.0.6.5 (Krueger, 2019), a wrapper tool around FASTQC and CUTADAPT, using settings --fastqc --retain unpaired. Sequence quality and adapter removal were confirmed with FastQC reports.

Quality and adapter-trimmed reads were aligned to A. comosus reference genome v.3 (Ming et al., 2015) using BOWTIE2 (Langmead & Salzberg, 2012) with the --very-sensitive-local option to increase sensitivity and accuracy. Samtools (Li et al., 2009) was then used to remove low-quality mapping and sort alignments by position, and PCR duplicates were marked using MarkDuplicates from PICARDTOOLS v.2.25 (Picard Toolkit, 2019). Summary statistics of the mapping step were generated using samtools stats. Variants were called using FREEBAYES v1.3.2-dirty (Garrison & Marth, 2012), and sites marked as MNP/complex were decomposed and normalized using the script 'vcfallelicprimitives' from vCFLIB (Garrison, 2012). Next, AN/AC field was calculated using BCFTOOLS v.1.7 (Li, 2011) and variant calls were filtered using VCFLIB (Garrison & Marth, 2012) and bcftools. Given that freebayes does not perform automatic variant filtering steps, we identified sets of parameters that generate reliable final SNP sets, based on two independent criteria: the highest transition/ transversion ratios as reported by SNPSIFT (SnpEff Cingolani et al., 2012) and the lowest $\pi_{\rm N}/\pi_{\rm S}$ (see Section 2.7). After a detailed evaluation, we used the following criteria to generate two high-quality SNP sets, one for each bait set: we considered genotype calls with per-sample coverage below 10x-as missing (NA) and excluded variants (i) marked as indels or neighbouring indels within a distance of 3 bp, (ii) with depth of coverage at the SNP level lower than $500 \times$, (iii) with less than 10 reads supporting the alternate allele at the SNP level or (iv) with more than 40% missing data. All genes in the Bromeliad1776 that passed the filtering criteria were included in the SNP set, regardless of their function. Summary statistics of the final SNP sets were generated using the script vcf2genocountsmatrix.py, namely the total number of SNPs, the proportion of on-target SNPs and the proportion of SNPs in some specific genomic contexts, with

A. *comosus* genome v.3 as a reference. The full data processing script align_and_trim.sh and the vcf2genocountsmatrix.py script are both available at https://github.com/giyany/Bromeliad1776.

2.5 | Bait specificity and efficiency

To explore bait specificity, we calculated the percentage of highquality trimmed reads on-target using samtools stats and BEDTOOLS INTERSECT v2.25.0 (Quinlan & Hall, 2010) using the script calculat_ bait_target_specifity.sh (available from https://github.com/giyan y/Bromeliad1776). Targets for Bromeliad1776 were defined as the bait sequences plus their 500-bp flanking regions. Targets for Angiosperms353 were defined using orthogroups to *A. comosus*: gene annotations from the bait set were used to assign genes to orthogroups using ORTHOFINDER (Emms & Kelly, 2019). When several orthogroups were found for a single Angiosperms353 gene, we included all, resulting in 559 *A. comosus* genes assigned to orthogroups. Within the orthogroups, targets were again defined as exonic regions plus their 500 bp flanking regions.

To provide insights into determinants of bait capture success, we calculated bait efficiency for all baits of Bromeliad1776. For each bait, efficiency was calculated as the number of high-quality reads uniquely mapping to each bait target region, averaged over samples. We then tested for the correlation of capture efficiency to several bait characteristics (copy number, GC content, number and size of exons in targeted gene, size of baits and phylogenetic distance to A. *comosus*) with a generalized linear model or Kruskal-Wallis test in R v.4.0.3 (R Core Team, 2020) using a negative binomial family.

2.6 | Phylogenomic analyses

We inferred phylogenomic relationships for all samples using two methods: a concatenation method, and a coalescent-based species tree estimation. The latter method was included as concatenation methods do not account for gene tree incongruence, which may result in high support for an incorrect topology (Kubatko & Degnan, 2007), especially in the presence of notable incomplete lineage sorting. In addition, gene tree incongruence analysis provides insight into molecular genome evolution, including the extent of incomplete lineage sorting and other genomic processes such as hybridization and introgression (Galtier & Daubin, 2008; Wendel & Doyle, 1998).

We used the variant and nonvariant genotypes to create a phylip matrix with VCF2PHYLIP v.2.0 (Ortiz, 2019) and constructed a maximum-likelihood species tree for each bait set with RAXML-NG v.0.9.0 (Kozlov et al., 2019), using 250 bootstrap replicates and a GTR model with an automatic MRE-based bootstrap convergence test. Next, we constructed a species tree using ASTRAL-III v.5.7.7 (hereafter: ASTRAL, Zhang et al., 2018). For both the Angiosperms353 and the Bromeliad1776 sets, we separated the matrix into independent genomic windows, defining each window as a gene according to the known exons and a 500-bp flanking region. For Angiosperms353,

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we extracted the 559 genes (assigned to orthogroups as explained above) as genomic windows using bedtools intersect. For Bromeliad1776, genomic windows were extracted using the *A. comosus* gene sequences included in bait design. All loci and all accessions were included in species tree inference regardless of the percentage of missing data, since taxon completeness of individual gene trees is important for statistical consistency of this approach, and we expected only low levels of fragmentary sequences (Mirarab, 2019; Nute et al., 2018). After excluding genes with zero coverage, 269 genes and 1600 genes were included in species tree inference for Angiosperms353 and Bromeliad1776, respectively.

For each gene, a maximum-likelihood gene tree was inferred using PARGENES (Morel et al., 2019) with RAXML-NG (Kozlov et al., 2019), using a GTR model with an automatic MRE-based bootstrap convergence test. Loci with insufficient signal may reduce the accuracy of species tree estimation (Mirarab, 2019), hence, in all gene trees, nodes with a bootstrap support smaller than 10 were collapsed using Newick utilities (Junier & Zdobnov, 2010). A species tree was then generated in ASTRAL with quartet support and posterior probability for each tree topology. The number of conflicting gene trees was calculated using phyparts and visualized using the script phypartspiecharts.py (available from https://github.com/mossmatters/MJPythonNotebooks).

2.7 | Population structure and nucleotide diversity estimates

To explore the genetic structure within the *Tillandsia* species complex, we focused on five species from 15 localities (Table S3 and Figure S1). We first used PLINK v.1.9 (Chang et al., 2015) to filter out SNPs in linkage disequilibrium. Population structure was further explored through individual ancestry analysis, with identity-by-descent matrix calculated by plink and inference of population structure using ADMIX-TURE v.1.3. with K values ranging from one to ten, and 30 replicates for each K, using a block optimization method (Alexander & Lange, 2011). A summary of the ADMIXTURE results was obtained and presented using pong (Behr et al., 2016). The set of LD-pruned biallelic SNPs was further filtered to allow a maximum of 10% missing data and used to perform a principal components analysis (PCA) with SNPRELATE V.1.20.1 (Zheng et al., 2012). Finally, for each Tillandsia species, we used the strategy of Leroy et al. (2021) to compute synonymous (π_c) and nonsynonymous (π_{N}) nucleotide diversities and Tajima's D, from fasta sequences using seq_stat_coding (Leroy et al., 2021).

3 | RESULTS

3.1 | Higher mapping rates and capture efficiency for taxon-specific set

On average, 4,401,958 (803,464–12,693,516) paired-end reads per accession were generated per Angiosperms353 library and 2,962,023 (1,282,762–6,298,880) per Bromeliad1776 library. Overall, the mapping rates to the *A. comosus* reference genome were higher for libraries enriched with Bromeliad1776, with an average mapping rate of 82.3% (61.8%–95.9%) and 42.8% (22.1%–77.9%), for Bromeliad1776 and Angiosperms353, respectively (Figure S2, Table S4). Higher mapping rates were recorded for subfamilies Bromelioideae and Puyoideae, as compared to Tillandsioideae, for both the Angiosperms353 and Bromeliad1776 sets (see Figures S3 and S4, respectively). This may reflect the effect of reference bias, and in the case of Bromeliad1776, it may be further amplified by our kit design based on *A. comosus* (subfamily Bromelioideae). Bait specificity was high for Bromeliad1776 with on average 90.4% reads on-target (76.5%–94.2%), while for Angiosperms353 bait specificity was 14.0% (4.6%–30.1%; see Figure S2). Mapping rates and bait specificity were positively correlated for both bait sets (GLM, p < .01).

3.2 | Bait efficiency depends on the genomic context

We investigated factors that may influence bait efficiency, starting with the contribution of gene copy number variation. We assumed three categories regarding the number of paralogs per orthogroup: single-copy, low-copy (i.e. less than five copies) and high-copy (i.e. five or more copies). The number of gene copies had a significant effect on bait efficiency and post hoc Dunn's test supported significant differences in efficiency for comparisons between low-copy and high-copy, and between single-copy and low-copy ($P = 2.8^{-44}$). Low-copy genes exhibit the lowest enrichment success, suggesting that the bait efficiency is not simply correlated with the number of gene copies (Figure 1). We also recovered a significant effect of the intragenic GC content and GC content of the baits on bait efficiency (GLM, $P = 1.5^{-68}$). Finally, we investigated the possible link between efficiency and gene structure. Average exon sizes ($P < 2.0^{-16}$) and total number of exons per gene ($P = 1.1^{-89}$) were also positively correlated with enrichment success. The size of the smallest exon for all targeted genes was however not correlated with bait efficiency. Sequence similarity, measured as per cent of identity between Tillandsia sequences and those of A. comosus, was positively correlated with capture success ($P = 4.8^{-13}$; Figure 1).

3.3 | Both kits provided a large number of SNPs

After variant calling and filtering, we identified 47,390 and 209,186 high-quality SNPs for the Angiosperms353 and the Bromeliad1776 bait sets, respectively. On average, missing data represented 23.7% of genotype calls per individual in Angiosperms353, but only 6.3% for the Bromeliad1776 kit. The differences in amount of missing data are likely associated with the higher mean depth per site across the Bromeliad1776 kit (6602), as compared to Angiosperms353 (3437). Focusing on the subgenus *Tillandsia*, we identified 15,622 SNPs for Angiosperms353 (including a total of



FIGURE 1 Effects of (a) putative gene copy number, (b) gene GC content, (c) average exon size, and (d) per cent of identity on bait efficiency in Bromeliad1776 bait set, measured as the number of high-quality reads uniquely mapping to bait target region across samples. Continuous variable was binned and y-values higher than 1000 excluded for visualization in b-d

18.9% missing data) compared to 65,473 polymorphic sites (2.9% missing data) for Bromeliad1776. In both full data sets and the subset including only *Tillandsia* samples, Bromeliad1776 recovered more variants in intronic regions compared with Angiosperms353. Angiosperms353 recovered a large proportion of off-target SNPs, whereas in Bromeliad1776 approximately 15% of the SNPs were recovered from flanking regions (Table 1). We discuss ascertainment bias that may rise due to the nonrandom selection of markers in the supporting information.

3.4 | Similar phylogenomic resolution in concatenation method, Bromeliad1776 outperforms Angiosperms353 for species tree reconstruction

The Angiosperms353 and Bromeliad1776-based maximumlikelihood phylogenetic trees recovered the same backbone phylogeny of Bromeliaceae, clustering subfamily Tillandsiaoedeae and the subgenus *Tillandsia* with high bootstrap values (Figure S5). Neither set obtained high support for interpopulation structure for *Tillandsia gymnobotrya*, but highly supported nodes separated *T. fasciculata* accessions from Mexico and from other locations, and the populations of *T. punctulata* for the Bromeliad1776 data set were similarly separated. The tree topologies were identical, with the notable exception of the placements of *Tillandsia biflora* and *Racinaea ropalocarpa* and the genus *Deuterocohnia* (Figure S5, purple arrow). Overall, internal nodes are strongly supported for both sets, except for *Hechtia carlsoniae* as sister to Tillandsioideae, which is poorly supported for both sets. While several internal nodes are slightly less supported for the Angiosperms353 set, overall these results demonstrate the efficacy of both kits in phylogenomic reconstruction using concatenation approaches, indicating that as few as 47 k SNPs within variable regions provide reliable information to resolve phylogenetic relationships within the recent evolutionary radiation of *Tillandsia*.

Species trees as inferred with ASTRAL for both data sets likewise provided an overall strong local posterior support (Figure 2, see also Figures S8 and S9). Several nodes however exhibit lower local posterior support values for the Angiosperms353 tree than for the Bromeliad1776 tree. The topology for the Bromeliad1776 ASTRAL tree was similar to the ML tree, but differed again by placing *Deuterocohnia* as sister taxa to *Puyoideae* only. In the Angiosperms353 tree, the topology differed from both ML trees and the ASTRAL Bromeliad1776 tree in several nodes. *H. carlsoniae* was placed as a sister taxa to all other subfamilies in the Angiosperm353 phylogeny. Notably, the placement of *Catopsis* and *Glomeropitcrania* differed,

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as well as the placement of *Cipurosis subandinai*, *T. biflora* and *R. ropalocarpa*. Several internal nodes were poorly supported, such as the node separating the tribe Catopsideae and core Tillandsioideae, and the nodes separating Tillandsioideae from all other subfamilies. The differences in topology between the Angiosperms353 ASTRAL tree to all other trees (ML trees and Bromeliad1776 ASTRAL tree) together with the low posterior support suggest lower resolution power and a poor fit of this data set for resolving a species tree.

The length and average size of the input gene trees different among sets, with average window length of 304.6 bp and 819.9 bp and average gene tree support of 16.9 and 38.9 for Angiosperms353 and Bromeliad1776 bait sets, respectively (Figure 2). An examination of gene tree concordance constructed with Bromeliad1776 data set allowed us to identify variable levels of gene tree conflict among nodes (Figure 2). Gene tree discordance was especially high for the split between Tillandsioideae and other subfamilies, as well as for the split between Puyoideae and taxa assigned to Bromelioideae. Furthermore, gene tree discordance and the proportion of uninformative gene trees were especially high for splits among clades within the K.1 and K.2 clades of subgenus Tillandsia. A similar analysis with Angiosperms353 yielded evidence for gene tree discordance, but a considerable number of gene trees were reported to be noninformative (grey part of the pie charts), especially within subgenus Tillandsia (Figure 2).

3.5 | Strong interspecific structure, but little evidence for within-species population structure

After LD-pruning and retaining maximum 10% missing data, 1025 and 32,941 biallelic SNPs were included for the *Tillandsia* PCA analysis of the Angiosperms353 and Bromeliad1776 data sets, respectively. Overall, both data sets provided evidence for interspecific structure, but not for population structure, with Bromeliad1776 resulting in border-line higher resolution (slightly better separating *T. foliosa* from *T. fasciculata*). The percentage of explained variance was higher in the Bromeliad1776 set (19.3% and 16.5% for PC1 and PC2) as compared to the Angiosperms353 data set (14.5% and 11.8%, see Figures 3 and S6). Based on these two PCAs, we found no evidence for spatial genetic structure within each species, since accessions did not cluster by geographic origin on the two PCs presented, or any other PCs we investigated (see Figure S6).

In addition to PCA, we performed ADMIXTURE analyses based on 9804 and 42,613 variants for the Angiosperms353 and Bromeliad1776 sets, respectively (Figure 4). We used a crossvalidation strategy to identify the best *K* and found clear support for K = 5 for the Bromeliad1776 set (Figure S7). In contrast, the CV pattern for the Angiosperms353 set varied widely, providing limited information about the best *K*. Lowest CV values were however observed for K = 9 with locally low values for K = 5 and K = 3 (Figure S7). We further investigated the ADMIXTURE bar plots at different values of *K*. For K = 5, very similar patterns can be observed for both sets, with the recovered clusters reflecting the

TABLE 1 Number and characteristics of the variants obtained for Angiosperms353 and Bromeliad1776

⊥W	IL	EY	R	ESO	UR	CES	
Off-target SNPs		35,478 (74.8%)	8601 (4.11%)		11,461 (73.4%)	3480 (5.3%)	
Flanking SNPs		3488 (7.4%)	37,661 (18.0%)		1129 (7.22%)	10,588 (16.2%)	
On-target SNPs		8424 (17.8%)	162,924 (77.9)%		3032 (19.4%)	51,405 (78.5%)	
SNPs in intergenic regions		2386 (5.1%)	2503 (1.2%)		835 (5.3%)	870 (1.3%)	
SNPs in intronic regions		4376 (9.2%)	35,790 (17.1%)		1442 (9.2%)	9967 (15.2%)	
SNPs in exonic regions		40,628 (85.7%)	170,893 (81.7%)		13,345 (85.5%)	54,636 (83.5%)	
Site mean depth		3447	6601.7		1837.8	3914.9	
SNP Nr.		47,390	209,186		15,622	65,473	
indv Nr.		70	72		38	40	
	intragenic vcf	Angiosperms353	Bromeliad1776	pop-level vcf	Angiosperms353	Bromeliad1776	

Bromeliad1776

Angiosperms353



FIGURE 2 Coalescent-based species trees generated ASTRAL-III for samples enriched with Bromeliad1776 (left) and Angiosperms353 (right, flipped for mirroring), on 269 and 1600 genes for each set, respectively. Node values represent local posterior probabilities (pp) for the main topology and are equal to 1 unless noted otherwise. Pie charts at the nodes show levels of gene tree discordance: the percentages of concordant gene trees (blue), the top alternative bipartition (green), other conflicting topologies (red) and uninformative gene trees (grey). At bottom, length and average bootstrap support for gene trees from either data set, according to the design of the bait set used for enrichment: Angiosperms353 (right) and Bromeliad1776 (left). Each gene was considered a single genomic window

expected species boundaries. The main difference between the two data sets was the ability of the Bromeliad1776 set to reach a more consistent solution ('consensus') among 30 runs, especially at large *K*, as compared to the runs based on the Angiosperms353 bait set. The Bromeliad1776 was also able to distinguish between different sampling localities of *T. punctulata* and of *T. fasciculata* at K = 7-8 (Figure 4).

3.6 | Distinct diversities hint at different demographic processes

Nucleotide diversity estimates were calculated for the Bromeliad 1776 data set only, due to difficulties obtaining a reliable SNP set with Angiosperms 353 (see Section 2.4). Averaged levels of nucleotide diversity at synonymous sites $\pi_{\rm S}$ greatly varied

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FIGURE 3 Principal component analysis (PCA) plot for samples of Tillandsia subgenus Tillandsia enriched with two bait sets: (a) Angiosperms353 (1025 variants); (b) Bromeliad1776 (32,941 variants). Colours indicate different species according to legend



FIGURE 4 Population structure of 5 Tillandsia subgenus Tillandsia species from 14 sampling locations inferred with the ADMIXTURE software. Samples were enriched with either of two bait sets: Angiosperms353 (9804 variants after LD-pruning) and Bromeliad1776 (42,613 variants after LD-pruning), showing values of K = 2 to K = 9. Colours represent genetically differentiated groups, while each accession is represented by a vertical bar



FIGURE 5 Distribution of Tajima's D and synonymous (π_s) nucleotide diversity within each species for the Bromeliad 1776 kit

among species, from 4.1×10^{-3} to 8.1×10^{-3} for *T. foliosa* and *T. fasciculata*, respectively (Table S5; Figure 5). Given the recent divergence of these different species and their roughly similar life history traits, they are expected to share relatively similar mutation rates; hence, the observed differences in $\pi_{\rm S}$ are expected to translate into differences of long-term $N_{\rm e}$. Looking at the distribution of $\pi_{\rm S}$ across genes, we found broader or narrower distributions depending on the species, which explains the observed

differences in averaged π_s , as typically represented by the median of the distribution (vertical bars, Figure 5). Most species exhibit distributions of Tajima's *D* (Figure 5) that are centred around zero, with the notable exception of *T. punctulata*. The distribution of this species is shifted towards positive Tajima's *D* values, therefore indicating a recent population contraction, suggesting that this species experienced a unique demographic trajectory as compared to the other species.

4 | DISCUSSION

4.1 | A taxon-specific bait set performs marginally better for phylogenomics

In this study, we compared the information content and performance of a taxon-specific bait set and a universal bait set for addressing questions on evolutionary processes at different scales in a highly diverse Neotropical plant group, including recently radiated clades. We found that the taxon-specific kit provided a greater number of segregating sites, yet contrary to our expectations, the abundance of information content did directly translate to a greater resolution power.

The universal and taxon-specific sets performed comparably when investigating macroevolutionary patterns: the inferred species trees are remarkably consistent between the two bait sets (Figures 2 and S5). Notably, both sets were sufficiently informative to reconstruct the relationships among the fastest radiating clades. These results resonate with previous comparative works (e.g. in Burmeistera, Bagley et al., 2020; in Buddleja, Chau et al., 2018; and in Cyperus, Larridon et al., 2020), where taxon-specific markers provided higher gene assembly success, but a comparable number of segregating sites for phylogenetic inference, indicating that universal bait sets are nearly as effective as taxon-specific bait sets, even in fast evolving taxa. The main advantage of the bromeliad taxon-specific set is its ability to provide additional resolution for deeper examination of gene tree incongruence (Figure 2), currently a fundamental tool in phylogenomic research (Edwards, 2009; Morales-Briones et al., 2021; Pease et al., 2016).

The taxon-specific bait set performed marginally better to address hypotheses at more recent evolutionary scales and provided arguably clearer evidence for inference of species genomic structure using clustering methods. In fact, genetic markers obtained from both data sets provided sufficient information to infer species but no geographic structure, suggesting that *Tillandsia* could be characterized by high gene dispersal among populations. Considering that the Angiosperms353 kit has shown potential to provide within-species signal, as recently demonstrated by Beck et al. (2021) on *Solidago ulmifolia*, and to estimate demographic parameters from herbarium specimen (Slimp et al., 2021), we would expect the taxon-specific set to accurately reveal a geographical genetic structure. However, the present study is generally based on small sample sizes per species (n = 4-8), mostly sampled within a limited geographic range, limiting our ability to draw robust conclusions on the levels of intraspecific population structure.

The Bromeliad1776 kit provided a substantially larger number of segregating sites (more than 200 k vs. 47 k in Angiosperms353; Table 1, Figure S2) due to higher enrichment success, following the expectation for higher sequence variation in custom-made loci (Figure 1, see also Bragg et al., 2016; de La Harpe et al., 2019; Kadlec et al., 2017). We accordingly found that rates of molecular divergence are distinctly correlated with enrichment success in our sampling (Figure 1), following the expectation that a universal kit will provide fewer segregating sites.

However, the difference in resolution power between the kits cannot be ascribed solely to the different numbers of SNPs, but rather to the length and variability of the obtained regions. The topology obtained with the Angiosperm353 data set under the multispecies coalescent model was substantially different from all other inferred trees and the input gene trees provided a low power to detect patterns of gene tree discordance (Figure 2). We additionally observed that the highly conserved regions targeted by Angiosperms353 are shorter in comparison to Bromeliad1776 targets and thus result in shorter input windows for species tree inference (Figure 2). Hence, the patterns of gene tree discordance in the Angiosperms353 data set likely indicate incorrect gene tree estimation or other model misspecifications, rather than a biological signal. Specifically, coalescence-based methods are sensitive to gene tree estimation error (Zhang et al., 2018) and perform better with gene trees estimated from unlinked loci long enough and variable enough to render sufficient signal per gene tree-this is especially true for data sets with many taxa. The high rates of uninformative genes trees, found in almost half of the intergenic nodes in the Angiosperms353 data set, are expected with increased levels of gene tree error, which in turn reduce the accuracy of ASTRAL (Mirarab, 2019; Sayyari & Mirarab, 2016). In contrast, the Bromeliad1776 ASTRAL tree (Figure 2, left and Figure S9) resolved phylogenetic relationships among taxa with high posterior probability and a topology similar to the ML tree. Gene tree discordance analysis revealed high incongruence around certain nodes, possibly reflecting rapid speciation events.

Since inference of phylogenetic relationships under the multispecies coalescent and exploration of gene tree discordance are both pivotal to phylogenomic research (Degnan & Rosenberg, 2009; Edwards et al., 2016; Pease et al., 2016), a taxon-specific kit provides a clear advantage especially in recent rapid radiations, where gene tree conflict and incomplete lineage sorting are expected to be prevalent (Dornburg et al., 2019; Kubatko & Degnan, 2007; Roch & Warnow, 2015). In that regard, inference of the species tree with the Bromeliad1776 is a tool to drive further hypotheses concerning evolutionary and demographic processes in the evolution of *Tillandsia*. Moreover, the features of the loci targeted provide an important opportunity to study selection (see Section 4.3).

4.2 | Insights on Bromeliaceae phylogeny and demographic processes in *Tillandsia*

Both bait sets resolved the phylogeny of Bromeliaceae, including the fastest evolving lineages of the subfamily Tillandsioideae. The results generally agreed with previous findings of the relationships among taxa (Givnish et al., 2011, 2014). Several findings that contrast with the expected known phylogeny may point at a complexity of genomic processes in the evolutionary history of Bromeliaceae subfamilies. Both the ML tree and species tree did not support a monophyly of the subfamily Pitcairnioideae, which was represented by four samples and two genera in our phylogeny: *Deuterochonia* and *Pitcarnia*. Rather, the genus *Deuterochonia* was sister to subfamily Puyoideae or sister to both Puyoideae and Bromelioideae subfamilies, inconsistent with the results of Barfuss et al. (2016) and Granados Mendoza et al. (2017). Interestingly, in a visualization of gene tree discordance we found high levels of incongruence and a high percentage of trees supporting an alternative topology in the node splitting the genera, indicating that several genomic processes such as hybridization and incomplete lineage sorting may have accompanied divergence in this group, contributing to the phylogenetic conflict and extending the challenges in resolving these evolutionary relationships. Within the core Tillandsioideae, the tribes Tillandsieae and Vrieseeae were found to be monophyletic, in accordance with previous work on the subfamily (Barfuss et al., 2016). Finally, within our focal group Tillandsia subgenus Tillandsia, clade K as suggested by Barfuss et al. (2016) and clades K.1 and K.2 as proposed by Granados Mendoza et al. (2017) were all well supported, further in agreement with their interpretation of Mexico and Central America as a centre of diversity for subgenus Tillandsia. Within Tillandsia, incongruence was prominent at the recent splits within clade K.1. and clade K.2 as expected in a recent rapid radiation, a result of high levels of incomplete lineage sorting, hybridization and introgression (Berner & Salzburger, 2015).

When applied to methods in population genetics, we obtained some evidence for a difference in demographic processes and in the level of genetic variation among species. This was especially true for the taxon-specific bait set: for example, the bait set differentiated between populations of T. punctulata and T. fasciculata, but not T. gymnobotrya in a maximum-likelihood tree and ancestry analysis (Figures 4 and S5), indicating differences in interpopulation genetic structure among species. The evidence for different demographic processes in these species extended to estimates of Tajima's D, where lower values may indicate a recent bottleneck. In addition, we found a unique distribution of nucleotide diversity for T. foliosa, possibly reflecting a low effective population size for this endemic species in contrast to the closely related, but widespread T. fasciculata. In all cases, our limited sampling given the large size of the family constrains our ability to draw conclusions of a 'true' phylogeny and to account for population structure. Our finding however suggests that nuclear markers obtained with a target capture technique can highlight genomic processes and be further applied to address guestions in population genomics with a wider sampling scheme.

4.3 | Future prospects and implications for research in Bromeliaceae and rapid radiations

Beyond the scope of this study, the availability of a bait set kit for Bromeliaceae provides a prime genetic resource for investigating several topical research questions on the origin and maintenance of Bromeliaceae diversity. Manifold studies of bromeliad phylogenomics set forth the challenges of resolving species-level phylogenies with a small number of markers, particularly in young and speciose groups (Goetze et al., 2017; Granados Mendoza et al., 2017; Loiseau MOLECULAR ECOLOGY RESOURCES

et al., 2021; Versieux et al., 2012). This particularly curated bait set allows highly efficient sequencing across taxa: within our study, we found high mapping success with 82.3% average read mapping. As expected, we documented a difference in enrichment success among taxa, explained by divergence time to the reference used for bait design (see Figure S4), suggesting possible deviations from the assumptions of nonrandomly distributed missing data that may mislead phylogenetic inference (Lemmon et al., 2009; Streicher et al., 2016; Xi et al., 2016). However, given the large enrichment success, downstream analysis with deliberate methodology can account for possible biases and provide robust inference with strict data filtering (Molloy & Warnow, 2018; Streicher et al., 2016). Hence, target enrichment with Bromeliad1776 can produce large data sets with consistent representation between taxa, allowing repeatability between studies and retaining the possibility for global synthesis by including sequence baits orthologous to the universal Angiosperms353 bait set. Moreover, with specific knowledge of the loci targeted in this set, the ability to obtain the same sequences across taxa and experiments and to differentiate genic regions with the use of A. comosus models, this bait set offers a broad utility for research in population genomics.

Another important feature in the Bromeliad1776 set is the inclusion of genes putatively associated with key innovative traits in Bromeliaceae with a focus on C3/CAM shifts. Little is known about the molecular basis of the CAM pathway, an adaptation to arid environments which evolved independently and repeatedly in over 36 plant families (Chen et al., 2020; Heyduk et al., 2019; Silvera et al., 2010). CAM phenotypes are considered key adaptations in Bromeliaceae, associated with expansion into novel ecological niches. In Tillandsia, C3/CAM shifts were found to be particularly associated with increased rates of diversification (Crayn et al., 2004; Givnish et al., 2014; de La Harpe et al., 2020). The Bromeliad1776 bait set offers opportunities to address specific questions on the relationship between rapid diversification and photosynthetic syndromes in this clade, including testing for gene sequence evolution. Additionally, the inclusion of multicopy genes, combined with newly developed pipelines for studying gene duplication and ploidy (Morales-Briones et al., 2021; Viruel et al., 2019), is beneficial for studying the role of gene duplication and loss in driving diversification. With the increasing ubiquity of target baits as a genomic tool, we expect to see additional pipelines and applications emerging, further expanding the utility of target capture for both macro-and microevolutionary research.

5 | CONCLUSIONS

Even as whole-genome sequencing becomes increasingly economically feasible, target capture is expected to remain popular due to its extensive applications in research. We found that evaluating the differences in resolution power between universal and taxon-specific bait sets is far from a trivial task, and we attempted to lay out a methodological roadmap for researchers wishing to reconstruct the VILEY MOLECULAR ECOLO

complex evolutionary history of rapidly diversifying lineages. While a taxon-specific set offers exciting opportunities beyond phylogenomic and into research of molecular evolution, its development is highly time-consuming, requires community-based knowledge and may cost months of work when compared with out-of-the-box universal kits. Our results suggest that universal kits can continue to be employed when aiming to reconstruct phylogenies, in particular as this may offer the possibility to use previously published data to generate larger data sets. However, for those wishing to deeply investigate evolutionary questions in certain lineages, a taxon-specific kit offers certain benefits during data processing stages, where knowledge of the design scheme and gene models is extremely useful, and the possible return of costs is especially high for taxa emerging as model groups. We furthermore encourage groups designing taxonspecific kits to include also universal probes, furthering the mission to complete the tree of life.

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AUTHOR CONTRIBUTIONS

CL, MP and GY conceived the study. CL provided funding. TK coordinated sample collection, MdLH, VGJ and GY collected data. MHJB and WT identified species. GY designed bait kit, with guidance from JH and MP. CGC, JV, NR, MHJB and GY performed molecular work. GY and TL analysed the data using feedback from JV and OP. GY wrote the manuscript with significant input from all co-authors.

OPEN RESEARCH BADGES

This article has earned an Open Data badge for making publicly available the digitally-shareable data necessary to reproduce the reported results.

DATA AVAILABILITY STATEMENT

Targeted sequencing reads generated for this project are available at NCBI-SRA under BioProject PRJNA759878; for accession numbers, see Table S4. The probe set and the relevant supporting information are available in Dryad (https://doi.org/10.5061/dryad.mpg4f4r11). The bioinformatics scripts are available at https://github.com/giyan y/Bromeliad1776/tree/main/MS_2021_scripts.

ORCID

Gil Yardeni Dhttps://orcid.org/0000-0002-6848-7156 Margot Paris Dhttps://orcid.org/0000-0001-7328-3820 Michael H. J. Barfuss Dhttps://orcid.org/0000-0001-7172-9454 Christian Lexer Dhttps://orcid.org/0000-0002-7221-7482 Ovidiu Paun Dhttps://orcid.org/0000-0002-8295-4937

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SUPPORTING INFORMATION

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Supporting information

including Supporting Figures, supporting information and supporting tables

Supplemental Information for:

Taxon-specific or universal? Using target capture to study the evolutionary history of a rapid radiation

Gil Yardeni, Juan Viruel, Margot Paris, Jaqueline Hess, Clara Groot Crego, Marylaure de La Harpe, Norma Rivera, Michael H. J. Barfuss, Walter Till, Valeria Guzmán-Jacob, Thorsten Krömer, Christian Lexer, Ovidiu Paun and Thibault Leroy

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Figure S1 Map of sampling locations for *Tillandsia* subgenus *Tillandsia* accessions within Mexico.



Figure S2 Mapping rates (A) and percentage of reads matching bait sequences (B) for Bromeliad samples enriched with one of two bait sets: Angiosperms353 and Bromeliad1776. Reads were mapped against *Ananas comosus* reference for both bait sets. Targets were defined as bait locations and flanking 500 base-pairs. Bromeliad1776 targets were defined as the regions used for bait design and Angiosperms353 targets were defined as *A. comosus* orthologous regions matching the genes used for bait design.



simplified phylogenetic tree (by assembly) for Bromeliaceae samples

Figure S3 A simplified phylogenetic tree, with branches colored according to read mapping percentage for samples enriched with Angiosperms353.



Figure S4 A simplified phylogenetic tree, with branches colored according to read mapping percentage for samples enriched with Bromeliad1776.



Figure S5 Maximum-likelihood (ML) phylogenetic tree inferred with RAxML-NG, based on variants called for data sets enriched with Bromeliad1776 bait set (left) and Angiosperms353 bait set (right, flipped for mirroring). Branch lengths were calculated by number of substitutions per site. Internal nodes are marked and colored according to bootstrap support. Nodes which differed among trees are colored purple and have been marked by an arrow.



Figure S6 Principal Component Analysis (PCA) plot for samples of *Tillandsia* subgenus *Tillandsia* enriched with two bait sets: A. Angiosperms353 (1,025 variants after LD-pruning) B. Bromeliad1776

(32,941 variants after LD-pruning). Colors indicate different species (following the scheme in Supporting Figure S5) and shapes represent different geographic origins (populations).



Figure S7 Admixture cross-validation errors (top) detected for values of K between 2 and 9 for A. Angiosperms353 data set and B. Bromeliad1776 data set.
MOLECULAR ECOLOGY RESOURCES



Figure S8 Coalescent-based species trees generated ASTRAL-III for samples enriched with Angiosperms353 using 269 genes. Node values represent local posterior probabilities (pp) for the main topology.

MOLECULAR ECOLOGY RESOURCES



Figure S9 Coalescent-based species trees generated ASTRAL-III for samples enriched with Bromeliad1776 using 1600 genes. Node values represent local posterior probabilities (pp) for the main topology.

MOLECULAR ECOLOGY RESOURCES

Supporting information: ascertainment bias

The non-random selection of markers for target capture may introduce ascertainment bias, with implications for population genomics methods (Heslot et al., 2013). An absence or misrepresentation of rare SNPs is an indication of such bias and may further result in loss of valuable information and misinterpretation of values, such as Fst and heterozygosity (Lachance & Tishkoff, 2013). To assess the extent of ascertainment bias that may rise in the use of Bromeliad1776, we assessed differences in SNP discovery by comparing whole genome data and target capture data in three Tillandsia samples, using the ratio of heterozygous to homozygous sites per LG as a measure to examine differences in SNP discovery.

Briefly, for each sample we obtained both whole-genome sequencing data and targeted sequencing data, produced with the bromeliad1776 bait-set. All accessions were reference mapped to the A. comosus v.3 reference (Ming, 2015). Variants were then called for each data type separately using freebayes v1.3.2-dirty (Garrison & Marth, 2012) - one variant call file for each data type, containing all three samples. Each vcf file was filtered to retain mean genotype depth > 4 and sites with 70% missing data using vcftools (Danecek et al., 2011). The ratio of heterozygous to homozygous sites was calculated for each individual and each LG (chr) using vcflib (Garrison, 2012).

The ratio heterozygous to homozygous sites was higher for target capture data sequencing in almost all species and loci, indicating high discovery of heterozygous sites. However, the differences in ratio were strongly correlated with sequencing depth (P < 0.003) and species (P < 0.003) and differences among species were more prominent than variation among data-types, indicating the former as causes for dissimilarities in SNP discovery, rather than marker selection (see figure below).



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Angiosperm_gene	NA	AA	A	M	6176	AA	AA	AA	AN	MA	6175	A	A	MA	AN	Ą	M	A	M	AN	AA	AA	AA	MA	NA	NA	AA	AA	NA	M
gene_families_CAM C3	٩N	AN	NA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	NA	NA	AN	AN	AN	NA	٩N	AN	AN	AN	NA	AN
MAD_not_selection_CAM shifta_	AN	AN	٩N	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	٩N	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	٩Z
Diff_expressed_CA DC3	yes	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	ΑN	AN	AN	AN	٩N	AN	AN	AN	AN	AN	AN	AN	AN	٨A	AN	AN	yes	ΝA	yes
High_copy.Broc_An an_Tilla.	ou	ou	AN	ou	ou	ou	ou	ou	ou	ou	ou	ou	0L	ou	ou	ou	ou	Q	ou	yes	ou	ou	ou	ou	ou	ou	ou	yes	ou	0 L
Low_copy.Broc_Ana n_Tilla.	92	2	AN	yes	yes	2	2	2	2	2	2	2	2	8	2	6	yes	2	2	e e	8	2	2	92	0L	yes	yes	2	0L	2
Single_copy.Broc_A nan_Tilla.	yes	yes	AN	Q	2	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	2	yes	yes	е И	yes	yes	yes	yes	yes	QL	QL	Q	yes	yes
emanes	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02
gene	Aco000722	Aco000724	Aco000727	Aco000731	Aco000735	Aco000736	Aco000746	Aco000748	Aco000753	Aco000754	Aco000759	Aco000767	Aco000778	Aco000793	Aco000794	Aco000795	Aco000798	Aco000809	Aco000814	Aco000816	Aco000822	Aco000823	Aco000834	Aco000836	Aco000843	Aco000868	Aco000907	Aco000950	Aco000965	Aco000985

9zi2_nox9_nim	132	53	497	44	51	310	278	66	133	325	155	61	159	35	1916	59	403	1367	915	54	124	271	27	106	428	26	113	228	146	113
total_exonic_size	2890	1783	2466	1797	3521	1278	1220	2001	1722	1101	950	764	1512	1077	1916	2169	1213	1367	2424	2370	1475	1108	1353	1833	1235	2270	2743	1559	1934	1355
ລແລຄີເລດີຣແດະລີແ	11	8	m	14	11	m	m	~	2	m	4	4	4	8		11	2	-	5	2 L	4	2	16	4	2	ъ	6	e	2	2
eziz_noxe_egereva	262.727	222.875	822.000	128.357	320.091	426.000	406.667	285.857	344.400	367.000	237.500	191.000	378.000	134.625	1916.000	197.182	606.500	1367.000	1212.000	474.000	368.750	554.000	84.563	458.250	617.500	454.000	304.778	519.667	386.800	271.000
ədAj	NA	10_Glucogenesis_specific_dayC3	NA	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	NA	NA	05_Chloroplasts_activity	00_#Ming2019_SI_gene	02_Aquaporins	NA	NA	NA	NA	05_Chloroplasts_activity	NA	NA	00_#Ming2019_S1_gene	NA	NA	NA	00_#16_calciumdependent_protK	NA	00_#W_StomatalMovement_ABA_r esponsive_binding- element_F101b_Abscisic_acid_sig nal	NA	NA	NA	NA
circadian_clock																														
ysis_glycol		yes		yes																										
ogulluhoq_ləs_soq	NA	NA	NA	NA	PREDICTED: Glycine max histidine kinase 2- like (LOC100781655)_ transcript variant X3_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	AN N	NA	NA	NA	NA
stronord_bionovslt SQ_binia_Dia	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Malate I ransterase Assimilation_Carboh ydrates										yes							yes													
circadian_metabolis m_Wai2017																										yes				
anthocyanin_SI_Ana nas											yes									yes										
markers																														
draught_res																														
aquaporin_reg												yes																		
stomata_func																										yes				
CAM- related_Acomosus_ 7102pm																								yes						
Angiosperm_gene	MA	M	AN	M	¥	M	M	A	AN	AA	AN	AN	7572	4890	AN	6363	A	AN	AA	AA	MA	AA	6389	AN	6401	M	AN	MA	AA	MA
MAD_2sailims1_anag C3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	AN
MAD_noticelection_CAM stifts_	ΝA	AN	yes	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
Diff_expressed_CA DC3	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	AN
high_copy.Broc_An an_Tilla.	ou	Q	ou	Q	yes	ou	0L	Q	Q	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	QL	Q	Q	ou	ou
Low_copy.Broc_Ana n_Tilla.	92	yes	2	92	ę	2	2	2	2	2	yes	yes	2	2	2	2	2	2	2	yes	92	9	2	2	2	e	2	2	2	2
Single_copy.Broc_A nan_Tilla.	yes	0L	yes	yes	2	yes	yes	yes	yes	yes	Q	QL	yes	yes	yes	yes	yes	yes	yes	Q	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
emanpes	-G02	-G02	-G02	.G02	-G02	-G02	.G02	-G02	.G02	.G02	.G02	.G02	.G02	.G02	.G02	-G02	-G02	.G02	.G02	.G02	.G02	.G02	.G02	-G02	-G02	-G02	-G02	-G02	-G02	.G02
gene	Aco000993	Aco000997	Aco001001	Aco001003	Aco001020	Aco001042	Aco001049	Aco001055	Aco001068	Aco001089	Aco001100	Aco001106	Aco001112	Aco001128	Aco001146	Aco001178	Aco001181	Aco001199	Aco001201	Aco001216	Aco001220	Aco001222	Aco001246	Aco001261	Aco001317	Aco001326	Aco001329	Aco001339	Aco001350	Aco001352

sziz_noxs_nim	89	372	313	180	342	132	4	1811	1379	1103	111	491	44	254	245	35	680	27	2345	210	516	330	434	114	170	4	272	191	170	49	377
ອຊເຮັວແມດສອີເຊເຊ	2251	1121	1304	1407	1145	778	1513	1811	1379	1103	1403	491	1845	577	1274	1254	1384	1581	2345	1164	1304	1263	1578	396	2374	2399	1124	2234	1447	3220	377
orio organization		01		10							10										01		~		10	_					
nr_exons_per_gene	5 11	0	0	<u>"</u>	~		~			1	<u> </u>	1	9 17	~	~	12		15		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	0		0	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	3	0	~			13	
aziz_noxa_agasiava	204.636	560.50	652.000	281.400	381.66	259.33	216.14;	1811.000	1379.000	1103.000	280.600	491.000	108.529	288.500	424.66	104.500	692.000	105.400	2345.000	388.000	652.000	421.000	526.000	132.000	474.800	266.556	374.66	372.33	482.33	247.692	377.000
əd/y	A	A	AV	AV	AV	AV	10_Glucogenesis_specific_dayC3	AV	٨٨	AV	AV	٨٨	AV	AV	AV	AV	AA	AV	AV	AV	A	11_Glycolysis_night_C4_malate_p athway	AA	06_Drough_resistance_genes_LEA	A	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	٨٨	AV	01d_Auxin_reponse_factor	AA
circadian_clock																															
glucogenesis_glycol ysis_							/es															/es				/es	/es				
oອິnjinuod jəs sod	PREDICTED: Oryza sativa Japonica Group homeobox-leucine zipper protein ROC7 (LOC4344614)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Vitis vinifera aspartic proteinase PCS1 (LOC100251245)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA									
filavonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates																															
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana san																															
markers																															
qraught_res																								es							
aquaporin_reg																															
stomata_func																														es	
related_Acomosus_ 8102gniM																															
-MA2	-	7	42	7	7	7	7	7	7	7	7	Ŧ	99	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7		7
Angiosperm gene	Ž	Ž	26	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	A 53	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž
_ettine	ž	ž	ž	ž	ž	ž	ž	Ż	ž	ž	ž	ź	ž	ž	ž	ž	Ż	ž	ž	ž	ž	ž	ź	ž	ž	ž	ž	ž	ż	ž	ž
MC3 Selection CAM	٩N	Ž	Z	Z	Ž	Ž	Ž	ž	Ž	Ž	Ž	ZN N	Z	Z	Ž	ye	Ž	Ž	Ž	Ž	Ž	Ň	ν	Ž	Ž	Ž	Ž	Ž	Z	Ž	Ž
an_Tilla. Diff_expressed_CA	NA	AN	AN	NA	AN	yes	AN NA	AN NA	AN	AN	NA	yes	AN	yes	AN	AN	AN	yes	A N	AN	AN	AN .	AN	NA	AN	AN	AN	, yes	AN	AN	yes
nn high_copy.Broc_An	yes	ou	ou	ou	0L	2	e L	0L	е Г	ou	ou	ou	ou	Q	2	2	2	2	0L	0L	ou	yes	ou	e	е Г	e L	NA	yes	ou	e 2	0L
Low_copy.Broc_Ana	2	8	yes	2	2	2	yes	2	2	2	2	yes	2	2	2	2	2	2	2	2	8	6	2	yes	2	yes	A	2	2	yes	2
A_oonB.voo_elgni2	2	yes	2	yes	yes	yes	2	yes	yes	yes	yes	QL	yes	yes	2	yes	2	yes	2	٩N	2	yes	2	yes							
edname	LG02	LG05	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18
әиәб	Aco001366	Aco001384	Aco001395	Aco001399	Aco001415	Aco001416	Aco001430	Aco001431	Aco001432	Aco001435	Aco001437	Aco001473	Aco001478	Aco001482	Aco001508	Aco001521	Aco001534	Aco001542	Aco001543	Aco001545	Aco001553	Aco001560	Aco001566	Aco001571	Aco001579	Aco001580	Aco001608	Aco001618	Aco001621	Aco001637	Aco001647

sziz_noxs_nim	59	164	105	196	2918	93	71	551	127	134	124	277	16	518	323	104	1112	48	70	243	32	79	367	25	35	1763	2108	36	06	130	1235
total_exonic_size	1902	1198	2090	1533	2918	895	871	1224	861	1539	1108	4262	2492	1230	1313	2118	1112	1540	1567	1036	1831	1405	1266	1389	1786	1763	2108	1190	2135	1390	1235
	10	4	2	4	-	4	m	2	m	4	2	2	17	2	2	80	-	16	9	2	8	7	5	12	18	1	1	7	~	2 2	-
	.200	.500	.571	.250	000:	:750	.333	000	000:	.750	.600	.400	588	000	.500	.750	.000	.250	.167	000:	.875	.714	000:	.750	.222	:000	:000	000	000	:000	000
average_exon_size	190	299	298	383	2918	223	290	612	287	384	221	852	146	615	656	264	1112	96	261	518	228	200	633	115	66	1763	2108	170	305	278	1235
əd/q	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	01b_Abscisic_acid_signal	NA	NA	NA	NA	00_#MB_PHYE/B	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	06_Drough_resistance_genes_LEA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	00_#W_SucroseTransporter_SWE ET11/12	NA	NA	NA
circadian_clock																															
glucogenesis_glycol sisy			yes										yes								yes										
ogulluhoq_ləs_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
filavonoid_anthocya 29_aimia_Picaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	AL B_F_acyl-glucose-dependent anthocyanin 7-o- olucosvitransferase	NA	NA	NA	NA	NA	NA	NA
Asimilation_Carboh Assimilation_Carboh ydrates																															
circadian_metabolis m_Wai2017																												yes			
anthocyanin_SI_Ana aas																															
markers												yes																			
qraught_res																				yes											
aquaporin_reg																															
stomata_func							yes																								
CAM- related_Acomosus_ Ming2015																															
Angiosperm_gene	AA	AA	AA	A	A	6550	AA	AA	5357	AA	A	A	A	A	A	6450	AA	6034	5858	AA	AA	5138	AA	AN	5945	AA	AN	AA	6717	AA	A
gene_families_CAM C3	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	NA	AN	AN	AN	AN	AN
Pos_selection_CAM 	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	NA	AN	AN	AN	AN	AN
Diff_expressed_CA MC3	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	NA	NA	AN	yes	AN	AN	AN
High_copy.Broc_An an_Tilla.	ou	Q	yes	ou	ou	ou	AN	ou	Q	ou	ou	Q	Q	Q	ou	ou	ou	ou	ou	Q	2	2	Q	ou	ou	ou	0 L	Q	ou	ou	2
Low_copy.Broc_Ana. n_Tilla.	2	e	2	2	2	2	A	6	2	yes	2	yes	yes	2	2	2	2	2	yes	2	yes	2	2	yes	yes	6	2	2	2	2	2
Single_copy.Broc_A nan_Tilla.	yes	yes	2	yes	yes	yes	AN	yes	yes	2	yes	2	2	yes	yes	yes	yes	yes	2	yes	2	yes	yes	ou	Q	yes	yes	yes	yes	yes	yes
əmanpəz	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18	LG18
деле	Aco001651	Aco001675	Aco001686	Aco001691	Aco001693	Aco001703	Aco001707	Aco001718	Aco001742	Aco001744	Aco001767	Aco001769	Aco001770	Aco001780	Aco001783	Aco001791	Aco001803	Aco001826	Aco001830	Aco001848	Aco001853	Aco001855	Aco001857	Aco001858	Aco001863	Aco001881	Aco001894	Aco001900	Aco001903	Aco001926	Aco001934

	9	m	8		4	m	6	5	5	~	1	6	5		~	0	5	2	m	0	~	m	0	2	2	6	4	0	4	0	-
əziz_noxə_nim	4	4	ñ	34.	17	ۍ ا	191	31!	11	64	^{ئن}	575	17	60	49	2	22	80	8	83(12	25;	14	11;	42	ň	26	30(1	18(÷
ezia_exonic_size	2401	864	3376	2784	1807	1340	1919	1104	2243	647	1357	1286	2224	4079	3445	1038	1730	1978	3427	830	1240	1902	1750	1930	2129	1920	1219	2454	595	1605	1113
ur_exons_per_gene	14	۳ ۱	24	["]	L	Ő	1	n n	2		~		۳ ۱	14		4	۳ ۳	7		-	⁶	4	9	L 10	~	LC LC	m	(^m)		9	5
average_exon_size	171.500	288.000	140.667	928.000	361.400	148.889	1919.000	368.000	320.429	647.000	169.625	643.000	741.333	291.357	1722.500	259.500	576.667	282.571	428.375	830.000	248.000	475.500	291.667	386.000	709.667	384.000	406.333	818.000	297.500	267.500	123.667
ədify	01b_Abscisic_acid_signal	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	NA	11_Glycolysis_night_C4_malate_p athway	NA	06_Drough_resistance_genes_LEA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	04_Oxygen_evolving_enhancer_O EE	NA	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
circadian_clock																															
glucogenesis_glycol ysis_		yes	yes			yes		yes			yes							yes		yes											
oɓnjimuod jəs sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
filavonoid_anthocya 29_aimia_pS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																se															
circadian_metabolis m_Wai2017 malateTransferase																~															
anthocyanin_SI_Ana nas																															
markers																															
draught_res										yes																					
aquaporin_reg																															
stomata_func	yes																														
related_Acomosus_																															
CAM-	A	4	4	4	A	483	×.	×.	A	4	4	4	4	4	4	A	×.	A	A	A	469	A	A	A	A	A	A	A	A	A	4
MAD_23eilinst_ang C3 Andiosperm gene	IN N	N V	N V	N A	N N	1A 64	N V	N N	N N	N V	N V	N V	N V	N V	N V	Z A	N N	N N	N V	N V	t≱ I	IA N	N A	N N	N V	N N	N N	N V	N V	N N	N N
pos_selection_CAM shifts	Z V	Z V	Z A	Z A	Z V	Z A	Z A	Z A	Z A	Z A	Z A	Z A	Z A	ves N	Z A	Z A	Z A	Z A	Z V	Z V	Z V	ves N	Z V	Z V	Z V	Z V	Z V	Z V	Z V	Z A	2
MC3 Diff_expressed_CA	A N	Z V	A N	A N	A N	A N	A N	A N	es D	A N	A N	A N	A N	IA V	A N	A N	A N	A N	es P	A N	A N	IA y	A N	A N	es 2	es D	A N	A N	es	Z A	es
High_copy.Broc_An an_Tilla.	2	2	2	2	2	2	 _0	2	ō V	2	2	2	2	2	2	 	 _0	2	0	2	2	2	2	2	0 7	0	0	2	0	2	0 2
Low_copy.Broc_Ana n_Tilla.	ves n	les n	g	g	u Q	u Q	u Q	n sə	n sə	ves n	g	g	g	g	u Q	u sə,	u Q	n sə	les n	0	g	u Q	u Q	u Q	۲ و	les n	u Q	u Q	les n	g	- 0
Alngle_copy.Broc_A nan_Tilla.	0 V	0	es n	es n	es n	es n	es n	ō V	0 ×	0	es n	u se	es n	es n	es n	0 ×	es n	ō V	0	es n	es n	es n	es n	es n	es n	ō	es n	es n	0	es n	es n
emenpez	G18 n	G18 n	G18 y	G18 y	G18 y	518 y	318 y	304 n	304 n	304 n	304 y	304 y	304 y	304 y	304 y	304 n	304 y	304 n	304 n	304 y	GO4 V	G04 y	G04 V	G04 y	304 y	304 n	G04 y	G04 y	204 n	304 y	304 V
	941 L(945 L(954 L(958 L(967 LC	976 LC	994 LC	015 LC	037 LC	055 LC	071 LC	118 LC	171 LC	187 LC	196 LC	227 LC	247 LC	248 L(253 L(268 L(270 LC	284 L(286 L(296 L(305 L(324 L(356 L(358 L(366 L(378 L(400 LC
0eue	Aco001!	Aco001!	Aco001!	Aco001!	Aco001!	Aco001!	Aco001!	Aco002(Aco002(Aco002(Aco002(Aco002:	Aco002:	Aco002:	Aco002:	Aco002	Aco002	Aco002:	Aco002:	Aco002:	Aco002:	Aco002:	Aco002:	Aco002:	Aco002;	Aco002;	Aco002;	Aco002;	Aco002;	Aco002:	Aco0024

əziz_noxə_nim	53	177	36	484	294	102	306	1112	55	395	398	339	449	15	53	443	140	59	236	77	409	327	60	48	986	52	11	18	191	129
total_exonic_size	3020	744	1285	1792	1539	1813	2352	1112	929	2460	398	1395	1835	1020	3054	443	2626	1557	1272	369	1828	1377	996	1320	986	2347	1152	1677	1333	3737
nr_exons_per_gene	17	2	9	2	m	2	m		4	m	1	m	e	9	6		2	7	m	е	2	e	4	8	1	14	6	9	e	4
average_exon_size	177.647	372.000	214.167	896.000	513.000	362.600	784.000	1112.000	232.250	820.000	398.000	465.000	611.667	170.000	339.333	443.000	525.200	222.429	424.000	123.000	914.000	459.000	241.500	165.000	986.000	167.643	128.000	279.500	444.333	934.250
əd/q	AA	06_Drough_resistance_genes_LEA	00_#W_FructoseTransporter_SWE ET17	AV	AV	00_#W_StomatalMovement_ethyle	10_Glucogenesis_specific_dayC3	A	A	A	10_Glucogenesis_specific_dayC3	AV	10_Glucogenesis_specific_dayC3	A	10_Glucogenesis_specific_dayC3	A	00_#MB_NIA	A	A	AA	AN	AA	AA	00_#04_carbonic_anhydrase	A	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	A	A	A
circadian_clock		0																		4	4	4								
glucogenesis_glycol							yes			yes	yes		yes		yes											yes	yes			
ogulluhoq_ləs_zoq	Arabidopsis thaliana Nucleoporin interacting component (Nup93/Nic96-like) family protein mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris mitochondrial uncoupling protein 5 (LOC104896063) mRNA	PREDICTED: Glycine max glucose-6- phosphate isomerase 1_chloroplastic (LOC100818441) mRNA	NA	PREDICTED: Beta vulgaris subsp. vulgaris dicarboxylate transporter 2_chloroplastic (LOC104904059) mRNA	NA	NA
attoroid_anthocya filavonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_flavonol synthase	NA	NA	NA	NA	NA	AA	NA	NA
MalateTransferase_ Assimilation_Carboh ydrates																														
circadian_metabolis m_Wai2017			yes			yes																								
anthocyanin_SI_Ana nas																														
markers																	yes													
qı.saght_res		yes																												
aquaporin_reg																														
CAM- related_Acomosus_ Ming2015_ stomata_func																								yes						
Angiosperm_gene	AN	AA	AA	AA	AA	AA	A	AA	A	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	6379	AA	AA	AA	AA	AA	AN	AA	AA	AA	AA
gene_families_CAM C3	NA	AN	AA	AN	AN	AA	AN	AN	AA	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	NA	AN	NA	AN	AN	NA	AN	AN	AN	AA
MAD_non_CAM 	ΝA	ΑN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	NA	yes	AN	AN	AN	AN	NA	yes	ΑN	NA	AA	AN	ΝA	AN	AN	AN	AN
Diff_expressed_CA MC3	AN	٩N	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	yes	AN	yes	AN	NA	NA	٩N	yes	AN	NA	NA	٩N	AN	AN	AN
high_copy.Broc_An I.Sli1_ns	ou	٩N	ou	QL	Q	Q	ę	Q	yes	Q	Q	оц	QU	Q	ę	Q	Q	AN	QL	ou	ou	ou	QL	ę	AN	ou	ou	Q	e e	e E
Low_copy.Broc_Ana n_Tilla.	yes	AA	Q	2	ę	yes	yes	ę	2	ę	2	2	yes	yes	yes	ę	yes	AA	ę	01	QL	ou	0L	2	MA	yes	yes	e	ę	2
Single_copy.Broc_A nan_Tilla.	2	ΑN	yes	yes	yes	2	2	yes	2	yes	yes	yes	2	2	2	yes	2	AN	yes	yes	yes	yes	yes	yes	AN	ou	2	yes	yes	yes
əmsnpəz	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06
деле	Aco002415	Aco002475	Aco002476	Aco002484	Aco002493	Aco002499	Aco002508	Aco002524	Aco002530	Aco002531	Aco002546	Aco002547	Aco002572	Aco002583	Aco002605	Aco002616	Aco002647	Aco002667	Aco002669	Aco002671	Aco002677	Aco002683	Aco002697	Aco002732	Aco002736	Aco002739	Aco002744	Aco002760	Aco002775	Aco002797

9zi2_nox9_nim	452	65	155	580	240	169	329	2510	71	53	125	151	166	46	136	60	61	131	155	379	333	65	20	e	119	48	1334	65	229	445
ezia_oinoxe_latot	1874	2661	1822	2839	1882	1615	835	2510	3809	1573	3292	2181	1664	4893	2578	1253	2470	1397	1936	1177	1775	1073	2192	2061	3984	1739	1334	1265	725	1037
ang ng n	2	3	80	2	2	Q	2	1	13	80	2	4	2	44	9	9	12	9	9	ю	e	9	20	11	4	2	1	2	2	2
əziz_noxə_əgerəva	937.000	887.000	227.750	1419.500	941.000	323.000	417.500	2510.000	293.000	196.625	1646.000	545.250	332.800	111.205	429.667	208.833	205.833	232.833	322.667	392.333	591.667	178.833	109.600	187.364	000.966	248.429	1334.000	253.000	362.500	518.500
ąłką	NA	NA	NA	NA	00_#20_hypothetical_protein	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	10_Glucogenesis_specific_dayC3	00_#W_MalateTransporter_ALMT_ 10_Glucogenesis_specific_dayC3	NA	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	11_Glycolysis_night_C4_malate_p athway	NA	01b_Abscisic_acid_signal	NA	NA	00_#Zizka_AGT1_#04_carbonic_a nhydrase	NA	10_Glucogenesis_specific_dayC3	01b_Abscisic_acid_signal	01b_Abscisic_acid_signal
circadian_clock																														
glucogenesis_glycol ysis_										yes				yes			yes				yes							yes		
ogullufioq_las_soq	NA	PREDICTED: Glycine max cullin-3A-like (LOC100794520)_mRNA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris alamine-IRNA ligase_ chloroplastic/mitochondrial (LOC104903847)_ transcript variant X1_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oryza sativa Japonica Group cDNA clone.J033097J24_full insert sequence	NA	NA	NA	NA	NA	NA
rtlavonoid_anthocya filavonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates ydrates																														
circadian_metabolis m_Wai2017															/es															
anthocyanin_SI_Ana asn																														
markers																										/es				
draught_res																														
aquaporin_reg																														
stomata_func																							yes						yes	yes
-MAJ related_Acomosus_ ZI0SpniM					yes																									
Angiosperm_gene	AV	AV	A	Ą	A,	Ą	343	Ą	AN AN	Ą	AN.	AN AN	AN AN	Ą	A)	260	4	Ą	AN AN	Ą	Ą	477	Ą	A)	A.	AN AN	A	AN A	٩ı	₹
MAD_26 C3 C3	A N	4 A M	4 A	A A	A A	A A	A A	A A	4 A	4 A	A	AN	AN	A A	A A	A A	4 A	A A	AN	A P	A A	AA	A A	A A	A A	4 A	A A	A A A	4 PN	4 A
pos_selection_CAM shifts	NA I	AM	- AN	AN	AN	AN	AN	AN	AN	AM	AM	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AM	AN	NA I	NA I	NA I	AN
Diff_expressed_CA MC3	4 V	4 A	4 V	A A	A A	A N	A P	A P	A A	/es	A A	A P	A P	A P	A A	4 A	4 A	A A	A P	A P	A P	AA	A	A A	A A	A A	4 V	A A	4 P	/es
High_copy.Broc_An an_Tilla.	1 01	0L	1 01	6	- NA	1	0	0L	ę	or	0	1	6	0	6	6	6	6	6	1	ves I	6	2	ves 1	0	2	1 01	0L	0	10
Low_copy.Broc_Ana n_Tilla.	0	0	0	2	AN	2	2	2	yes	yes	2	2	2	yes 1	2	yes 1	yes r	2	2	2	02	2	yes 1	6	2	yes	0	yes	6	2
A_oopy.Broc_A nan_Tilla.	yes	yes	yes	yes	AN	yes	yes	yes	2	2	yes	yes	yes	2	yes	2	2	yes	yes	yes	2	yes	2	2	yes	2	yes	2	yes	yes
əmsnpəz	.G06	.G06	.G06	G06	G06	G06	.G06	.G06	.G06	.G06	G06	G06	G06	.G06	GOG	.G06	.G06	G06	G06	.G06	.G06		.G06	.G06		GOG	G17	G17	G17	G17
gene	Aco002844 L	Aco002868 L	Aco002869 L	Aco002875 L	Aco002885 L	Aco002887 L	Aco002912 L	Aco002939 L	Aco002940 L	Aco002942 L	Aco002964 L	Aco002968 L	Aco002978 L	Aco002990 L	Aco003023	Aco003024 L	Aco003031 L	Aco003034 L	Aco003091 L	Aco003094 L	Aco003097 L	Aco003098 L	Aco003126	Aco003131 L	Aco003135 L	Aco003139 L	Aco003181 L	Aco003188 L	Aco003190 L	Aco003191 L

əziz_noxə_nim	88	73	285	67	1529	260	314	58	68	110	316	178	2087	348	48	127	46	54	134	53	56	60	36	1046	76	120	67	308	71	1370	44
eziz_pinoxe_latot	1051	2871	1215	1800	1529	260	1267	1454	1789	3212	1725	22.79	2087	805	2947	2372	1781	4978	1107	2698	2717	1178	1386	1046	2880	1316	2070	1416	745	1370	1536
nr_exons_per_gene	9	13	m	9	1	1	7	80	10	6	5	7	-	2	10	9	10	30	m	12	12	6	7	1	80	4	10	m	2	1	11
average_exon_size	175.167	220.846	405.000	300.000	1529.000	260.000	633.500	181.750	178.900	356.889	862.500	325.571	2087.000	402.500	294.700	395.333	178.100	165.933	369.000	224.833	226.417	130.889	198.000	1046.000	360.000	329.000	207.000	472.000	372.500	1370.000	139.636
jhbe	NA	NA	03_VATPase	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	NA	01d_Auxin_reponse_factor	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA
circadian_clock																															
glucogenesis_glycol visy								yes	yes							yes	yes	yes				yes	yes		yes						
oົກາແກ່ກັດຊ_les_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Oryza sativa Japonica Group cDNA clone:J023046C06_full insert sequence	NA	NA	PREDICTED: Vitis vinifera transcriptional corepressor SEUSS (LOC100241984)_ transcript variant X1_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
filovonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	AA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
malateTransferase_ Assimilation_Carboh ydrates			yes																												
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana aas																															
markers																															
aduaporin_reg																															
stomata_tunc																					s										
CAM- related_Acomosus_																					ye										
Angiosperm_gene	NA	AA	AN	AN	AA	AN	AN	AN	AA	AA	A	AA	AN	A	AN	AN	AA	AN	AN	7331	NA	NA	NA	NA	AA	AN	6507	AA	NA	AN	4796
gene_families_CAM C3	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
MAD_not_selection_CAM 	ΝA	AN	AN	yes	AN	AN	AN	AN	AN	yes	AN	AN	AN	NA	AN	AN	AN	AN	AN	AN	AN	٨A	٩N	AN	AN	AN	AN	AN	NA	AN	AN
Diff_expressed_CA DC3 DMC3	AN	yes	AN	AN	٩N	yes	AN	AN	٩N	AN	AN	AN	٩N	AN	NA	٩N	AN	AN	AN	٩N	٩N	٩A	٩N	yes	٩N	yes	٩N	AN	yes	ΔN	٩N
High_copy.Broc_An an_Tilla.	ou	0L	ou	QU	ou	AN	ou	ou	QU	yes	ou	ou	ou	ou	ou	ou	ou	Q	ou	ou	ou	ou	ou	Q	0L	yes	Q	ou	ou	ou	ou
Low_copy.Broc_Ana n_Tilla.	yes	yes	yes	2	2	AA	2	2	yes	2	2	yes	2	6	yes	yes	yes	yes	2	e	yes	2	2	2	yes	2	2	2	QL D	2	2
Single_copy.Broc_A nan_Tilla.	ou	QL	2	yes	yes	AN	yes	yes	0L	2	yes	Q	yes	yes	e P	2	Q	Q	yes	yes	ou	yes	yes	yes	QL	Q	yes	yes	yes	yes	yes
emsnpez	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17
деле	Aco003192	Aco003218	Aco003220	Aco003224	Aco003228	Aco003251	Aco003266	Aco003271	Aco003277	Aco003279	Aco003284	Aco003299	Aco003301	Aco003312	Aco003313	Aco003317	Aco003321	Aco003326	Aco003337	Aco003341	Aco003358	Aco003363	Aco003393	Aco003414	Aco003425	Aco003430	Aco003453	Aco003454	Aco003456	Aco003459	Aco003463

	Ţ.	~	~	10	~	10	-		_	~	-	~			N	10		10	-	~	-	10	<u> </u>	10	10	÷	~	-+	~	10	10
esi2_noxe_nim	26	282	87	66	1125	215	101	494	2261	135	161	395	191	290		55	64	926	1481	51	51	З	1190	26	666	155	62	2384	435	66	165
total_exonic_size	1070	1158	513	1390	2615	1487	1374	1641	2261	1201	2743	2185	2050	1376	1990	1690	1288	1963	1481	1213	4267	769	1190	1197	1654	1520	2631	2384	1198	948	2402
	9	e	m	5	2	2	e	m	-	2	2	m	m	5	9	0	D D	2	-	6	4	9	-	∞	2	4	5	-	2	80	9
nr_exons_per_gene	33	8	8	8	8	8	00	8	8	8	57	33	ŝ	8	57	20 1	00	00	8	82	36 1	57	8	25	8	8	50 1	8	8	8	33
average_exon_size	178.33	386.00	171.00	695.00	1307.50	743.50	458.00	547.00	2261.00	240.20	391.85	728.33	683.33	688.00	331.66	169.00	257.60	981.50	1481.00	134.77	304.75	128.16	1190.00	149.62	827.00	380.00	219.25	2384.00	599.00	118.50	400.33
ąłką	٧N	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	11_Glycolysis_night_C4_malate_p athway	NA																
circadian_clock																															
glucogenesis_glycol ysis																			yes											yes	
oɓnijnµod"]əs ⁻ sod	NA	NA	PREDICTED: Glycine max histidine kinase 2- like (LOC100781655)_ transcript variant X3_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA																		
- filavonoid_anthocya nin_Pitcaima_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_L_Flavonoid 3- hydroxylase																		
Malate I ransterase Assimilation_Carboh ydrates																															
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana asn																															
markers																															
qraught_res																															
aquaporin_reg																															
stomata_func																															
related_Acomosus_																															
	955	4	407	∢	∢	∢	134	∢	4	∢	∢	∢	∡	4	4	∢	277	4	4	∢	4	4	∢	168	4	∢	264	∢	∢	∢	<
Andiosnetm dene	V 66	z 4	ور ح	Z A	Z A	Z A	کر ۲	Z V	Z V	Z A	Z A	Z A	z v	Z A	Z A	Z V	A 75	Z A	Z V	Z A	Z A	Z V	Z A	2 <u>:</u>	z v	Z A	2 <u>2</u>	Z A	Z A	Z V	Z V
stiide_com	Z ∢	z ∢	z ∢	Z d	Z ⊲	Z ⊲	Z d	Z ∢	Z d	Z ⊲	Z ⊲	Z ⊲	z d	z ∢	Z ⊲	Z ⊲	Z d	Z ∢	Z ∢	z d	Z ⊲	Z ∢	Z ∢	Z ⊲	z ∢	z ∢	z d	z d	Z d	Z ∢	Z d
MC3 CAM	ż	ż	Ż	2 s	ż	ż	Ż	ż	ż	Ż	Ż	Ż	Ż	Ż	2 s	2 s	ż	Ż	Ż	2 s	Ż	2 s	ż	Ż	ż	Ż	Ż	Ż	Ż	ż	Ż
AD hazzanza tiil	ź	ž	ž	ye	ž	ž	ž	ž	ź	ž	ž	ž	Ż	ž	ye	ye	ž	ž	ž	ye	ž s	v ye	ž	ž	ž	ž	Ż	ž	ž	ž	ž
High conv.Broc An	ou	0 L	2	s no	e e	0L	ou	ou	ou	2	2	2	6	0 2	s no	ou	ou	ou	s no	2	ye	Ň	0u	2	0 L	e e	6	e e	e l	s no	s no
Low copy.Broc Ana	8	8	8	ye	90	90	2 10	90	200	8	8	8	8	8	ye	8	8	5	ye	9	2	-N	90	8	8	90	8	90	90	ye	ye.
A copy.Broc A	7 yet	7 yet	7 yet	7 no	7 yet	7 no	7 yet	7 yet	7 yet	7 no	7 yet	2	5 NA	5 ye	5 ye	5 ye	5 ye	5 ye	5 ye	5 ye	5	5 no									
Seaname	2 LG1) LG1	3 LG1	7 LG1	5 LG1	7 LG1	3 LG1	3 LG1	7 LG1	3 LG1	(LG1	3 LG1	5 LG1	3 LG1	3 LG1) LG1	1 LG1	7 LG1	3 LG1	3 LG1	7 LG1.) LG1.	LG1.	2 LG1	5 LG1.	3 LG1.	3 LG1.	2 LG1.	3 LG1.	3 LG1.	7 LG1.
gene	Aco003472	Aco00348(Aco00350:	Aco003507	Aco003515	Aco003517	Aco003518	Aco00353{	Aco003547	Aco003556	Aco003571	Aco003578	Aco003605	Aco00363:	Aco00363{	Aco003635	Aco003654	Aco003687	Aco00368	Aco003685	Aco003757	Aco00376(Aco00376	Aco003762	Aco003785	Aco003795	Aco003796	Aco003802	Aco003806	Aco00382(Aco003857

9zi2_nox9_nim	210	350	65	11	162	44	2099	650	745	1331	106	560	151	33	33	3872	164	56	1253	1415	166	497	73	57	32	31	296	1991	194	1787
total_exonic_size	2518	1798	2070	1567	1560	3780	2099	650	1725	1331	1098	1166	3058	2305	2244	3872	1269	1216	1253	1415	2322	1716	3516	949	181	3602	3020	1991	1152	1787
ur_exons_per_gene	e	7	6	2 L	4	17	1	1	2		9	7	9	14	14	1	4	8			2	2	10	2	2	24	7	1	e	
average_exon_size	839.333	899.000	230.000	313.400	390.000	222.353	2099.000	650.000	862.500	1331.000	183.000	583.000	509.667	164.643	160.286	3872.000	317.250	152.000	1253.000	1415.000	1161.000	858.000	351.600	189.800	90.500	150.083	1510.000	1991.000	384.000	1787.000
əd/q	NA	10_Glucogenesis_specific_dayC3	00_#Ming2019_Anthocyanin_biosy nthesis	00_#Ming2019_Anthocyanin_biosy nthesis	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	00_#W_SucroseTransporter_10_Gl ucogenesis_specific_dayC3	00_#W_SucroseTransporters_SUT 1_10_Glucogenesis_specific_dayC 3	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	AA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	01b_Abscisic_acid_signal
circadian_clock																														
glucogenesis_glycol ysis		yes						yes										yes						yes						
oɓnjintiod_les_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris CWF19-like protein 2 (LOC104905381)_ transcript variant X1_ mRNA	NA	NA	PREDICTED: Glycine max protein argonaute 1- like (LOC100778754)_ mRNA	NA	NA	NA	NA
styondra, bionovalt 29_ simison9_ nin	AA	AA	NA	ALB_F_Flavonoid 3- hydroxylase	AA	AA	AA	AA	A	AA	AA	AA	AA	AA	A	AA	AA	AA	A	AA	AA	AA	A	AA	AA	AV	AA	AA	NA	A
ydrates ydrates ydrates		_									_																	_	_	
circadian_metabolis m_Wai2017														yes	yes															
anthocyanin_SI_Ana nas			yes	yes																										
draught_res																														
aquaporin_reg																														
stomata_func																														es
related_Acomosus_ Ming2015																														
Angiosperm_gene	ĄA	Ą	Ą	Å	Ą	5449	Ą	Ą	Ą	Ą	802	Å	Å	Å	Ą	Ą	Ą	Ą	Å	Ą	Ą	ĄĄ	Ą	٩A	Ą	Ą	Å	Ą	Ą	Ą
gene_families_CAM C3	4 A	4 A	A	4 A	Z A	A A	A	A A	4 A	AA	A A	A	A	A	Z A	A A	AA	AA	A	Z A	AA	AA	Z V	A P	AA	4 A	AA	AA	A	AA
MAD_noi_selection_CAM 	AM	AN	AM	AM	AM	AM	AN	NA L	AN	AM	AM	AM	AM	AN	AM	ves h	AM	AM	AM	AM	AM	A P	AN	AA I	AM	AM	AM	AM	AM	AM
Diff_expressed_CA CSM	AN	AN	AN	ves I	AN	AN	AN	NA I	AN	AN	AN	AN	AN	/es	AN	NA J	AN	AN	AN N	AN	AN	NA I	AN	NA I	/es	AN	AN	AN	AN	AN
High_copy.Broc_An an_Tilla.	ou	e e	6	6	or O	on Or	04	04	04	6	or or	6	6	0	02	04	6	6	0	02	ou	ou	2	ou	NA	yes I	6	ou	ou	6
Low_copy.Broc_Ana n_Tilla.	0	yes r	yes r	yes r	2	2	2	2	2	2	2	2	2	yes r	yes r	2	2	2	2	2	02	ou	2	- ou	- M	6	2	02	02	yes
A_oorgy.Broc_A nan_Tilla.	yes	2	2	2	yes	yes	yes	yes	yes	yes	yes	yes	yes	2	e e	yes	yes	yes	yes	yes	yes	yes	yes	yes	NA	01	yes	yes	yes	2
əmanpəz	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15	.G15
gene	Aco003860 L	Aco003871 L	Aco003873 L	Aco003885 L	Aco003924 L	Aco003927 L	Aco003928 L	Aco003937 L	Aco003946 L	Aco003984 L	Aco004017 L	Aco004039 L	Aco004109 L	Aco004131 L	Aco004135	Aco004155 L	Aco004156 L	Aco004162 L	Aco004170 L	Aco004181 L	Aco004198 L	Aco004199 L	Aco004202 1	Aco004218 L	Aco004222 L	Aco004236 L	Aco004250 L	Aco004281 L	Aco004283 L	Aco004290 L

9zi2_nox9_nim	61	2198	13	61	138	447	215	505	415	304	689	247	52	168	316	116	602	25	58	385	116	568	635	254	315	687	224	51	44	51
ezia_pinoxe_latot	1414	2198	1612	1395	1959	1361	1229	1150	1370	618	689	1092	1160	2040	2515	1922	1330	1189	1248	1479	1149	1402	635	1590	2045	3490	818	4133	1756	2318
21126 ⁻ 124 ⁻ 21	5	1	~	7	m	2	m	2	5	2	-	m	- 00	9	2	4	2	4	4	5	4	5	-	m	m	2	2	1	7	LS
nr exons der gene	00	8	36	36	8	00	57	8	8	8	8	8	8	00	00	00	8	20	8	8	20	8	8	00	57	00	8	27 1	57	33 1
average_exon_size	282.80	2198.00	230.28	199.28	653.00	680.50	409.66	575.00	685.00	309.00	689.00	364.00	145.00	340.00	1257.50	480.50	665.00	297.25	312.00	739.50	287.25	701.00	635.00	530.00	681.66	1745.00	409.00	375.72	250.85	154.53
əd/q	02_Aquaporins	NA	NA	00_#21_Malate_dehydrogenase	10_Glucogenesis_specific_dayC3	NA	01b_Abscisic_acid_signal	NA	NA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	02_Aquaporins	NA	10_Glucogenesis_specific_dayC3	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3							
circadian_clock																														
glucogenesis_glycol ysis					ves																/es									/es
oອິnijnµod" jəs ⁻ sod	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris mitochondrial dicarboxylate/fricarboxylate transporter DTC (LOC104906718)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max histidine kinase 2- like (LOC100781655)_transcript variant X3_ mRNA	NA	NA
filavonoid_anthocya nin_Pircaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	AA	NA	NA
Assimilation_Carboh ydrates																														
circadian_metabolis m_Wai2017																														
antrocyanin_51_Ana																														
markers																														
draught_res						-				Se	se												Se		-					
aquaporin_reg	es										~	es																		
stomata_func	~						Se																							
related_Acomosus_ Ming2015				St			×																							
CAM-				ye											_			93	20				_	_			ß			
Angiosperm_gene	NA	AN M	AN I	MA	AN N	NA I	MA	MA	M	¥	AN N	M	A A	AN	AN N	NA I	MA	286	52	AN M	A	MA	AN N	AN N	NA I	NA I	109	A	NA	AN M
_shirta MAD_seilims1_eneg	NA	AN V	NA N	NA	NA	NA	NA	NA	NA	AN AN	NA	NA	NA N	NA	NA	NA	NA	NA	NA	AN V	AN N	NA	NA	NA	NA	NA	NA	NA N	NA	AN V
pos_selection_CAM	AN	AN	yes	NA	NA	AN	NA	NA	AN 	NA	AN	A N	A N	NA	NA	AN	AN 	NA	AN NA	AN	NA	NA	NA	NA	AN	NA	NA	NA	NA	ΔN
an_Tilla. Diff_expressed_CA	ΝA	ΝA	AN	NA	NA	NA	NA	NA	yes	NA	NA	NA	yes	NA	yes	NA	yes	NA	NA	ΝA	NA	NA	NA	NA	NA	NA	NA	AN	yes	ΔN
high_copy.Broc_An	ou	2	e e	e L	e L	0L	0L	e E	e E	AN	2	2	2	ę	е Г	0L	yes	6	e E	2	2	e L	6	e L	0L	е Ц	6	yes	ou	8
Low_copy.Broc_Ana	yes	2	yes	yes	yes	2	yes	2	2	¥	2	yes	2	2	2	2	2	2	2	2	2	2	yes	2	2	2	2	2	yes	yes
A_oon8.vqoo_elgni2	0L	yes	2	2	2	yes	2	yes	yes	AN	yes	2	yes	yes	yes	yes	2	yes	yes	yes	yes	yes	2	yes	yes	yes	yes	e e	QL	2
emanpes	LG05	LG05	L G05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05
әиәб	Aco004297	Aco004304	Aco004321	Aco004349	Aco004370	Aco004374	Aco004375	Aco004393	Aco004398	Aco004401	Aco004406	Aco004430	Aco004447	Aco004448	Aco004452	Aco004465	Aco004471	Aco004476	Aco004483	Aco004488	Aco004489	Aco004512	Aco004532	Aco004555	Aco004564	Aco004579	Aco004585	Aco004612	Aco004613	Aco004638

əziz_noxə_nim	134	60	167	330	29	287	48	29	232	309	739	293	78	264	33	74	269	1913	1217	1442	757	1073	199	65	54	172	211	50	69	69	56
ezia_exonic_size	1671	825	1834	2231	2224	2564	955	1532	1493	1116	1754	5131	1900	1165	986	1528	1474	1913	1217	1442	2465	2156	1155	1370	5419	1109	2697	1483	1450	2650	2092
nr_exons_per_gene	7	9	2	2	12	ъ	7	ß	4	m	2	ß	6	2	4	80	m	1	-	-	2	2	m	80	21	m	2	15	6	4	10
average_exon_size	238.714	137.500	917.000	1115.500	185.333	512.800	136.429	306.400	373.250	372.000	877.000	1026.200	211.111	582.500	246.500	191.000	491.333	1913.000	1217.000	1442.000	1232.500	1078.000	385.000	171.250	258.048	369.667	539.400	98.867	161.111	662.500	209.200
jAbe	NA	09_Circadian_clock	NA	NA	NA	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	00_#MB_PhytC	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	00_#W_StomatalMovement_RootP hototropism2	NA
circadian_clock		yes																													
glucogenesis_glycol ysis																yes				yes				yes				yes			
oɓnjinuod"jəs"sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris protein DETOXIFICATION 33 (LOC104898970) mRNA
filevonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates																															
circadian_metabolis m_Wai2017																														'es	
anthocyanin_SI_Ana nas																															
araught_res								les				yes																			
aquaporin_reg																															
stomata_func																															
related_Acomosus_ Ming2015																															
Angiosperm_gene	MA	AN	AN	AN	6383	AN	6506	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	NA	AN	AN	AN	AN	AN	A	6527	NA	AN	AN	6492	A	AA
gene_families_CAM C3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN
MAD_noticelection_CAM 	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN
Diff_expressed_CA CM	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	yes	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
nA_ooy.Broc_An an_Tilla.	ou	AN	ou	Q	ou	Q	ou	ou	ou	Q	Q	Q	ou	Q	ou	ou	ou	ou	QU	Q	e	ou	Q	Q	yes	ou	ou	ou	ou	yes	Q
Low_copy.Broc_Ana n_Tilla.	2 2	AN N	2	2	2	e.	g	yes	2	2	2	yes	2	2	2	yes	2	2	2	yes .	e.	2	2	yes	2	2	2	yes	2	2	yes
Single_copy.Broc_A nan_Tilla.	yes	AN	yes	yes	yes	yes	yes	92	yes	yes	yes	2	yes	yes	yes	2	yes	yes	yes	6	yes	yes	yes	6	2	yes	yes	6	yes	ę	2
edname	-G05	-G05	-G05	-G05	-G05	.G05	-G05	-G05	-G05	-G05	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	.G07
gene	Aco004644 1	Aco004646	Aco004662 1	Aco004672 1	Aco004679	Aco004700 1	Aco004708 1	Aco004773 1	Aco004804 1	Aco004808	Aco004821 1	Aco004827	Aco004844 1	Aco004853 1	Aco004854 1	Aco004855 1	Aco004857 1	Aco004859 1	Aco004860 1	Aco004861 1	Aco004864 1	Aco004888 1	Aco004899 1	Aco004902 1	Aco004919 1	Aco004920	Aco004926 1	Aco004930	Aco004946 1	Aco004947 1	Aco004960

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əziz_noxə_nim	298	35	20	1220	28	1991	82	2012	1700	22	220	56	44	02	1271	22	120	43	1220	197	86	188	4	20	150	310	1937	41	131	134	20
total_exonic_size	1455	1453	1592	1220	1833	1991	1069	2012	1700	1838	636	1620	1322	2811	1271	1722	816	1815	1220	1272	1054	1793	1330	2348	1388	1275	1937	1628	1735	1382	1507
ur_exons_per_gene	m	6	9	-	12		9	-	-	80	2	9	9	9	-	10	m	4	-	4	ы	4	11	9	3	m	-	12	4	4	6
average_exon_size	485.000	161.444	265.333	1220.000	152.750	1991.000	178.167	2012.000	1700.000	229.750	318.000	270.000	220.333	468.500	1271.000	172.200	272.000	453.750	1220.000	318.000	210.800	448.250	120.909	391.333	462.667	425.000	1937.000	135.667	433.750	345.500	167.444
ədvi	NA	00_#29_Malate_dehydrogenase	NA	NA	AN	NA	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	09_Circadian_clock	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA								
circadian_clock		0															yes														
glucogenesis_glycol sisy							yes			yes								yes										yes			
oßniluhoq_ləs_zoq	NA	NA	NA	NA	PREDICTED: Glycine max thiosulfate/3- mercaptopyruvate sulfurtransferase 2-like (LOC100798053)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Glycine max RNA polymerase II-associated protein 3-like (LOC100790717)_ mRNA
- filavonoid_anthocya nin_Pitcatmia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
malateTransferase_ Assimilation_Carboh ydrates																															
circadian_metabolis m_Mai2017																	yes														
markers anthocyanin_SI_Ana nas																															
draught_res																															
aquaporin_reg																															
stomata_func																															
-MAJ related_Acomosus_ <u>8102015</u>		/es																													
wudiozbeuu-deue	355	A	A	A	A	A	A	A	A	A	A	A	A	A	A	533	A	A	A	A	439	A	866	A	A	A	A	A	A	A	A
gene_families_CAM C3 Angiography	4A 5	A N	A A	Z A	A A	A A	Z A	Z A	Z A	A A	A A	A A	A A	A N	Z A	4A 6	Z A	A A	Z A	A A	AA 6	A N	4A 5	Z A	A N	A A	Z A	A A	A N	A N	A A
MAD_noi_selection_CAM 	A A	AN	A A	A A	A A	A A	A A	A A	A A	A A	A A	A A	A A	A A V	A A	A A	A A	A A	A A	A A	A A	NA P	A A	A A	A A	A A	A A	A A	AA P	AA P	A A
Diff_expressed_CA MC3	4 A	A P	les l	4 A	4 A	4 A	4 A	4 A	4 A	4 A	/es	ves h	/es	les l	4 A	4 A	4 A	4 A	4 A	4 A	4 A	AA P	4 A	les l	A A	4 A	4 A	AA	AA P	AA P	4 A
High_copy.Broc_An an_Tilla.	ę	6	/es	2	2	2	2	2	2	02	AN V	0	OL OL	01	2	2	2	02	2	<u>د</u>	0	1 01		02	0L	2	2	0L	0	1 01	ог.
Low_copy.Broc_Ana n	2	yes r	02	2	2	2	2	2	2	2	- M	2	2	yes I	2	2	yes r	2	2	2	2	- ou	2	2	02	2	2	02	- ou	- ou	02
Single_copy.Broc_A nan_Tilla.	yes	2	2	yes	yes	yes .	yes	yes	yes	yes .	AN	yes	yes .	e.	yes	yes .	2	yes .	yes	yes	yes .	yes	yes	yes	yes						
əmsnpəz	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	.G07
деле	Aco004989	Aco004996	Aco005022	Aco005037	Aco005040	Aco005041	Aco005042	Aco005047	Aco005049	Aco005054	Aco005055	Aco005078	Aco005083	Aco005101	Aco005103	Aco005104	Aco005108	Aco005109	Aco005110	Aco005112	Aco005118	Aco005119	Aco005125	Aco005127	Aco005134	Aco005140	Aco005155	Aco005164	Aco005168	Aco005173	Aco005209

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əziz_noxə_nim	302	111	1433	61	395	125	385	145	9	69	728	415	495	65	109	16	45	38	2282	39	153	926	48	401	223	321	1235	111	48	127	476
ezia_exonic_size	1170	2385	1433	1759	1211	2916	1669	1934	4749	2023	1600	1168	1320	4530	986	2904	1124	1224	2282	4377	1440	926	1158	1732	1525	1365	1235	1221	2549	1359	1131
ur_exons_per_gene	ŝ	4		[∞]		4	m	7	17	9	2			8	4	25	7	6		9	20		[∞]		en en	e	1	9	19	4	2
average_exon_size	390.000	596.250	1433.000	219.875	605.500	729.000	556.333	276.286	279.353	337.167	800.000	584.000	660.000	566.250	246.500	116.160	160.571	136.000	2282.000	729.500	288.000	926.000	144.750	866.000	508.333	455.000	1235.000	203.500	134.158	339.750	565.500
ədAj	AN N	AN	A	10_Glucogenesis_specific_dayC3	A	A	AV	AV	AV	A	10_Glucogenesis_specific_dayC3	35_Chloroplasts_activity	35_Chloroplasts_activity	A	06_Drough_resistance_genes_LEA	00_#W_HexoseTransporter_GLUT 5/8-like_transporter	AA	AV	A	AV	A	AA	00_##06_carbonic_anhydrase	AV	A	AV	AV	A	A	٨٨	01b_Abscisic_acid_signal
	~	~	-		-	-		-	-					-			-	-		-	-	-		-			-	-	-	-	
circadian clock																															
glucogenesis_glycol				yes							yes																				<u> </u>
oອິກແກນod Jəs sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
tllavonoid_anthocya nin_Pitcaimia_PS	NA	NA	ALB_F_anthocyanidin 3-O- glucosyltransferase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_anthocyanin 3 -o-beta- glucosyltransferase	ALB_F_dihydroflavonol 4- reductase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh												es	es										es								
circadian_metabolis m_Wai2017 m_metabolise																'es															
anthocyanin_SI_Ana nas																															
markers																															
qraught_res															yes																
aquaporin_reg																															
stomata_func																															yes
-MAJ related_Acomosus_ ZI0SpniM																															
	A	A	4	4	4	4	A	4	4	721	A	4	4	4	A	A	271	326	A	4	4	4	4	4	A	A	4	×	4	A	4
Andiosnetm dene	A N	Z V	Z V	Z V	Z V	Z V	Z V	Z V	Z V	22 V	Z V	Z A	Z A	Z A	Z V	Z V	A 52	A 6(Z V	Z V	Z V	Z A	Z V	Z V	Z V	Z V	Z V	Z V	Z V	Z V	Z V
stiits_	Z V	z ∢	Z A	se	Z A	Z V	Z V	Z V	Z V	Z A	se	Z A	Z A	Z A	Z A	z v	Z V	Z V	Z V	Z A	Z A	se	Z A	Z A	Z V	Z V	Z V	Z A	SS N	z ∢	Z A
	z	z	z	×	z	s	z	z	s	z	ž	s	s	s	z	z	z	z	z	z	z	ž	z	z	z	z	s	z	×	z	s s
angn Copyreilla. An hazzaraza Mil	Ž	ž	ž	ž	ž) ye	ž	Ň	s ye	Ž	⊿ V	ye	ye ve	ye ve	Ž	ž	Ň	Ň	ž	Ž	Ž	ž	ž	ž	ž	ž) ye	ž	N/ Si	ž	A ye
	ŭ	Ĕ	ž	ž	ŭ	s nc	ŭ	ч	yε	ž	Ż	s nc	s nc	s nc	s nc	s nc	л Ч	ч Ч	ž	s nc	ž	2 Z	s nc	ž	ŭ	ŭ	ч	ž	yε	Ĕ	Ż
Low conv.Broc Ana	0U	90	<u> </u>	9 	90	ye	00	00	2	<u> </u>	Ž	ye	ye	ye	ye	ye	ou ;;	90	90	ye	9 	2	ye	9	00 .,	90	00	90	2	е 2	Ž
A_oong.koo_slgni2	7 yes	7 yes	7 yes	7 yes	7 yes	6	7 yes	7 yes	2	1 yes	AN L	2	2	2	2	2	l yes	1 yes	1 yes	2	1 yes	1 yes	2	1 yes	l yes	1 yes	1 yes	l yes	2	l yes	AN L
əmsnpəz	LG07	LG07	LG07	LG07	LG07	LG07	LG07	LG07	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11	LG11
gene	Aco005229	Aco005233	Aco005239	Aco005251	Aco005262	Aco005283	Aco005287	Aco005291	Aco005343	Aco005353	Aco005354	Aco005358	Aco005359	Aco005366	Aco005373	Aco005379	Aco005384	Aco005385	Aco005390	Aco005393	Aco005397	Aco005399	Aco005402	Aco005409	Aco005439	Aco005444	Aco005457	Aco005478	Aco005505	Aco005508	Aco005513

əziz_noxə_nim	128	139	710	1481	18	23	1952	152	611	225	116	119	47	39	82	427	279	267	503	570	129	48	2411	32	231	182	52	794	39	19	67
ezia_cinoxe_latot	1366	1539	710	1481	096	326	1952	1143	4148	1167	1728	2390	1810	2088	1212	1075	1135	1386	1198	1435	1172	1679	2411	1999	2195	1119	1508	794	1839	1121	1324
our_exons_per_gene	3	9	H	1	9	4	1	m	2	m	∞	4	16	15	∞	2	2	m	2	2	ю	10	1	10	5	ю	12	1	10	7	9
average_exon_size	455.333	256.500	710.000	1481.000	160.000	81.500	1952.000	381.000	2074.000	389.000	216.000	597.500	113.125	139.200	151.500	537.500	567.500	462.000	599.000	717.500	390.667	167.900	2411.000	199.900	439.000	373.000	125.667	794.000	183.900	160.143	220.667
ədAş	NA	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	NA	NA	NA	00_#33_Malic_enzyme	11_Glycolysis_night_C4_malate_p athway	NA	03_VATPase	NA	NA	NA	06_Drough_resistance_genes_LEA	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	NA	03_VATPase	NA						
circadian_clock																															
yucogenesis_glycol ysis		yes												yes													yes				
ດອີກເງກນດຜີງອຣີsod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris NADP-dependent malic enzyme (LOC104883143)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ationovali filevonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	ALB_L_anthocyanidin 3-O- glucosyltransferase	ALB_F_isoflavone reductase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates ydrates																						yes								yes	
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana san																															
markers																															
draught_res			/es			/es																				/es		/es			
aquaporin_reg																															
stomata_func																															
CAM- related_Acomosus_ Ming2015													yes																		
Angiosperm_gene	٩A	٩A	Ą	AA	Ą	Ą	Ą	Ą	Ą	Ą	Ą	Ą	AA	4A	958	Ą	Ą	Ą	Ą	٩A	٩A	٩A	٩A	3488	٩A	٩A	٩A	ĄĄ	5554	٩A	Ą
MAD_sainims_eng C3	A A	A A	AA	A A	A A	A A	A A	A A	A A	A A	A A	A A	AN	A A V	AA 6	/es	A A	A A	A A	AA P	AA P	AA P	A A V	AA AA	A A	AN	4 A	A A	AA 5	AA P	A
pos_selection_CAM shifts	NA I	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA I	AN	AN	AN	AN	AN	NA I	NA I	NA I	NA I	AN	AN	NA I	AN	AN I	NA I	NA I	AN
Diff_expressed_CA C3	A N	A A	A A	A M	A A	A M	A M	A M	A M	A M	A A	A A	AN	NA I	A A	A A	A A	A A	A A	NA I	NA I	l sə/	NA I	A M	A A	A M	A A	NA I	AA I	NA I	/es
High_copy.Broc_An an_Tilla.	ou	ou	6	02	AN	AN	ou	04	04	6	6	6	2	yes	ou ou	02	02	or O	ou	ou	ou	ou)	ou	02	ou	ou	ou	ou	ou	ou	6
Low_copy.Broc_Ana n_Tilla.	0	yes	2	yes	MA	AN	0	2	2	2	2	2	yes	ou Qu	yes	yes	2	2	0	0	uo I	- 01	0	2	01	yes	02	ou	ou	yes	2
A_ooy.Broc_A nan_Tilla.	yes	Q	yes	2	AN	AN	yes	yes	yes	yes	yes	yes	2	Q	e	e	yes	Q	yes	yes	yes	ou	yes								
əmsnpəz	.G11	.G11	G11	.G11	G11	G11	.G11	G11	.G11	G11	G11	G11	.G11	G11	.G11	.G11	.G11	G11	.G11	.G11	.G11	.G11	G11	.G11	.G16	.G16	.G16	.G16	.G16	.G16	.G16
әиәб	Aco005520 L	Aco005552 L	Aco005561 L	Aco005562 L	Aco005564 L	Aco005567 L	Aco005570 L	Aco005587 L	Aco005599 L	Aco005614 L	Aco005616 L	Aco005623 L	Aco005631 L	Aco005646 L	Aco005654 L	Aco005657 L	Aco005667 L	Aco005669 L	Aco005671 L	Aco005673 L	Aco005684 L	Aco005715 L	Aco005746 L	Aco005794 L	Aco005821 L	Aco005826 L	Aco005867 L	Aco005868 L	Aco005891 L	Aco005908 L	Aco005915 L

əziz_noxə_nim	61	61	570	451	39	134	28	29	186	170	116	386	31	31	62	349	406	61	64	2138	41	1136	123	1325	164	48	122	55	60
etal_exonic_size	1732	1906	1170	1315	2238	1673	1471	3656	2503	1130	3008	803	2397	2528	2135	1879	1713	1604	1847	2138	1695	1136	2692	1325	1217	1170	1435	2145	1079
nr_exons_per_gene	6	6	2	⁰	15	2	17	21	8	4	11	5	6	10	11	_ س_	~ ~	-	11	1	13		~		_ ~ _	8	9	16	7
aziz_noxa_agerave	192.444	211.778	585.000	657.500	149.200	334.600	86.529	174.095	312.875	282.500	273.455	451.500	266.333	252.800	194.091	626.333	571.000	229.143	167.909	2138.000	130.385	1136.000	384.571	1325.000	405.667	146.250	239.167	134.063	154.143
əd/q	11_Glycolysis_night_C4_malate_p athway	11_Glycolysis_night_C4_malate_p athway	NA	NA	11_Glycolysis_night_C4_malate_p athway	NA	00_#34_Malic_enzyme	NA	NA	NA	NA	06_Drough_resistance_genes_LEA	11_Glycolysis_night_C4_malate_p athway	11_Glycolysis_night_C4_malate_p athway	10_Glucogenesis_specific_dayC3	NA	NA	00_#17_Malate_dehydrogenase	NA	NA	NA	NA	NA	NA	NA	00_##05_carbonic_anhydrase	NA	10_Glucogenesis_specific_dayC3	NA
circadian_clock																													
ysis_ glucogenesis_glycol	yes	yes			yes								yes	yes	yes													yes	
ດອີກແກນດປ່ີງອະີsod	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris NADP-dependent malic enzyme (LOC104883143) mRNA	PREDICTED: Glyčine max kinesin-4-like (LOC100777089)_ transcript variant X4_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris sodium/pyruvate cotransporter BASS2_ chloroplastic (LOC104902128)_mRNA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris carbonic anhydrase_chloroplastic-like (LOC104902037) mRNA	NA	PREDICTED: Beta vulgaris subsp. vulgaris glucose-1-phosphate adenylytiransferase large suburit 3_chloroplastic/amyloplastic (DC104883901)_transcript variant X1_ ImRNA	NA
Vuraies	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
m																													
circadian_metabolis																													
anthocyanin_SI_Ana																													
นรายเรื่อง					-															-					-				
aquaporin_reg												ye	-																
stomata_func																													
Ming2015							10											(0								(0			
CAM-				-	-		ye			,c			-			-		ye	e.							ye			
Angiosperm_gene	AN	AN	NA	AN	A	AN	AN	AN	AN	520(AN	AN	AN	٩Ŋ	AN	AN	AN	AN	693	NA	MA	AN	AN	AN	714:	NA	AN	NA	688
	ΝA	ΝA	AN	AN	A N	AN	٩N	NA	NA	AN 	AN	NA	NA	NA	NA	NA	NA 	NA	AN	AN	٩N	ΝA	NA	AA	A N	NA	AN	NA	ΝA
MC3MA3MA3MA3	ΝA	ΝA	NA	AA	A A	AA	AN	AN	NA	yes	AN	NA	NA	A A	A N	NA	yes	NA	NA	ΝA	AN	ΝA	NA	NA	yes	ΥN	NA	₹Z	NA
Diff_expressed_CA	٩N	٩N	yes	A N	۲ ۲	AN	NA	AN	٩N	٩N	٩N	yes	٩N	A N	A N	yes	yes	٩N	٩N	yes	AN	٩N	٩N	AN	۲ ۲	AN	٩N	٩N	٩N
- Aligh_copy.Broc_An AliT_na	оц	ę	Q	2	yes	ę	Q	6	е С	Q	Q	2	2	2	2	e e	ę	e	Q	ou	e e	ę	2	2	2	Q	2	ou	оц
Low_copy.Broc_Ana nn	yes	yes	2	2	2	2	yes	yes	2	yes	2	2	yes	yes	yes	yes	2	yes	e	Q	2	2	2	2	2	2	e	yes	e E
A_copy.Broc_A nan_Tilla.	0L	e	yes	yes	2	yes	0L	2	yes	2	yes	yes	2	2	2	2	yes	2	yes	yes	yes	yes	yes	yes	yes	yes	yes	e e	yes
edname	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16	LG16
gene	Aco005930	Aco005931	Aco005947	Aco005956	Aco005968	Aco005975	Aco005989	Aco005991	Aco006015	Aco006030	Aco006043	Aco006056	Aco006063	Aco006064	Aco006068	Aco006084	Aco006096	Aco006122	Aco006129	Aco006140	Aco006144	Aco006150	Aco006157	Aco006164	Aco006172	Aco006181	Aco006186	Aco006199	Aco006225

əziz_noxə_nim	54	22	356	160	39	1508	139	119	17	104	349	18	41	2159	339	12	626	68	9	1118	154	2582	158	409	318	1988	36	1229	123	333
esia_oinoxe_latot	1 2961	489	1969	2110	1108	1508	2620	1 3164	2782	1324	1157	1347	2845	2159	1087	1395	626	1338	1746	1118	1097	2582	1 1571	1258	1792	1988	3 2786	1229	1337	748
ut_exons_per_gene	14						ů,	14	1.1	L 10		1	ដ			0	1	ω	16		, ["]		4	~~			16		Ű	
əziz_noxə_əgɛıəvɛ	211.500	163.000	656.333	1055.000	184.667	1508.000	436.667	226.000	185.467	264.800	578.500	122.455	284.500	2159.000	543.500	155.000	626.000	167.250	97.000	1118.000	219.400	2582.000	392.750	629.000	597.333	1988.000	154.778	1229.000	222.833	374.000
ədify	AA	A	L0_Glucogenesis_specific_dayC3	AA	AA	AA	10_Glucogenesis_specific_dayC3	AA	10_Glucogenesis_specific_dayC3	AA	AA	٩٨	10_Glucogenesis_specific_dayC3	A	AA	10_Glucogenesis_specific_dayC3	A	A	A	A	L0_Glucogenesis_specific_dayC3	A	A	AA	AA	A	10_Glucogenesis_specific_dayC3	AA	AA	٨٨
circadian_clock	2	_2	-1	2	2	2	-		-	2	_2	2	-	2	2	7	~	2		2	-	2	2	~	~	2		~	~	2
ysisənəgooulg ysis			/es				/es		/es				/es			/es					/es						/es			
oßnijnµod"jəs"sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris adenylate kinase 5_chloroplastic (LOC104901827)_transcript variant X1_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Vdrates	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
circadian_metabolis m Wai2017																														
markers anthocyanin_SI_Ana nas																														
draught_res																														
aquaporin_reg																														
stomata_func																														
related_Acomosus_ Ming2015																									-					
Angiosperm_gene	5943	6667	MA	M	5821	AN	AN	MA	MA	5200	AA	5870	MA	NA	4951	AN	AN	5950	NA	AN	MA	AN	NA	NA	NA	NA	MA	NA	AN	6164
gene_families_CAM C3	AN	AN	AN	AN	V	AN	AN	AN	AN	V	AN	: VA	AN	AN	, VA	AN	AN	AN	AN	AN	AN	AN	AN	NA	NA	AN	AN	AN	AN	AN
Pos_selection_CAM shifts	٩N	٩N	٩N	٩N	AN	٩N	AN	yes	AN	٩N	٩N	٩N	٩N	AN	٩N	yes	٩N	٩N	AN	٩N	٩N	٩N	AN	ΑN	ΑN	ΑN	٩N	٩N	٩N	ΑN
Diff_expressed_CA MC3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	/es	A	AN	AN	AN	AN	/es	AN	٩N	AN	AN	AN	AN	AN	٩N	AN	AN	AN	٩	٩N
High_copy.Broc_An an_Tilla.	4 ou	ou	yes h	ou	ou	ou	ou	ou	yes h	ou	v ou	ou	00	ou	ou	ou	v v	ou	ou	ou	AN	ou	ou	a ou	a ou	00	yes	u ou	1 ou	uo I
Low_copy.Broc_Ana. n_Tilla.	2	yes	2	2	2	2	yes	2	2	2	yes	2	yes	2	2	yes	yes	2	yes	2	A	2	2	0	01	2	2	2	2	2
Single_copy.Broc_A nan_Tilla.	sə,	e	Q	'es	'es	'es	Q	'es	e	sə,	e	es	e	'es	'es	g	Q	/es	e	es	٩N	'es	sə,	sə,	sə,	sə,	e	sə,	/es	se/
edusme	.G16 y	.G14 r.	.G14 r.	-G14 y	.G14 y	-G14 y	.G14 r.	-G14 y	.G14 r.	.G14 y	.G14 r.	-G14 y	.G14 r.	.G14 y	-G14 y	.G14 r	.G14 r	.G14 y	.G14	.G14 y	.G14	-G14 y	.G14 r.	-G14 y	-G14 y	.G14 y				
gene	Aco006227 1	Aco006252 1	Aco006253 1	Aco006280 1	Aco006311 1	Aco006312 1	Aco006319 1	Aco006345 1	Aco006349 1	Aco006380 1	Aco006394 1	Aco006403 1	Aco006406	Aco006409 1	Aco006416 1	Aco006436	Aco006438 1	Aco006440 1	Aco006453 1	Aco006461 1	Aco006467	Aco006469 1	Aco006470 1	Aco006479 1	Aco006487 1	Aco006523 1	Aco006524 1	Aco006529 1	Aco006536	Aco006540 1

	8	24	18	75	49	1	47	66	16	88	22	88	31	29	48	33	8	8	51	80	10	25	т	56	18	59	13	75	60	42	96
əziz_noxə_nim	ĕ			23.	4			-	10	6		-		1 T	1	5		ñ			10	ä		ю́	1	12:	Ĥ	14.	1	`	ñ
total_exonic_size	1477	1545	1879	2375	1178	1784	2566	3021	1016	2011	1042	1881	1969	1289	2541	1354	1610	2083	1664	571	1270	1359	370	1803	1407	1229	677	1475	2469	2461	1846
ut_exons_per_gene	~	13	22			9	10	12	1		6	5	14	6	m	m	~	۳ ا	12	4	~	e e	5	~	2	1		1	4	13	
average_exon_size	738.500	118.846	85.409	2375.000	589.000	297.333	256.600	251.750	1016.000	1005.500	208.400	209.000	140.643	257.800	847.000	451.333	230.000	694.333	138.667	142.750	635.000	226.500	185.000	901.500	201.000	1229.000	225.667	1475.000	617.250	189.308	615.333
эdб	NA	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	04_Oxygen_evolving_enhancer_O EE	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	00_#Ming2019_Anthocyanin_biosy nthesis	06_Drough_resistance_genes_LEA	NA	NA	NA	06_Drough_resistance_genes_LEA	NA	AN	NA	NA							
circadian_clock																															
glucogenesis_glycol sisy		yes	yes									yes					yes														
oົກາແກ່ກັດຊ_les_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Populus trichocarpa hypothetical protein (POPTR_0001s35130g) mRNA_ complete cds	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris aspartate aminotransferase_cytoplasmic (LOC104906385)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
- Tilsvonoid_anthocya filsaimia_PS nin	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_L_dihydroflavonol 4- reductase	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh Vdrates																es															
circadian_metabolis m_Wai2017 malateTransferase																>															
anthocyanin_SI_Ana san																					es	es									
markers																					~										
qısınght_res																							yes				yes				
aquaporin_reg																															
stomata_func																															
related_Acomosus_ Ming2015																															
	4	4	A	4	A	A	947	668	A	4	536	4	032	A	A	A	A	4	4	A	×	A	A	A	A	A	4	375	A	4	4
MAC_2amilies_change CC	N N	Z Z	Z A	Z A	Z A	Z Z	IA 6	IA 5	es N	Z Z	N 6	Z A	IA 5	Z Z	N	N	N N	N N	Z A	es N	N N	Z A	N	N	N	N	Z A	IA 6	N	es	z A
pos_selection_CAM 	A	Z A	A	Z A	Z A	Z A	AA N	A P	AA V	Z A	Z A	Z A	se/	Z A	AA	A A	A A	A	A A	AA V	A	Z A	AA	AA	AA	AA	Z A	A N	A A	A V	Z A
WC3	4	÷ ح	4	4	4	s:	A	A F	A A	4	4	4	A	4	4	4	4	4	4	A	۔ ح	4	A	ے ح	ي ح	ي ح	4	4 V	4	4	4
Algn_copy.Broc_An an_Tilla.	2 o	2 o	2 o	2 o	2 o	es ye	0 N	ů v	ů v	2 o	2 o	z o	2 o	2 o	2 o	2 o	ů v	2 0	z o	° v	2 o	2 o	v v	2 o	2 o	ů v	ź o	ů v	ů v	2 o	2 o
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Low conv.Binc Ana	2	2	2	2	2	2	ou	ye	8	2	2	2	2	2	8	2	8	2	2	9	2	2	ye	2	2	02	ye	ou	ou	ye	2
A_oong.goopy.Broc_A	yes	yes	yes	yes	yes	8	yes	92	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes	2	yes	yes	yes	2	yes	yes	2	yes
edname	LG14	LG14	LG14	LG14	LG14	LG14	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG22	LG22	LG22	LG22	LG22	LG22	LG22	LG22
ðeue	Aco006549	Aco006583	Aco006586	Aco006591	Aco006594	Aco006606	Aco006629	Aco006642	Aco006659	Aco006675	Aco006679	Aco006692	Aco006693	Aco006698	Aco006711	Aco006719	Aco006733	Aco006735	Aco006741	Aco006754	Aco006755	Aco006769	Aco006847	Aco006861	Aco006874	Aco006886	Aco006923	Aco006939	Aco006949	Aco006978	Aco006993

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əziz_noxə_nim	43	4	117	364	257	65	424	60	133	152	78	119	142	4	329	124	159	247	442	139	126	158	46	260	619	46	92	75	1700	67	37
eziz_pinoxe_latot	3394	2948	2460	2151	1089	1634	1129	2861	2079	1907	5305	2134	1873	066	2350	1216	1830	944	2044	4596	3062	1786	2393	601	1920	1880	3941	1306	1700	3138	1052
ang_per_gene	12	17	2	7	m	8	2	17	e	2	24	2	m	m	4	m	2	m	m	2	2	4	14	2	2	6	22	2	1	9	8
average_exon_size	282.833	173.412	351.429	1075.500	363.000	204.250	564.500	168.294	693.000	381.400	221.042	426.800	624.333	330.000	587.500	405.333	366.000	314.667	681.333	656.571	612.400	446.500	170.929	300.500	960.000	208.889	179.136	186.571	1700.000	523.000	131.500
дbe	NA	03_VATPase	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	01b_Abscisic_acid_signal	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA
circadian_clock																															
ysis_glycol						yes														yes						yes					
ogulluhoq_ləs_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Populus trichocarpa transducin family protein (POPTR_0016s13950g) mRNA_ complete cds	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
- filsvonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	ALB_F_leucoanthocyanidin dioxygenase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
-malateTransterase Assimilation_Carboh ydrates		yes																													
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana nas																															
markers																															
qraught_res														yes																	
aquaporin_reg																															
related_Acomosus_ Ming2015 stomata_func																							yes								
CAM-	7	7	7		7	7	20	18	7	7	7	7	7	7	7	7	7	89	7	7	7	7	7	8	7	7	92	148	7	16	48
Angiosperm_gene	A N	A N	⊿ Z	Z ₹	⊿ Z	⊿ Z	A 66	A 63	A N/	⊿ Z	NZ VZ	∆7	⊿ Z	⊿ Z	A N	A N	A N/	A 65	⊿Z	A N	A NZ	A NZ	∆ ∡	A 67	A N	A N	A 49	A 53	A NZ	A 60	₽ 60
stiite_	SS N	Z V	Z V	z v	Z V	Z V	Z V	Z V	N SS	Z V	Z A	Z V	Z V	Z V	Z V	Z V	A N	Z V	Z V	Z V	N V	N V	Z V	Z V	Z V	Z V	Z V	Z V	Z V	Z V	Z V
BOM BOM CA	ss ye	z v	z v	z v	z v	z v	z v	Z V	es ye	z v	z v	z v	z v	z v	z v	Z V	N V	z v	z v	z v	Z V	Z V	z v	Z V	Z V	z v	z v	z v	Z V	Z V	z v
Algh_copy.Broc_An an_Tilla.	ہ ۲	2 0	2 0	2 0	es N	2 0	2 0	2 0	es yı	2 0	_ Z _ 0	2 0	2 0	N AI	2 0	2 0	2 0	2 0	2 0	2 0	2 0	v o	2 0	2 0	2 0	2 0	2 0	2 0	z o	2 0	2 0
Low_copy.Broc_Ana n_Tilla.	es n	¢ o	<u> </u>	<u> </u>	× م	es n	ē o	es n	0 X	o o	<u> </u>	e o	¢ o	N N	ē o	ē o	ū o	es n	o o	es n	ū Q	ē Q	es n	ē o	ē o	ē o	es n	o o	ū Q	é Q	<u>c</u>
Alngle_copy.Broc_A nan_Tilla.	0 V	u sə.	u sə.	u sə	0	0	es n	0 V	u Q	es n	les n	es n	es n	A N	es n	les n	les n	0	es n	2	u sə.	u sə.	0	u sə.	les n	es n	0	u sə.	les n	es n	es
amsnpaz	323 n	323 y	523 y	323 y	523 n	523 n	523 y	G23 n	323 n	G23 y	G23 y	523 y	523 y	523 A	G23 y	G23 y	323 y	G23 n	G23 y	G23 n	323 y	323 y	G23 n	523 y	G23 y	G23 y	323 n	523 y	G23 y	523 y	523 y
әиәб	Aco007014 Lt	Aco007033 Lt	Aco007035 Lt	Aco007041 Lt	Aco007046 Lt	Aco007054 Lt	Aco007057 Lu	Aco007065 Lt	Aco007085 Lt	Aco007096 Lt	Aco007098 Lt	Aco007115 Lt	Aco007119 L(Aco007198 Lt	Aco007204 Lu	Aco007212 Lu	Aco007214 Lu	Aco007234 Lu	Aco007241 Lu	Aco007248 Lt	Aco007258	Aco007277 Lu	Aco007291 Lt	Aco007294 Lu	Aco007304 Lu	Aco007306 Lt	Aco007307 Lt	Aco007319 Lt	Aco007326 Lt	Aco007376 Lt	Aco007384 Lt

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əziz_noxə_nim	132	2126	95	181	69	128	166	1316	8	8	22	124	486	132	32	144	446	347	140	1484	37	63	62	586	24	142	3146	111	45	85
etal_exonic_size	1575	2126	3144	2685	2284	1566	1253	1316	1709	1671	2225	1140	1557	1145	2822	1763	446	1405	1537	1484	3164	1808	1529	1556	2223	829	3146	2649	3304	1597
ur_exons_per_gene	m		12	LO LO	LC				17	13	19	цл	m	4	21	۳ ۱			LC	1	11	10	10		17	4		12	25	9
average_exon_size	525.000	2126.000	262.000	537.000	456.800	223.714	626.500	1316.000	100.529	128.538	117.105	228.000	519.000	286.250	134.381	587.667	446.000	702.500	307.400	1484.000	287.636	180.800	152.900	778.000	130.765	207.250	3146.000	220.750	132.160	266.167
дуе	10_Glucogenesis_specific_dayC3	AA	VA	AV	00_#W_StomatalMovement_RootP nototropism2	AA	AV	A	A	10_Glucogenesis_specific_dayC3	AA	AA	AV	AV	10_Glucogenesis_specific_dayC3	AA	AV	A	10_Glucogenesis_specific_dayC3	AN	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	AA	AA	00_#36_Malic_enzyme	٨٨	AV	٨٨	ИА	AA
circadian_clock	-			-	01		-				-	2	-						1	2				-		~			2	
glucogenesis_glycol ysis	yes									yes					yes				yes		yes	yes								
oɓnjintiod_ləs_soq	NA	NA	PREDICTED: Oryza sativa Japonica Group homeobox-leucine zipper protein ROC7 (LOC4344614) mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris NAD-dependent malic enzyme 59 kDa proformmitochondrial (LOC104888560) mRNA	NA	NA	NA	NA	NA
filavonoid_anthocya nin_Pircaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates																														
circadian_metabolis m_Wai2017 malateTransferase_					/es																									
anthocyanin_SI_Ana san					~																									
markers																														
qraught_res																														
aquaporin_reg																														
stomata_func																														
related_Acomosus_																									es					1
	<	4	4	4	4	4	4	4	4	4	4	∢	4	4	∢	4	4	4	A	A	4	4	4	4	A A	591	∢	∢	A	<
gene_families_CAM C3	N N	N N	Z A	N N	N N	N A	Z A	N N	N N	N N	N N	N N	N N	N	N N	N N	Z A	N N	N N	N N	N N	N	N N	Z A	Z V	4N 41	N N	N N	A N	
pos_selection_CAM 	AN	AN	AN	AN	AN	AN	AN AN	AN	AN	AN	ves N	AN	AN	AN	AN	AN	AN AN	AN	ves N	NA N	AN	AN	AN	AN	AN AN	AN	AN	AN	NA N	AN
	_	_	4	SE	A	<	<	_	SE	_	۲ ۲	-	_	_	4	_	se	_	A	SS	-	_	SE	_	4	4	SE	4	SS	SS
High_copy.Broc_An an_Tilla.	/es N.	Z Z	es N.	10 yé	/es N.	N N	Z Q	Z Q	10 YE	ž Ž	N AN	JO Z	2 Z	Z Z	'es N.	Z Z	√A y€	Z Z	/es N	to yt	N N	2 Z	JO YE	Z Q	Z Q	0 N	10 YE	Z Z	to yé	Jo ye
nnnnn	~			u s:	~		-	-	u s:	s:	4	-	-				4	-	~		-	u s:	s:	-	SX SX	s:	-			s:
.slliT_nsn	ž	2	2	٧٤	ч	ž	2	ž	×	ž	Ż.	2 Z	ž	2	2	2	Ž	ž	ŭ	л С	ц Ц	yέ	×	ц Ц	×	×٤	ž	ž	u c	×٤
Single_copy.Broc_A	12 no	12 yes	12 no	12 no	12 no	12 yes	12 yes	12 yes	12 no	12 no	12 NA	12 yes	12 yes	12 yes	12 no	12 yes	12 NA	38 yes	00 8C	38 yes	JB yes	00 8C	01 BC	38 yes	01 28	00 8C	38 yes	38 yes	38 yes	00 BC
) LG1	3 LG1	3 LG1) LG1	LG1	3 LG1	5 LG1	7 LG1	5 LG1	3 LG1	3 LG1) LG1	4 LG1	3 LG1	2 LG1	3 LG1) LG1	1 LGC) LGC	3 LGG	r LGG) LGG	5 LGG) LG0	- LGG) LGC	5 LGG	7 LGC	2 LGC) LGC
âene	Aco007400	Aco007415	Aco007425	Aco007440	Aco007441	Aco007445	Aco007445	Aco007457	Aco007465	Aco007465	Aco007485	Aco007490	Aco007494	Aco007496	Aco007502	Aco007506	Aco007505	Aco007534	Aco007535	Aco007546	Aco007561	Aco007570	Aco007575	Aco007580	Aco007622	Aco007625	Aco007645	Aco007647	Aco007652	Aco007655

əziz_noxə_nim	386	785	166	809	2558	49	198	41	1301	111	155	59	29	48	70	102	122	32	353	200	514	193	282	227	1391	85	210	152	2132	66	56
total_exonic_size	2280	785	1909	808	2558	1851	1186	1213	1301	1520	1403	2029	743	2509	988	1213	2256	2644	865	606	1150	1673	832	1205	1391	4897	2061	733	2132	1869	3041
	e		m	-	-	20	2	2	-	~	4	16	m	7	8	9	4	7	2	m	5	4	2	m	1	6	4	m		8	17
erage_erage_erage	760.000	785.000	636.333	809.000	2558.000	92.550	593.000	242.600	1301.000	217.143	350.750	126.813	247.667	358.429	123.500	202.167	564.000	377.714	432.500	303.000	575.000	418.250	416.000	401.667	1391.000	544.111	515.250	244.333	2132.000	233.625	178.882
əd/q	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	NA	00_#Ming2019_Anthocyanin_biosy nthesis	02_Aquaporins	NA	00_#17_Malate_dehydrogenase	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	00_#01_carbonic_anhydrase	NA	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	NA	01b_Abscisic_acid_signal	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3							
circadian_clock																															
ysis_ glucogenesis_glycol												yes						yes												yes	yes
oßnijnµod~jəs [–] sod	NA	NA	NA	NA	NA	PREDICTED: Glycine max actin-related protein 4-like (LOC100795390)_ mRNA	NA	NA	NA	Beta vulgaris subsp. vulgaris malate dehydrogenase_cytoplasmic /L.OC104887939] mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
filavonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MalateTransferase_ Assimilation_Carboh ydrates																															
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana nas							yes																								
draught_res		/es																	/es												
aquaporin_reg								yes																							
stomata_func																					yes										
CAM- related_Acomosus_ Ming2015										yes						yes															
Angiosperm_gene	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	7111	AA	AA	AA	AA	5447	AA	AA	AA	AA	AA	AA	AA	5148	AA	NA	A
gene_families_CAM C3	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN						
MAD_not_selection_CAM 	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	yes	AN	yes	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
Diff_expressed_CA MC3	yes	AN	AN	yes	AN	AN	AN	AN	AN	NA	AN	yes	yes	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN
nA_ooy.Broc_An an_Tilla. an_Tilla.	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	Q	QL	yes	ou	ou	ou	yes	ou	ou	ou	ou	QU	ou	ou	QL	ou	ou	ou	ou	2
Low_copy.Broc_Ana n_Tilla.	Q	yes	2	2	2	9	9	yes	2	yes	92	yes	2	2	2	2	2	2	2	2	2	2	2	9	Q	yes	2	2	2	Q	yes
Single_copy.Broc_A nan_Tilla.	yes	2	yes	yes	yes	yes	yes	2	yes	2	yes	2	yes	2	yes	yes	yes	2	yes	yes	yes	yes	yes	yes	yes	2	yes	yes	yes	yes	2
edusme	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21	LG21
gene	Aco007664	Aco007670	Aco007671	Aco007678	Aco007684	Aco007686	Aco007699	Aco007718	Aco007730	Aco007734	Aco007753	Aco007762	Aco007777	Aco007782	Aco007800	Aco007803	Aco007818	Aco007825	Aco007828	Aco007832	Aco007857	Aco007859	Aco007876	Aco007882	Aco007890	Aco007901	Aco007906	Aco007911	Aco007924	Aco007928	Aco007953

		_																-												_	
əziz_noxə_nim	56	2810	23	8	44	178	350	177	1919	328	16	36	26	1433	96	158	107	172	20	09	1580	20	20	37	127	136	396	1967	68	1616	51
total_exonic_size	3541	2810	3298	2236	2653	1317	1659	2211	1919	1688	3394	2009	2957	1433	3111	1197	2524	466	2287	1554	1580	1950	1253	2501	1409	1585	1266	1967	1474	1616	2297
ur_exons_per_gene	13	F	13	15	13	4	m	цл		4	12	16	[∞]		14	m	11	N	12	^o		12		20	m	4	m		~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	F	50
average_exon_size	272.385	2810.000	253.692	149.067	204.077	329.250	553.000	442.200	1919.000	422.000	282.833	125.563	369.625	1433.000	222.214	399.000	229.455	233.000	190.583	259.000	1580.000	162.500	179.000	125.050	469.667	396.250	422.000	1967.000	184.250	1616.000	114.850
дуе	01d_Auxin_reponse_factor	٨٨	10_Glucogenesis_specific_dayC3	AV	٨٨	AV	AV	AA	AA	00_#MB_MS	AA	10_Glucogenesis_specific_dayC3	00_#W_ProtonPump_AVP1	AA	00_#W_StomatalMovement_AHA2	AA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	A	AA	10_Glucogenesis_specific_dayC3	00_#W_ProtonPump_VHA-A	٨٨	٨٨	A	AA	A	٨٨	AN
circadian_clock	0	~	1	2	2	2	2					-		2		2	1	1		1	2	2	-	0	2	~	2			~	
ysisangooulg ysis			/es									es					'es	'es	es	/es			/es								
oອິnijnµod"jəs ⁻ sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	V	NA	NA	NA	NA	y	V	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
attoroid_anthocya	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates																															
circadian_metabolis m_Wai2017 malateTransferase_													/es		ves									ves							
anthocyanin_SI_Ana san																															
markers										yes																					
draught_res																															
aquaporin_reg																															
stomata_func	yes																														
related_Acomosus_ Mina2015																															
Angiosperm_gene	AA	AA	AA	5489	A	A	AA	AA	AA	A	A	A	A	A	A	Ą	A	A	AA	AA	A	3405	A	AA	A	AA	AA	AA	A	AA	1889
gene_families_CAM C3	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	AN	AN						
pos_selection_CAM shifts	AN	NA	NA	AN	NA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	AN	yes	AN						
Diff_expressed_CA MC3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	yes	AN	AN	AN	AN	AN	yes	AN	٩N
High_copy.Broc_An an_Tilla.	ou	ou	yes	ou	ou	ou	ou	ou	ou	AN	ou	ou	yes	ou	yes	ou	ou	ou	ou	ou	02	e e	e e	ou	ou	ou	ou	ou	e e	ou	2
Low_copy.Broc_Ana n_Tilla.	yes	6	0	yes	yes	2	8	2	2	M	yes	8	8	8	6	6	yes	yes	yes	2	2	2	2	2	6	01	2	2	2	6	yes
Single_copy.Broc_A nan_Tilla.	g	sə,	Q	g	g	'es	'es	'es	'es	۲Þ.	g	,es	g	,es	g	,es	Q	g	g	'es	'es	'es	'es	'es	'es	'es	'es	'es	'es	sə/	g
emanee	G21 n	G21 y	G21 n	G21 n	G21 n	G21 y	G21 y	G21 y	G21 y	G21 N	G21 n	G21 y	G19 n	G19 y	G19 n	G19 y	G19 n	G19 n	G19 n	G19 y	G19 y	G19 y	G19 y	G19 y	G19 y	G19 y	G19 y	G19 y	G19 y	G19 y	G19 n
əuəɓ	Aco007973 L	Ac0007974 L	Aco007975 L	Aco008032 L	Ac0008037 L	Aco008046 L	Aco008062 L	Aco008066 L	Aco008078 L	Aco008099 L	Aco008105 L	Aco008126 L	Aco008167 L	Aco008175 L	Aco008192 L	Aco008206 L	Aco008234 L	Aco008236 L	Aco008246 L	Aco008257 L	Aco008287 L	Aco008292 L	Aco008298 L	Aco008300 L	Ac0008315 L	Aco008321 L	Aco008330 L	Aco008331 L	Aco008348 L	Ac0008394 L	Aco008399 L

əziz_noxə_nim	56	540	168	1538	20	92	127	52	113	48	93	143	36	527	2831	128	223	59	35	122	10	524	245	151	1178	308	27	121	558	35	290
eziz_pinoxe_latot	3419	1405	1371	1538	3632	1498	1436	1133	1412	2724	2172	1484	2025	1557	2831	2772	1228	3096	3162	3344	898	524	1451	2787	1178	1552	4572	1523	1949	1454	1629
nr_exons_per_gene	14	2	4	-	19	ы	ы	ъ	4	16	7	4	10	2	-	10	4	14	10	14	ß	н г	e	7	F	e	6	2	2	13	e
average_exon_size	244.214	702.500	342.750	1538.000	191.158	299.600	287.200	226.600	353.000	170.250	310.286	371.000	202.500	778.500	2831.000	277.200	307.000	221.143	316.200	238.857	179.600	524.000	483.667	398.143	1178.000	517.333	508.000	304.600	974.500	111.846	543.000
эdб	01d_Auxin_reponse_factor	NA	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	05_Chloroplasts_activity	NA	NA	10_Glucogenesis_specific_dayC3	NA	00_#30_Malate_dehydrogenase	NA	04_Oxygen_evolving_enhancer_O EE	NA	10_Glucogenesis_specific_dayC3	NA													
circadian_clock																															
yucogenesis_glycol sisy					yes	yes					yes																			yes	
ດອີກເຫຼານດີ ງອຣ sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Oryza sativa Japonica Group homeobox-leucine zipper protein ROC7 (LOC434614) mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ationovali filosonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
MalateTransferase_ Assimilation_Carboh ydrates								yes													yes										
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana san																															
աջլkers																															
draught_res																															
aquaporin_reg																															
Ming2015 stomata_func	yes																														
CAM- related_Acomosus_																			yes												
Angiosperm_gene	AA	AA	¥	AN	AA	AA	AA	7324	A	¥	AA	A	AN	AA	¥	¥	¥	AN	AA	AN	Ą	A	AA	¥	¥	¥	AN	AA	AA	6859	¥
MAD_aene_families_CAM C3	ΝA	٩N	٩N	AN	AN	AN	AN	AN	٩N	AN	ΥN	٩N	ΝA	ΝA	٩N	٩N	٩N	AN	AN	ΝA	٩N	٩N	ΝA	٩N	٩N	٩N	٩N	ΝA	ΝA	ΑN	AN
MAD_notzelection_CAM	ΝA	ΑN	AN	AN	AN	AN	AN	AN	AN	AN	AN	ΝA	ΝA	AN	AN	AN	AN	AN	AN	ΝA	AN	ΝA	ΝA	AN	٩N	AN	yes	AN	AN	AN	AN
AD_bessed_CA	ΝA	ΑN	AN	AN	AN	AN	AN	AN	AN	AN	AN	ΝA	yes	AN	AN	AN	AN	yes	AN	ΝA	AN	yes	ΝA	AN	٩N	AN	AN	ΝA	ΝA	ΑN	AN
High_copy.Broc_An	yes	ou	ę	Q	ę	AN	е	е	e L	yes	yes	ou	QL	0L	e	e	e	Q	e L	QL	QL	٩N	QL	e	ę	ę	e.	ou	ou	ę	Q
Low_copy.Broc_Ana	Q	Q	ę	ę	yes	AA	8	ę	e	ę	ę	2	yes	ę	e	e	e	yes	yes	01	yes	AA	6	e	ę	ę	ę	8	QL	yes	2
A_oongle_copy.Broc_A	0L	yes	yes	yes	2	AN	yes	yes	yes	2	2	yes	6	yes	yes	yes	yes	e	e	yes	e	٩N	yes	2	yes						
emsnpez	LG19	LG19	LG19	LG19	LG19	LG19	LG19	LG19	LG19	LG19	LG19	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09							
gene	Aco008426	Aco008429	Aco008430	Aco008431	Aco008441	Aco008446	Aco008452	Aco008453	Aco008459	Aco008460	Aco008491	Aco008510	Aco008513	Aco008564	Aco008568	Aco008569	Aco008573	Aco008578	Aco008626	Aco008682	Aco008684	Aco008685	Aco008698	Aco008715	Aco008738	Aco008744	Aco008752	Aco008775	Aco008777	Aco008784	Aco008787

	~	~	-	<u><u></u></u>	~			<u><u></u></u>	10	<u> </u>	-					<u> </u>	10	~	~	~	0	~	~	10	~	Þ	~	n.	-		
əziz_noxə_nim	2630	43	6	1652	198	54	204	512	506	200	1430	15	61	2594	104	120	125	213	140	33	50	1130	1928	475	83	57	1589	117	161	65	394
ezia_exonic_size	2630	2752	2293	1652	1841	3640	1260	1108	1589	451	1430	681	770	2594	773	935	1568	1535	1226	2542	2031	1130	1928	1038	1993	1608	1589	1109	1392	1966	2805
nr_exons_per_gene		17	'			11							~							14	12	-			11	12					
average_exon_size	2630.000	250.182	327.571	1652.000	368.200	330.909	420.000	554.000	794.500	225.500	1430.000	227.000	192.500	2594.000	193.250	311.667	313.600	383.750	306.500	363.143	169.250	1130.000	1928.000	519.000	181.182	134.000	1589.000	221.800	464.000	245.750	701.250
jAbe	AA	AA	10_Glucogenesis_specific_dayC3	AA	AV	00_#W_StomatalMovement_ATP- binding_cassette_B14	00_#Ming2019_Anthocyanin_biosy hthesis	A P	AV	11_Glycolysis_night_C4_malate_p	AV	AA	02_Aquaporins	AA)2_Aquaporins	04_Oxygen_evolving_enhancer_O	AV	AA)2_Aquaporins)1d_Auxin_reponse_factor	AA	AA	AA	AA	AA	10_Glucogenesis_specific_dayC3	AA	A	05_Chloroplasts_activity	L0_Glucogenesis_specific_dayC3	A
	2	2		2	2		0 5		2	0 1-1	2	~	0		0	ОШ	2	2	0	0	2				2	н	2	2		-	
circadian_clock																															
glucogenesis_glycol ysis			yes							yes																yes				yes	
oßnijnµod"jəs ⁻ sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
								nidi	. <u>e</u>																						
styoortina_biorovalit 29_aimia_pri	NA	NA	NA	NA	NA	NA	NA	STA_F_coumaroyl- :anthocya n 3-o-glucoside-6 -o- coumaroyltransferase 2	ALB_F_anthocyanin 5-aromat acyttransferase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																se													se		
circadian_metabolis m_Wai2017 malateTransferase						/es										~													~		
anthocyanin_SI_Ana nas							es																								
markers																															
draught_res																															
aquaporin_reg													es		es				es												
stomata_func															~					se											
related_Acomosus_																				Y											
	7	7	7	7	7	7	7	7	7	7	7	58	7	7	7	7	7	7	7	7	4	7	7	44	7	7	7	7	7	7	4
Angiosperm gene	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	Ž	A 59	Ž	۲Z ۲	Ž d	Ž	Ž	Ž	Ž d	۲N ۲	NZ T	۲۷ ۲۷	۲۷ ۲	A 57	S S	Ž	Ž	Ž	Ž	Ž	Ž
	ž	s S	ž	Ż	ž	ž	ž	ž	Ż	ž	ž	ž	ž	ž	ž	Ż	ž	ž	ž	ž	Ž	s N	ź	ž	A ye	ž	ž	ž	ž	ž	Ž
MC3 MC3	٩N	yes		Z	Z	Z	Z	٩Z	Z	Z	Z	٩N	٩N	٩N	٩Z	٩Z	٩Z	٩Z	٩N	٩N	٩N	ye	٩N	٩Z	٩N	٩N	٩Z	٩Z	٩Z	٩N	٩N
an_rilla. Diff_expressed_CA	AN	AN	A N	A N	A N	ΝA	٩N	NA	A N	A N	AN	AN	AN	ΝA	٩N	AN	AN	AN	ΝA	ΝA	yes	ΝA	AN	ΥN	٩N	ΝA	٩N	AN	AN	AN	NA
High_copy.Broc_An	Q	6	2	2	2	yes	6	NA	2	2	ę	Q	٩N	8	2	٩N	8	2	e e	8	yes	ou	оц	2	2	0L	2	0L	0L	0L	2
Low_copy.Broc_Ana	2	2	yes	2	2	6	8	AA	yes	2	ę	8	AA	ę	yes	¥	2	2	yes	yes	입	입	6	ę	yes	yes	ę	2	2	yes	2
Single_copy.Broc_A nan Tilla.	yes	yes	2	yes	yes	2	yes	٩N	2	yes	yes	yes	٩N	yes	2	٩N	yes	yes	e	6	0	yes	yes	yes	e	2	yes	yes	yes	2	yes
edusme	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG09	LG22
деле	Aco008789	Aco008802	Aco008830	Aco008834	Aco008854	Aco008863	Aco008872	Aco008881	Aco008882	Aco008884	Aco008903	Aco008910	Aco008925	Aco008929	Aco008932	Aco008947	Aco008949	Aco008951	Aco008952	Aco008955	Aco008957	Aco008992	Aco009049	Aco009059	Aco009070	Aco009080	Aco009124	Aco009125	Aco009134	Aco009143	Aco009185

əziz_noxə_nim	30	21	140	126	1193	74	36	481	461	33	84	262	11	362	123	77	45	64	77	603	167	80	530	254	198	44	44	996	616	365
total_exonic_size	1403	4260	1150	2626	1193	1528	1309	1801	2046	2511	1449	1760	1630	882	1250	709	5599	1582	704	1880	1557	3219	530	683	1329	2117	1314	2015	2154	2127
ur_exons_per_gene	12	23	4	5	-	8	9	2	m	15	8	m	13	5	9	9	33	m	m	2	ß	15		2	4	14	13	5	2	4
aziz_noxa_agerave	116.917	185.217	287.500	1313.000	1193.000	191.000	218.167	900.500	682.000	167.400	181.125	586.667	125.385	441.000	208.333	118.167	169.667	527.333	234.667	940.000	311.400	214.600	530.000	341.500	332.250	151.214	101.077	1007.500	1077.000	531.750
ədáj	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	10_Glucogenesis_specific_dayC3	03_VATPase	NA	NA	01b_Abscisic_acid_signal	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	NA	NA
circadian_clock																														
glucogenesis_glycol ysis		yes							yes	yes	yes				yes											yes	yes			
oßnijntiod_fəs_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max lysine-specific demethylase rbr-2-like (LOC100819576)_ mRNA	NA	NA	NA	NA	PREDICTED: Solanum tuberosum heat shock cognate protein 80-like (LOC10260008)mRNA	NA	NA	NA	NA	NA	NA	NA	NA
stronovalt S9_aimia319_nin	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_flavone 3 -o- methyltransferase 1	NA	NA	NA	AN	NA	NA	NA	NA	NA	NA	NA	NA
Asimilation_Carboh Assimilation_Carboh ydrates																yes														
circadian_metabolis m_Wai2017																														
anthocyanin_SI_Ana nas																														
draught_res markers																														
aquaporin_reg																														
stomata_func																			es											
related_Acomosus_																														
	216	A1	A,	A	A.	913	068	A.	A.	A	A	A	A	A.	393	Ą	۲.	٩	٩	A	۲	٩	A,	A1	A1	Ą	572	A	Ą	đ
gene_families_CAM C3	AA 6	Z A	A	4 A	A	AA 6	AA 6	A	A	A	4 A	A	4 A	ves /	AA 6	AA	A A	Z A	Z A	AA	Z A	A A	Z A	Z A	Z A	A A	AA 6	Z A	AA	4
MAD_notection_CAM shifts_	NA F	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA V	AN	AN	NA 1	AN	AN	AN	yes h	AN	AN	AN	NA L	AN 1	AN	AN	AN 1	AN
Diff_expressed_CA MC3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	ves	/es	AN	AN	AN	AN	AN	AN	AN	AN	/es	/es	AN	AN	AN	AN	AN	AN
High_copy.Broc_An an_Tilla.	1 01	ves I	6	6	6	1	1	0L	/es	AM	6	2	6	01	6	A A	6	6	6	6	101	ves I	01	01	0	1	0L	2	01	2
Low_copy.Broc_Ana n_Tilla.	yes I	6	2	2	2	2	6	6	6	- N	ves 1	2	2	2	6	AN	ves 1	2	2	2	6	6	2	2	6	2	6	2	0	2
A_oopy.Broc_A nan_Tilla.	2	2	yes	yes	yes	yes	yes	yes	2	AN	2	yes	yes	yes	yes	AN	2	yes	yes	yes	yes	2	yes .	yes .	yes .	yes	yes	yes	yes	yes
əmanpəz	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	.G22	G14	G14
anag	Aco009215 L	Aco009217 L	Aco009219 L	Aco009231 L	Aco009247 L	Aco009256 L	Aco009272 L	Aco009273 L	Aco009274 L	Aco009281 L	Aco009282 L	Aco009283 L	Aco009289 L	Aco009291 L	Aco009299 L	Aco009301 L	Aco009310 L	Aco009322 L	Aco009346 L	Aco009353 L	Aco009366 L	Aco009370 L	Aco009371 L	Aco009385 L	Aco009388 L	Aco009392 L	Aco009409 L	Aco009425 L	Aco009446 L	Aco009453 L

							-								-	-	-	-												
əziz_noxə_nim	21	35	28	737	67	622	116	238	182	13	155	2039	81	127	566	162	115	238	31	609	16	641	260	162	685	55	72	14	152	125
ezia_oinoxe_laiot	1615	1643	626	737	1297	1370	3126	1644	182	250	1721	2039	867	1511	566	2711	2579	1398	2105	1588	767	641	1725	856	2066	1944	8476	938	1944	1618
ut_exons_per_gene	2	8	6		4	5	14	з	-	2	9		2	20	-	ŝ	7	e	17	10	4		5	5	2	15	24	10	ъ	4
average_exon_size	323.000	205.375	104.333	737.000	324.250	685.000	223.286	548.000	182.000	125.000	286.833	2039.000	173.400	302.200	566.000	542.200	368.429	466.000	123.824	794.000	191.750	641.000	862.500	428.000	1033.000	129.600	353.167	93.800	388.800	404.500
adái			_specific_dayC3				_specific_dayC3		ance_genes_LEA	ance_genes_LEA								_specific_dayC3	ht_C4_malate_p				Oscillator_cycling	ance_genes_LEA	_specific_dayC3	_specific_dayC3				
	٧N	NA	10_Glucogenesis	NA	NA	NA	10_Glucogenesis	AN	06_Drough_resist	06_Drough_resist	NA	10_Glucogenesis	11_Glycolysis_ni athway	NA	NA	NA	00_#W_Circadiar _DOF_F1	06_Drough_resist	10_Glucogenesis	10_Glucogenesis	NA	NA	NA	NA						
circadian_clock																														
glucogenesis_glycol visi			yes				yes											yes	yes						yes	yes				
oßnijntiod_les_sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Bela ungaris subgaris subgaris glucose-1.phosphate adentylytransferase large subuni 3. chiorophastic/amtylophastic (LOC104883901)_transcript/variant X1_ mRNA	NA	NA	NA	NA
filevonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																														
circadian_metabolis m_Wai2017 malateTransferase																							yes							
anthocyanin_SI_Ana nas																														
markers																														
draught_res									yes	yes														yes						
aquaporin_reg													-										-							
related_Acomosus_ Ming2015																														
CAM-	¥	942	960	4	A	4	A	A	A	¥	4	4	4	4	110	4	A	4	4	4	4	4	4	4	4	A	A	501	A	4
gene_families_CAM C3 Andiosperm.gene	N N	44 46	4A 66	N V	N V	N	N	N N	N	N N	Z A	Z A	Z A	Z A	4A 6.	N N	N N	N N	N N	Z A	N V	N N	Z A	N N	Z A	N V	N N	4A 66	N AL	Z V
MAD_noi_selection_CAM 	AN	AN	AN	AN	AN	AN	AN	yes h	AN	AN	AN	yes h	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
MC3 Diff_expressed_CA	es	4	4	4	es	A	A	A	A	-	A	A	4	4	4	4	A	A	A	A	4	A	4	A	4	- I	es	A	A	4
High_copy.Broc_An an_Tilla.	no y	∠ ou	∠ ou	∠ ou	no y	∠ ou	yes N	uo N	∠ ou	ou	∠ ou	∠ ou	∠ ou	2 Q	2 OU	∠ ou	∠ ou	∠ ou	∠ ou	∠ ou	∠ ou	∠ ou	2	∠ ou	∠ ou	 0	no y	⊿ ou	∠ ou	ou
Low_copy.Broc_Ana n_Tilla.	/es	ves	/es	/es	/es	ę	Q.	0L	ves	/es	ę	ę	ę	ę	ę	ę	¢.	ę	ę	ę	ves	/es	ę	/es	/es	/es	ves	ę	ę	ę
Single_copy.Broc_A nan_Tilla.	ot	e e	0	Q	0	l sə	0	l sə/	oc oc	OC OC	les t	les t	ies t	r sə	'es	'es r	'es r	r sə	l sa	les t	e e	Q Q	res r	Q	0	Q	of C	l sə/	l sə/	l sə
emanpez	.G19 r	.G01	.G01 r	.G01 r	.G01 r	.G01 y	.G01 r	.G01 y	.G01	.G01	.G01 y	.G01 y	.G01 y	.G01	.G01 r	.G01 y	.G01 r	.G01 r	.G01 r	.G01 r	.G01	.G01 y	.G01							
gene	Aco009463 1	Aco009469 1	Aco009474 1	Aco009477	Aco009484 1	Aco009499 1	Aco009508 1	Aco009511 1	Aco009513 1	Aco009514 1	Aco009532 1	Aco009549 1	Aco009551 1	Aco009559 1	Aco009566 1	Aco009569 1	Aco009577 1	Aco009587 1	Aco009588 1	Aco009592 1	Aco009599 1	Aco009600 1	Aco009612 1	Aco009627	Aco009639 1	Aco009644 1	Aco009645 1	Aco009647	Aco009654	Aco009662 1

sziz_noxs_nim	43	344	42	71	131	138	63	488	161	264	113	116	175	112	202	198	200	39	47	1112	796	1415	640	84	69	345	1460	12	1985	2285
esia_pinoxe_latot	2104	1313	1241	915	1505	1300	3120	1453	1557	1664	1832	3177	1898	1079	1165	2106	2386	2197	2897	1112	2516	1415	1690	3480	1211	1277	1460	880	1985	2285
ur_exons_per_gene	13	2	10	m	m	m	20	10	9	m	4	9	m	4	m	9	4	14	20	1	2	1	5	10	2	m	-	7	-	F-
average_exon_size	161.846	656.500	124.100	305.000	501.667	433.333	156.000	726.500	259.500	554.667	458.000	529.500	632.667	269.750	388.333	351.000	596.500	156.929	144.850	1112.000	1258.000	1415.000	845.000	348.000	173.000	425.667	1460.000	125.714	1985.000	2285.000
əd/ù	NA	NA	09_Circadian_clock	10_Glucogenesis_specific_dayC3	NA	01d_Auxin_reponse_factor	AN	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	11_Glycolysis_night_C4_malate_p athway	00_#32_Malic_enzyme	NA	10_Glucogenesis_specific_dayC3	NA	NA	00_#MB_PEPC_10_Glucogenesis_ specific_dayC3_	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	NA
сігсадіал_сіоск																														
glucogenesis_glycol sisy				ves														/es			/es				/es	/es				
oßnijnµod"jəs"sod	PREDICTED: Beta vulgaris subsp. vulgaris histone acetyltransferase GCN5 (LOC104894583) mRNA	NA	NA	NA	NA	NA	PREDICTED: Glycine max protein argonaute 1- like (LOC100778754)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris phosphoenolpyruvate carboxylase 1 (LOC104903486)_mRNA	NA	NA	NA	NA	NA	NA
filavonoid_anthocya Alavonoid_anthocya Alaimia_PS	A	AA	AA	AA	AA	AA	AV	AA	AA	AA	STA_L_flavonoid glucosyl- ransferase	AA	AA	AA	AV	AA	AA	AA	AA	AA	AA	AA	AA	A	AA	AA	AA	AA	AN	AN
Assimilation_Carboh ydrates ydrates		-	yes h	-			-			-	0, 1	-		-		-			-	~	-	-				-	-	-		
circadian_metabolis m_Wai2017																														
anthocyanin_S_Ana san																														
markers																								yes						
qı.anght_res																														
aquaporin_reg																														<u> </u>
ST020nd						yes																								<u> </u>
CAM- related_Acomosus_																			yes											
9n9p_mn9q2oipnA	AN	AA	AA	AA	AA	AA	A	A	A	AA	AA	AA	AA	6528	A	A	A	A	A	AA	AA	AA	AA	NA	AA	AA	AA	AA	A	¥
gene_families_CAM C3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	NA	ΑN	AN	AN	AN	AN	AN
pos_selection_CAM shifts	AN	AN	AN	AA	AN	AN	AN	AA	AA	AA	AA	AN	AA	AN	AA	AN	AA	AA	AN	AN	AA	AN	AN	NA	AN	AN	AN	AN	AN	AN
Diff_expressed_CA MC3	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	ΑN	AN	AN	AN	NA	ΥN	AN	AN	yes	AN	AN
nA_ooy.Broc_An an_Tilla. an_Tilla.	ou	ou	ou	ou	ou	AN	yes	2	ou	Q	ou	ou	ou	Q	2	2	2	yes	AN	0L	0 L	ou	Q	ou	0L	ou	ou	AN	Q	2
Low_copy.Broc_Ana n_Tilla.	e	2	2	2	2	A	2	2	2	2	yes	2	2	2	2	2	2	2	A	2	yes	2	2	yes	yes	2	2	AA	2	2
Single_copy.Broc_A nan_Tilla.	yes	yes	yes	yes	yes	AN	2	yes	yes	yes	2	yes	yes	yes	yes	yes	yes	2	AN	yes	2	yes	yes	Q	2	yes	yes	AN	yes	yes
emanpez	LG01	LG01	LG01	LG01	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG10	LG25	LG25	LG25
əuəɓ	Aco009673	Aco009686	Aco009689	Aco009713	Aco009744	Aco009779	Aco009780	Aco009790	Aco009794	Aco009801	Aco009807	Aco009813	Aco009822	Aco009889	Aco009903	Aco009914	Aco009924	Aco009949	Aco009967	Aco009980	Aco009989	Aco010002	Aco010013	Aco010025	Aco010028	Aco010030	Aco010034	Aco010086	Aco010087	Aco010088

əziz_noxə_nim	1433	126	83	107	155	41	86	20	704	62	247	1358	1184	19	30	1169	1253	77	478	120	153	229	276	353	644	162	119	203	51	80
etal_exonic_size	1433	938	1959	860	1119	835	747	1931	704	1063	1255	1358	1184	1760	1826	1169	1253	858	1735	1129	1370	2230	1092	139	1785	1678	1922	1225	4439	2377
nr_exons_per_gene	1	4	12	۳ ۱	4	4	4	19	-	4	4		Ч	15	9		1	20	5	4	e construction de la constructio	4	e	5	5	4	٣	4	26	10
aziz_noxa_agerave	1433.000	234.500	163.250	286.667	279.750	208.750	186.750	101.632	704.000	265.750	313.750	1358.000	1184.000	117.333	304.333	1169.000	1253.000	171.600	867.500	282.250	456.667	557.500	364.000	369.500	892.500	419.500	640.667	306.250	170.731	237.700
əd/q	NA	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	11_Glycolysis_night_C4_malate_p athway	NA	NA	00_##28_Malate_dehydrogenase	02_Aquaporins	NA	00_#W_CircadianOscillator_WD_re peat-containing_protein_RUP2	00_#W_ProtonPump_VHA- F_03_VATPase	NA	NA	NA	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	NA	NA	NA	NA	NA	NA
circadian_clock																														
glucogenesis_glycol ysis											yes											yes								
oɓnijnµod"]əs ⁻ sod	NA	NA	NA	NA	NA	Populus trichocarpa hypothetical protein (POPTR_0002s25930g) mRNA_ complete cds	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris malate dehydrogenase [NADP]_ chloroplastic (LOC104884197)_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
outaites	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_malonyl-coenzyme a: anthocyanin 3-o-glucoside-6 -o- malonyltransferase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
And the Carbon Carboh Carboh																														
circadian_metabolis m_Wai2017																	yes	yes												
anthocyanin_SI_Ana antocyanin_SI_Ana																														
markers																														
qraught_res				es			es																es	es						
aquaporin_reg															es								~							
stomata_func															~															
related_Acomosus_ 2102gniM														s																
-MA2		5							g	5				ye																
Angiosperm_gene C3	NA	641	AA	A	AA	NA	AN	645	733	556	₽ ₽	AN	AN	NA	NA	NA	AN	A A	A	AN	AN	AA	AN	AN	AA	A A	A A	AA	AN	¥
gene_fanilies_CAM	NA	AN	yes	AN	AN	AN	AN	AN	NA	AN	A N	NA	ΥN	NA	NA	NA	NA	A N	AN	NA	NA	NA	AN	NA	AN	AN	AN	AN	ΥN	AA
MAD_nos_selection_CAM	AN	AN	NA	AN	AN	AN	AN	NA	AN	AN	AN	NA	٩N	NA	ΝA	AN	AN	A N	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	AN	AA
AD_iff_expressed_CA	٩N	٩N	AN	AN	AN	AN	AN	AN	AN	AN	A N	AN	ΝA	AN	٨A	٩N	AN	A N	AN	AN	AN	yes	AN	AN	AN	A N	A N	AN	yes	yes
- High_copy.Broc_An fill_ns	оц	ę	Q	Q	Q	0Ľ	Q	ou	2	Q	Q	Q	2	ou	ou	оц	0Ľ	<u>e</u>	2	Q	Q	yes	yes	Q	ou	Q	Q	Q	оц	2
Low_copy.Broc_Ana nn	2	2	yes	yes	2	yes	yes	2	yes	yes	2	e	2	Q	yes	2	2	2	2	e	2	e	2	yes	2	2	2	2	yes	yes
Single_copy.Broc_A nan_Tilla.	yes	yes	2	2	yes	2	2	yes	2	2	yes	yes	yes	yes	0	yes	yes	yes	yes	yes	yes	8	2	2	yes	yes	yes	yes	2	2
edname	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG25	LG03	LG03
gene	Aco010113	Aco010116	Aco010122	Aco010134	Aco010136	Aco010148	Aco010160	Aco010172	Aco010193	Aco010197	Aco010215	Aco010217	Aco010230	Aco010232	Aco010251	Aco010261	Aco010278	Aco010280	Aco010296	Aco010298	Aco010300	Aco010310	Aco010312	Aco010315	Aco010319	Aco010322	Aco010340	Aco010341	Aco010367	Aco010377

		-				-			-					-	-		-		-		-			-			1.7				-
əziz_noxə_nim	44	140	51	2201	167	39	925	83	1979	488	177	247	28	2342	420	278	362	1658	239	158	169	15	351	139	125	461	125	23	31	45	20
ezia_cinoxe_latot	1287	1198	1805	2201	2618	1138	2406	1295	1979	1124	1473	1833	1729	2342	1409	766	894	1658	1115	1752	1298	1359	1897	1651	1917	1002	2413	1426	2580	1388	1299
anger_gere	12	3	5	1	6	6 1) 2	8	1) 2	3	4	5	1) 2) 2) 2	1) 2	5	5	12) 2	6	3) 2	8	6	9 (2 11	8
average_exon_size	107.250	399.333	361.000	2201.000	436.335	126.444	1203.000	161.875	1979.000	562.000	491.000	458.250	345.800	2342.000	704.500	383.000	447.000	1658.000	557.500	350.400	259.600	113.250	948.500	275.167	639.000	501.000	301.625	237.667	430.000	126.182	162.375
ədiQ	10_Glucogenesis_specific_dayC3	02_Aquaporins	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3	NA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	00_#W_MalateTransporter_ALMT_ 10_Glucogenesis_specific_dayC3	NA	NA	NA	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	NA
circadian_clock																															
glucogenesis_glycol ysis_	yes		yes					yes			yes		yes								yes							yes	yes		
oßnijmuod" jəs [—] sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Populus trichocarpa Argonaute 4 family protein (POPTR_0001s22710g) mRNA_ complete cds	NA	NA	NA	NA	NA	NA	NA	NA	NA
Vurates	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_dihydroflavonol 4- reductase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
malateTransferase Modiaco_Carboh Modiaco_Carboh																															
circadian_metabolis m_Wai2017																								yes							
anthocyanin_SI_Ana asn																															
ացւէթւշ																															
draught_res															yes	yes															
aquaporin_reg		yes																													
-MA- related_Acomosus_ <u>8102pmiM</u> onn_tatemote																															
Angiosperm_gene	AM	Ą	Å	Ą	Ą	5974	Ą	Ą	Ą	Ą	Å	Å	Å	Å	Ą	Ą	Ą	Ą	Ą	Ą	Ą	Ą	Ą	Ą	AM	Ą	3320	Ą	Ą	989	3303
gene_families_CAM C3	NA I	AN	AN	AN	AN	AN AN	NA	NA I	NA	AN	AN	AN	AN	AN	AN	NA I	yes I	NA	AN	AN	AN	AN	AN	AN	NA I	NA	NA (AN	NA	AN 6	AN
MAD_not_selection_CAM shifts	NA	AA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	NA	NA	AN	AN	AN	AN
Diff_expressed_CA C3	NA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	yes	NA	AN	NA	AN	AN
High_copy.Broc_An an_Tilla.	ou	ou	g	e.	e.	ou ou	ou	on D	0 L	e.	e	e	2	g	yes	e Q	QL	QL	e e	e.	e.	e e	e.	Q	ou	ou	ou	QU	Q	on	e e
Low_copy.Broc_Ana n_Tilla.	e	yes	yes	2	2	2	2	2	2	2	yes	2	yes	2	2	yes	2	2	2	2	2	yes	2	yes	e	yes	2	Q	yes	yes	e
A_oopy.Broc_A nan_Tilla.	yes	QL	2	yes	yes	yes	yes	yes	yes	yes	2	yes	2	yes	2	2	yes	yes	yes	yes	yes	e e	yes	2	yes	Q	yes	yes	ou	2	yes
emsnpez	-G03	.G03	.G03	.G03	.G07	.G07	.G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	-G07	.G10	.G10	.G10	.G10	.G10	.G10	-G10	-G10	-G10	.G10	.G10	.G10	.G10
әиәб	Aco010381 1	Aco010390 L	Aco010438 L	Aco010466 L	Aco010544 L	Aco010549 L	Aco010557 L	Aco010572 L	Aco010579 L	Aco010590 L	Aco010614 L	Aco010619 L	Aco010620 L	Aco010624 L	Aco010634 L	Aco010638 L	Aco010641 L	Aco010642 L	Aco010678 L	Aco010696 L	Ac0010710 L	Aco010716 1	Aco010721 L	Aco010725 1	Aco010731 1	Aco010740 L	Ac0010747 1	Aco010748 L	Ac0010756 L	Aco010770 1	Aco010774 1

əziz_noxə_nim	286	523	654	79	60	212	174	85	1133	225	71	395	583	58	50	109	647	191	86	157	230	114	617	605	59	125	629	805	965	277	1625
total_exonic_size	591	1142	1755	1839	2576	1049	673	1619	1133	1087	561	1790	1372	1069	1584	2801	1475	2098	3405	1025	975	283	1482	1690	2216	1761	629	1647	2037	1609	1625
ur_exons_per_gene	2	5	7	10	14	m	2	4	1	m	9	m	7	6	~	11	2	9	17	4	m	7	5	5	10	9	1	2	5	e	-
aziz_noxa_agerava	295.500	571.000	877.500	183.900	184.000	349.667	336.500	404.750	1133.000	362.333	93.500	596.667	686.000	118.778	226.286	254.636	737.500	349.667	200.294	256.250	325.000	141.500	741.000	845.000	221.600	293.500	629.000	823.500	1018.500	536.333	1625.000
çıbe	NA N	AN	AA	AV	10_Glucogenesis_specific_dayC3	32_Aquaporins	36_Drough_resistance_genes_LEA	AA	AV	32_Aquaporins	04_Oxygen_evolving_enhancer_O	AV	AA	AA	10_Glucogenesis_specific_dayC3	00_#W_CircadianOscillator_Pseud o-response_regulator7	AA	NA	30_#W_StomatalMovement_Phosp nolipase_C	AA	11_Glycolysis_night_C4_malate_p athway	36_Drough_resistance_genes_LEA	AV	AV	AN	AN	06_Drough_resistance_genes_LEA	AA	01d_Auxin_reponse_factor	AA	AN
circadian_clock																															
glucogenesis_glycol ysis					yes										yes						yes										
ogullufioq_ləz_zoq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
gyondrae_bionovalt 29_aimiao)19_nin	AA	A	A	A	A	A	A	A	A	AV	AV	A	AA	AA	AA	AV	A	AV	A	ALB_F_anthocyanidin synthase	A	A	A	A	A	A	A	AV	A	AA	A
ydrates ydrates ydrates		_						_			yes I						_														
circadian_metabolis m_Wai2017																/es			/es												
anthocyanin_SI_Ana asn																															
markers																															
draught_res							/es															/es					/es				
aquaporin_reg						/es				sə/																					
stomata_func																													/es		
related_Acomosus_ Ming2015																															
Angiosperm_gene	Ą	Ą	Å	3038	Å	Ą	Ą	5919	Ą	Ą	Ā	Å	Ą	5926	Ą	Å	Ā	Å	Å	Ą	Å	Å	Å	Å	Ą	Ą	Ą	Ā	Å	Ą	₹
MAD_2amilies_CAM C3	A A V	A A	A A	AA 6	A A	A A	A A	AN AN	A A	A	A A	A A	A A	A A	A A	A A	A A	A A	A A	A	A A	A A	A A	A A	A A	A A	A A	A A	A A	A A	A A
pos_selection_CAM 	NA I	A A	A A	A M	A M	A M	A M	A N	A M	A A	A A	A M	A A	4 A	A A	A A	A N	A A	A A	A A	A A	A A	A M	A A	A M	A M	A N	A A	A M	A A	A A
Diff_expressed_CA MC3	es 1	4 A	4 A	4 A	4 A	A A	A A	A P	A A	4 A	4 A	4 A	4 A	4	4 A	A A	A P	A A	4 A	4 A	4 A	4 A	4 A	4 A	es 1	A N	A P	A A	4 A	A A	4
high_copy.Broc_An an_Tilla.	ر د	Q	Q	Q	Q	Q	0	0	0	4 A	Q	Q	2 Q	Q	4 A	Q	0	Q	Q	'es	Q	Q	Q	Q	o V	0	0	0	Q	Q	2
Low_copy.Broc_Ana. n_Tilla.	/es	2	2	2	2	es r.	'es	Q	2	4	g	2	2	g	4	'es,	Q	Q	'es	ğ	2	,es	2	2	les r	2	2 Q	Q	2	Q	
Single_copy.Broc_A nan_Tilla.	or V	'es	'es	'es r	'es r	0 V	v v	'es r	'es r	4 A	'es	,es	'es	'es	4 A	٥ ک	'es r	'es	0 V	g	'es	Q	'es r	'es	ol V	'es	'es r	'es	'es r	'es	'es
edusme	G10 r.	G10 y	G10 y	G10 y	G10 y	G10 r.	G10 r.	G10 y	G10 y	G04	G04 y	G04 y	G04 y	G04	G04	G04	G04 y	G04 y	G04	G04	G04 V	G04	G04	G04	G04	G04 y	G04 y	G01 y	G01 y	G01 y	G01
ðeueß	Aco010779 L	Aco010780 L	Aco010787 L	Aco010792 L	Aco010811 L	Aco010816 L	Aco010827 L	Aco010835 L	Aco010847 L	Aco010977 L	Aco010980 L	Aco010982 L	Aco011000 L	Aco011010 L	Ac0011011 L	Aco011012 L	Aco011025 L	Aco011032 L	Aco011047 L	Aco011051 L	Aco011056 L	Aco011067 L	Aco011075 L	Aco011098 L	Aco011105 L	Aco011162 L	Aco011172 L	Aco011192 L	Aco011198 L	Ac0011204 L	Aco011238 L
9zi2_nox9_nim	57	246	276	981	50	1670	100	141	604	151	46	69	210	133	1760	241	249	56	68	77	49	48	5	62	221	247	344	59	70	112	74
--	-----------	-----------	-----------	-----------	-------------	-------------	--------------------------------	-----------	-----------	-----------	-----------	-------------	-----------	-------------	-----------	-------------	-----------	--------------------------	---	-------------	-------------	-----------	-----------	--------------------------------	--------------------------------	---	-----------	-------------	--------------------------------	-------------	--------------------------------
total_exonic_size	1410	1375	1313	2221	1276	1670	1512	1840	1444	1474	1252	1230	1101	1399	1760	2686	1264	3299	3613	1117	1254	2675	4787	1784	2067	1280	2218	1667	1667	1338	1832
	6	m	m	5	6	1	9	2	2	m	12	9	m	ى د	-	4	e	15	17	4	6	6	19	8	4	4	5	12	13	4	6
average_exon_size	156.667	458.333	437.667	1110.500	141.778	1670.000	252.000	368.000	722.000	491.333	104.333	205.000	367.000	279.800	1760.000	671.500	421.333	219.933	212.529	279.250	139.333	297.222	251.947	223.000	516.750	320.000	1109.000	138.917	128.231	334.500	203.556
edĄ	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	01d_Auxin_reponse_factor	NA	03_VATPase	NA	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	NA	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3
circadian_clock																															
glucogenesis_glycol ysis							yes																	yes	yes	yes			yes		yes
oßniintrod_les_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Solanum tuberosum protein HUA ENHANCER 2-like (LOC102587942)_ transcript variant X3_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
filovonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Asimilation_Carboh Assimilation_Carboh ydrates																				yes											
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana san																															
markers draught_res																															
aquaporin_reg																															
stomata_func																		es													
related_Acomosus_																															
eue0_meqsoibnA	961	A	۲	AL AL	679	AL AL	A	A	AL AL	A	791	034	A	A.	A.	AL AL	A	A	4	A	404	A	A	A	A	4	A	406	A1	Ą	۲
MAD_sailims1_eneg C3	AA 6	AN	AN	AN	AA 6	AN	A A	AN	AN	A	A A	AA AA	AA	A	A	AA	AN	AN	AN	Z A	NA 6	AN	AA N	A A V	A A	AA	AN	AA 6	AN	A A	A
pos_selection_CAM shifts	AN	AN AN	AN	AN	AN	ves h	AN	AN	AN	AN	AN N	AN	AN	AN	AN	AN	A P	AN	AN	AN	AN	AN	ves h	NA P	AN	AN AN	AN	AN	AN	AN	AN
Diff_expressed_CA C3	- AV	- AN	A A	l sə/	NA I	AA V	I AN	/es	- AN	A A	A A	A A	- AN	- AN	- AN	- AN	I AN	I AN	- AN	/es	NA I	l sə	NA J	NA I	A A	- AN	NA N	NA I	NA I	- 47	Ā
High_copy.Broc_An an_Tilla.	م م	0	Q	ŏ	0	0	01	ر د	0	2	2	2	2	2	2	0	2 01	'es	Q	v v	0	v of	es h	0	0	2	Q	0	0	1 01	2
Low_copy.Broc_Ana n_Tilla.	p L	6	2	/es r	6	/es r	/es r	6	2	2	2	2	2	2	2	2	2 Q	02	les L	2	ę.	/es r	0	/es r	2	2	2	6	/es r	ę	/es
Single_copy.Broc_A nan_Tilla.	/es r	/es	'es	2 Q	'es	02	0	'es r	'es r	'es	'es	'es	'es	'es	'es	'es r	'es r	6	Q Q	/es	/es r	of V	0,	OL OL	/es	'es r	/es	'es	Q	/es r	
emsnpez	G01 y	G01 y	G01 V	301 r	G01 V	301 r	301 r	301 y	301 y	301 y	301 y	G01 V	G01 V	301 V	301 y	301 y	306 y	306 r	306	306 V	306 V	306 r	306 r	306 r	306 y	306 V	306 V	306 V	306	G08 V	308
gene	Aco011239	Aco011246	Aco011261	Aco011262	Aco011283 L	Aco011299 L	Aco011300 L	Aco011306	Aco011332	Aco011338	Aco011346	Aco011349 L	Aco011352	Aco011371 L	Aco011378	Aco011401 L	Aco011462	Aco011464 L	Ac0011466	Aco011496 L	Ac0011515 L	Aco011516	Ac0011527	Ac0011528	Aco011530	Aco011531	Aco011560	Aco011590 L	Aco011609	Ac0011644 L	Aco011651 L

əziz_noxə_nim	1868	208	27	190	367	21	625	51	77	63	2186	55	55	60	189	194	161	56	259	61	200	120	166	31	39	558	425	84	112	213
etal_exonic_size	1868	1391	1209	666	1578	2442	2166	1073	1167	1447	2186	2190	1161	3009	1432	1719	3675	3852	1253	2321	1108	3723	1416	3737	1754	1330	2340	2202	1397	026
ang_per_gene	1	en e	9	en la	en la	6	2	9	5	6	1	15	4	12	2	4	9	16	e	7	e	9	2	23	11	2	e	2	2	2
average_exon_size	1868.000	463.667	201.500	333.000	526.000	271.333	1083.000	178.833	233.400	160.778	2186.000	146.000	290.250	250.750	286.400	429.750	612.500	240.750	417.667	331.571	369.333	620.500	283.200	162.478	159.455	665.000	780.000	440.400	199.571	485.000
əd⁄u	AN N	AN	AV	32_Aquaporins	A	11_Glycolysis_night_C4_malate_p athway	AN	AV	NA	11_Glycolysis_night_C4_malate_p athway	AN	NA	AN	AN	AN	AN	AN	01d_Auxin_reponse_factor	AN	00_#W_CircadianOscillator_Reveill e1	AV	00_#W_HexoseTransporter_MSSP -like_transporter	AA	AA	AN	AA	AN	06_Drough_resistance_genes_LEA	NA	06_Drough_resistance_genes_LEA
circadian_clock					_							_	-								-							0	-	
glucogenesis_glycol sisy						yes				yes																				
ogulluhoq_ləs_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Vitis vinifera putative tRNA pseudouridine synthase Pus10 (LOC100242087)_ transcript variant X1_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max protein argonaute 1- like (LOC100778754)_mRNA	NA	NA	NA	NA	NA	NA
ມາເມີ່ອງເຮັ້ອງ ເຊື່ອງ ເຊື່ອ	NA	NA	NA	NA	ALB_L_malonyl-coenzyme a: anthocyanin 3-o-glucoside-6 -o- malonyltransferase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																														
circadian_metabolis m_Wai2017																				yes		yes								
anthocyanin_SI_Ana antocyanin_SI_Ana																														
markers																														
qraught_res																												es		es
aquaporin_reg				yes																										
stomata_func																		es												
related_Acomosus_ Ming2015																		>												
CAM-								35	8																					
Angiosperm_gene	MA	¥	A A	A A	NA	AN N	NA	675	63(AN N	AN N	NA	MA	MA M	AN N	M	¥	M	AN	AN 1	AA	MA	A	MA	¥	MA	¥.	NA	M	AA
 MAD zailims1 gene	٩N	٩Z	Z	Z	Ž	Z	٩N	Z	Z	Z	٩Z	_N N	٩Z	٩Z	٩Z	٩Z	Z	⊿ Z	٩N	AN	AN	٩Z	٩Z	٩Z	٩Z	٩N	٩Z	٩N	٩Z	٩Z
MC3 MAD_nction_CAM	ΡN	ZA	A N	A N	AN N	Z	ΡN	A Z	A Z	A N	A N	AN N	ΡN	Ϋ́	Ϋ́	Z	yes	yes	ΝA	AN	AN	AN	A N	A N	AN	AN	AN	ΝA	ΥN	ΔA
AD_besserged_CA	ΡN	٩N	yes	۲ ۲	A N	٩Z	ΥN	٩ _Z	۲ ۲	۲ ۲	AN	AN NA	yes	yes	yes	٩Z	ΥN	AN	ΝA	AN	AN	AN	AN	ΥN	yes	ΥN	ΥN	ΝA	ΥN	AN
High_copy.Broc_An	0L	6	A N	٩N	NA	2	8	2	2	2	2	ou	8	yes	٩N	0L	e e	yes	ou	Q	2	Q	2	yes	e e	е С	0L	ou	0L	0
Low_copy.Broc_Ana	2	2	A	¥	¥	2	9	2	2	2	2	2	yes	2	¥	2	2	2	2	2	2	yes	2	2	yes	2	2	yes	2	yes
A_oony.Broc_A Single_copy.Broc_A	yes	yes	AN	AN	AN	yes	yes	yes	yes	yes	yes	yes	2	2	٩N	yes	yes	2	yes	yes	yes	e	yes	e	2	yes	yes	QL	yes	2
emanpes	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03
деле	Aco011671	Aco011681	Aco011700	Aco011705	Aco011709	Aco011710	Aco011720	Aco011724	Aco011740	Aco011789	Aco011792	Aco011813	Aco011817	Aco011837	Aco011838	Aco011860	Aco011881	Aco011886	Aco011896	Aco011903	Aco011912	Aco011916	Aco011917	Aco011930	Aco011960	Aco011969	Aco011974	Aco011976	Aco011977	Aco011978

	_											_			_																
əziz_noxə_nim	66	617	140	159	65	217	1055	1322	20	8	9	139	190	56	116	31	71	119	23	149	138	957	76	438	89	133	76	1370	6	94	144
eziz_oinoxe_lstot	1989	617	1445	1644	2376	3040	2304	1322	1901	732	727	3107	2210	3988	2418	5374	409	1663	1960	1902	1246	2008	1407	3280	594	2301	3050	1370	1093	2085	1779
ur_exons_per_gene	8		4	4	4	20	2	1	13	m l	9		20	15	~	16	4	4	11	2 C	4	2	~	^m	4	4	8	1	8	10	4
average_exon_size	248.625	617.000	361.250	411.000	594.000	608.000	1152.000	1322.000	146.231	244.000	121.167	443.857	442.000	265.867	302.250	335.875	102.250	415.750	178.182	380.400	311.500	1004.000	201.000	1093.333	148.500	575.250	381.250	1370.000	136.625	208.500	444.750
jdbe	AA	06_Drough_resistance_genes_LEA	02_Aquaporins	AA	10_Glucogenesis_specific_dayC3	AA	AA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	AA	AV	AV	01d_Auxin_reponse_factor	AV	00_#MB_XDH	10_Glucogenesis_specific_dayC3	AV	A	AA	AA	AA	AV	AA	AA	AA	10_Glucogenesis_specific_dayC3	AA	L0_Glucogenesis_specific_dayC3	L0_Glucogenesis_specific_dayC3	AA
circadian_clock																															
glucogenesis_glycol ysis_					yes			yes	yes								yes										yes		yes	yes	
oßnijnµod"jəs ⁻ sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max protein argonaute 1- like (LOC100778754)_mRNA	NA	NA	NA	NA	NA	NA	NA
tites on the subject of the subject	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																															
circadian_metabolis m_Wai2017																															
anthocyanin_I2_ninsyoothna san																															
markers																/es															
qraught_res		yes								yes																					
aquaporin_reg			yes																												
stomata_func														/es																	
related_Acomosus_ Ming2015																															
CAM-					_			_	_		49							_	8	_			59		67	_		_		_	
Angiosperm_gene	۹ N	⊿N	⊿	۹N م	۸ ۸	AN A	AN A	۸ N	۹ N	⊿ N	A 66	۲ ۲	⊿ V	⊿	۲ ۲	۲ ۲	۹ N	۸ ۸	A 52	√Z ∀	⊿N N	۸ ۸	A 65	AN NA	A 73	۸ N	⊿N A	⊿N P	A NA	۸	Z ⊲
stiids_	² ∢	z ∢	z v	N Si	z ∡	z v	z v	z ∡	z ∡	z v	Z ∢	Ż ∢	z v	z v	2 ∢	2 ∢	z v	z ∡	z ∡	² ∢	z ∢	z ∢	z v	2 V	ν ν	² ∢	2 V	2 V	2 V	N Si	_2` ∢
MC3 WC3	z	Ż	Ż	λe	Ż	z	ż	ż	ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	ż	Ż	ż	Ż	Ż	Ż	Ż	ż	Ż	Ż	ż	Ż	У€	Ż
an_Tilla. Diff_expressed_CA	s yes	AN NA	AA	NA	NA	yes	AN	AN	NA	NA	A N	A N	NA	S NA	AN	NA	AN	AN	NA	ΝA	NA	NA	NA	S NA	ΝA	NA	ΝA	AN	AN	ΥN	AN
high_copy.Broc_An	ye	ou "	ou "	ou	ou ș	s no	ou	ou ș	ou ș	0L	ou "	0L	0L	ye	ou	ou "	s no	ou	ou	ou	ou	ou	0L	ye	ou	ou	ou ș	ou	s no	on "	ou
Low_copy.Broc_Ana	2	yee	yes	2	ye	yes	6	ye	ye	2	yet	2	2	2	2	yes	ye	2	2	2	2	2	2	2	01	2	yet	2	ye	ye	2
Single_copy.Broc_A	2	2	2	yes	2	2	yes	6	2	yes	2	yes	yes	2	yes	2	2	yes	yes	yes	yes	yes	yes	2	yes	yes	8	yes	2	2	yes
edname	LG03	LG03	LG03	LG03	LG03	LG03	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG02	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01
0eue	Aco011994	Aco012009	Aco012014	Aco012041	Aco012049	Aco012057	Aco012085	Aco012095	Aco012114	Aco012160	Aco012179	Aco012217	Aco012218	Aco012234	Aco012256	Aco012270	Aco012284	Aco012292	Aco012294	Aco012308	Aco012311	Aco012319	Aco012352	Aco012380	Aco012389	Aco012398	Aco012400	Aco012404	Aco012412	Aco012435	Aco012441

	4	8		0	ы	0	9	N	4	ß	6	N	ß	4	6	4		0	ß	<u>∞</u>	6		-	0	H	L H	N	6	0	œ	-
əzis_noxə_nim	48	39	5	33(ŭ	5(12(162	151	615	8	5	13		16	36	193	1229	6	8		25	265:	6	4	13.	202	13	18:	108	26:
ezia_oinoxe_lstot	2095	3086	1328	1271	1987	1055	2031	1354	1514	3593	840	631	1268	892	1745	1157	1937	1229	2430	3420	2283	1790	2651	2137	2319	1755	2020	1378	1000	1088	2287
nr_exons_per_gene		11		0			9	Ű					L				1	1		17	1				12		4				
average_exon_size	698.333	181.529	221.333	423.667	283.857	175.833	338.500	225.667	1514.000	1197.667	210.000	315.500	253.600	446.000	290.833	578.500	1937.000	1229.000	303.750	201.176	175.615	596.667	2651.000	267.125	193.250	292.500	505.000	689.000	333.333	1088.000	762.333
jAbe	A	A	A	.1_Glycolysis_night_C4_malate_p	.0_Glucogenesis_specific_dayC3	A	A	.0_Glucogenesis_specific_dayC3	A	A	A	06_Drough_resistance_genes_LEA	A	06_Drough_resistance_genes_LEA	A	A	A	A	A	A	AA	AA	A	A	.0_Glucogenesis_specific_dayC3	A	A	A	.0_Glucogenesis_specific_dayC3	A	AA
		2	2	0 1	-	2	2	-			2	0	2		2	2	~	2	2	2	2		2	~	-	2	2	2	-	~	2
circadian_clock																															
glucogenesis_glycol				yes	yes			yes																	yes				yes		
oßnijnuod" jəs" sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max uridine-cytidine kinase C-like (LOC100781286)_mRNA	NA	NA	PREDICTED: Solanum tuberosum ATPase family AAA domain-containing protein 3C (LOC102578202) _ MRNA	NA	NA	NA	NA	NA	NA	NA
gyantine_bionovalit 29_aimiasurg_nin	٨	٨	A	LB_F_leucoanthocyanidin ioxygenase	A	A	A	A	Α	٨	LB_F_chalcone isomerase	٩	Δ	A	Α	Α	Α	Α	A	Δ	A	LB_L_flavonoid glucosyl- ansferase	A	A	LB_F_isoflavone reductase	A	٩	A	A	A	A
Assimilation_Carbon ydrates	2	2	2	40	2	2	2	2	2	2	4	2	2	2	2			2		2		4.5	2	2	4	2	2	2	2	2	2
circadian_metabolis m_Wai2017 malateTransferase_																															
antrocyanin_Si_Ana																															
markers																															
qraught_res												yes		yes																	
aquaporin_reg																															
stomata_func																															
CAM- related_Acomosus_ Ming2015																															
Angiosperm_gene	AN	Ą	A	AA	AN	5894	AA	AN	AA	AA	AA	Ą	AN	AA	AA	AA	AA	AA	AA	6544	A	A	A	NA	AN	6139	AN	AN	AA	6387	AA
MAD_families_CAM C3 C3	ΝA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	AN	AN	AN	AN
pos_selection_CAM 	٨A	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
Diff_expressed_CA MC3	٩N	٩N	/es	٩N	AN	٩N	٩N	٩N	٩N	٩N	AN	٩N	٩N	٩N	٩N	٩N	٩N	٩N	/es	٩Ņ	٩v	٩Ņ	AN	AN	٩N	AN	٩N	AN	٩N	٩N	٩V
High_copy.Broc_An an_Tilla.	ou	ou	ou	yes	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	AN	ou	ou
Low_copy.Broc_Ana n_Tilla.	e	yes	2	2	yes	2	9	2	2	2	2	2	2	2	2	2	2	Q	2	yes	2	yes	2	yes	yes	2	2	2	AA	2	6
Single_copy.Broc_A nan_Tilla.	/es	Q	'es	g	Q	/es	/es	/es	/es	/es	/es	/es	'es	/es	'es	/es	/es	'es	'es	ę	'es	g	'es	ę	Q	/es	/es	/es	Ą	/es	'es
əmanpəz	LG13 y	LG13 r	LG13 y	LG13 r	LG13 r	LG13 y	LG13 y	LG13 y	LG13 y	LG13 y	LG13 y	LG13 y	LG13 y	LG13 y	LG13 y	LG05 r	LG05 y	LG05 r	LG05 y	LG05 r	LG05 r	LG05 y	LG05 y	LG05 y	LG05	LG03 y	LG03 y				
әиәɓ	Aco012460	Aco012463	Aco012466	Aco012471	Aco012481	Aco012483	Aco012488	Aco012491	Aco012511	Aco012530	Aco012547	Aco012577	Aco012622	Aco012641	Aco012644	Aco012651	Aco012700	Aco012704	Aco012715	Aco012740	Aco012743	Aco012745	Aco012760	Aco012767	Aco012772	Aco012775	Aco012776	Aco012793	Aco012797	Aco012808	Aco012817

sziz_noxs_nim	222	133	57	182	44	59	127	329	50	55	56	85	31	1838	1103	63	71	753	60	62	197	1505	L340	442	389	33	1148	69	302	422	60
	044	392	901	279	230	158	533	329	133	322	125	508	132	338	103	869	781	555	265	026	976	505 1	340 1	142	375	270	550 1	200	441	940	503
total_exonic_size	10	18	0,	52	52	21	15		4	18	8	26	35	18	11	16	27	11	52	0,	16	11	13	14	11	12	26	16	14	10	16
ur_exons_per_gene	ŝ	8	9	5	9	14	9	1	30	11	14	10	22	1	1	10	5	2	8	9	m	1	1	1	2	11	2	8	e	e	6
average_exon_size	348.000	236.500	150.167	455.800	371.667	154.143	255.500	329.000	147.767	165.636	244.643	250.800	156.000	1838.000	1103.000	169.800	556.200	777.500	283.125	161.667	658.667	1505.000	1340.000	1442.000	687.500	115.455	1325.000	200.000	480.333	646.667	178.111
ədily	02_Aquaporins	NA	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	AN	10_Glucogenesis_specific_dayC3	01d_Auxin_reponse_factor	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
circadian_clock													_							_	_	_									
glucogenesis_glycol ysis_					yes	yes	yes			yes		yes																			
oßniiutroq_ləs_soq	NA	Glycine max seed maturation protein PM37 (PM37)_mRNA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max cullin-associated NEDD8-dissociated protein 1 (LOC100816200) mRNA	NA	NA	NA	PREDICTED: Glycine max protein argonaute 1- like (LOC100778754)_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
filevonoid_anthocya	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
malateTransferase_ Assimilation_Carboh vdrates																															
circadian_metabolis T102iaW_m																															
anthocyanin_SI_Ana asn																															1
markers																															1
draught_res								yes																							1
aquaporin_reg	yes																														1
stomata_func											yes																				1
CAM- related_Acomosus_ Ming2015																															
aua6_uuadsoi6uv	۲Þ	A1	536	A	Ą	A.	۲	Ą	٩ĭ	A1	A1	٩	۲	A,	A1	702	A	A1	A.	848	۲	۲	۲A	A1	A1	Ą	A1	096	٩	Ą	123
gene_families_CAM C3	A A	Z A	4 P	A A	A A	Z A	A A	A A	A A	Z A	A A	A N	A A	A A	Z A	4 P	Z A	Z A	4	AA 6	A A	A A	A A	Z A	Z A	A A	A A	AA 5	Z A	Z A	4
pos_selection_CAM _shifts_	A A	4 A	4 A	4 A	4 A	A	4 A	A P	A A	4 A	A A	AA P	4 A P	A A	4 A	4 A	4 A	4 A	4 A	4 A	A A	4 A	AA P	4 A	4 A	4 A	4 A	A P	A A	4 A	4
Diff_expressed_CA MC3	I AN	A A	4 A	A N	A A	A A	A I	A I	4	A A	A N	I VI	I AV	A I	A A	A A	es	A A	es 1	A N	A I	A N	I AN	A A	A A	es 1	A A	I AN	A A	A A	4 F
High_copy.Broc_An an_Tilla.	A N	2	2	2	2	0	es 1	A L		2	es 7	es 1	es 1	0	2	2	c c	2	es y	2	0	2	2	2	2	6	2	2	2	2	-
Low_copy.Broc_Ana n_Tilla.	4 A	ies II	g	<u>_</u>	es n	'es	0	Ā	res n	0	0	io y	0	<u> </u>	0	0	es n	9	p Q	0	9	0	0	0	9	g	<u>_</u>	9	9	9	
A_oopy.Broc_A nan_Tilla.	A N	0	es u	es u	0	0	0	A N	0	es	0	0	0	es	es	es	0	es	0	es n	es	es n	es	es	es	es n	es	es	es	es	es L
emsnpes	303 N	303 n	303 y	303 y	303 n	303 y	325 n	325 n	325 n	325 y	325 y	325 y	325 n	325 y	325 n	325 y	325 y	325 y	325 y	325 y	325 y	325 y	325 y	325 y	325 y	325 y	324 y				
21/26	2825 LG	2837 LG	2850 LG	2862 LG	2869 LG	2915 LG	2924 LG	2927 LG	2941 LG	2946 LG	2988 LG	2992 LG	3001 LG	3003 LG	3014 LG	3015 LG	3023 LG	3026 LG	3034 LG	3037 LG	3038 LG	3074 LG	3080 LG	3083 LG	3096 LG	3100 LG	3121 LG	3126 LG	3128 LG	3134 LC	3158 LG
6090	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01	Aco01.	Aco01	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.	Aco01.

əziz_noxə_nim	86	44	197	26	29	402	2792	175	734	186	104	275	13	61	114	77	111	1916	149	100	51	128	76	140	192	241	119	37	35	541
total_exonic_size	613	2150	197	866	3312	1325	2792	2347	734	2158	3994	1675	1398	1410	1750	318	2345	1916	1114	591	3437	2837	2731	1066	2440	1532	1634	1473	2642	2916
	e	19	-	4	12	2	1	ъ	-	m	15	m	6	5	2	m	8	-	m	m	11	4	7	ъ	m	e	4	11	24	<i>т</i>
average_exon_size	204.333	113.158	197.000	249.500	276.000	662.500	2792.000	469.400	734.000	719.333	266.267	558.333	155.333	282.000	350.000	106.000	293.125	1916.000	371.333	197.000	312.455	709.250	390.143	213.200	813.333	510.667	408.500	133.909	110.083	972.000
ədáj	NA	11_Glycolysis_night_C4_malate_p athway	06_Drough_resistance_genes_LEA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	01d_Auxin_reponse_factor	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	02_Aquaporins	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	00_#W_StomatalMovement_Histidi ne_Kinase_HK5	NA	00_#W_StomatalMovement_Respo nseRegulator2	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA
circadian_clock																														
glucogenesis_glycol ysis_		yes		yes						yes			yes							yes								yes		
ogulluhoq_ləs_soq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Solanum tuberosum protein HUA ENHANCER 2-like (LOC102587942) transcript variant X3_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max histidine kinase 2- like (LOC100781655)_ transcript variant X3_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA
stronovalt S9_aimia319_nin	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_leucoanthocyanidin reductase	NA	NA	NA	NA	NA	NA
Asimilation_Carboh Vdrates Vdrates																														
circadian_metabolis m_Wai2017																					yes		yes							
anthocyanin_SI_Ana asn																														
markers																														
qraught_res			yes																											
aquaporin_reg														yes																
stomata_func									yes																					
related_Acomosus_ Ming2015																														
Angiosperm_gene	A	A	¥	A	A	A	AM	A	A	A	AA	AM	AA	Ā	¥	A	A	¥	¥	Ą	AM	A	A	A	Ā	A	A	A	5454	¥
gene_families_CAM C3	AN	AN	AN	AN	A	AN	AN	AN	AN	AN N	AN	AN	AN	AN	AN N	AN	AN	¥.	A N	AN	AN	A	A	AN	AN	AN	AN	AN	AN N	A
MAD_not_selection_CAM 	AN	AN	AN	AN	yes	AN	yes	AN	AN	AN	NA	NA	AN	NA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
Diff_expressed_CA MC3	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	NA	AN	NA	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN
nA_ooy.Broc_An an_Tilla.	ou	ou ou	AN	AN N	e e	ou	ou	QL	AN	2	ou	Q	ou	ou	ou	e e	e e	2	e e	AN	yes	e e	02	ou ou	ou	ou	ou	ou ou	ou ou	e
Low_copy.Broc_Ana n_Tilla.	yes	yes	AA	AN	yes	2	8	2	AN	yes	yes	Q	yes	yes	Q	yes	2	6	2	AA	e	2	yes	2	9	2	2	yes	yes	8
Single_copy.Broc_A nan_Tilla.	2	2	AN	AN	2	yes	yes	yes	AN	2	02	yes	2	e	yes	2	yes	yes	yes	AN	2	yes	2	yes	yes	yes	yes	2	2	yes
emanpes	G24	G24	G24	G24	G24	G24	G24	G24	G24	G24	.G24	G24	G24	G24	G24	G24	G15	G15	G15	G15	G15	G15	G15	G15	G15	G20	G20	G20	G20	G20
әиәб	Aco013178 L	Aco013202 L	Aco013204 L	Aco013205 L	Aco013210 L	Aco013213 L	Aco013214 L	Aco013224 L	Aco013227 L	Aco013253 L	Ac0013267 L	Aco013270 L	Aco013283 L	Aco013293 L	Aco013305 L	Aco013309 L	Aco013351 L	Aco013353 L	Aco013355 L	Aco013390 L	Ac0013412 L	Aco013414 L	Aco013421 L	Aco013473 L	Aco013474 L	Aco013489 L	Aco013510 L	Aco013517 L	Aco013524 L	Aco013533 L

9zi2_nox9_nim	871	59	303	41	56	68	224	263	55	290	236	48	41	247	1514	93	81	388	623	771	2141	219	254	24	103	30	45	135	101
esia_pinoxe_latot	2844	1190	1616	849	1730	1552	1253	1311	1354	3899	2284	3028	2198	2046	1514	1765	3693	1569	1747	1882	2141	1189	1393	1209	1221	1170	1383	2307	3853
nr_exons_per_gene	3	9	4	9	10	10	3	2	14	4	2	10	11	e	1	e	14	e	2	2	Т	e	2	11	9	e	10	8	6
average_exon_size	948.000	198.333	404.000	141.500	173.000	155.200	417.667	655.500	96.714	974.750	1142.000	302.800	199.818	682.000	1514.000	588.333	263.786	523.000	873.500	941.000	2141.000	396.333	696.500	109.909	203.500	390.000	138.300	288.375	428.111
ədAj	NA	NA	AN	10_Glucogenesis_specific_dayC3	NA	11_Glycolysis_night_C4_malate_p athway	02_Aquaporins	AN	10_Glucogenesis_specific_dayC3	00_#MB_PhyA	AN	00_#W_CircadianOscillator_TF_PI F3	AA	AN	AN	AN	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	AN	AN	AN	AN	10_Glucogenesis_specific_dayC3	NA	NA	NA
circadian_clock																													
glucogenesis_glycol ysis				yes		yes			yes									yes	yes	yes						yes			
oິກາແກກດູ ໂອະ_soq	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris glucose-1-phosphate adenylytransferase large subunit 3_chloroplastic/amyloplastic (LO-104883901)_transcript variant X1_ (LO-104883901)_transcript variant X1_	NA	NA	NA	PREDICTED: Solanum tuberosum guanine nucleotide-binding protein-like NSN1 (LOC102593978) mRNA	NA	NA	NA	PREDICTED: Glycine max nuclear export mediator factor NEMF-like (LOC100803745)_ transcript variant X3_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Oryza sativa Japonica Group homeobox-leucine zipper protein ROC7 (LOC4344614) mRNA
tilavonoid_anthocya filavonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																													
circadian_metabolis m_Wai2017												/es																	
anthocyanin_Si_Ana nas																													
markers										es																			
draught_res										~																			
aquaporin_reg							es																				-		
stomata_func							ž																						
related_Acomosus_ Ming2015																													
CAM-		90											36			35								86	57				
Angiosperm_gene C3	NA	48(AN N	MA	AN Y	M	AN .	AN Y	AN NA	AN Y	MA	AN	600	MA	MA	62	AN N	AN N	AN N	MA	AN A	AN N	MA	61	475	MA	AN Y	¥	AN N
_shirta MAD seilims1_eneg	NA	NA	NA	NA	NA	NA	NA 1	NA	NA N	NA	NA.	NA NA	NA	S NA	NA.	NA.	S NA	NA	NA	NA	NA	NA	NA.	NA.	NA.	NA	NA	N	NA
Pos_selection_CAM	NA	NA	NA	NA	, NA	NA	NA	NA	NA N	NA	NA	NA	AN	ye	NA	NA	ye	NA	NA	NA	NA	NA	NA	NA	AN	NA	"NA	AN NA	NA
an_Tilla. Diff_expressed_CA	ΑN	٩N	٩N	AN	yes	ΔN	ΝA	AN	AN NA	ΝA	AN	AN	AN	AN NA	AN NA	AN	NA	A N	٩N	AN NA	٩N	AN	NA	AN	AN	ΝA	yes	A N	A Z
n_Tilla. High_copy.Broc_An	ou	ou	оц Ц	NA	on D	e u	ou	Q	о С	on D	ou	ou	ou	ou	ou	Q	оц	e u	e	Q	0L	0L	ou	Q	ou	ou	e e	e 2	yes
nan_Tilla. Low_copy.Broc_Ana	8	2	8	AA	yes	yes	92	2	yes	yes	2	6	yes	yes	2	2	2	yes	yes	yes	2	8	2	2	yes	8	yes	2	2
A_oopy.Broc_A) yes) yes) yes	NA (ou C	ou	3 yes	} yes	е ~	on ~	} yes	} yes	ou ~	9 ~	} yes	} yes	} yes	е ~	0 ~	e ~	3 yes	} yes	} yes	} yes	е ~	} yes	ou t	t yes	ou t
emanes	LG20	LG20	LG20	LG20	LG20	LG20	LG13	LG13	LG15	LG13	LG15	LG13	LG13	LG15	LG15	LG13	LG13	LG15	LG15	LG15	LG13	LG15	LG15	LG13	LG13	LG13	LG24	LG24	LG24
gene	Aco013536	Aco013538	Aco013550	Aco013584	Aco013587	Aco013594	Aco013623	Aco013628	Aco013633	Aco013637	Aco013642	Aco013643	Aco013654	Aco013659	Aco013678	Aco013680	Aco013682	Aco013691	Aco013692	Aco013695	Aco013717	Aco013718	Aco013719	Aco013720	Aco013735	Aco013744	Aco013769	Aco013776	Aco013825

əziz_noxə_nim	45	48	178	111	367	78	45	140	101	239	446	45	61	495	179	446	116	17	44	65	224	260	243	204	791	272	1622	127	158	1601	736
etal_exonic_size	2262	1627	1373	1537	1302	2925	4018	1299	1684	1800	2065	1388	1801	2020	1602	1947	2401	5217	3228	445	2857	598	1234	1473	2707	272	1622	1096	1076	1601	2662
ut_exons_per_gene	2	10	9	~	e	2	21	4	9	4		4	6	e co	ß	e	10	16	18	2	2	2	°	4	2			LC L	4	1	2
average_exon_size	452.400	162.700	228.833	219.571	434.000	585.000	191.333	324.750	280.667	450.000	1032.500	347.000	200.111	673.333	320.400	649.000	240.100	326.063	179.333	222.500	408.143	299.000	411.333	368.250	1353.500	272.000	1622.000	219.200	269.000	1601.000	1331.000
ədify	NA	NA	NA	00_##19_Malate_dehydrogenase	00_##14_Phosphoenolpyruvate_ca rboxylase_kinase	01d_Auxin_reponse_factor	NA	02_Aquaporins	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	04_Oxygen_evolving_enhancer_O EE	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	AM	03_VATPase	10_Glucogenesis_specific_dayC3	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	00_#Ming2019_Anthocyanin_biosy nthesis	NA	NA
circadian_clock	-		-																				-								-
ysis ysis																															
oິກາແກ່ງດີ ເອຣີ sod	NA	MA MA	NA	Beta vulgaris subsp. vulgaris malate dehydrogenase_cytoplasmic (LOC104887939) mRNA	AA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Solanum tuberosum heat shock cognate protein 80-like (LOC102600008)_ mRNA	NA	NA yes	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
ydrates flavonoid_anthocya Picaimia_PS nin_Picaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_anthocyanidin synthase	NA	NA	NA	NA	NA	NA	NA	ALB_L_chalcone isomerase	NA	NA
												yes							yes												
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana nas																													yes		
markers																															
draught_res																						sə,				'es					
aquaporin_reg								es																							
stomata_func						es																									
related_Acomosus_ Ming2015				Sé	Sé	<u>خ</u>																									
-MAD		96	_	×	×	_	36	_		-	-	-	_	_	-	-	-		_	_	_	_					_	20			_
Angiosperm_gene C3	-NA	1 64	NA N	N N N N N N N N N N N N N N N N N N N	MN V	NA	1 29	_N 	_N 	_N 	NA N	N N	MM	MN V	N⊿	N⊿	_N N	vN √	_N N	MN V	_N 	_N 	-NP	VN	-NA	vN √	vN √	65	v⊿N V	JN V	AN NA
shifta MAD alilies CAM	٩N	⊿N N	N N	N N	NA	NA	NA N	N	N	NA *	NA N	N N	N⊿ N	N	NA	NA	N	Ň	NA	NA	N	N	⊿N	v Z	٩N	N⊿ N	N⊿ N	N	NA	v⊿ N	√N ,
Pos_selection_CAM	ΨN	ΔN	AN	N N N	NA	ΔN	A N	NA	A N	yes	NA NA	A N	NA	NA	AN	AN	A N	AN NA	A N	AN	AN	NA	٩N	٩N	ΑN	NA	NA	NA	AN	ΔN	ΑN
AD_iff_expressed_CA	yes	ΨN	ΝA	A N	AN	ΝA	ΥN	AN	AN	AN	yes	A N	yes	AN	AN	AN	ΥN	NA	ΥN	AN	AN	AN	٩N	٩N	ΝA	AN	AN	AN	AN	AN	AN
High_copy.Broc_An	0L	0L	2	2	٩N	6	0L	2	2	2	yes	2	2	Q	Q	Q	6	yes	0L	٩N	Q	0L	2	2	0L	e e	0L	6	ou	8	ou
Low_copy.Broc_Ana	yes	e	e	yes	A	yes	yes	yes	2	yes	2	2	2	2	2	2	2	2	yes	AA	yes	2	e	2	e	2	2	2	2	9	9
A_ooy.Broc_A elliT_nen	6	yes	yes	2	AN	6	ę	2	yes	2	2	yes	yes	yes	yes	yes	yes	2	ę	AN	2	yes	yes	yes	yes	yes	yes	yes	yes	yes	yes
əmsnpəz	LG08	LG08	LG08	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG13	LG13	LG13	LG13	LG13	LG13	LG05
әиәб	Aco013826	Aco013898	Aco013901	Aco013935	Aco013938	Aco013950	Aco013951	Aco013954	Aco013958	Aco013959	Aco013965	Aco013974	Aco013975	Aco013992	Aco014001	Aco014023	Aco014027	Aco014051	Aco014055	Aco014058	Aco014061	Aco014063	Aco014077	Aco014086	Ac0014118	Aco014120	Aco014214	Aco014228	Aco014232	Aco014241	Aco014257

9zi2_nox9_nim	94	161	256	1669	647	1457	210	1883	77	3179	50	38	54	589	355	235	72	1619	68	135	48	117	98	1259	376	445	251	71	98	142	41
9zi2_oinox9_l6101	1054	2530	1403	4055	1581	1457	1436	1883	888	3179	8159	1473	4156	1492	1602	942	2005	1619	1527	1730	1636	2746	750	1259	2883	1448	1161	984	2048	1686	844
ut_exons_per_gene	5	ю	4	5	5	1	4	1	4		26	6	15	2	e	2	10	1	9	4	13	ß	e	1	4	e	en co	4	6	4	4
average_exon_size	210.800	843.333	350.750	2027.500	790.500	1457.000	359.000	1883.000	222.000	3179.000	313.808	163.667	277.067	746.000	534.000	471.000	200.500	1619.000	254.500	432.500	125.846	549.200	250.000	1259.000	720.750	482.667	387.000	246.000	227.556	421.500	211.000
ədAj	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	NA	03_VATPase	NA	NA	11_Glycolysis_night_C4_malate_p athway	00_#W_CircadianOscillator_GIGA NTEA_09_Circadian_clock	00_#W_StomatalMovement_Synta xin_plant_121	NA	06_Drough_resistance_genes_LEA	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	04_Oxygen_evolving_enhancer_O EE	VN	00_#38_Pentatricopeptide	NA	03_VATPase	NA	NA	NA	NA
circadian_clock																															
glucogenesis_glycol sisy	yes											yes					yes		yes	yes	yes										
oິກາແກ່າວຕ່_ໂອະ_ຂວດ	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Populus trichocarpa hypothetical protein (POPTR_0002s25930g) mRNA_ complete cds
filevonoid_anthocya	NA	NA	NA	NA	ALB_L_flavonoid glucosyl- transferase	ALB_L_flavonoid glucosyl- transferase	NA	NA	NA	NA	ALB_L_cyanidin 3-o-rutinoside 5- o-glucosyltransferase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh									es														es					es			
mMai2017													s	s																	
ssn													¥6	Ye																	
markers																															
quangut_res																s															
aquaporin_reg																ye															
stomata_func																															
related_Acomosus_																									s						
CAM-																									ye:						
Angiosperm_gene	AA	AA	A	¥	¥	A	AA	AA	AA	¥	¥	¥	¥	AA	AA	AN	AN	Ą	¥	AN	AN	AA	AA	AN	AN	AA	AA	674	¥	AN	NA
MAD_seilimst_eneg	AN	AN	AN	AN	٩ ۲	AN	AN	AN	AN	AN	٩Ŋ	AN	AN	AN	AN	ΝA	ΑN	Ϋ́	AN	AN	AN	AN	AN	ΝA	AN	AN	ΥN	AN	AN	Å	AN
MAD_not_selection_CAM	ΑN	ΥN	ΝA	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	ΝA	ΥN	AN	٩N	ΥN	AN	AN	AN	ΝA	yes	AN	ΥN	ΥN	٩N	٩N	ΑN
Diff_expressed_CA MC3	ΑN	ΑN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	٩N	٩N	AN	AN	AN	ΝA	AN	AN	yes	ΑN	yes	٩N	ΑN
high_copy.Broc_An A_n_Iilla.	٩N	ou	ou	Q	Q	ou	ou	ou	ou	Q	Q	Q	Q	ou	ou	yes	ou	Q	Q	yes	ou	ou	QU	ou	ou	Q	ou	ou	Q	ou	ou
Low_copy.Broc_Ana n_Tilla.	AA	01	0	2	yes	yes	8	2	2	2	yes	yes	8	yes	2	ou	yes	8	2	Q	yes	e E	yes	ou	8	2	yes	ou	yes	6	yes
Single_copy.Broc_A nan_Tilla.	AN	yes	yes	yes	2	2	yes	yes	yes	yes	2	2	yes	8	yes	ou	Q	yes	yes	Q	Q	yes	2	yes	yes	yes	Q	yes	2	yes	2
emenpez	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G05	.G07	.G07	.G07	.G07	.G07	.G07	.G07	.G07	.G07	.G07	.G07	.G20	.G08	.G08	-G08	.G08
gene	Aco014274 L	Aco014278 1	Ac0014285 L	Aco014286 L	Aco014301 L	Aco014304 L	Ac0014314 L	Ac0014315 L	Ac0014317 L	Ac0014321 L	Aco014334 L	Aco014342 L	Ac0014347 L	Aco014352 L	Aco014364 L	Aco014393 L	Aco014402 L	Ac0014404 L	Aco014406 L	Ac0014415 L	Ac0014417 L	Aco014433 L	Aco014452 L	Ac0014474 L	Aco014488 L	Aco014493 L	Ac0014555 L	Ac0014579 L	Ac0014581 L	Aco014582 1	Aco014590 [

əziz_noxə_nim	125	44	06	1697	98	11	61	160	1874	46	47	684	1319	215	222	62	34	56	287	178	45	122	704	210	144	55	48	53	446	1172
ezia_pinoxe_latot	1727	4436	2278	1697	373	1532	1154	2644	1874	1770	1600	1565	1319	863	2215	1395	1720	4550	287	1704	1049	1864	704	1377	1053	977	1989	1146	2377	1172
ang pergene	ß	25	10	-	5	N	ъ	2		12	ß	2	-	m	9	80	11	17	н,	m	6	9	-	ъ	9	ъ	13	8	ю	F
ezi2_noxe_egereve	345.400	177.440	227.800	1697.000	186.500	766.000	230.800	528.800	1874.000	147.500	320.000	782.500	1319.000	287.667	369.167	174.375	156.364	267.647	287.000	568.000	116.556	310.667	704.000	275.400	175.500	195.400	153.000	143.250	792.333	1172.000
ədíq	NA	00_#MB_RPB2	NA	NA	04_Oxygen_evolving_enhancer_O EE	00_#22_Malate_dehydrogenase	02_Aquaporins	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	01d_Auxin_reponse_factor	NA	NA	NA	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	NA
circadian_clock																														
glucogenesis_glycol ysis											yes			yes	yes	yes	yes					yes			yes	yes	yes	yes		
ogullutioq_las_zoq	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris malate dehydrogenase_chloroplastic-like (LoC104908004)_transcript variant X2_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
filavonoid_anthocya Sq_ainnia_pi	AA	AA	AA	AA	AA	A	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	NA	AA	ALB_F_anthocyanidin reductase	AA	AA	AA	AA	AA
Assimilation_Carboh ydrates					yes 1														_	_									_	
circadian_metabolis m_Wai2017																														
anthocyanin_SI_Ana san																														
mærkers dræught_res		yes																					es							
aquaporin_reg							yes																							
stomata_func																		yes												
CAM- related_Acomosus_ Ming2015						yes																								
Angiosperm_gene	AA	AA	5500	AA	A	AA	AA	AA	AA	5551	AA	AA	AA	AA	AA	5318	5296	AA	AA	AA	5304	AA	AA	AA	AA	AA	AA	NA	NA	A
gene_families_CAM C3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	NA N	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
MAD_noticelection_CAM ethics	ΝA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	NA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	ΝA	AN
Diff_expressed_CA DC3 DMC3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	NA	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	٩N
High_copy.Broc_An an_Tilla.	ou	yes	Q	Q	AN	ou	ou	ou	Q	Q	yes	Q	ou	ou	ou	ou	Q	yes	AN	Q	ou	ou	ou	ou	ou	ou	ou	ou	ou	2
Low_copy.Broc_Ana n_Tilla.	92	2	2	2	A	yes	yes	2	2	2	2	2	2	92	yes	9	yes	2	M	8	8	yes	yes	8	9	2	yes	Q	92	2
Single_copy.Broc_A nan_Tilla.	yes	2	yes	yes	AN	e e	9	yes	yes	yes	2	yes	yes	yes	QL	yes	2	2	AN	yes	yes	2	9	yes	yes	yes	2	yes	yes	yes
emanpez	LG08	LG08	LG08	LG08	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG14	LG14	LG14	LG14	LG14	LG14	LG14	LG14	LG14	LG14	LG14	LG14	LG04	LG04	LG04
әиәб	Aco014592	Aco014603	Aco014616	Aco014628	Aco014682	Aco014690	Aco014693	Aco014697	Aco014716	Ac0014745	Aco014753	Aco014755	Aco014770	Aco014781	Aco014791	Aco014801	Aco014810	Aco014831	Aco014837	Aco014842	Aco014855	Aco014864	Ac0014875	Aco014884	Aco014888	Aco014895	Aco014899	Ac0014931	Aco014937	Aco014942

əziz_noxə_nim	150	1385	570	215	1310	38	345	423	172	954	269	41	366	14	94	130	22	136	360	21	209	40	17	121	378	207	68	564	47	566	31
total_exonic_size	2178	1385	2265	2161	1310	2735	1807	1545	2191	1973	1115	4082	1312	3822	2523	1378	1013	2841	1153	4295	1172	1735	631	1362	1684	2721	1353	1152	1928	1246	1252
anag_aer_gene	7	F	2	9	-	23	2	e	m	2	m	16	2	15	10	m	10	7	e	21	m	14	2	ى ك	2	m	2	5	15	2	4
average_exon_size	311.143	1385.000	1132.500	360.167	1310.000	118.913	903.500	515.000	730.333	986.500	371.667	255.125	656.000	254.800	252.300	459.333	101.300	405.857	384.333	204.524	390.667	123.929	315.500	272.400	842.000	907.000	193.286	576.000	128.533	623.000	313.000
ρη	NA	01d_Auxin_reponse_factor	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	11_Glycolysis_night_C4_malate_p athway	01b_Abscisic_acid_signal	NA	NA	NA	NA	NA	00_#W_ProtonPump_VHA- B_03_VATPase	NA	11_Glycolysis_night_C4_malate_p athway												
circadian_clock																															
glucogenesis_glycol visi															yes							yes									yes
oßniintrod_les_soq	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max kinesin-4-like (LOC100777089)_ transcript variant X4_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA													
filovonoid_anthocya filosonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA													
circadian_metabolis m_Wai2017																													yes		
anthocyanin_SI_Ana asn																															
markers																															
draught_res																															
aquaporin_reg																															
CAM- related_Acomosus_ Ming2015 stomata_func														yes									yes								
Angiosperm_gene	NA	AA	AA	AA	AA	5528	AA	AA	AA	AA	AA	6732	AA	AA	AA	AA	5642	4848	AA	AN	AA	AA	AA	AA	AA	AA	5430	AA	NA	AA	AA
gene_families_CAM C3	AN	AA	AN	AN	AA	AN	AA	AN	AN	AN	AN	AN	AN	AN	yes	yes	AN	AN	AN	AN	AN										
MAD_no_selection_CAM 	ΝA	AN	AA	AA	AN	AA	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AA	AN	AN	AN	AN							
Diff_expressed_CA MC3	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	٩N	٩N	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	٩N								
High_copy.Broc_An an_Tilla.	ou	ę	Q	Q	Q	QL	QU	ou	QL	ę	ę	ę	ę	Q	Q	Q	ou	QU	ou	ou	ou	yes	AN	QU	ou	Q	ę	Q	Q	оц	Q
Low_copy.Broc_Ana nn	ou	ę	ę	ę	ę	ę	ę	e E	ę	2	2	yes	2	yes	yes	2	6	2	e	yes	2	ę	AA	ę	yes	yes	2	2	ę	ę	yes
Single_copy.Broc_A nan_Tilla.	yes	2	yes	2	2	yes	yes	yes	yes	ę	yes	2	AN	yes	92	9	yes	yes	yes	yes	2										
əmsnpəz	LG04	LG13	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG01	LG24	LG24	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05	LG05						
деле	Aco014951	Aco014959	Aco014967	Aco015009	Aco015014	Aco015020	Aco015031	Aco015035	Aco015042	Aco015045	Aco015047	Aco015060	Aco015072	Aco015073	Aco015090	Aco015107	Aco015108	Aco015128	Aco015141	Aco015171	Aco015180	Aco015184	Aco015194	Aco015197	Aco015198	Aco015199	Aco015201	Aco015211	Aco015226	Aco015235	Aco015240

			-			1										-	1													
əziz_noxə_nim	56	235	44	111	159	8	549	136	525	199	44	887	2051	852	456	105	1973	1448	85	1337	75	114	5	659	119	384	1421	22	101	274
ezia_oinoxe_latot	1483	1222	2475	1201	1196	2844	2492	1153	1129	1725	941	1951	2051	1832	1429	678	1973	1448	1708	1337	1374	1530	235	659	1983	1743	1421	3016	2529	1160
ur_exons_per_gene	12		14			5	e	m			11					m	1	Ч	~		5				LO LO	m		12	0	~
average_exon_size	123.583	611.000	176.786	240.200	299.000	316.000	830.667	384.333	564.500	345.000	85.545	975.500	2051.000	916.000	714.500	226.000	1973.000	1448.000	244.000	1337.000	152.667	218.571	117.500	659.000	396.600	581.000	1421.000	251.333	281.000	580.000
ədáj	IA	IA	0_Glucogenesis_specific_dayC3	IA	IA	0_Glucogenesis_specific_dayC3	IA	IA	IA	IA	P	0_Glucogenesis_specific_dayC3	PI	IA	IA	P	P	IA	.0_Glucogenesis_specific_dayC3	IA	IA	IA	IA	P	IA	10_#W_StomatalMovement_Carbo dioxide_insensitive3_CD13_11_ Siycolysis_night_C4_malate_pathw	P	IA	P	IA
_	2	2		2	2	-	2	2	2	2	2		2	2	2	2	2	2	1	2	2	2	2	2	2	0 - 0 a	2	2		2
circadian clock																														
glucogenesis_glycol			yes			yes						yes							yes											
oguliuhoq_ləɛ_zoq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Oryza sativa Japonica Group homeobox-leucine zipper protein ROC7 (LOC4344614)_mRNA	NA
vanates Mavonoid_anthocya Picaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																														
circadian_metabolis m_Wai2017																										/es				
anthocyanin_SI_Ana asn																														
markers																														
draught_res																														
aquaporin_reg																														
stomata_func																														
related_Acomosus_																														
	50	4	⊲	4	4	4	4	4	⊲	⊲	94	₫	⊿	4	4	164	٩	4	4	4	4	4	060	⊲	4	4	4	4	4	4
Andiosperm dene	₽ 60	Z ⊲	Z ⊲	Z d	Z d	Z d	Z d	Z d	Z d	Z ⊲	۲ 21	Z d	Z ⊲	Z d	Z d	P 50	Z d	Z d	Z d	Z ⊲	Z ⊲	Z ⊲	₽	Z d	Z d	Z d	Z ⊲	Z ⊲	Z d	Z ⊲
stiins_	Z d	z a	z a	z a	z a	Z d	Z d	Z d	z a	z a	z a	z a	z a	z a	z a	z a	z a	z a	z s	z a	z a	z a	z a	z a	Z d	ਟਂ ਰ	z a	z s	z a	z d
MC3 Telection CAM	Ž	Ž	Ž	Ž	Ž	Ž	Ň	Ž	× N	Ž	Ž	Ż	Ž	Ž	Ž	Ż	Ž	Ž	ye	Ž	Nr v	Ž	Ž	ž	Ž	Ž	Ž	s ye	Ž	Ń
an_Tilla. AD bessered CA	NA	AN	A N	NA	NA	NA	NA	NA	ye	NA	AN NA	A A	A A	NA	NA	NA	NA	NA	NA	AN	yee	AN	AN	yes	NA	A N N	NA	yet	NA V	NA
n_Tilla. high_copy.Broc An	0L	0 L	u u	6	6	ou "	ou	ou	ou ,	6	0L	0 	6	6	е Р	ou	ou	оц	ou "	0L	on "	6	6	0L	0L	01	6	0 	ye	ou
nan_Tilla. Low_copy.Broc_Ana	2	2	yes	2	2	yes	2	2	yes	2	2	yes	2	2	2	2	9	2	yes	2	yee	2	2	2	2	yes	2	yec	8	2
A_oong. Koo_elgni2	yes	yes	2	yes	yes	2	yes	yes	2	yes	yes	2	yes	yes	yes	yes	yes	yes	2	yes	2	yes	yes	yes	yes	2	yes	2	2	yes
edname	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG20	LG23	LG23	LG23	LG23	LG23	LG23	LG23	LG23	LG23	LG23	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03	LG03
gene	Aco015263	Aco015297	Aco015298	Aco015317	Aco015319	Aco015324	Aco015329	Aco015338	Aco015340	Aco015349	Aco015352	Aco015377	Aco015387	Aco015404	Aco015411	Aco015420	Aco015422	Aco015434	Aco015436	Aco015443	Aco015453	Aco015495	Aco015513	Aco015521	Aco015530	Aco015541	Aco015546	Aco015555	Aco015577	Aco015588

27/5 10/2 10/11	52	L40	126	112	51	41	33	947	40	180	350	124	296	36	227	122	L44	57	136	269	53	69	36	194	124	396	357	228	102	155
ezis uoxe uim		~	~				_	0, N	~	5											10			~		~		5		
ezia_pinoxe_latot	546	1783	3815	1791	1759	1580	2805	947	1493	2480	1455	3390	1146	1487	1355	1877	1526	1441	1407	2433	1085	881	1599	1677	2331	1667	2032	2228	1400	1628
ur_exons_per_gene	4	ß	2	6	6	4	22	1	12	H	2	~	m	13	m	m	4	2	9	4	10	4	14	2	2	2	4	H	5	4
aziz_noxa_agerave	137.000	356.600	544.714	199.000	195.444	395.000	127.682	947.000	124.417	2480.000	727.500	484.286	382.667	114.385	451.667	625.667	381.500	720.500	234.500	608.250	108.500	220.250	114.214	838.500	1165.500	833.500	508.000	2228.000	280.000	407.000
ədiğ	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	00_#W_HexoseTransporter_MSSP -like_transporter	NA	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	00_#Ming2019_Anthocyanin_biosy nthesis
сігсадіал_сіоск																														
glucogenesis_glycol ysis_	yes	yes							yes					yes		yes							yes						yes	
ogulluhoq_ləs_zoq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Populus trichocarpa adenosylhomocysteinase family protein (POPTR_0017s08610g) mRNA_ complete cds	NA	NA	NA
nin_pricaima_ps	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_chalcone synthase
Assimilation_Carboh Assimilation_Carboh Atrates																														
circadian_metabolis m_Wai2017												yes																		
anthocyanin_SI_Ana asn																														/es
markers																														
qraught_res																														
aquaporin_reg																														
stomata_func																														
related_Acomosus_ 8102pniM																														
CAM-	_	_	_	_	32	7	02	_	_				94	_	_	_	7	_		_	73	28	_	_	7	_	1		7	_
Angiosperm gene	Ž	Ž	Ž	Ž	A 49	Ž	A 55	s S	Ž	Ž	Ž	Ž	₽ 22	Ž	Ž	Ž	Ž	Ž	Ž	Ž	4 72	4 70	Ž	Ž d	NN T	Z d	Z ∡	2 d	NZ d	Ž
stiins	Z ⊲	² ∢	Z ⊲	Z d	Z ⊲	2 ∢	N N	A V€	Z ⊲	Z ⊲	Z ⊲	Z ⊲	Z ⊲	Z d	Z ⊲	Z ⊲	² ∢	² ∢	N S	Z ⊲	² ∢	Z d	Z ⊲	Z ⊲	۲ ۷	Z ∡	Z V	2 s	2 d	z ⊲
WC3	Z d	z a	z a	z a	z a	z a	A Ye	z d	z a	z a	z a	z a	z a	z a	z a	z a	Z d	z v	۹ ۲	z a	z a	z a	z a	z d	Z d	Z d	Z A	۹ ۳	Z d	z d
and as the second as the secon	ź	ź s	Ż	Ż	ž	ž	ź	ź	ž	ž	ž	ž	ž	Ż	ź	ž	ž	ye	ž	Ż	Ż	ź	ź	ź	ź	ź	ź	ź	ż	ź
.slliT_n .slliT_n	2 d	, ye	u L	2	s nc	s nc	s nc	, nc	, nc	2	2	s nc	2	2	2 J	s nc	, nc	2	2	2	2	2	s nc	2	u uc	, nc	is nc	ž	s nc	ž
Low conv.Broc Anal	Ž	2	s no	s no	ye	ye	ye	s no	s no	s no	s no	ye	s no	s no	s no	ye	s no	s no	ye	s no	s no	s no	ye	s s	ye	s no				
Single_copy.Broc A	3 NA	9 9	3 ye	9 yet	01 6	01 6	0 lo	9 ye	9 ye	9 ye	9 ye	01 6	9 ye	1 ye	1 ye	2 10	2 ye	2 ye	2 ye	2 ye	1 ye	1 ye	1 1	1 yet	1 yet	1 yet	1 10	1 ye	1 10	7 ye
emennez	9 LG0	2 LG0	3 LG0	3 LG1	5 LG1	1 LG1	7 LG0	1 LG0) LG0	1 LG0	2 LG0	9 LG0	9 LG0	2 LG0	5 LG0	7 LG2	4 LG2	4 LG2	3 LG2	9 LG2	7 LG2	7 LG2) LG2	0 LG2	7 LG2	3 LG2	2 LG2	9 LG2	1 LG2) LG1
gene	Aco015585	Aco015592	Aco01559:	Aco01565	Aco015685	Aco01571	Aco01572	Aco01574	Aco01576(Aco015761	Aco015775	Aco015775	Aco015795	Aco015842	Aco015885	Aco01597	Aco016004	Aco016014	Aco016015	Aco016025	Aco016047	Aco01605	Aco01607(Aco01608(Aco016087	Aco01610:	Aco016112	Aco01613(Aco01615;	Aco01620(

əziz_noxə_nim	2318	22	69	602	462	203	51	132	34	38	46	91	61	1568	167	227	74	86	22	707	200	120	61	614	1628	1406	160	272	356	359
total_exonic_size	2318	1248	1408	602	1102	1323	975	816	607	1404	1465	1696	3666	1568	2191	1152	4939	1935	2246	1858	1109	1309	2816	614	1628	1406	2968	1486	1128	1498
ur_exons_per_gene	1	e	6	-	2	2	9	m	4	8	2	2	19	-	m	m	10	œ	20	2	m	9	8	1	1	-	4	2	2	2
average_exon_size	2318.000	416.000	156.444	602.000	551.000	661.500	162.500	272.000	151.750	175.500	209.286	242.286	192.947	1568.000	730.333	384.000	493.900	241.875	112.300	929.000	369.667	218.167	352.000	614.000	1628.000	1406.000	742.000	743.000	564.000	749.000
ədáj	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	02_Aquaporins	NA	11_Glycolysis_night_C4_malate_p athway	NA	NA	00_#12_10_Glucogenesis_specific _dayC3	NA	NA	NA	00_#W_StomatalMovement_Phosp holipase_Da1	NA	00_#10_Glucogenesis_specific_da	NA	NA	NA	00_#W_CircadianOscillator_CCA1/ LHY	01d_Auxin_reponse_factor	NA	NA	NA	NA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA
circadian_clock																														
glucogenesis_glycol ysis				yes						yes																				
oɓnijnµod"]əs ⁻ sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris NAD-dependent malic enzyme 59 kDa coformmitochondrial (LOC10488560) mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
gyondrae_bionovalt 29_aimiao#_nin	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_isoflavone reductase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
malateTransferase_ Assimilation_Carboh ydrates											-																			
circadian_metabolis m_Wai2017																	yes						yes							
anthocyanin_SI_Ana nas																														
markers																														
qraught_res																													yes	yes
aquaporin_reg								yes																						
stomata_func																								yes						
related_Acomosus_													yes						yes											
Angiosperm_gene	NA	NA	MA	MA	AN	AA	5660	NA	7024	MA	AA	5639	AN	MA	AA	AA	AA	5116	AN	AA	AN	AA	AA	AA	NA	AA	AA	AA	MA	AA
MAD_eailims_eng C3	NA	NA	NA	NA	yes	AN	NA	NA	NA	AN	NA	AN	AN	NA	NA	ΝA	NA	NA	NA	NA	AN	AA	AA	AN	NA	AN	NA	NA	NA	NA
MAD_not_selection_CAM shifts_	٩N	AN	٨A	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	٩N	AN	AN	٩N	AN	AN	yes	AN	yes	AN	AN	٩N	AN	AN
Diff_expressed_CA DC3 DC3	AN	yes	yes	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	٩N	٩N	AN	AN	٩N	AN	AN	AN	٩N	٩N	AN	AN
High_copy.Broc_An an_Tilla.	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	yes	ou	ou	ou	ou	ou	ou	AN	ou	ou	ou	ou	yes	yes
Low_copy.Broc_Ana n_Tilla.	ou	yes	yes	yes	e	e e	2	yes	92	2	yes	2	2	2	2	2	2	2	yes	2	e	2	2	AA	2	2	2	2	QL	ou
Single_copy.Broc_A nan_Tilla.	yes	02	2	2	yes	yes	yes	2	yes	yes	2	yes	yes	yes	yes	yes	2	yes	e	yes	yes	yes	yes	AN	yes	yes	yes	yes	e L	0L
əmanpəz	.G17	.G03	.G03	.G03	.G03	.G03	.G03	.G03	G03	G10	G10	G10	.G10	G10	G10	G11	.G11	G09	.G09	G09	G08	.G08	.G08	G08	G08	.G17	G17	G17	.G17	.G17
апар	Aco016245 L	Aco016255 L	Aco016258 L	Aco016261 L	Aco016318 L	Aco016323 L	Aco016352 L	Aco016357 L	Aco016360 L	Aco016390 L	Aco016393 L	Aco016395 L	Aco016429 L	Aco016437 L	Aco016438 L	Aco016511 L	Aco016554 L	Aco016562 L	Aco016569 L	Aco016575 L	Aco016607 L	Aco016636	Aco016649 L	Aco016654 L	Aco016662 L	Aco016690 L	Aco016697 L	Aco016708 L	Aco016710 L	Ac0016712 L

	45	82	33	95	55	47	99.	32	12	72	6	16	23	36	37	24	49	60	67	11	45	14	10	72	44	95	57	26	83	24	73
əziz noxə nim	1	1	~	1		, 15	2	~	1	23		5	-		-	10	-		2	1		0	4	1	1	1	-		15	5	с С
fotal_exonic_size	1206	866	1828	1544	1776	1547	1470	2598	1609	2372	1905	1900	1939	1332	2430	1644	1679	4067	2189	1269	5104	2872	1306	1790	2243	1553	2562	803	1583	1707	2139
ur_exons_per_gene	e	4	6	en en	20		4	2	-		~	۳ ا	9		~	4	11	27	20	20	12	۳ ۳	5	m l	9	e	15	2		~	4
average_exon_size	402.000	249.500	203.111	514.667	355.200	1547.000	367.500	371.143	229.857	2372.000	272.143	633.333	323.167	190.286	347.143	411.000	152.636	150.630	437.800	253.800	425.333	957.333	653.000	596.667	373.833	517.667	170.800	160.600	1583.000	569.000	534.750
эdĄ	AN	00_#18_Malate_dehydrogenase	AN	01d_Auxin_reponse_factor	36_Drough_resistance_genes_LEA	AN	AN	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	AN	AV	AV	AV	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	AA	AA	AA	10_Glucogenesis_specific_dayC3	AN	AA	AN	AN	AA	AN	AN	10_Glucogenesis_specific_dayC3	AV	AN	AA	AN
circadian_clock																														-	
glucogenesis_glycol sisy								yes	yes					yes	yes				yes								yes				
oɓnjinuod"jəs"sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
stronoralit SQ_ainia_proventi SQ_ainia_pr	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																															
malateTransferase																															
SBN 2017-10-1010-0010-0010-0010-0010-0010-00																															
draught_res markers					S																										
aquaporin_reg					ye																										
elated_Acomosus_		0		ye:																											
-MAC		ye:	53														22	5			90							9			
Angiosperm_gene	AA	AN	646	AN	A	A	AN	AA	AA	٩ ۲	513	٩ ۲	٩ ۲	A A	A A	AA	999	265	AN A	AA	556	AN AN	AN AN	AN AN	AA	AA	AA	769	٩ ۲	Ч.	¥
2010 CAMM 2010 C	AN	AN	AN	NA	AN	AN	AN	AN	AN	AN NA	A N	A N	A N	A N	A N	AN	AN	AN	AN	AN	AN	AN	AN	A N	AN	AN	NA	AN	AN NA	Υ Z	AN N
MC3 MAD_nos_selection_CAM	ΔN	٩N	ΔN	ΔN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	٩N	٩N	ΔN	AN	AN	ΔN	ΝA	yes	AN	AN	Ϋ́	ΔA
Diff_expressed_CA	ΑN	ΥN	AN	AN	AN	AN	AN	AN	AN	AN	AN	A N	yes	AN	AN	AN	AN	AN	AN	Ϋ́	ΥN	yes	AN	AN	AN	yes	AN	AN	AN	٩N	yes
High_copy.Broc_An	Q	AN	ę	е Г	е Р	Q	ou	yes	yes	e e	ę	ę	2	2	yes	Q	QU	Q	yes	ę	е Ц	yes	e e	ę	Q	QU	Q	Q	e e	ę	2
Low_copy.Broc_Ana	9	AA	yes	yes	2	2	2	2	2	2	yes	2	yes	2	2	2	6	yes	2	2	yes	2	2	2	8	6	2	2	2	2	2
A_oong.copy.Broc_A nan_nia.	yes	AN	ę	Q	yes	yes	yes	2	e	yes	2	yes	2	yes	2	yes	yes	2	e	yes	QL	ę	yes	yes	yes	yes	yes	yes	yes	yes	yes
emanpes	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG17	LG04	LG04	LG04	LG04	LG04	LG04	LG04	LG02	LG02	LG02	LG02	LG02	LG02	LG08	LG08	LG08	LG08	LG08	LG08	LG08	LG08
деле	Aco016722	Aco016727	Aco016732	Aco016748	Aco016764	Aco016768	Aco016769	Aco016773	Aco016774	Aco016784	Aco016803	Aco016807	Aco016809	Aco016819	Aco016848	Aco016862	Aco016876	Aco016888	Aco016897	Aco016898	Aco016907	Aco016943	Aco016948	Aco016978	Aco016979	Aco016986	Aco016993	Aco017006	Aco017008	Aco017030	Aco017042

sziz_noxs_nim	427	86	154	38	48	311	44	226	194	1937	57	2033	183	234	1268	125	144	1808	244	06	152	152	152	80	1583	1054	271	20	124	1802
total_exonic_size	1727	1825	1179	810	1467	793	2704	2720	1716	1937	1453	2033	1542	2802	1268	1532	1326	1808	1626	1906	1802	1389	1458	1081	1583	2563	1938	3511	3188	1802
ur_exons_per_gene	2	6	ß	6	12	2	19	4	e	1	2	1	9	2	-	2	e	H	4	7	e	4	e	ß	1	2	2	22	6	1
average_exon_size	863.500	202.778	235.800	000.06	122.250	396.500	142.316	680.000	572.000	1937.000	726.500	2033.000	257.000	1401.000	1268.000	306.400	442.000	1808.000	406.500	272.286	600.667	347.250	486.000	216.200	1583.000	1281.500	969.000	159.591	354.222	1802.000
ədAş	NA	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	11_Glycolysis_night_C4_malate_p athway	NA	00_#Ming2019_Anthocyanin_biosy nthesis	NA	01b_Abscisic_acid_signal	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	00_#MB_phosphoribulokinase-like protein (PRK) gene	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
circadian_clock																														
glucogenesis_glycol sisy		yes			yes	yes	yes								yes															
oßniintroq_ləs_soq	NA	PREDICTED: Beta vulgaris subsp. vulgaris glucose-1-phosphate adenylytiransferase small subunit_chloroplastic/amyloplastic (LOC104903071)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Solanum tuberosum ATPase family AAA domain-containing protein 3C (LOC102578202)_mRNA	NA	PREDICTED: Glycine max protein argonaute 1- like (LOC100778754)_ mRNA	NA	NA						
- filavonota_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	STA_L_Flavonoid 3- hydroxylase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh Assimilation_Carboh ydrates																														
circadian_metabolis m_Wai2017																														
anthocyanin_SI_Ana san									/es																					
draught_res																			yes											
aquaporin_reg																														
stomata_func											es																			
related_Acomosus_											~																			
S	Į.	A	¥	460	Ā	Ā	Ā	Ā	Ā	Ā	Ā	Ą	Ą	Ā	Ā	Ā	Ā	Ā	Ā	Ā	Ă	Ā	Ā	779	4	Ą	Ā	Ā	4	4
MAD_22 C3 Aprilography appro-	N V	Z A	Z V	IA 5	N N	Z Z	N N	Z A	Z Z	N N	N N	N N	N N	N V	N V	N V	N N	N N	N N	N	N N	N N	N N	IA 6	N N	N N	N N	N N	N N	z ≰
pos_selection_CAM shifts	es N	Z V	Z A	Z A	Z A	Z Ę	Z Ş	Z A	Z Ş	Z A	Z A	A N	A A	Z A	Z A	Z A	Z A	Z Ą	N A	A N	Z A	A A	Z A	Z A	Z A	'es	A N	Z A	A N	Z A
Diff_expressed_CA MC3	JA V	∠ ¢	A A	A N	A N	A A	4 A	A A	4 A	A N	A N	A N	A N	A A	A A	A A	A A	A A	A A	A N	'es	A N	A A	A N	A N	JA y	A N	A N	A N	∠ ₹
High_copy.Broc_An an_Tilla.	2 0	2	2	2	2	es N	2	2	2	2	A A	2	0	2	2	2	2	2	2	4 01	<u>ر</u>	2	2	2	2	0	0	es N	4	2
Low_copy.Broc_Ana n_Tilla.	0	les L	<u>e</u>	02	2	p Q	/es n	p p	ves n	Q	A	0	02	2	2	2	2	p p	Q.	/es	e e	Q	2	Q	2	2 Q	e Q	0ť V	5	2
Single_copy.Broc_A nan_Tilla.	/es	ę	/es	/es r	/es r	2	2 Q	/es	2 Q	/es	AN	/es r	/es r	/es	/es	/es	/es	/es	/es	0	/es	/es	/es r	/es	/es r	/es r	/es r	6	/es r	/es
əmsnpəz	G14)	G14 1	G14)	G14 >	G14)	G14 r	G14 r	G14 >	G18 r	G18	G18	G18)	G18)	G03	G03	G03	G03	G03	G03	G03 1	G01	G01)	G01 >	G01)	G01)	G01)	G01)	C09 r	G22	G22
gene	Aco017062 L	Aco017076 L	Aco017100 L	Aco017111 L	Aco017115 L	Aco017128 L	Aco017133 L	Aco017138 L	Aco017169 L	Aco017171 L	Aco017183 L	Aco017195 L	Aco017212 L	Aco017240 L	Aco017241 L	Aco017259 L	Aco017266 L	Aco017276 L	Aco017282 L	Aco017286 L	Aco017324 L	Aco017325 L	Aco017331 L	Aco017335 L	Aco017336 L	Aco017339 L	Aco017365 L	Aco017433 L	Aco017479 L	Aco017482 L

	64	26	23	15	10	75	œ	43	61	40	12	8	46	32	40	16	18	90	8	65	63	31	57	94	26	95	68	32	92	36	62
əzis noxə nim		~			1	~						ő				1	-	-	4				14	1			о О	24			
ezia_exonic_size	2803	1415	487	985	1404	1377	2151	1225	1279	670	1563	1741	1248	2613	1711	1279	2317	1471	1291	1534	4560	3181	1457	1014	2264	1103	2235	2432	2781	1799	2001
ut_exons_per_gene	11	۳ ۱	5	2	4	e	8	2	4		20	4	~	~	2	4	20	20		8	13	23	1	3	13	4	5		6	8	1
əziz_noxə_əgsıəvs	254.818	471.667	243.500	197.000	351.000	459.000	268.875	612.500	319.750	335.000	312.600	435.250	156.000	373.286	342.200	319.750	463.400	294.200	645.500	191.750	350.769	138.304	1457.000	338.000	174.154	275.750	1117.500	2432.000	309.000	224.875	181.909
əd⁄u	AN	00_#23_Lactate_dehydrogenase	00_#24_hypothetical_protein	00_#25_hypothetical_protein	00_#26_Lactate_dehydrogenase	AV	00_#W_VacuolarAcidInvertase_AI	AA	AV	AV	01b_Abscisic_acid_signal	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	01d_Auxin_reponse_factor	AA	AA	00_#W_CircadianOscillator_casein kinase2_subunit_beta	A	10_Glucogenesis_specific_dayC3	00_#W_StomatalMovement_ATP- binding_cassette_C4	AV	٨٨	٨٨	10_Glucogenesis_specific_dayC3	01d_Auxin_reponse_factor	٨٨	AA	٨٨	10_Glucogenesis_specific_dayC3	AN
circadian_clock	-2					-			-														2	~		0	~			1	
glucogenesis_glycol ysis_												'es	/es	/es						/es					/es					'es	
oອິnjinuod jes sod	PREDICTED: Vitis vinifera cell division control protein 48 homolog C (LOC100261441) mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	VA	NA	Populus trichocarpa Argonaute 4 family protein (POPTR_0001s22710g) mRNA_ complete cds	NA	NA	NA	NA	NA	NA	NA	NA	NA
guntus bionovalt S9 pinio pini	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_flavonol synthase	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates																															
circadian_metabolis m_Wai2017 malateTransferase							es											se			es										
มารามาราวารเหตุ							×											~			×										
markers																															
qraught_res																															
aquaporin_reg																															
stomata_func											/es				/es											/es					
related_Acomosus_ 2102pm Bing2015		/es	/es	/es	/es																										
Anglosperm_gene	A	4	A	4	4	A	₹	428	4	371	≤	A	A	A	A	A	A	4	≤	₹	A	A	A	A	₹	A	A	₹	A	A	A
gene_families_CAM C3	N	N	N	N N	N N	N N	N N	1A 5	N A	A N	N	N N	N	N	N N	N	N N	N N	N	N	N	N	N AL	IA N	N N	N AL	N N	N N	N	N N	N N
pos_selection_CAM 	A P	A A	A A	A A	A A	A N	A A	A A	4 A	4	A A	A A	A A	A A	A A	A	Z A	4 A	A A	4 A	A	A A	A P	A P	A A	A A	A A	A A	A A	A N	les 2
WC3	4	4	4	4	2	∠ ∀	∠	4	4	4	4	4	4	2	2	4	4	4	4	4	2	∠	4	4	∠	4	4	4	4	4	A
angride (402 mg/m) angride (402 mg/m) angride (40 mg/m) angride (4	Ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	Ż	SS N/	Ż	Ż	Ż	2 v	Ż	Ż	SS N/	Ż	Ń O	A N	Ż	2 0	Ż	Ż	Ż	Ň	Ż
.sliit_n .bliit_n	Ĕ	s II	N S	S DI	NI S	ŭ	S DI	Ĕ	Ĕ	Ĕ	Ĕ	s II	Ĕ	ž	Ĕ	Ĕ	Ĕ	Z a	Ĕ	ы S	ž	s S	ŭ i	Z d	s: Z	s:	Ĕ	Ĕ	s Di	ŭ	Ĕ
.slliT_nsn	s nc	yε	yε	yε	yε	s nc	yε	2 2	2 2	2 2	2 2	yέ	2 20	2	2 20	2 UC	2 2	Ż	2 2	γ€	2	У€	s nc	Ż	Ύ€	y€	s nc	2 L	y€	s nc	2
Single_copy.Broc A	2 ye	2 no	2 no	2 no	2 no	2 ye	2 no	2 ye	2 ye	9 ye	9 yet	4 10	4 ye	4 10	5 ye	5 ye	5 ye	1 NA	1 ye	1 1	9 3	3	4 ye	6 N	0U 6	0U 6	9 ye	9 yet	0L 6	1 ye	1 ye
Segname	I LG2	i LG2:	i LG2:	, LG2:	t LG2:	LG2	t LG2:	I LG2:	i LG2:	r LG0	i LGO	I LG1	, LG1	t LG1	LG0	: LGO	LG0	, LG2	LG2	LG2:	I LG2:) LG2	1 LG0) FG0	C LGO	LG1	, LG1	i LG1	I LG1	LG0	LG0:
gene	Aco017488	Aco017525	Aco017526	Aco017527	Aco017528	Aco017531	Aco017533	Aco017540	Aco017546	Aco017554	Aco017556	Aco017624	Aco017637	Aco017688	Aco017701	Aco017705	Aco017761	Aco017767	Aco017802	Aco017829	Aco017858	Aco017860	Aco017874	Aco017939	Aco017945	Aco017965	Aco017967	Aco017975	Aco017983	Aco017991	Aco018002

əziz_noxə_nim	260	74	56	122	84	617	4	1400	115	339	614	4	584	677	677	142	656	33	43	9	71	66	229	538	170	44	155	377	153	170
ezia_pinoxe_latot	2024	1287	3076	1394	3431	617	923	1400	1862	743	614	504	584	677	677	1165	1802	1292	2172	2620	1181	2230	1200	1200	659	2351	1188	377	1771	1353
ur_exons_per_gene	2	~	12	4	10	-	7	1	m	2	1	e				m	2	80	10	10	e	10	ю	2	2	19	4		m	2
aziz_noxa_agerave	1012.000	183.857	256.333	348.500	343.100	617.000	131.857	1400.000	620.667	371.500	614.000	168.000	584.000	677.000	677.000	388.333	901.000	161.500	217.200	262.000	393.667	223.000	400.000	600.000	329.500	123.737	297.000	377.000	590.333	676.500
əd/q	06_Drough_resistance_genes_LEA	NA	01d_Auxin_reponse_factor	11_Glycolysis_night_C4_malate_p athway	00_#10_Glucogenesis_specific_da yC3	01b_Abscisic_acid_signal	01d_Auxin_reponse_factor	00_#Ming2019_Anthocyanin_biosy nthesis	NA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	06_Drough_resistance_genes_LEA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	NA	06_Drough_resistance_genes_LEA	11_Glycolysis_night_C4_malate_p athway	NA	NA	NA	NA
circadian_clock																														
ysis_nycol				yes														yes								yes				
oອິກIJmJod Jəs Sod	NA	PREDICTED: Beta vulgaris subsp. vulgaris adenylate kinase 2. chloroplastic (LOC104898822)_transcript variant X1_ mRNA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris phosphoenolpyruvate carboxylase 1 (LOC104903486) mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Solanum tuberosum guanine nucleotide-binding protein-like NSN1 (LOC102593978)_mRNA	NA	NA	NA	NA	NA	NA	NA	NA
ationovali filavonoid_anthocya ficaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
malateTransferase_ Assimilation_Carboh ydrates																														
circadian_metabolis m_Wai2017																														
anthocyanin_SI_Ana nas								yes																						
markers																														
draught_res	yes									yes	yes	yes	yes	yes	yes						yes				yes					
aquaporin_reg																														<u> </u>
Ming2015 stomata_func			yes			yes	yes																							
CAM- related_Acomosus_					yes	-											-													-
Angiosperm_gene	AA	M	A	¥	AA	¥	A	AA	A	A	A	Ą	¥	¥	¥	A	¥	5840	AA	AA	AA	6036	AA	AA	A	AA	AA	A	¥	¥
gene_families_CAM C3 C3	٩N	A N	AN	٩Z	AN	٩ _Z	AN	AN	AN	AN	AN	٩N	٩N	٩Z	٩Z	AN	٩	٩Z	AN	AN	AN	NA	ΝA	ΝA	AN	AN	٩N	٩N	٩N	AN
MAD_notice MAD_notice athing	AN	٩Z	AN	AN	٩N	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	Å	AN	AN	AN	AN	AN	ΝA	ΝA	AN	AN	AN	AN	٩N	AN
AD_bszegreed_AD_bs	AN	۲ ۲	AN	AN	٩N	AN	AN	AN	AN	AN	AN	AN	AN	AN	Å	AN	Å	AN	yes	yes	AN	AN	ΝA	ΝA	AN	AN	AN	yes	٩N	AN
High_copy.Broc_An	ou	e	2	٩Z	e 2	٩Z	ę	ę	ę	Q	ou	ou	0L	e L	2	ę	2	2	е Ц	yes	0 L	ou	ou	ou	Q	ou	еu	ę	ou	2
Low_copy.Broc_Ana	yes	2	yes	A	yes	A	yes	2	2	yes	yes	yes	yes	yes	yes	2	2	2	2	2	2	yes	01	QL	2	yes	2	e	ę	2
A_oopy.Broc_A nan nan	9	yes	2	AN	ę	AN	2	yes	yes	8	6	6	2	2	2	yes	yes	yes	yes	6	yes	e.	yes	yes	yes	e e	yes	yes	yes	yes
emanpes	LG01	LG01	LG11	LG11	LG11	LG11	LG11	LG12	LG12	LG01	LG01	LG01	LG01	LG01	LG01	LG16	LG07	LG07	LG01	LG01	LG01	LG21	LG06	LG06	LG06	LG06	LG06	LG06	LG06	LG06
əuəɓ	Aco018009	Aco018038	Aco018061	Aco018084	Aco018093	Aco018101	Aco018117	Aco018141	Aco018176	Aco018265	Aco018268	Aco018269	Aco018270	Aco018272	Aco018273	Aco018321	Aco018350	Aco018356	Aco018440	Aco018451	Aco018452	Aco018478	Aco018512	Aco018514	Aco018517	Aco018526	Aco018527	Aco018533	Aco018556	Aco018557

əziz_noxə_nim	67	167	125	50	303	440	432	49	258	122	26	87	137	117	72	62	1637	680	1598	9	44	56	57	45	365	11	125	59	39	102
total_exonic_size	1774	2036	1708	1667	1749	1144	2247	2006	1658	2117	2070	2053	2381	1381	1219	526	1637	680	1598	789	1268	3509	1058	3493	365	497	4495	2258	1327	2548
ur_exons_per_gene	11	e	ы	10	4	2	m	11	4	4	6	10	m	2	4	m	1	1		6	10	14	5	12	1	4	6	16	8	80
əziz_noxə_9gs19vs	161.273	678.667	341.600	166.700	437.250	572.000	749.000	182.364	414.500	529.250	230.000	205.300	793.667	690.500	304.750	175.333	1637.000	680.000	1598.000	87.667	126.800	250.643	211.600	291.083	365.000	124.250	499.444	141.125	165.875	318.500
ədí	00_#W_ProtonPump_VHA- C_03_VATPase	NA	NA	NA	NA	00_#Ming2019_Anthocyanin_biosy nthesis	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	01b_Abscisic_acid_signal	NA	NA	10_Glucogenesis_specific_dayC3	01d_Auxin_reponse_factor	09_Circadian_clock	NA	00_#Versieux_Leafy	00_#Versieux_Leafy	NA	10_Glucogenesis_specific_dayC3	NA	10_Glucogenesis_specific_dayC3
circadian_clock																														
ysis_glycol									yes							yes					yes							yes		yes
oßnijintiod_les_sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Solanum tuberosum heat shock cognate protein 80-like (LOC102600008)_ mRNA	PREDICTED: Solanum tuberosum heat shock cognate protein 80-like (LOC10260008)_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
gyononala pinonovali 29. pinia pinonovali	AA	AA	A	A	A	ALB_F_flavanone 3-hydroxylase	A	A	AV	A	A	A	A	A	AA	A	A	A	A	A	A	AA	AA	AA	A	A	A	A	ALB_F_dihydroflavonol 4- eductase	A
Asimilation_Carboh ydrates																														
circadian_metabolis m_Wai2017	yes																						yes							
anthocyanin_SI_Ana san						yes																								
markers																									yes	yes				
draught_res																														
related_Acomosus_ Ming2015																		yes				yes								
CAM-	A	A	A	279	4	A	A	744	4	A	A	652	A	A	347	A	A	4	4	531	A	A	A	A	A	A	₹	4	A	A
gene_families_CAM C3	N N	N N	Z A	AN 7	Z A	Z A	N N	A 4	Z A	N N	N N	4A 6	N N	N N	AA 5	N N	N N	N N	N N	4A 6	N N	N N	N N	N N	N N	N N	N N	N N	N AL	Z A
MAD_roselection_CAM 	A P	AM	A AV	AM	AM	A A	AM	AM	A AV	AN	A A V	AM	AM	AM	A P	AM	AM	AM	AM	AN	AM	AN	AM	ves h	AM	A AV	A AV	AM	AN	AN
Diff_expressed_CA CM	NA I	- 4	- AN	NA I	- AN	- AN	NA I	NA I	'es	- AN	NA I	L AN	NA I	NA I	NA I	NA I	NA I	- AN	A A	- AN	- AN	NA I	- V	NA J	I AN	I AN	I AN	A A	- AN	- A
high_copy.Broc_An_an_Tilla.	Q	e e	0L	2 Q	2 2	2 Q	2	2	ies y	les l	/es	g	2 Q	2 Q	0 2	A A V	2	2	2	2	g	/es	e e	Q.	A A V	A A V	2	2	02	2
Low_copy.Broc_Ana n_Tilla.	/es r	6	0.	6	2	2	6	6	٥ ک	Q A	ν γ	6	6	ę.	p L	A	6	/es r	2	2	/es r	٥ ۷	6	/es r	Ă	A	6	/es r	/es r	/es
Single_copy.Broc_A nan_Tilla.	01	ves I	ves r	ves I	ves t	ves t	ves 1	ves I	e D	2	- 01	ves I	ves I	ves I	ves I	AM	ves I	6	ves 1	ves 1	0.	0	ves I	01	AM	- AV	ves I	6	01	0
emanpez	G01	G01	G01	G01	G01	G22	G22	G22	G22	G22	.G22	G14	G14	G14	G14	G13	G08	G08	G20	G12	G12	G02	G02	G20	G20	G20 I	G20	G20	G20	G06
əuəɓ	Aco018567 L	Aco018571 L	Aco018578 L	Aco018579 L	Aco018598 L	Aco018609 L	Aco018625 L	Aco018626 L	Aco018637 L	Ac0018645 L	Ac0018648 L	Aco018665 L	Aco018673 L	Ac0018674 L	Aco018695	Aco018780 L	Aco018851 L	Aco018853 L	Aco018892 L	Aco018949 L	Aco018974 L	Aco018978 L	Aco018982 L	Aco019042 L	Aco019058 L	Aco019059 L	Aco019060 L	Aco019065 L	Aco019068 L	Aco019096 L

	6	10	6	- 41	-	LO	6	10	0		4	10	3	0	0	-	0	e	2	2	10	10	47	0	2	ŝ	4		ŝ
əziz_noxə_nim	Ř	25	325	46⁄	2	66	125	1805	14:	4	ڻ ا	2135	ۍ ۲	14(14(б 	2	34	6	2,	135	25	14	345	102	ž	13,	8.	Ř
ezia_cinoxe_latot	1051	2479	1735	1790	4882	2946	1513	1805	1294	1096	4488	2135	1382	1276	1740	1581	2154	1445	1519	1374	1967	2005	2186	1954	734	3172	728	3188	921
ou	2	15	m	3	26	12	9	1	m G	8	30	1	12	4	5	9	17	en e	6	4	5	80	11	m a	m N	14	m	5	e
average_exon_size	150.143	165.267	578.333	895.000	187.769	245.500	252.167	1805.000	431.333	137.000	149.600	2135.000	115.167	319.000	348.000	263.500	126.706	481.667	168.778	343.500	393.400	250.625	198.727	651.333	244.667	226.571	242.667	637.600	307.000
дbe	10_Glucogenesis_specific_dayC3	NA	00_#Ming2019_Anthocyanin_biosy nthesis	NA	NA	NA	NA	NA	NA	NA	NA	NA	09_Circadian_clock	02_Aquaporins	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	01d_Auxin_reponse_factor	NA	NA	06_Drough_resistance_genes_LEA
circadian_clock																													
glucogenesis_glycol sisy	yes																		yes										
oßnijnµod"jəs ⁻ sod	NA	NA	NA	NA	PREDICTED: Glycine max cleavage and polyadenylation specificity factor subunit 1-like (LoC100801803)_ transcript variant X1_ mRNA	PREDICTED: Glycine max cleavage and polyadenylation specificity factor subunit 1-like (LoC100801803)_ transcript variant X1_ mRNA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max protein XAP5 CIRCADIAN TIMEKEEPER-like COC100814574)_ transcript variant X3_ mRNA	NA	NA	NA	PREDICTED: Glycine max T-complex protein 1 subunit alpha (LOC100805255)_ mRNA	NA	NA	NA	NA	NA	Oryza sativa Japonica Group cDNA clone.J033097J24_ full insert sequence	NA	NA	NA	NA	NA	NA
rtlavonoré_bionovsli 29_ منام_21	NA	NA	STA_F_Flavonoid 3- hydroxylase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates ydrates																													
circadian_metabolis m_Wai2017													yes																
markers anthocyanin_SI_Ana nas			yes																										
qraught_res																													s
aquaporin_reg														s															
stomata_func														¥												s			
related_Acomosus_ Ming2015																										*			
-MAQ	A)41	4	4	<	4	257	4	4	265	A	4	A	4	4	4	4	4	4	578	4	4	4	4	4	4	4	4	4
Anaiosnerm anne	Z V	A 60	2 V	Ž V	Z ∢	2 V	A 52	2 ∢	2 ∢	A 62	Z V	Z V	2 V	Z A	Z V	Z V	Z V	Z V	Z V	A 55	Z V	2 V	2 V	Z V	Z ∢	Z V	Z V	Z A	Ž
MAD_notices shirts_	A N.	A N	AI N	Z Z	Z Z	A Z	A.	A N	es N	AI N	A.	Z Z	N N	A N	A.	A.	AI N	A.	A N.	IA N.	IA N.	A N	A N	A.	A N	Z.	A N	N A	N N
MC3 WC3 WC3 CW	N N	Z Z	N SE	Z	Z	z	Z Z	Z Z	, A	Z A	N SE	Z	Z	z	Z A	SS N	Z A	Z Z	Z Z	N N	N N	N SE	Z A	z	SS N	Z	N SE	SS N	z
Algn_copy.Broc_An an_Tilla.	2 0	2 0	~ ~	2 0	2 0	2 0	2 0	2 0	2 0	2 0	× 0	2 0	2 0	z o	2 0	~ ~	2 0	2 0	2 0	es N	2 0	× ۲	es N	2 0	× 0	2 0	× ۲	ہ ک	 0
Low_copy.Broc_Ana n_Tilla.	ū o	es n	es n	, c o	es	u sə	es n	o o	o o	¢.	ē o	, c	ũ Q	es n		es n	es n	ē o	¢ o	ō Ž	ē o	es n	يخ د	<u> </u>	o o	es n	ē o	es n	
Single_copy.Broc_A nan_Tilla.	res n	0	o 2	ies n	2	2 Q		'es	'es	'es	res n	les n	les n	ر م	'es	o o		ies n	res n	0	res n	0 V	0	u sə,	res n	2	res n	م م	'es
emsnpez	306 y	G13 n	313 n	303 V	203	203	305 n	305 y	305 V	305 y	306 y	303 V	G07 y	307 r	G10 y	200 u	- 605	520 y	520 y	305 n	G07 y	522 n	G12 n	G03 y	G10 y	G10 n	G21 y	321 r	G09 V
anag	019116 L(019211 L(019275 L(019302 L(019314 L(019315 L(019356 L(019360 L(019362 L(019382 L(019394 L(019493 L(019534 L(019543 Lt	019586 L(019600 L(019622 L(019691 L(019702 L(019777 L(019822 L(019932 L(019983 L(020038 L(020099 L(020108 L(020123 L(020124 Lt	020155 L(
	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco	Aco

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əziz_noxə_nim	712	68	1033	1778	177	1772	20	42	18	47	51	10	237	83	1715	189	1796	170	13	224	23	37	143	123	3314	47	207	8	508	1232	154
ezia_oinoxe_latot	3211	1910	4367	1778	2440	1772	2022	1800	962	3852	1559	3597	1706	1993	1715	2853	1796	1490	1483	1728	2919	217	1726	1092	3314	1931	919	901	1046	1232	1273
ur_exons_per_gene	2	~	۳ ا		20		14	10	9	19	13	24	۳ ا	11		m (1	4	12	2	13	2	9	20	1	17	e e	ŝ			9
average_exon_size	1605.500	272.857	1455.667	1778.000	488.000	1772.000	144.429	180.000	160.333	202.737	119.923	149.875	568.667	181.182	1715.000	951.000	1796.000	372.500	123.583	864.000	224.538	108.500	287.667	218.400	3314.000	113.588	306.333	180.200	523.000	1232.000	212.167
jAbe	A	A	AA	A	A	A	A	A	A	A	.0_Glucogenesis_specific_dayC3	AA	A	AA	A	A	A	IA	.0_Glucogenesis_specific_dayC3	A	A	12_Aquaporins	A	.0_Glucogenesis_specific_dayC3	A	A	.0_Glucogenesis_specific_dayC3	.0_Glucogenesis_specific_dayC3	A	A	.0_Glucogenesis_specific_dayC3
circadian_clock		2	2	2	2	2	2	2	2		1	2	2	2	2	2	~	2	1	2	2	0	2	-	2	2	1	1		~	
sisk																															
glucogenesis_glycol											yes								yes					yes			yes	yes			yes
oົກາແກງດີ ເອຣີ sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	Arabidopsis thaliana DNA/RNA polymerases superfamily protein mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
- filavonoid_anthocya 29_nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
circadian_metabolis m_Wai2017																															
anthocyanin_SI_Ana asn																															
markers																															
draught_res																															
aquaporin_reg																						yes									
stomata_func																															
CAM- related_Acomosus_ Ming2015																															
Anglosperm_gene	٩Þ	686	Ą	Ą	AN	Ą	Ą	AV	Ą	A,	A1	A,	A,	4	Ą	Ą	Ą	Ą	Ą	AV	A	AN A	A)	Ą	AV	٩A	933	AN AN	Ą	٩,	4
gene_families_CAM C3	AA P	4A	4 A	4 A	AA	4 A	4 A	4 A	4 A	4 A	4 A	4 A	4 A	les l	4 A	4 A	4 A	4 A	4 A	4 A	4 A A	A A	4 A	4 A	A A	AA P	AA 5	4 A	4 A	4 A	4 A
pos_selection_CAM 	AA I	4 A	4 A	4 A	A A	4 A	A P	A P	A A	4 A	4A	4A	4 A	AA	es 1	A A	A P	A A	4 A	A A	AA	AA I	A A	A A	A A	l sə	AA I	A M	4 A	A A	A A
MC3 Diff_expressed_CA	es 2	4	4	4	4	4	4	4	se	4	∠	se	4	4	Ā	4	Ā	4	4	∠	4	A	∠	4	4	A	A	A	se	4	_∠
High_copy.Broc_An an_Tilla.	× م	0	0	0	2 0	2 0	2 0	0	A N	0	_ Z	es y	0	0	2 0	2 0	2 0	2 0	0	_ Z	2	N N	_ Z	2 0	2 0	0. V	0	0	<u>م</u>	z o	
Low_copy.Broc_Ana n_Tilla.	es n	0	0	0	0	0	0	0	Z A	es n	0	0	0	es n	0	0	0	0	0	0	es n	A	0	0	0	es n	и 0	es n	0	0	 0
nan_join_ienc_	Ň	s:	i S	i S	s:	i Si	i Si	SS D.	Z V	×	s:		s:	×	i Si	i Si	i S	i Si	i S	s:	Ň	۲ ۷	i Si	i Si	s:	Ň	u s:	Ň	u s:	u Si	s
9msnpez	500 no	309 ye	318 ye	310 ye	310 ye	311 ye	307 ye	307 ye	311 N/	319 no	302 y€	302 no	319 ye	on 905	302 ye	302 ye	315 ye	315 ye	315 ye	322 ye	322 ng	322 N,	316 ye	309 ye	322 ye	324 no	313 ye	315 nG	315 ye	315 ye	310 ye
	62 LG	63 LG	78 LG	17 LG	23 LG	59 LG	00 LG	13 LG	26 LG	75 LG	00 LG	10 LG	32 LG	43 LG	16 LG	30 LG	28 LG	33 LG	38 LG	70 LG	71 LG	75 LG	00 FG	43 LG	81 LG	62 LG	89 LG	08 LG	48 LG	51 LG	30 LG
gene	Aco0201	Aco0201	Aco0201	Aco0203	Aco0203	Aco0203	Aco0204	Aco0204	Aco0204	Aco0204	Aco0205	Aco0205	Aco0205	Aco0205	Aco0206	Aco0206	Aco0207	Aco0207	Aco0207	Aco0207	Aco0207	Aco0207	Aco0208	Aco0208	Aco0208	Aco0209	Aco0209	Aco0210	Aco0211	Aco0211	Aco0212

əziz_noxə_nim	349	53	127	459	27	151	1142	56	59	28	166	137	269	58	85	2	6	1067	116	56	673	33	307	284	5	480	74	410	62	24
esia_pinoxe_latot	1868	515	1311	1930	2443	1109	1142	2615	2105	1351	1479	2693	2258	1884	1588	814	893	1067	889	3076	1445	1853	2395	1983	696	1195	1571	1500	1060	2138
nr_exons_per_gene	e	m	4	2	10	4	1	12	13	7	7	2 L	4	ى ك	9	7	4	1	2	20	2	12	m	4	9	2	8	7	5	11
əziz_noxə_əgsıəva	622.667	171.667	327.750	965.000	244.300	277.250	1142.000	217.917	161.923	193.000	739.500	538.600	564.500	376.800	264.667	116.286	223.250	1067.000	177.800	153.800	722.500	154.417	798.333	495.750	161.500	597.500	196.375	750.000	212.000	194.364
əd/i	NA	10_Glucogenesis_specific_dayC3	NA	NA	01b_Abscisic_acid_signal	NA	NA	01d_Auxin_reponse_factor	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	NA	NA	NA	11_Glycolysis_night_C4_malate_p athway	NA	NA	00_#W_ProtonPump_VHA- H_03_VATPase	NA	NA	10_Glucogenesis_specific_dayC3	06_Drough_resistance_genes_LEA	NA	10_Glucogenesis_specific_dayC3	NA	NA
circadian_clock																														
glucogenesis_glycol sisy		yes												yes	yes				yes						yes			yes		
oßnijnµod~jəs ⁻ sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max leucinetRNA ligase_chloroplastic/mitlochondrial (LOC100781232)_transcript variant X1_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
maliato Transferace proteination. Catboh ydrates filavonoid_anthocya nin_Pitcaimia_PS	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
circadian_metabolis m_Wai2017																						yes								
markers anthocyanin_SI_Ana nas																														
aquaporin_reg draught_res																										yes				
stomata_func					yes			yes																						
CAM- related_Acomosus_ Ming2015																														
Angiosperm_gene	AA	AA	AA	AA	AA	AA	AA	AA	6373	AA	AA	AA	AA	AA	AA	5849	AN	AA	AA	AN	AA	AA	AA	5162	AA	AA	AA	AA	6221	¥
gene_families_CAM C3	٨A	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	NA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
Pos_selection_CAM _shifts_	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN
Diff_expressed_CA DC3 DC3	yes	AN	AN	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	yes	AN	AN	AN	yes	AN	AN	AN	AN	AN	yes	AN	AN	yes
High_copy.Broc_An an_Tilla.	ou	AN	Q	0L	Q	QU	ou	ou	ou	ou	Q	Q	0L	ou	Q	ou	ou	ou	yes	Q	ou	ou	ou	ou	yes	AN	Q	Q	0L	e e
Low_copy.Broc_Ana. n_Tilla.	yes	A	2	2	yes	2	2	yes	yes	2	2	2	2	yes	yes	2	2	2	2	yes	yes	yes	2	2	2	AA	2	2	2	yes
Single_copy.Broc_A nan_Tilla.	2	AN	yes	yes	2	yes	yes	2	2	yes	yes	yes	yes	2	2	yes	yes	yes	2	2	2	2	yes	yes	2	AN	yes	yes	yes	2
emanpez	LG10	LG12	LG14	LG06	LG06	LG16	LG16	LG16	LG17	LG17	LG18	LG23	LG21	LG14	LG14	LG14	LG14	LG07	LG23	LG10	LG13	LG13	LG04	LG04	LG05	LG05	LG04	LG04	LG04	LG08
ອນອຍິ	Aco021241	Aco021278	Aco021294	Aco021318	Aco021330	Aco021372	Aco021378	Aco021382	Aco021395	Aco021408	Aco021447	Aco021534	Aco021544	Aco021597	Aco021598	Aco021600	Aco021616	Aco021664	Aco021721	Aco021839	Aco021905	Aco021924	Aco021999	Aco022001	Aco022068	Aco022074	Aco022095	Aco022109	Aco022112	Aco022148

əziz_noxə_nim	105	1292	45	81	115	142	206	187	29	124	210	28	30	22	311	30	572	606	272	2762	370	41	673	222	51	114	126	182	93	96
total_exonic_size	1284	1292	1591	802	1126	3442	1655	1537	1883	2290	2648	1415	1368	781	1834	1699	572	1310	2994	2762	1447	1251	2036	1208	1387	1481	2033	582	2016	1901
	3	1	4	4	m	9	4	m	12	m	ъ	10	80	9	m	6	+	7	m		5	6	2	m	9	4	7	2	7	5
erage_exon_erage	428.000	1292.000	397.750	200.500	375.333	573.667	413.750	512.333	156.917	763.333	529.600	141.500	171.000	130.167	611.333	188.778	572.000	655.000	998.000	2762.000	723.500	139.000	1018.000	402.667	231.167	370.250	290.429	291.000	288.000	380.200
əd/j	NA	NA	NA	00_#W_ProtonPump_VHA- G_03_VATPase	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	00_#15_calciumdependent_protK	NA	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	00_#W_VacuolarAcidInvertase_AI	00_#W_VacuolarAcidInvertase_AI						
circadian_clock																														
glucogenesis_glycol ysis									yes										yes			yes						yes		
oßnijnuod_jəs_sod	NA	NA	Populus trichocarpa adenosylhomocysteinase family protein (POPTR_0017s08610g) mRNA_ complete cds	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
gyontine_bionovall 29_aimiao19_nin	ALB_F_anthocyanin 5-aromatic acyltransferase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh ydrates																														
circadian_metabolis m_Wai2017				yes																									yes	yes
anthocyanin_SI_Ana nas																														
markers																														
qraught_res																														
aquaporin_reg																														
Ming2015 -																														
CAM- related Acomosus											yes																			
Angiosperm_gene	NA	AN	A	AN	AA	AN	6284	¥	¥	¥	¥	5299	¥	6449	AA	AN	¥	Ą	¥	¥	5940	AN	¥	5328	6274	AA	¥	¥	AN	AN
MAD_seilims1_eneg	ΝA	AN	ΥN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
MAD_notzelection_CAM	ΝA	ΥN	ΥN	AN	AN	AN	AN	AN	٩N	٩N	AN	AN	AN	AN	AN	AN	AN	AN	yes	٩N	AN	AN	AN	AN	AN	AN	AN	٩N	yes	٩N
Diff_expressed_CA MC3	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN
- high_copy.Broc_An an Tilla.	AN	Q	6	Q	оц	ou	Q	Q	e e	e	e e	e.	Q	AN	ou	ou	AN	Q	e	e	Q	Q	Q	оц	ou	Q	Q	٩N	e E	ou
Low_copy.Broc_Ana n_Tilla.	AA	2	yes	yes	2	e	2	2	yes	2	2	2	2	AA	2	2	AA	2	2	2	yes	yes	2	2	2	2	2	¥	yes	yes
Single_copy.Broc_A nan_Tilla.	ΝA	yes	2	2	yes	yes	yes	yes	2	yes	yes	yes	yes	AN	yes	yes	AA	yes	yes	yes	2	9	yes	yes	yes	yes	yes	AN	e	e
amanpaz	LG08	LG08	LG17	LG16	LG16	LG16	LG08	LG02	LG02	LG02	LG22	LG18	LG18	LG18	LG09	LG01	LG01	LG18	LG03	LG03	LG03	LG01	LG01	LG24	LG24	LG08	LG08	LG06	LG20	LG20
ອນອຍິ	Aco022172	Aco022185	Aco022207	Aco022226	Aco022281	Aco022288	Aco022306	Aco022383	Aco022384 1	Aco022402	Aco022525	Aco022558	Aco022561	Aco022563	Aco022583	Aco022694	Aco022696	Aco022713	Aco022846	Aco022847	Aco022851	Aco022874	Aco022875	Aco022927	Aco022932	Aco022947	Aco022956	Aco023000	Aco023030	Aco023036

	əziz_nox9_nim	86	457	585	113	437	86	161	485	137	152	49	101	37	1280	406	158	66	39	61	72	339	107	728	1928	304	209	34	35	31	1730
M 2 M 2 M 3 M 3 M 4 <td></td> <td>519</td> <td>333</td> <td>288</td> <td>327</td> <td>300</td> <td>986</td> <td>816</td> <td>023</td> <td>409</td> <td>185</td> <td>583</td> <td>182</td> <td>304</td> <td>280</td> <td>190</td> <td>323</td> <td>358</td> <td>0.75</td> <td>444</td> <td>441</td> <td>472</td> <td>275</td> <td>728</td> <td>928</td> <td>124</td> <td>416</td> <td>450</td> <td>457</td> <td>0.75</td> <td>730</td>		519	333	288	327	300	986	816	023	409	185	583	182	304	280	190	323	358	0.75	444	441	472	275	728	928	124	416	450	457	0.75	730
	total exonic size		1	1	1	2	1	1	1	1	1	1	2	1	1		2		1	1	1	1	1		1	1	1			6	1
1 1	ur_exons_per_gene	3	5	2	4	2	6	4	2	4	4	10	4 1	10	1	8	9	5	80	7	8	2	9	1	-	2	2	e e	2	3 22	1
	average_exon_size	173.000	666.500	644.000	331.750	1150.000	220.667	454.000	511.500	352.250	296.250	158.300	311.71	130.400	1280.000	730.000	387.167	179.000	134.375	206.286	180.125	736.000	212.500	728.000	1928.000	562.000	283.200	150.000	91.400	139.773	1730.000
	çhbe	02_Aquaporins	00_#Ming2019_Anthocyanin_biosy nthesis	00_#Ming2019_Anthocyanin_biosy nthesis	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	NA	NA	03_VATPase	06_Drough_resistance_genes_LEA	NA	NA	NA	06_Drough_resistance_genes_LEA	NA	NA	NA
und matrix matrix <td>circadian_clock</td> <td></td>	circadian_clock																														
0 0	ylucogenesis_glycol glucogenesis_glycol						yes											yes													
θ δ	oɓnjintiod_ləs_zoq	NA	NA	NA	NA	NA	PREDICTED: Beta vulgaris subsp. vulgaris glucose-1-phosphate adenylytransferase small subunit_chloroplastic/amyloplastic (L.CC.104903071, mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Populus trichocarpa Argonaute 4 family protein (POPTR_0001s22710g) mRNA_ complete cds	NA
3023303 102 <	yonace	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $																							yes								
$ \begin{array}{c c c c c c c c c c c c c c c c c c c $	circadian_metabolis																														
1 1	markers anthocyanin_SI_Ana		yes	yes																											
No. No. <td>qısınght_res</td> <td></td> <td>se</td> <td></td> <td></td> <td></td> <td>se</td> <td></td> <td></td> <td></td>	qısınght_res																							se				se			
Constraint Constra	aquaporin_reg	es																						ž				× ا			
Occurrent Constrained Comme Gene Gene Gene Constrained Constraine Constraine Const	stomata_func	~																													
Control Control Control Control Control 00023363 LGG0 M M M M M M 000233133 LG19 MS M M M M M M M 000233133 LG19 Ves M	related_Acomosus_ Ming2015																														
Open consistent Consent Consistent Conse		A	₹	A	A	A	A	A	A	A	A	013	A	802	A	₹	₹	₹	977	₹	978	A	A	A	A	A	₹	A	A	A	A
Generation Genera		Z Z	Z A	Z A	Z A	Z A	Z A	z z	Z A	Z A	Z Z	A A	Z Z	A 4	Z	Z A	Z Z	Z A	9 4	Z Z	A 6	Z Z	Z	Z Z	Z Z	Z Z	Z Z	Z A	Z	Z Z	Z
Openance	NAJ_norselection_com	Z Z	Z A	Z A	Z A	Z A	Z A	z z	Z A	Z Z	Z Z	Z A	Z Z	Z Z	Z Z	Z A	Z Z	Z Z	Z Z	Z Z	Z Z	Z Z	Z Z	Z Z	Z Z	Z Z	Z Z	Z Z	Z	Z Z	sa
gene gene no no <th< td=""><td>MC3 MC3 WC3</td><td>A N</td><td>Z A</td><td>Z A</td><td>Z A</td><td>Z A</td><td>A</td><td>A</td><td>es</td><td>A</td><td>A</td><td>Z A</td><td>es N</td><td>A N</td><td>Z A</td><td>Z A</td><td>Z A</td><td>Z A</td><td>Z A</td><td>es 🗸</td><td>A</td><td>A A</td><td>A N</td><td>N N</td><td>Z A</td><td>A</td><td>Z A</td><td>A</td><td>es 🗸</td><td>A A</td><td>A V</td></th<>	MC3 MC3 WC3	A N	Z A	Z A	Z A	Z A	A	A	es	A	A	Z A	es N	A N	Z A	Z A	Z A	Z A	Z A	es 🗸	A	A A	A N	N N	Z A	A	Z A	A	es 🗸	A A	A V
Openance	High_copy.Broc_An an_Tilla.	A N	2	2	2	2		2	0	2	2	2	ē Ā	 _0	 	2	2	2	2	0	0	2	0	A N	0	2	2	2	0 7	2	2
genne genne genne 0.0023063 LG07 NA 1 0.0023063 LG07 NA 1 0.00230308 LG03 NA 1 0.00230308 LG03 NA 1 0.00230308 LG09 Yes 1 0.002303135 LG19 Yes 1 0.0023135 LG10 Yes 1 0.0023135 LG11 Yes 1 0.0023315 LG11 Yes 1 0.0023315 LG11 Yes 1 0.0023313 LG10 Yes 1 0.0023313 LG11 Yes 1 0.0023313 LG11 Yes 1 0.0023313 LG21 Yes 1 0.0023313 LG21 Yes 1 0.002331 LG24 Yes 1 0.0023353 LG06 Yes 1 0.0023353 LG06 Yes 1	Low_copy.Broc_Ana n_Tilla.	AA AA	les n	les n	Q	Q	les n	0	les n	u Q	u Q	u Q	u sə,	u Q	u Q	Q	g	u sə,	g	les n	u Q	Q	les n	∠ ₹	0	0	0	les n	les n	u sə/	u Q
gene gene 0.00236/2 LG0/7 I 0.002308/2 LG0/9 I 0.0023175 LG11 I 0.0023175 LG11 I 0.0023190 LG10 I 0.0023191 LG10 I 0.0023319 LG10 I 0.0023369 LG14 I 0.0023369 LG14 I 0.0023369 LG24 I 0.0023369 LG14 I 0.0023369 LG24 I 0.0023851 LG20 I 0.0023851 LG20 I 0.0023851 LG20 <td>Single_copy.Broc_A nan_Tilla.</td> <td>A AV</td> <td>6</td> <td>Q Q</td> <td>/es</td> <td>/es</td> <td>2 2</td> <td>es r.</td> <td>Q Q</td> <td>/es</td> <td>/es</td> <td>/es</td> <td>٥ ک</td> <td>'es r</td> <td>'es</td> <td>/es</td> <td>/es</td> <td>6</td> <td>les L</td> <td>6</td> <td>/es</td> <td>les r.</td> <td>6</td> <td>AM</td> <td>les r.</td> <td>/es</td> <td>les r.</td> <td>e e</td> <td>6</td> <td>ر د</td> <td>'es</td>	Single_copy.Broc_A nan_Tilla.	A AV	6	Q Q	/es	/es	2 2	es r.	Q Q	/es	/es	/es	٥ ک	'es r	'es	/es	/es	6	les L	6	/es	les r.	6	AM	les r.	/es	les r.	e e	6	ر د	'es
gene gene gene gene gene gene gene gene	əmsnpəz	307	200 L	200	605	G19 >	G19 r	G11)	G10 r	302 y	G02 >	G16 >	318 r	524 y	324 y	521 >	304	306	309	309	309 >	G19 >	G24 r	G14 P	G14 >	G20)	G20 >	320 r	522 r	G14 r	314 y
	gene	:0023062 Li	20023087 Li	:0023089 L	:0023092 L	co023132 L	20023139 L	0023175 L	:0023190 L	co023264 L	co023275 L	:0023302 L	co023369 Li	co023410 L	co023418 L	c0023513 L	:0023525 Li	co023573 L	:0023597 L	:0023600 L	:0023607 L	co023620 L	co023631 L	co023654 L	:0023656 L	c0023689 L	:0023810 L	co023812 L	20023961 Li	0024014 L	:0024020 Li

əziz_noxə_nim	71	181	5	2252	164	39	95	13	1064	146	191	1388	1499	2072	220	77	201	60	101	86	65	15	77	193	348	56	125	1205	48	1637	14
esia_oinoxe_faiot	3264	2610	1524	2252	1179	1285	3003	1818	1064	940	2967	1388	1499	2072	1047	3045	2446	1365	1113	2283	1264	6372	1070	1357	2095	2965	2185	1205	2200	1637	3416
ur_exons_per_gene	21	з	20		5	6	16	7	1	۳ ا	4				5	19	2	10	2	۳ ا	8	46	20	e co	2	14	7		13	1	23
average_exon_size	155.429	870.000	304.800	2252.000	589.500	142.778	187.688	259.714	1064.000	313.333	741.750	1388.000	1499.000	2072.000	523.500	160.263	1223.000	136.500	222.600	761.000	158.000	138.522	214.000	452.333	1047.500	211.786	312.143	1205.000	169.231	1637.000	148.522
ədAş	11_Glycolysis_night_C4_malate_p athway	NA	10_Glucogenesis_specific_dayC3	NA	NA	10_Glucogenesis_specific_dayC3	10_Glucogenesis_specific_dayC3	02_Aquaporins	NA	10_Glucogenesis_specific_dayC3	NA	00_#Ming2019_Anthocyanin_biosy nthesis	NA	NA	06_Drough_resistance_genes_LEA	00_#10_Glucogenesis_specific_da yC3	NA	NA	NA	NA	NA	NA	NA	NA	NA	01d_Auxin_reponse_factor	NA	NA	NA	NA	01b_Abscisic_acid_signal
circadian_clock																															
glucogenesis_glycol	yes		yes			yes	yes			yes						yes															
oguliuhoq_ləz_zoq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	PREDICTED: Glycine max adagio protein 1-like (LOC100805523)_ mRNA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Voriates	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	ALB_F_chalcone isomerase	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Assimilation_Carboh																															
circadian_metabolis m_Wai2017																															
antnocyanin_5i_Ana nas												s																			
markers												<u>></u>																			
draught_res															se																
aquaporin_reg								es							×																
stomata_func								~																		s					ŝ
related_Acomosus_ Ming2015																s s										У€					¥
CAM-													-			ye					9		8						9		
Angiosperm_gene	NA	AA	A	AA	A	AA	AA	AA	AA	¥	¥	¥	¥	A	A	A	AA	613	AA	¥	565	A	678:	AA	AA	ΝA	AA	AA	617	NA	AA
MAD_sellimst_eneg	ΝA	AN	AN	A N	AN	AN	AN	AN	AN	AN	AA	AA	¥ Z	AA	AA	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	ΝA	AN	AN	AN	AN	ΥN
MAD_noiselection_CAM	٩N	٩N	٩N	٩N	٩N	٩N	٩N	ΥN	٩N	AN	٩N	٩Z	¥ Z	A N	٩N	٩N	AN	٩N	٩N	٩N	٩N	٩N	٩N	٩N	٩N	٩N	٩N	٩N	٩N	٩N	٩N
AD_iff_expressed_CA	٩N	ΑN	AN	yes	AN	AN	AN	AN	yes	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	AN	٩N	yes	AN	AN	AN	NA	AN	yes	AN	ΑN	AN
High_copy.Broc_An an_Tilla.	ou	ou	ou	ou	ou	ou	yes	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	ou	yes	ou	ou	ou	ou	ou	ou	ou	ou	ou
Low_copy.Broc_Ana n_Tilla.	yes	Q	yes	yes	e	2	2	yes	2	yes	2	yes	2	2	2	6	2	2	2	yes	Q	2	Q	e	9	Q	2	2	yes	Q	8
Single_copy.Broc_A nan_Tilla.	ou	yes	2	2	yes	yes	2	2	yes	2	yes	2	yes	yes	yes	yes	yes	yes	yes	2	yes	2	yes	yes	yes	yes	yes	yes	QL L	yes	yes
emanpes	_G20	-G20	-G21	-G05	-G01	-G07	.G11	.G03	-G01	-G01	G01	.G19	_G19	-G24	.G15	-G04	.G08	-G01	-G10	-G06	_G17	-G10	-G05	-G06	-G20	-G24	-G24	-G24	-G19	-G10	-G01
деле	Aco024092	Aco024146	Aco024224	Aco024279	Aco024340	Aco024368	Aco024370	Aco024440	Aco024489	Aco024553	Aco024634	Aco024663	Aco024665	Aco024749	Aco024760	Aco024818	Aco024860	Aco024898	Aco025098	Aco025121	Aco025167	Aco025277	Aco025306	Aco025351	Aco025372	Aco025401	Aco025404	Aco025405	Aco025417	Aco025467	Aco025560

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	əziz_noxə_nim	70	44	66	62	46	145	467	509	12	173	810	7	64	85	70	124	46	69	173	139	1343	295	124	35	115	111	140	88	102	137
	fotal_exonic_size	1123	3081	2093	3 1776	t 2623	1759	2 1686	1204	845	1119	3498	9 884	1435	506 t	t 558	t 1445	1844	487	3 2733	1535	1343	980	t 2604	1333	1447	\$ 4004	3 723	1116	1030	1 2271
ŝ	ur_exons_per_gene	~	16	- ^w	"	- F	2,			14				0,	7	~	7	0,							10	2,					
	average_exon_size	140.375	162.158	261.625	222.000	187.357	351.800	843.000	602.000	120.714	279.750	1749.000	98.222	159.444	226.250	139.500	361.250	204.889	162.333	911.000	511.667	1343.000	326.667	651.000	133.300	289.400	667.333	241.000	223.200	206.000	567.750
	ədAı	AA	AA	AA	10_Glucogenesis_specific_dayC3	0_#W_StomatalMovement_NHX1/ NHX2_01b_Abscisic_acid_signal	AA	AA	AA	09_Circadian_clock	AA	AA	11_Glycolysis_night_C4_malate_p athway	10_Glucogenesis_specific_dayC3	AA)1d_Auxin_reponse_factor	AA	L0_Glucogenesis_specific_dayC3	AA	10_Glucogenesis_specific_dayC3	AA	AA	14_Oxygen_evolving_enhancer_O	AA	ЧА	AA	11_Glycolysis_night_C4_malate_p athway	L0_Glucogenesis_specific_dayC3	AA	L0_Glucogenesis_specific_dayC3	A
	_	2	2	2	1	02	2	2	2	0	2	2	10	1	~	0	~	1	~		2	~	0 0	2	2	~	6 1	-	2	1	
	circadian_clock									yes																					
1	ysis_ glucogenesis_glycol				yes								yes	yes				yes		yes							yes	yes		yes	
	oônijnuod‴jəs sod	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	Populus trichocarpa putative cathepsin B-like protease family protein (POPTR_0002s18500g) mRNA_ complete cds	NA	NA	NA	NA	NA	NA
1	κγοοrtina_biorovalî† 29_βinieotra	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
L	Assimilation_Carboh ydrates																						es								
	circadian_metabolis m_Wai2017					s																									
E	antnocyanin_51_Ana					~																									
	markers																														
	qraught_res																														
	aquaporin_reg																														
	stomata_func					es										/es															
	related_Acomosus_ 2102gniM																														
	auab_iuuadsoibuv	679	670	Ą	A	۲ı	A	Ą	857	AI.	825	Ą	A	۲	843	Al	۲Þ	A	Ą	A1	Ą	۲	AI.	Ą	٩	Al.	AI.	Ą	432	٩	A.
	gene_families_CAM C3	AA 6	AA B	AM	AN	A N	A A V	A A V	A A	A A	AA 6	AM	A A	AM	AA B	AN	A P	A A A	AA	AA	A A	AM	AN	AN	AN	AN	AN	Z A	AA 6	A A	4
	pos_selection_CAM 	A P	A A	4 A	4 A	A A	A P	A A	es 1	A A	4 A	4 A	4 A	A P	AA P	A A	AA P	A N	A A	4 A	es 1	A A	A P	A A	es	A P	A A	A A	4 A	A P	4
		۷ ۲	∠	s	∠	∠ 4	∠ ∀	∠ ₹	× م	۷ ۲	∠	∠	∠	Z V	۷ ۷	Z V	۷ ۷	Z V	s	∠	A A	Z V	×	∠	A	۷ ۲	∠	∠	∠	∠	
	Algh_copy.Broc_An an_Tilla.	Z 0	Z o	es yt	Z o	z o	Z o	z o	z o	Z o	z o	z o	z o	Z O	v v	z o	v v	v v	0 X	z o	z o	z o	Z o	z o	z o	v v	z o	es N	z o	Z 0	z o
F	ene_poly.eroc_market. .nn	ů c	u se	, v	u se	ت د	ů c	ů c	<u> </u>	ú c	<u> </u>	<u> </u>	c c	ú c	u se	u se	ŭ c	ů c	u se	u se	<u> </u>	ú c	ů c	Ċ.	Č O	c c	Č O	Ś.	<u> </u>	ù Se	<u> </u>
ŀ		s nc	ž	Ĕ	ž	<u>×</u>	s nc	s nc	s S	s nc	s S	s S	s S	s nc	, X	ž	s nc	s nc	<u> </u>	<u>×</u>	s S	s nc	s S	s S	S S	s nc	s S	Ĕ	s S	ž	s S
	Sinale conv.Broc A	J2 ye	23 no	33 no	32 no	I3 IIO	l3 ye)7 ye	23 ye	32 ye	24 ye	24 ye	L7 ye	J5 ye	00 8C)2 no	39 ye	24 ye	22 no)5 no	21 ye	24 ye	39 ye	22 ye	23 ye	34 ye	34 ye	35 no	74 ye	21 no)1 ye
	0.000000	3 LGC	39 LG2	.3 LG2	5 LGC	3 LG1	4 LG1	17 LGC	12 LG2	11 LGC	17 LG2	18 LG2	2 LG1)9 LGC	39 LGC	i0 LGC	3 LGC	0 LG2	102 P	3 LGC	t4 LG2	3 LG2	15 LGC	19 19	17 LG2	1 LGC	19 LGC	13 LGC	N LGC	15 LG2	4 LGC
	gene	Aco02562	Aco02576	Aco02577	Aco02585	Aco02606	Aco02606	Aco02609	Aco02648	Aco02663	Aco02664	Aco02664	Aco02665	Aco02680	Aco02686	Aco02704	Aco02711	Aco02721	Aco02729	Aco02735	Aco02748	Aco02761	Aco02769	Aco02772	Aco02776	Aco02785	Aco02795	Aco02838	Aco02839	Aco02855	Aco02869

sziz_noxs_nim	203	56	8	500	395	2255	59	2840	295	32	15	38	204
	940	666	381	543	026	255	325	340	121	964	020	125	305
total_exonic_size	16	56		16	0,	22	10	28	3	0,	10	17	
ou-ger_per_gene	3	14	e	2	2	1	10	1	e	2	9	9	2
average_exon_size	646.667	214.214	227.000	771.500	485.000	2255.000	132.500	2840.000	1140.333	482.000	170.000	237.500	402.500
ədAş	NA	01d_Auxin_reponse_factor	10_Glucogenesis_specific_dayC3	NA	NA	NA	10_Glucogenesis_specific_dayC3	NA	NA	01d_Auxin_reponse_factor	NA	10_Glucogenesis_specific_dayC3	NA
circadian_clock													
glucogenesis_glycol ysis_			yes				yes					yes	
oßnilutioq_les_eoq	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
styootine_bionovslit 29_simisoii9_nin	AA	AA	A	AA	A	AA	AA	AA	AA	AA	AA	AA	NA
Assimilation_Carboh ydrates										_	_		
circadian_metabolis 7102isW_m malateTensterase													
andugnt markers anthocyanin_SI_Ana anthocyanin_SI_Ana													
aduaponn_reg													
stomata_tunc		s								<i></i>			
related_Acomosus_		, Ye								ye			
-MAC													
Angiosperm_gene C3	NA	AA	AA	NA	AA	NA	NA	NA	MA	NA	AA	AA	¥
Zninz_ MAD_2eilims1_eneg	ΝA	ΝA	NA	NA	NA	NA	NA	NA	ΝA	ΝA	yes	ΝA	ΥN
MC3_MC3 MAD_non_CAM	ΝA	٩N	AN	NA	AN	NA	NA	NA	NA	ΝA	ΑN	٩N	AN
Diff_expressed_CA	٩N	٩N	٩N	ΑN	yes	ΝA	ΝA	ΑN	٩N	٩N	٩N	٩N	yes
High_copy.Broc_An	ou	ou	Q	ou	Q	ou	ou	ou	Q	ΝA	ou	Q	e E
Low_copy.Broc_Ana	8	yes	yes	8	2	8	yes	8	2	AA	yes	yes	e
A_oor&.vqoo_elgni2	yes	Q	Q.	yes	yes	yes	QL	yes	yes	AN	Q	Q.	yes
emsnpez	LG01	LG17	LG03	LG13	LG12	LG07	LG21	LG11	LG07	LG01	LG04	LG20	LG20
деле	Aco028698	Aco029197	Aco029846	Aco029912	Aco030202	Aco030327	Aco030333	Aco030647	Aco030651	Aco031044	Aco031251	Aco031276	Aco031754

Legend for table S1.		
gene	gene identifier	
seqname	sequence location	1
Single_copy.Broc_Anan_Tilla.	present in single copy category	output of clustering of transcriptome assemblies
Low_copy.Broc_Anan_Tilla.	present in low copy category (=<5 copies)	output of clustering of transcriptome assemblies
High_copy.Broc_Anan_Tilla.	present in high copy category (>5 copies)	output of clustering of transcriptome assemblies
Diff_expressed_CAMC3	Significant for differential Expression analysis genes between CAM and C3 species	de la Harpe et al., 2020
pos_selection_CAM_shifts	genes that underwent adaptive protein evolution during C3/CAM transitions	de la Harpe et al., 2021
gene_families_CAMC3	belonging to gene families with putative association to C3 vs CAM phenotype in Tillandsia spp	de la Harpe et al., 2021
Angiosperm_gene	orthologous to Angiosperm353 gene	citation - table 2
CAM-related_Acomosus_Ming2015	Putative CAM-related genes from pineapple genome assembly	citation - table 2
stomata_func	putatively associated with stomatal function	citation - table 2
aquaporin_reg	putatively associated with aquaporin regulation	citation - table 2
draught_res	putatively associated with drought-resistance	citation - table 2
markers	previously used marker in bromeliad phylogenies (phytc, prk, malate synthase, NADH1, PGIC, RBP2, XDH, LEAFY, AGT1, PEPC, PHYA, PHYAE/B)	citation - table 2
anthocyanin_SI_Ananas	genes regulating anthocyanin biosynthesis and self incompatibility in Ananas	citation - table 2
circadian_metabolism_Wai2017	genes coding for circadian expression or key roles in metabolism in Ananas	citation - table 2
malateTransferase_Assimilation_Carbohydrates	putatively associated with malate transferase in the vacuole, assimilation of inorganic carbon and compartmentalization of carbohydrates	citation - table 2
fllavonoid_anthocyanin_Pitcairnia_PS	genes orthologous to transcripts encoding for key enzymes in the flavonoid and anthocyanin biosynthesis pathways in Pitcairnia transcriptome	citation - table 2
pos_sel_portullugo	under positive selection within the portullugo clade (Caryophyllales)	citation - table 2
glucogenesis_glycolysis	putatively associated with glucogenesis and starch synthesis	citation - table 2
circadian_clock	putatively associated with circadian clock	citation - table 2
łype	defined as candidate genes, as follows: 1. Stomate opening/ closing genes (SOCG): 1.1 CO2- sensing HIGH LEAF TEMP (HLT 1.2 Abscissic acid signalling 1.3 K+/Ca2+/Cl2+ channels + Na+/H+ anti transporter 1.4 Auxin reponse factor (ARF4) 2. Aquaporins 3. V-ATPase 4. Oxygen evolving enhancer (OEE) 5. Chloroplasts activity 6. Drough resistance genes (LEA) 7. Mitochondrial pyruvate transporters 09. Circadian clock 10. Glucogenesis specific (day: C3 pathway) 11. Glycolysis night C4 malate pathway)	

Table S2 Categories of pathways and t source and number of genes in each ca	traits us ategory.	ed to choose genes of interest for the Bromeliad1776 bait set, including literature
category num	nber_genes	citation
Differentialy expressed between CAM/C3	190	Harpe, Marylaure De La et al. 2018. "Genomic Footprints of Repeated Evolution of CAM Photosynthesis in Tillandsioid Bromeliads." IN PRESS: 495812.
showing positive selection [dN/dS] along CAM shifts	22	Harpe, Marylaure De La et al. 2018. "Genomic Footprints of Repeated Evolution of CAM Photosynthesis in Tillandsioid Bromeliads." IN PRESS: 495812.
Delong in gene families putatively associated to CAM/C3 correlated trait syndrome	57	Harpe, Marylaure De La et al. 2018. "Genomic Footprints of Repeated Evolution of CAM Photosynthesis in Tillandsioid Bromeliads." IN PRESS: 495812.
Matching Angiosperm-353 set	281	Johnson, Matthew G et al. 2019. "A Universal Probe Set for Targeted Sequencing of 353 Nuclear Genes from Any Flowering Plant Designed Using K-Medoids Clustering" ed. Susanne Renner. Systematic Biology 68(4): 594–606
Putative CAM-related genes from pineapple genome assembly	31	Ming, Ray et al. 2015. "The Pineapple Genome and the Evolution of CAM Photosynthesis." Nature Genetics 47(12): 1435-42.
putatively associated with stomatal function	32	Christin, Pascal-Antoine et al. 2014. "Shared Origins of a Key Enzyme during the Evolution of C4 and CAM Metabolism." Journal of Experimental Botany 65(13): 3609–21. Winter, Klaus, and Joseph A. M. Holtum. 2014. "Facultative Crassulacean Acid Metabolism (CAM) Plants: Powerful Tools for Unravelling the Functional Elements of CAM Photosynthesis." Journal of Experimental Botany 65(13): 3425–41.
putatively associated with aquaporin regulation	21	Vera-Estrella, Rosario, Bronwyn J. Barkla, Julio C. Amezcua-Romero, and Omar Pantoja. 2012. "Day/Night Regulation of Aquaporins during the CAM Cycle in Mesembryanthemum Crystallinum." Plant, Cell & Environment 35(3): 485–501.
putatively associated with malate transferase in the vacuole, assimilation of inorganic carbon and compartmentalization of carbohydrates	32	Cosentino, Cristian et al. 2013. "Proteomic Analysis of Mesembryanthermum Crystallinum Leaf Microsomal Fractions Finds an Imbalance in V-ATPase Stoichiometry during the Salt-Induced Transition from C3 to CAM." Biochemical Journal 450(2): 407–15.
putatively associated with drought-resistance	52	Xiao, Benze, Yuemin Huang, Ning Tang, and Lizhong Xiong. 2007. "Over-Expression of a LEA Gene in Rice Improves Drought Resistance under the Field Conditions." Theoretical and Applied Genetics 115(1): 35–46.
putatively associated with circadian clock	8	McClung, C. Robertson. 2006. "Plant Circadian Rhythms." The Plant Cell 18(4): 792–803.
		Cushman, John C. et al. 2008. "Large-Scale MRNA Expression Profiling in the Common Ice Plant, Mesembryanthemum Crystallinum, Performing C3 Photosynthesis and Crassulacean Acid Metabolism (CAM)." Journal of Experimental Botany 59(7): 1875–94.
putatively associated with glucogenesis and starch synthesis	288	Antony, Edna et al. 2008. "Cloning, Localization and Expression Analysis of Vacuolar Sugar Transporters in the CAM Plant Ananas Comosus (Pineapple)." Journal of Experimental Botany 59(7): 1895–1908.
		Wada, Hajime, and Norio Murata. 2009. Lipids in Photosynthesis: Essential and Regulatory Functions. Springer Science & Business Media.
under positive selection within the portullugo clade (Caryophyllales), lineage contains multiple evolutionary origins of all known photosynthesis types	86	Goolsby, Eric W. et al. 2018. "Molecular Evolution of Key Metabolic Genes during Transitions to C4 and CAM Photosynthesis." American Journal of Botany 105(3): 602–13.
transcripts encode for key enzymes in the flavonoid and anthocyanin biosynthesis pathways in Pitcairnia transcriptome	119	Palma-Silva, C., M. Ferro, M. Bacci, and A. C. Turchetto-Zolet. 2016. "De Novo Assembly and Characterization of Leaf and Floral Transcriptomes of the Hybridizing Bromeliad Species (Pitcaimia Spp.) Adapted to Neotropical Inselbergs." Molecular Ecology Resources 16(4): 1012–22.
circadian expression or key roles in metabolism	41	Wai, Ching M. et al. 2017. "Temporal and Spatial Transcriptomic and MicroRNA Dynamics of CAM Photosynthesis in Pineapple." The Plant Journal 92(1): 19–30.
anthocyanin biosynthesis and self incompatibility in Ananas	21	Chen, Li-Yu et al. 2019. "The Bracteatus Pineapple Genome and Domestication of Clonally Propagated Crops." Nature Genetics 51(10): 1549-58.
		Machado, Talita Mota et al. 2020. "Systematics of Vriesea (Bromeliaceae): Phylogenetic Relationships Based on Nuclear Gene and Partial Plastome Sequences." Botanical Journal of the Linnean Society 192(4): 656–74.
		Schulte, Katharina, Michael H. J. Barfuss, and Georg Zizka. 2009. "Phylogeny of Bromelioideae (Bromeliaceae) Inferred from Nuclear and Plastid DNA Loci Reveals the Evolution of the Tank Habit within the Subfamily." Molecular Phylogenetics and Evolution 51(2): 327–39.
marker (nhvirc nrk malate svinthase NADH1 DGIC PRD3 YDH		Sass, Chodon, and Chelsea D. Specht. 2010. "Phylogenetic Estimation of the Core Bromelioids with an Emphasis on the Genus Aechmea (Bromeliaceae)." Molecular Phylogenetics and Evolution 55(2): 559–71.
LEAFY, AGT1, PEPC, PHYA, PHYAE/B)	13	Versieux, Leonardo M. et al. 2012. "Molecular Phylogenetics of the Brazilian Giant Bromeliads (Alcantarea, Bromeliaceae): Implications for Morphological Evolution and Biogeography." Molecular Phylogenetics and Evolution 64(1): 177–89.
		Heller, Sascha et al. 2017, "Barcoding of Bromeliaceae (Poales)." Genome 60(11): 943-45.
		Barfuss, Michael H. J. et al. 2016. "Taxonomic Revision of Bromeliaceae Subfam. Tillandsioideae Based on a Multi-Locus DNA Sequence Phylogeny and Morphology." Phytotaxa 279(1): 1–97.
		private correspondence
all	10	JI Comparison of the second seco

	sisylsns nøp-qoq ni	yes	yes	yes	yes	yes	yes	ou	yes	yes	yes	yes	yes	yes	yes	yes			_					
	collector	G. Yardeni	W. Welz 3132	Kamm s.n.	G. Noller 9106	W. & S. Till 7116	W. & S. Till 7004	KD. & R. Ehlers EM890701	M de la Harpe	M de la Harpe	G. Yardeni	W. & S. Till 7112	W. & S. Till 7043	M de la Harpe	M de la Harpe	G. Yardeni	no data	E. Trauner s.n.	no data (old holdings)	W. & S. Till 12012	W. Rauh 21147a	H. & I. Seethaler s.n.	W. & S. Till 15050	FJ. Hase s.n.
	əq\1_əlqms	silicagel dried	fresh	fresh	fresh	fresh	fresh	silicagel dried	silicagel dried	silicagel dried	silicagel dried	fresh	fresh	silicagel dried	silicagel dried	silicagel dried	fresh	fresh	fresh	fresh	fresh	fresh	fresh	fresh
	herbarium acc.	unknown	WU: 0006333, 0011189, 0013562	WU: 0013708	WU: 0006321	WU: 0013642	WU: 0013632, 0013754	WU: 0002124	unknown	unknown	unknown	WU: 0003058	WU: 0001725, 0003008	unknown	unknown	unknown	WU: HBV: WU-0027605 (photo)	WU: 0007683, 0009236	WU: 0004316, 0005675	WU: 0015907 (photo)	WU: 0008378	WU: 0001763, 0008630, 0010416	WU: 0008124	WU: 0008343, 0011768
	9771mo18_N	4	Ч	Ч	Ч	Ч	Ч	Ч	7	4	7	Ч	÷	9	9	4								
2	E2EoipnA_N	4	Ч	Ч	1	Ч	Ч	Ч	2	4	7	Ч	Ч	9	9	4								
illandsiá	locality code	fas_VER	ES GUA		SOL_GUA	PUN CR	HER_CR		MH124	MH027	lei_VER	ALA_CR	CAR CR	_ MH016	MH098	fol_VER								
subgenus 7	source	field collection	HBV: WU-0025390 (WU-B97/94)	HBV: WU-0025334 (WU-B99B53-1)	HBV: WU-0026950 (WU-B103/94)	HBV: WU-0024657 (WU-B179/91)	HBV: WU-0024655 (WU-B99/91)	HBV: WU-0024656 (WU-B108/94)	field collection (Sinergia)	field collection (Sinergia)	field collection	HBV: WU-0024715 (WU-B82/91)	HBV: WU-0000663 (WU-B84/91)	field collection (Sinergia)	field collection (Sinergia)	field collection	HBV: WU-0027605	HBV: WU-0023734 (WU-B5/95)	HBV: WU-0000137 (WU-BRO000135, WU-B144/80)	HBV: WU-0023999 (WU-B89/96)	HBV: WU-0025584 (WU-B97B277-1, HEID-103077)	HBV: WU-0024036 (WU-B204/91)	HBV: WU-B98B1-1	HBV: WU-0023998 (WU-B206/96)
Tillandsia	Сапирл	Mexico	Guatemala	Honduras	Guatemala	of td Costa Rica 2.	Costa Rica	Mexico	Mexico	Mexico	Mexico	n Costa Rica	Costa Rica	Mexico	Mexico	Mexico	Peru	Costa Rica	Brazil	Dominica	Peru	Jamaica	^{IS} Costa Rica	Venezuela
. For samples of 7	Ιοςαίκλ	Poza Azul Pinoltepec, Veracruz	Depto. Escuintla, Sta. Teresa Escuintla	no data	Depto. Sololá, Lago de Atitlán	Prov. Puntarenas, SW declivities c Cordillera de Tilaran, along the ros from Sta. Elena to Rancho Grande	Prov. Heredia, Barva north of Heredia	Estdo. Chiapas, Sumidero Cañon bei Tuxtla Gutierrez	San Felipe Usila, Oaxaca	Coatepec, Veracruz	Mexico, Veracruz, Cascada De Texolo	Prov. Alajuela, 2 km N San Ranior	Prov. Cartago, Turrialba, Centro Agronomico Tropical de Investigacion y Ensenanza (CATIE	San Andrés Tuxtla, Veracruz	San Felipe Usila, Oaxaca	Mexico, Veracruz, Cascada De Texolo	Depto. Amazonas, Bagua	Prov. San José	no data	Parish St. Joseph, road Layou - Pont Cassé	Depto. Junín below Tarma	Trelawny Parish	Prov. Puntarenas Bosque Esquina near La Gamba	Estdo. Sucre Peninsula Paria, Cerro la Cerbatana
in this study	edinî	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Tillandsieae	Cipuropsidinae	Catopsideae	Vrieseeae	Glomeropitcairnieae	Cipuropsidinae	Tillandsieae	Catopsideae	Glomeropitcairnieae
ons used Idicated	γlimsîdu≳	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	t Tillandsioideae	t Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae
st of accessi es are also ir	səicəds	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia gymnobotrye	Tillandsia gymnobotrye	Tillandsia leiboldiana	Tillandsia leiboldiana	Tillandsia leiboldiana	Tillandsia punctulata	Tillandsia punctulata	Tillandsia foliosa	Cipuropsis subandina	Catopsis nutans	Vriesea saundersii	Glomeropitcairnia penduliflora	Werauhia tarmaensis	Guzmania monostachia	Catopsis juncifolia	Glomeropitcairnia erectiflora
lity code	Di Anga Ang		MHJB-B1837	MHJB-B1838	MHJB-B1839	MHJB-B1840	MHJB-B1841	MHJB-B360				MHJB-B1842	MHJB-B323				MHJB-B1832	MHJB-B2	MHJB-B4	MHJB-B13	MHJB-B18	MHJB-B22	MHJB-B29	MHJB-B30
Tak loca	ssmple code							E L	P13, P14,	P15							B1832	B2	B4	B13	B18	B22	B29	B30

collector	H. Prinsler s.n.	K. Sasse s.n.	J. Utley & K. Burt- Utley 8940	F. G. Gruber	W. Till 18094 et al.; M.H.J. Barfuss 020221-43 et al.	E.M.C. Leme 8175 & L. Kollmann	E.M.C. Leme 8417 et al.	Horich s.n.	W. Rauh 69417	A. Weissenhofer s.n.	G. Palim s.n.	W. Rauh 69323	E.M.C. Leme 1830	W. Till 10045	W. Till 62, E. Haugg & H. Hromadnik	no data	W. & S. Till 6025	W. Till 21027, M.H.J. Barfuss 060204-10 & al.	W. Till 21077, M.H.J. Barfuss 060208-21b & al.	W. Till 21081, M.H.J. Barfuss 060208-22a & al.	W. Till 21123, M.H.J. Barfuss 060209-48 & al.
əd⁄q [—] əldmss	fresh	frash	fresh	fresh	silicagel dried	& silicagel dried	silicagel dried	silicagel dried	fresh	silicagel dried	silicagel dried	fresh	fresh	fresh	fresh	fresh	fresh	silicagel dried	silicagel dried	silicagel dried	silicagel dried
herbarium acc.	WU: 0003462-0003464, 0007342 WU: 0008802_0008048	WU: UUU88UZ, UUU8948, 0009245-0009247, 0012735-0012736, 0015103	WU: J. Utley & K. Burt- Utley 8940	WU: 0000452, 0007348, 0013882, 0014775	WU: 0011130-0011131	RB: E.M.C. Leme 8175 L. Kollmann	RB: E.M.C. Leme 841 / et al.	B: Horich s.n.	WU: 0012008-0012018	wu: A. weissennoter s.n. (photo)	B: B100162215- B100162217, GH 42669	HEID: 602934-602935	WU: E.M.C. Leme 1830	WU: W. Till 10045	WU: W. Till 62	WU: HBV: WU-B70/96	WU: W. & S. Till 6025	QCNE: W. Till 21027	QCNE: W. Till 21077	QCNE: W. Till 21081	QCNE: W. Till 21123
N_Brom1776																					
E2EoipnA_N																					
locality code																					
source	HBV: WU-0024525 (WU-B256/96)	HBV: WU-0032184 (WU-B229/95)	HBV: WU-0024096 (WU-B178/96)	HBV: WU-0024591 (WU-B266/96)	field collection	Leme: 8175	Leme: 8417	BGBM: B-021-14-74- 63	HBV: WU-0024778 (HEID-104552)	field collection	BGBM: B-289-33-00- 63	HBV: WU-0020269 (WU-BRO140825, WU-B12/6)	HBV: WU-0023621 (WU-B00B95-2)	HBV: WU-0025179 (WU-B23/93)	HBV: WU-B177/95	HBV: WU-0024486 (WU-B70/96)	HBV: WU-0024355 (WU-B70/91)	field collection	field collection	field collection	field collection
ζαμησο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο Ο	Ecuador	Bolivia	Mexico	Venezuela	Dominican Republic	Brazil	Brazil	Costa Rica	Peru	Venezuela or Colombia	Dominican Republic	Venezuela	Brazil	Argentina	Bolivia	Bolivia or Agentina	Paraguay	Ecuador	Ecuador	Ecuador	Ecuador
locality	no data	Depto. Santa Cruz	Estdo. Guerrero	Estdo. Lara, S Cubiro	Prov. La Altagracia Parque Nacional del Este, S of Boca de Yuma	Estdo. Minas Gerais, near Bahia border, Santa Maria do Salto, Talismã	Estdo. Minas Gerais, Gouvaia	no data	Depto. Lambayeque, Vally of Rio Saña (type locality)	no data	no data	Estdo. Bolívar La Escalera, Ciudad Guayana - Santa Elena de Uairén, immediately NW Cerro Venado	Estdo. Minas Gerais near Palácios	Prov. Tucumán, Depto. Trancas, 2 km N bifurcation to Gonzalo, road to San Pedro de Colalao	Depto. Tarija, near pass Cumbre del Condor, between Tarija and Narvaez	no data	Depto. Amambay, ca. 11 km W Cerro Corá, main road to Yley Yau	Prov. Carchi, Páramo del Ángel	Prov. Pichincha, ca. 13 km above Pifo, road to Papallacta pass	Prov. Napo, path Papallacta pass - Termas de Papallacta	Prov. Napo, Cordillera de los Guacamayos, road Cosanga – Cocodrillo
θάτ	Tillandsieae			Tilandsieae		Vrieseeae	Vrieseeae	Cipuropsidinae	Tilandsieae		Cipuropsidinae										
Viimetduz	Tillandsioideae	Duvoideae	Hechtioideae	Tillandsioideae	Bromelioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Tillandsioideae	Lindmanioideae	Tillandsioideae	Brocchinioideae	Bromelioideae	Pitcairnioideae	Pitcairnioideae	Puyoideae	Pitcairnioideae	Bromelioideae	Puyoideae	Puyoideae	Pitcairnioideae
species	Racinaea ropalocarpa	exel evid	Hechtia carlsoniae	Tillandsia biflora	Aechmea nudicaulis	Vriesea drepanocarpa	Waltillia hatschbachii	Jagrantia monstrum	Tillandsia rauhii	Connellia sp.	Zizkaea tuerckheimii	Brocchinia micrantha	Eduandrea selloana	Deuterocohnia Iongipetala	Deuterocohnia lotteae	Puya mirabilis	Pitcairnia paraguavensis	Greigia vulcanica	Puya glomerifera	Puya clava-herculis	Pitcairnia cosangaensis
di yns8 AND	MHJB-B57	MH 18-R 78	MHJB-B79	MHJB-B90	MHJB-B118	MHJB-B1586	MHJB-B1579	MHJB-B1604	MHJB-B92	MHJB-B133	MHJB-B148	MHJB-B150	MHJB-B173	MHJB-B174	MHJB-B175	MHJB-B381	MHJB-B452	MHJB-B543	MHJB-B558	MHJB-B559	MHJB-B590
sample code	357	178	379	<u> 061</u>	3118	31586	31579	31604	392	3133	3148	1150	3173	3174	3175	3381	3452	3543	3558	3559	3590

in pop-gen analysis

in bob-gen analysis						
collector	W. Till 21151, M.H.J. Barfuss 060212-51 & al.	W. Till 21152, M.H.J. Barfuss 060212-52b & al.				
sample_fype	silicagel dried	silicagel dried				
herbarium acc.	DCNE: W. Till 21151	QCNE: W. Till 21152				
9771mo18_N	0	0				
EdeoignA_N						
locality code						
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Vilisol	Prov. Napo, Estación Biológica Ec Jatun Sacha	Prov. Napo, Estación Biológica Ec Jatun Sacha			ssperms353 data-set	
əditi					s included in the Angio	
Viimeiduz	Bromelioideae	ss Bromelioideae		de (Wien Universität) cus Vindobonensis the University of	number of sample	data-set
səicəds	Aechmea zebrina	Aechmea tillandsioid	legend	WU = Institutional Cc HBV = Hortus Botani (Botanical Garden of Vienna)	N_Angio353	N_Brom1776
di ynß8 and	MHJB-B594	MHJB-B596				
sample code	3594	3596				

localities description limited: for full locality collection data, please contact the authors

Tabl	e S4 Number of reads, n	umbers and percer	Itage of read	mapping 1	to target in all s	amples for b	oth bait s	ets.		
epos	səicəds	bait_kit	Reads ⊃Q_gnivivius	Reads Reads	gniqqsM secoues	Reads Mapped HQ	Reads target	Percent on_target	Matrix recovered DDTA_dtpn91	Matrix recovered relative to total target
P1	Tillandsia fasciculata	Bromeliad1776	2669424	2153711 0.8	30680738616271	1926038	1763939	0.915838	1077237	0.42459
P2	Tillandsia punctulata	Bromeliad1776	3114626	2509191 0	.8056155056819	2234791	2034506	0.910379	1295465	0.46836
P3	Tillandsia punctulata	Bromeliad1776	3031356	2416439 0.7	79714787705568	2145604	1968306	0.917367	1349306	0.56325
Ρ4	Tillandsia punctulata	Bromeliad1776	3077884	2521473 0.8	31922288169405	2239837	2077502	0.927524	1069002	0.58665
P5	Tillandsia punctulata	Bromeliad1776	3260914	2704548 0.8	32938341826862	2411667	2268828	0.940772	1220583	0.46478
P6	Tillandsia gymnobotrya	Bromeliad1776	2270494	1874042 0.8	32538954077835	1662206	1566088	0.942174	1344222	0.53069
Ъ7	Tillandsia gymnobotrya	Bromeliad1776	1630016	1347428 0.8	32663483057835	1187509	1117364	0.940931	1327973	0.58444
Р8	Tillandsia gymnobotrya	Bromeliad1776	3565312	2912157 0.8	31680284923171	2606042	2397680	0.920047	751547	0.57738
Б9	Tillandsia gymnobotrya	Bromeliad1776	4391420	3584750 0	.8163077091237	3181017	2905918	0.913519	1334783	0.32676
P10	Tillandsia gymnobotrya	Bromeliad1776	3239560	2655668 0.8	31976194297991	2366246	2175200	0.919262	1337797	0.58034
P11	Tillandsia leiboldiana	Bromeliad1776	2807756	2339016 0.8	33305529397854	2070531	1902692	0.918939	1354655	0.58165
P12	Tillandsia leiboldiana	Bromeliad1776	3892048	3197777 0.8	32161807870818	2818092	2551399	0.905364	1294642	0.58898
P13	Tillandsia fasciculata	Bromeliad1776	2899466	2210876 0.7	76251144176204	1941225	1740558	0.896629	1296043	0.56289
P14	Tillandsia fasciculata	Bromeliad1776	2742836	2156627 0.7	78627632129664	1900077	1694722	0.891923	1118106	0.56350
P15	Tillandsia fasciculata	Bromeliad1776	2827008	2153745 0.7	76184609311328	1885606	1681074	0.891530	1361624	0.48613
P16	Tillandsia punctulata	Bromeliad1776	3334248	2686609 0.8	30576159901723	2384865	2184198	0.915858	1350965	0.59201
P17	Tillandsia punctulata	Bromeliad1776	4672066	3716587 0.7	79549111677789	3257097	3011345	0.924549	1357563	0.58738
P18	Tillandsia punctulata	Bromeliad1776	6074946	5032673 0	.8284309029249	4432691	4021146	0.907157	1311902	0.59024
P19	Tillandsia punctulata	Bromeliad1776	6256346	5154496 0.8	32388282233751	4558707	4149881	0.910320	1366049	0.57039
P20	Tillandsia punctulata	Bromeliad1776	6280070	5176383 0.8	32425562135454	4575244	4130192	0.902726	1274360	0.59393
P21	Tillandsia punctulata	Bromeliad1776	5965530	4997135 0.8	33766823735695	4416874	3989756	0.903299	1179268	0.55407
P22	Tillandsia punctulata	Bromeliad1776	5465612	4602836 0.8	34214466742242	4085739	3765890	0.921716	1301415	0.51273
P23	Tillandsia punctulata	Bromeliad1776	6044558	5053954 0.8	33611638766639	4470080	4025319	0.900503	1326100	0.56583
P24	Tillandsia gymnobotrya	Bromeliad1776	5748662	4803579 0.8	33559948384511	4217722	3895223	0.923537	1323329	0.57657
P25	Tillandsia gymnobotrya	Bromeliad1776	3891812	3127374 0.8	30357787066796	2748616	2532437	0.921350	1320943	0.57536
P28	Tillandsia gymnobotrya	Bromeliad1776	3760206	3101024 0.8	32469524276064	2732992	2544375	0.930985	1337747	0.57432
P29	Tillandsia gymnobotrya	Bromeliad1776	3146722	2517081 0.7	79990574318291	2229365	2057525	0.922920	1275798	0.58163
P30	Tillandsia foliosa	Bromeliad1776	3217278	2630344 0.8	31756814300785	2346838	2182993	0.930185	1327392	0.55469

relative to total target).57713).59152).58249).58998).59388).46992).58391).58517).57694).58437).52346).56753).57854).58789	0.56777).58106).54950	0.58197).55695).57395	0.59070).58994).46186).58556).59360).51659).55095	0.59071	0.59007	0.59135
Matrix recovered		0	0		0		0		5				0		0	0		0	2		0				0				0	
Matrix recovered JDTA_ftpn9l	1360496	1339738	1356962	1365932	1080812	1342997	1345898	1326968	1344054	1203965	1305328	1330651	1352150	1305873	1336429	1263840	1338541	1280979	1320084	1358608	1356860	1062287	1346781	1365281	1188150	1267191	1358623	1357153	1360100	1324318
Percent on_target	0.905743	0.923639	0.901224	0.889124	0.898658	0.883247	0.892310	0.889454	0.906795	0.898758	0.904290	0.901814	0.904529	0.905485	0.911508	0.764775	0.890458	0.906511	0.900128	0.921765	0.898689	0.864009	0.815601	0.913477	0.913298	0.908875	0.872378	0.901680	0.900540	0.877176
Reads target	2845417	1152773	2272335	2957134	1558150	3310614	2469330	2426229	1828287	2498905	1108880	2154929	2114382	1395022	1303779	1023982	2133997	1414385	2145572	2305674	1973375	1827226	976173	1660250	2321864	2203100	3553616	1846274	998171	968073
Reads Mapped HQ	3141529	1248078	2521387	3325897	1733864	3748232	2767346	2727773	2016208	2780397	1226244	2389550	2337550	1540635	1430354	1338932	2396516	1560251	2383630	2501369	2195838	2114823	1196876	1817506	2542284	2423985	4073484	2047593	1108414	1103624
gniqq&M 2230u29	0.7937545487546	.74751006625621	.80237151468969	.79340027493624	.81035956608162	.79513133850097	.79083815353063	.79277365616505	.78667718806974	.79256625209579	.80197412576084	.82863515186613	.83299581076809	.84952532659996	.82714980812966	74852994085225	.83090272533469	.84901467938568	.80781158032258	.92636603629919	.82774563615685	0.7748944562074	0.9126340482973	.85621201347622	.84056427540525	.83692273280842	.82413766432156	.85135594125342	.82963817432735	.61804282789647
Meads Reads	3551061	1403495 0	2838784 0	3791890 0	1964203 0	4278950 0	3158848 0	3110013 0	2305883 0	3167174 0	1386100 0	2655716 0	2613581 0	1722591 0	1595926 0	1560393 0	2684660 0	1741594 0	2687245 0	2807947 0	2443967 0	2400809	1532026	2022955 0	2817674 0	2708990 0	4603005 0	2295998 0	1235610 0	1256465 0
Reads CO_privivius	4473752	1877560	3537992	4779290	2423866	5381438	3994304	3922952	2931168	3996100	1728360	3204928	3137568	2027710	1929428	2084610	3231016	2051312	3326574	3031142	2952558	3098240	1678686	2362680	3352122	3236846	5585238	2696872	1489336	2032974
bait_kit	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776
səicəds	Tillandsia foliosa	Tillandsia foliosa	Tillandsia foliosa	Tillandsia fasciculata	Cipuropsis subandina	Tillandsia fasciculata	Tillandsia leiboldiana	Catopsis nutans	Vriesea saundersii	Glomeropitcairnia penduliflora	Werauhia tarmaensis	Guzmania monostachia	Catopsis juncifolia	Glomeropitcairnia erectiflora	Racinaea ropalocarpa	Puya laxa	Hechtia carlsoniae	Tillandsia biflora	Aechmea nudicaulis	Waltillia hatschbachii	Vriesea saundersii	Jagrantia monstrum	Tillandsia rauhii	connellia sp.	zizkaea tuerckheimii	Brocchinia micrantha				
әроэ	P31	P32	P33	P34	P35	P36	P37	P38	P39	P40	P41	P42	P43	P44	P46	P47	P48	P49	P50	P51	P52	P53	P54	P55	P56	P57	P58	P59	P60	P61

ואומנוזא רפכסעפרפd רפומנועפ נס נסנמו נמרקפנ	0.57579	0.53254	0.57055	0.56943	0.56343	0.56762	0.58271	0.56952	0.58330	0.35092	0.51453	0.54762	0.57640	0.55423																
Xatrix recovered DDTA_Atpn Matrix	1224849	1312276	1309692	1295884	1305524	1340233	1309890	1341597	807111	1183427	1259534	1325715	1274725	1311369																
Percent on_target	0.924127	0.907422	0.915005	0.765456	0.925281	0.916900	0.901064	0.905280	0.913505	0.903048	0.919840	0.918737	0.906014	0.915704	0.056317	0.053973	0.053260	0.055103	0.061225	0.067536	0.057729	0.061558	0.059452	0.065134	0.060620	0.051438	0.176557	0.163262	0.170460	0.237191
Reads target	3205162	2676037	2268130	653122	2032682	1062553	980259	2295847	940500	884110	2245036	3509240	1998581	1710295	30625	34229	30625	37341	36481	37044	26947	36876	48661	43349	39760	61429	216318	44598	119604	88323
Reads Reads	3468313	2949054	2478817	853246	2196826	1158854	1087891	2536062	1029551	979029	2440682	3819633	2205905	1867737	543799	634184	575012	677663	595852	548506	466786	599049	818492	665540	655895	1194227	1225200	273169	701653	372371
gniqqsM esuccss	0.95898513821218	0.89881233444819	0.89161563788192	0.70444261218329	0.92229717538589	0.82668871491988	0.90894330695768	0.91150132962799	0.91197874750947	0.81736326010449	0.93714769573139	0.93792861488489	0.73298541205372	0.76353967603887	0.2585140675274	0.24282658324123	0.22831097493059	0.27718970909788	0.29739818681803	0.31080012786016	0.321664896838	0.22740942977489	0.22171251601211	0.23583238898015	0.2527087978849	0.24700403626407	0.4054677026745	0.46430568456993	0.39852153541456	0.42175931706099
mapped Reads	3916783	3296876	2755169	1008156	2453613	1307309	1243369	2877174	1167196	1108289	2759139	4282734	2582743	2166356	1392546	1611675	1594717	1654093	1438587	1302899	1172888	1469809	1953403	1529174	1683405	3123699	1779661	406872	1034267	540493
sbaaЯ ეე_ ₀ nivivnus	4084300	3668036	3090086	1431140	2660328	1581380	1367928	3156522	1279850	1355932	2944188	4566162	3523594	2837254	5386732	6637144	6984846	5967368	4837242	4192080	3646304	6463272	8810522	6484156	6661442	12646348	4389156	876302	2595260	1281520
bait_kit	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Bromeliad1776	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353	Angiosperm353
səiəəqs	Eduandrea selloana	Deuterocohnia longipetala	Deuterocohnia lotteae	Tillandsia leiboldiana	Puya mirabilis	Pitcairnia paraguayensis	Greigia vulcanica	Puya glomerifera	Puya clava-herculis	Pitcairnia cosangaensis	Aechmea zebrina	Aechmea tillandsioides	Tillandsia gymnobotrya	Tillandsia gymnobotrya	Tillandsia fasciculata	Tillandsia punctulata	Tillandsia punctulata	Tillandsia punctulata	Tillandsia punctulata	Tillandsia gymnobotrya	Tillandsia leiboldiana	Tillandsia leiboldiana	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia fasciculata	Tillandsia punctulata				
əpoo	P62	P63	P64	P65	P66	P67	P68	P69	P70	P71	P72	P73	P104	P105	P1	P2	ЪЗ	P4	P5	P6	Ъ7	P8	6d	P10	P11	P12	P13	P14	P15	P16

Matrix recovered relative to total target

JOTA_dtpn recovered XittaM 0.191146 0.265955 0.072718 0.163339 0.209285 0.1925540.220054 0.187382 0.246498 0.275570 0.300527 0.225562 0.286261 0.209230 0.160371 0.189542 0.155775 0.169159 0.159483 0.176335 0.201984 0.182885 0.167531 0.089788 0.156262 0.071375 0.084325 0.059482 0.250832 0.202261 on_target Percent 59776 130470 313714 54806 371053 4338 22347 97300 57373 85929 20100 272328 259843 30395 18295 65905 483102 66784 82807 03932 37487 202194 59068 309219 119728 109928 59671 34571 98491 78222 Reads target 2252053 2960833 78065 707563 473579 242349 275539 L478490 820576 L410533 080756 1232773 591947 2308348 2128897 L425622 505300 19232 365852 763637 981304 453351 667191 282614 820664 096933 293946 923369 700484 315051 OH beqqm Reads 1872568 0.40432810773976 867951 0.4470319625296 3306543 0.43428333739614 3311952 0.46917083619014 4297243 0.46382659371066 2209450 0.45602005501673 347047 0.43531712383409 523333 0.4161184236682 1146704 0.39169033241813 1456270 0.37603480775686 953264 0.40306770930672 2115091 0.47900790068589 2469932 0.48693557290435 2175739 0.47970659424345 2066579 0.48868604404793 .672241 0.46197846363466 .906005 0.47312338558859 245404 0.40402400648824 884113 0.33287886197592 214269 0.29951496231733 1842660 0.45356221570211 2106478 0.43441170574935 407605 0.42869327982095 29964 0.38379956962804 113304 0.42644866988844 685286 0.27445846112687 1793811 0.29459562080334 727232 0.33880128707581 782848 0.48063726666347 3104148 0.42961274693251 รรววทรอ **Mapping** pəddeu Reads 265692 797228 78072 .257654 2927578 3082500 4631308 L941586 7613792 7225456 059160 1849036 3264762 1845072 950808 3872700 2496866 2365022 4415566 5089062 5072400 1535562 1228848 3619738 1028558 5098068 3709342 660056 054118 1062640 OQ_00ivivius Reads Angiosperm353 bait_kit **Slomeropitcairnia penduliflora** Guzmania monostachia illandsia gymnobotrya illandsia gymnobotrya rillandsia gymnobotrya rillandsia gymnobotrya rillandsia gymnobotrya Tillandsia gymnobotrya Cipuropsis subandina Verauhia tarmaensis Tillandsia leiboldiana rillandsia leiboldiana Tillandsia leiboldiana Tillandsia leiboldiana Tillandsia fasciculata rillandsia fasciculata Tillandsia fasciculata rillandsia punctulata rillandsia fasciculata rillandsia fasciculata 'illandsia fasciculata rillandsia leiboldiana Tillandsia punctulata illandsia punctulata rillandsia punctulata rillandsia punctulata 'illandsia punctulata 'illandsia punctulata /riesea saundersii səisəds Catopsis nutans P18 P19 P25 P26 P29 P30 P35 P36 P39 P40 P43 P46 epoo P20 P22 P23 P24 P27 P28 P31 P32 P33 P34 P37 P38 P42 P44 P47 P21 P41
Matrix recovered relative to total target

JOTA_dtpn recovered XittaM 0.186815 0.158113 0.075813 0.076652 0.145683 0.149758 0.122737 0.045783 0.091536 0.175858 0.151747 0.123441 0.154850 0.083228 0.075889 0.139001 0.157473 0.067055 0.150177 0.100036 0.1300460.141420 0.132032 0.081990 0.148757 0.078637 on_target Percent 75743 246326 L31170 14308 246268 84215 202852 50248 L34230 345820 49798 219439 85554 279360 35344 233522 16479 43930 108358 211401 247851 56761 75851 .11467 59534 47917 Reads target l643313 L508049 1768773 1068708 1213960 1131608 573923 L461202 991449 988144 1917582 L478586 603743 2487901 1377948 247365 644830 312517 1400381 742650 895673 788198 579454 450907 758237 804092 M beqqem Reads 2477695 0.52575609553218 .349628 0.63238951687118 L550197 0.44517824107445 963273 0.77254048071602 2616032 0.3814168295493 1915638 0.50393278644365 1761575 0.45908421615001 2354788 0.55175584281205 1684404 0.30010326492478 4158719 0.77912599350428 3942026 0.62542476088211 2375274 0.57957656506662 1059110 0.37406141174975 2357148 0.64803635593849 349521 0.60158276883355 812511 0.4527436730973 3445851 0.67418891331935 2140250 0.27977636192035 1846802 0.32469280099806 808566 0.43542509517128 2407049 0.5020412871017 1120431 0.28596955391617 706160 0.44802904090337 518183 0.59713856428692 566406 0.58687333041097 3029801 0.66119136615037 รรววทรอ **Mapping** pəddeu Reads 7649860 1794524 3801376 3918008 5612748 5337672 3637370 3808146 2134172 5687844 1153564 1582336 3482194 L246890 3858722 3837150 1267808 4712632 3302958 1098292 2831380 542430 2669070 243284 794638 111106 OQ_gnivivius Reads Angiosperm353 bait_kit Glomeropitcairnia erectiflora **Deuterocohnia longipetala** Pitcairnia paraguayensis Pitcairnia cosangaensis Aechmea tillandsioides Racinaea ropalocarpa Vriesea drepanocarpa **Deuterocohnia lotteae Brocchinia** micrantha Valtillia hatschbachii rillandsia leiboldiana zizkaea tuerckheimii Eduandrea selloana Aechmea nudicaulis Jagrantia monstrum Puya clava-herculis səicəds Hechtia carlsoniae Catopsis juncifolia Aechmea zebrina **Sreigia vulcanica** Puya glomerifera *Tillandsia biflora* Tillandsia rauhii Puya mirabilis connellia sp. Puya laxa P48 P49 P56 P59 P63 P65 P66 epoo P50 P52 P53 P54 P55 P57 P58 P60 P61 P62 P64 P67 P68 P69 P70 P72 P51 P71

Table S5 Averaged levels of nucleotide diversity at synonymous (π S) and non-synonymous (π N) for 5 *Tillandsia* subgenus *Tillandsia* species.

species	πS	πΝ	J ·	πΝ/πS	
T. fasciculata		0.008134	0.001061	0.130317	
T. foliosa		0.004188	0.000585	0.139684	
T. leiboldiana		0.005715	0.000716	0.125284	
T. punctulata		0.007411	0.001039	0.140215	
T. gymnobotrya		0.006449	0.000926	0.143588	

Chapter 2

Rapid radiation coupled with pervasive hybridization in the Neotropical *Tillandsia* subgenus *Tillandsia*

Gil Yardeni¹, Michael H. J. Barfuss¹, Walter Till¹, Matthew R. Thornton¹, Clara Groot Crego¹, Christian Lexer¹, Thibault Leroy^{1,2,*}, Ovidiu Paun^{1,*}

¹Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria. ²IRHS-UMR1345, Université d'Angers, INRAE, Institut Agro, SFR 4207 QuaSaV, 49071 Beaucouzé, France. *shared last authorship

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Abstract

The recent rapid radiation of Tillandsia subgenus Tillandsia (family Bromeliaceae) provides an attractive system for studying the drivers and limitations of species diversification. This species-rich Neotropical monocot lineage consists of predominantly epiphytic plants with tremendous phenotypic diversity. So far, phylogenetic resolution has been lacking for this genus, which is thought to have diversified within the last 3 million years during its expansion from South America into Central America. We used whole-genome resequencing data to explore the evolutionary history of 32 species of Tillandsia, including inferring phylogenomic relationships with a tree-based and a network approach. Our results indicate that co-occurrance does not predict relatedness between lineages and reveal significant deviations from a tree-like structure, coupled with pervasive gene tree discordance. Focusing on hybridization, Patterson's D (ABBA-BABA) and related statistics were used to describe the rates and timing of introgression events, whereas topology weighting uncovered high heterogeneity of the phylogenetic signal along the genome. High rates of hybridization within and between clades suggest that the expansion of the subgenus into Central America proceeded in several migration events, followed by episodes of diversification and gene flow. Network analysis supported a reticulated history during colonization of different ecological niches. This work provides an example of how hybridization and introgression, rather than being a complicating issue for phylogenomic inference, should be investigated as a key driver of genomic processes during rapid species diversification.

Keywords: *Tillandsia*, gene tree discordance, hybridization, phylogenomics, bromeliad, Neotropical diversity, species network

Rapid radiations are characterised by accelerated diversification, usually following dispersal into novel habitats. As a diversity of ecological spaces become available, a lineage can opportunistically adapt to quickly occupy them in a process termed adaptive radiation (Hughes et al. 2015; Linder 2008; Naciri and Linder 2020; Rundell and Price 2009). While not all rapid radiations are adaptive (i.e., not necessarily associated with an increase in species diversification or ecological occupancy; Givnish 2015; Schluter 2000; Stroud and Losos 2016), they are generally associated with climatic fluctuations, habitat heterogeneity, landscape fragmentation and/or orogenesis (Boschman and Condamine 2022; Hughes and Atchison 2015; Paun et al. 2016; Qian and Ricklefs 2000; Richardson et al. 2001; Valente et al. 2010). Both ubiquitous among angiosperms in general and in the Neotropics in particular, rapid radiations provide ample opportunities to investigate the mechanisms driving plant diversification and Neotropical biodiversity in particular (Drummond et al. 2012; Lagomarsino et al. 2016; Linder 2008; Pérez-Escobar et al. 2017; Richardson et al. 2001; Soltis et al. 2019).

Phylogenomic studies of recent, rapid radiations must however overcome significant challenges. Quick diversification coincides with limited phylogenomic signal due to low sequence divergence, increased probability of short internal branches, longer terminal branches, and incomplete reproductive barriers, impeding phylogenomic resolution (Giarla and Esselstyn 2015; Straub et al. 2014; Whitfield and Lockhart 2007). Moreover, frequent morphological innovation is often associated with phylogenetic conflict, stemming from complex population-level processes like changes in population size, incomplete lineage sorting (ILS) and reticulation (Oliver 2013; Parins-Fukuchi et al. 2021). Researchers traditionally viewed the problem as analytical noise when aiming to construct bifurcating species trees, yet an increasing amount of research indicates that such episodes of phylogenomic conflict represent microevolutionary processes which are fundamental to rapid species diversification. Hence, gene-tree conflict and non-bifurcating relationships in rapid radiations (Filiault et al. 2018; Malinsky et al. 2018; Parins-Fukuchi et al. 2021).

Hybridization particularly influences phylogenomic signals, augmenting rates of discordance, but has emerged as a key driver of species' diversification (e.g., Abbott et al. 2013; Seehausen 2004). Historically viewed as an uncommon event during speciation and mostly accounted for secondary contact in allopatric processes, ancestral and recent gene-

flow is now regarded as a fundamental evolutionary process (Barth et al. 2020; Linck and Battey 2019; Mallet et al. 2016; Taylor and Larson 2019). Not only does speciation frequently persist in the face of hybridization, ecological diversification may be prompted through adaptive introgression, a process in which advantageous alleles are incorporated from one gene pool to another. Gene flow between recently diverged species may increase their genetic variability and enrich the genomic substrate for natural selection to act on. In addition, introgression can introduce advantageous alleles upon which selection has already acted, thus catalyzing adaptive radiations (Abbott et al. 2013; Edelman et al. 2019; Harrison and Larson 2014; Meier et al. 2019; Suarez-Gonzalez et al. 2018).

The rapidly radiating and highly diverse Neotropical genus *Tillandsia* belongs to the Bromeliaceae family. It consists of approximately 600 species of predominantly epiphytic plants distributed from southeastern United States to central Argentina. *Tillandsia* exhibit tremendous morphological diversity of adaptive traits which allowed them to occupy disparate habitats, from tropical rainforests to deserts and from lowlands to highlands (Benzing 2000; Givnish et al. 2011). Adaptations such as adventitious roots, trichomes modified for water and nutrient absorption, a water-impounding leaf rosette tank habit and Crassulacean acid metabolism (CAM) photosynthesis appear to have undergone correlated and contingent evolution, resulting in adaptive syndromes (Givnish et al. 2014).

Subgenus *Tillandsia* is one of seven subgenera in the genus and exhibits a similar morphological range as the entire genus (Barfuss et al. 2016). The phylogenetic relationships within this exceptionally young radiation (likely < 3 Mya) had been poorly resolved and its evolution remains elusive, as previous work employing conserved plastid and nuclear markers encountered issues like inconsistent relationships, "fuzzy" clade and species boundaries (Barfuss et al. 2005; 2016; Chew et al. 2010; Granados Mendoza et al. 2017; Pinzón et al. 2016). Barfuss et al. (2016) and Granados Mendoza et al. (2017) identified a monophyletic clade 'K' within the subgenus, with members distinctly distributed in North and Central America. Rivera (2019) expanded upon the naming scheme to describe subclades K.1 and K.2 (see Supporting Table S1). Using an ancestral area reconstruction strategy, Granados Mendoza et al. (2017) further showed that clade K's ancestral area was likely Central and North American. Previous inferences estimated an Andean ancestor for *Tillandsia* subgenus *Tillandsia*, with continental islands formation playing an important role

in the evolution of the central American groups (Givnish et al. 2014; Till 2000; Winkler, 1990).

Here, we used whole-genome data to explore phylogenomic relationships and patterns of gene flow among 32 representative species of the recently and rapidly radiating *Tillandsia* subgenus *Tillandsia*. With sampling focused on Mexican groups within clade K, we inferred relationships between species and used a tree- and a network-based approach to shed light on the group's evolutionary history. We identify deviations from a tree structure and prevalent gene tree discordance, suggesting that phylogenomic inference in this group is complicated by the signature of microevolutionary processes. Finally, we used several variations of the D-statistic (Patterson's D) to characterise patterns of hybridization and gene flow that may have contributed to adaptive trait shift in this Neotropical rapid radiation.

Materials and Methods

Plant Material collection

We sampled a total of 69 individuals representing 33 species of Tillandsia subgenus Tillandsia and 2 species of Tillandsia subgenus Allardtia as outgroups. Within our ingroup sampling, 25 Tillandsia species represent the Central-American radiation (henceforth: K clades) and eight species represent South American Tillandsia (henceforth: SA subclades; Supporting Table S2). We sampled with the intention to represent a variety of morphological and physiological syndromes of the Mexican species (Supporting Table S1). One typical example of this physiological variation within species of the clade K is photosynthetic syndrome. The large K.2.3 clade includes species exhibiting CAM photosynthetic syndrome and varying distributions, endemic or widespread, extending into the Antilles. Clade K.2.2 is a small group of widespread C3 plants, while the other two clades, K.1 and K.2.1, include widespread or endemic species with intermediate CAM-C3 syndromes (K.1) or various CAM-like photosynthetic syndromes (K.2.1). Species within all clades are mainly epiphytic and ornithophilous. Finally, the South American sampling included epiphytic, saxicolous and tank forming xerophitic species, predominantly endemic to Peru (with the exception of Tillandsia adpressiflora; Supporting Tables S1-2). Voucher information for the samples is provided in Supporting Table S1. Leaves were cut lengthwise and immediately dried in

powdered silica gel. Fresh samples from the University of Vienna botanical collection were also included.

DNA library preparation

DNA extractions were performed as previously described (Yardeni et al. 2022) using a modified CTAB protocol (Doyle and Doyle, 1987) or the QIAGEN DNeasy® Plant Mini Kit (Qiagen, USA), and purified using the Nucleospin® gDNA cleanup kit from Macherey-Nagel (Hudlow et al. 2011) following the supplier's instructions. The extracts were subsequently diluted in water and quantified with a Qubit® 3.0 Fluorometer (Life Technologies, Carlsbad, CA, USA). Prior to library preparation, DNA extracts containing a maximum of 600ng of DNA were sheared at 4°C to a target average length of 400 bp using a Bioruptor® Pico sonication device (Diagenode, Denville, NJ, USA). Libraries were then prepared using a modified KAPA protocol with the KAPA LTP Library Preparation Kit (Roche, Basel, Switzerland). Sample cleaning, end repair reaction and A-tailing steps were carried out using the KAPA LTP library preparation kit following the supplier's instructions and adaptor ligation and adaptor fill-in reactions were added based on Meyer and Kircher (2010). Libraries were amplified using 8 cycles of PCR with additional cycles for samples of low amount or degraded DNA. Samples were either double indexed with a set of 60 dualindex primers, as recommended by Kircher et al. (2012) and described in Loiseau et al. (2019) or with Illumina TrueSeq PCR-free single index (Supporting Table 3). Finally, the libraries underwent a final size selection using AMPure Beads (Agencourt). Libraries were then pooled and sequenced at Vienna BioCenter Core Facilities on Illumina HiSeqV4 PE125 or on NovaSeqS1 PE150.

Data processing

The raw sequence data was demultiplexed using deML v.1.1.3 (Renaud et al. 2015) and bamtools 2.5.1 (Barnett et al. 2011). Statistics were then collected with samtools v.1.9 (Li et al. 2009). The data in BAM format was converted to fastq using bedtools v.2.29.2 (Quinlan and Hall 2010) and quality checked using fastqc v.0.11.9 (Andrews 2010). Reads were trimmed for adapter content and quality using trimgalore v.0.6.5 (Krueger 2019), a wrapper tool around fastqc and cutadapt, using the following settings: --fastqc --retain unpaired. Sequence quality and adapter removal were confirmed with FastQC reports.

Quality- and adapter-trimmed reads were aligned to a *Tillandsia fasciculata* reference genome (Clara Groot Crego et al. in prep.) using bowtie2 v.2.3.5.1 (Langmead and Salzberg 2012) with the --very-sensitive-local option to increase accuracy. Low-quality mapped reads were removed, alignments were sorted by position using samtools v.1.15.1 (Li et al. 2009) and PCR duplicates were marked using MarkDuplicates from PicardTools v.2.25.2 (Picard Toolkit 2018). When a single accession was sequenced twice on different lanes, the reads were merged after confirming relatedness with inference of KING kinship coefficient, indicating a duplicate or 1st-degree relationship (kinship > 0.177; Manichaikul et al. 2010). Samples with an average coverage below 2x were removed from subsequent analysis, as well as accessions for which a high kinship coefficients was inferred: for this step, a kinship coefficient was estimated using KING and when a 1st degree relationship among accessions was indicated, only one sample was retained (see Supporting Tables S2-3).

Next, variants were called using GATK HaplotypeCaller v.4.1.9.0 followed by joint calling with GenotypeGVCFs (Poplin et al. 2018). The resulting variant call file (VCF) was filtered to exclude indels and any SNPs 3bp or closer from indels using bcftools v.1.15 (Li 2011) and GATK SelectVariants (DePristo et al. 2011). Regions reported to contain transportable elements were excluded using bedtools intersect (Quinlan and Hall 2010). We used the transition/transversion ratio as a guideline to define the filtering parameter values leading to a set of SNPs exhibiting the highest ratio using SnpSift (Cingolani et al. 2012). The following parameters were finally used: MQ < 20, genotype depth (DP) < 4, QD < 4, FS > 40, SOR > 3), MAF < 0.045 and missing rate > 0.2. Summary statistics were generated using bcftools stats (Li 2011). The full data processing pipeline and description is available at https://github.com/giyany/TillandsiaPhylo.

Phylogenetic tree inference

We inferred phylogenetic relationships for all samples using a genome-wide concatenated matrix and a coalescent-based method using genomic windows. To infer a genome-wide concatenated phylogeny we first converted the VCF containing only variant sites to a FASTA file using vcf2phylip with the --resolve-IUPAC option (Ortiz 2019), followed by using the raxml_ascbias.py script to remove any variant sites exclusively resulting from assignment of heterozygotes (https://github.com/btmartin721/raxml_ascbias). We used IQ-TREE 1.6.12 (Nguyen et al. 2015) to construct a maximum-likelihood tree,

allowing IQ-TREE to estimate the best-fit model and assess branch-support using ultra-fast bootstrap estimation with 1,000 replicates. After removal of species that could not be delimited (see Supplementary note regarding *T. zoquensis*), we inferred maximum-likelihood trees on a whole-genome and chromosome-by-chromosome basis.

Next, we constructed a species tree using a summary method with ASTRAL-III v.5.7.8 (hereafter: ASTRAL, Zhang et al. 2018). The VCF file was separated into nonoverlapping windows of 100kb and a maximum-likelihood tree was inferred for each genomic window as described above, excluding genomic windows with fewer than 40 SNPs. Loci with insufficient signal may reduce the accuracy of species tree estimation (Mirarab 2019), hence, across all gene trees, nodes with a bootstrap support below 10 were collapsed using Newick utilities v. 1.1.0 (Junier and Zdobnov 2010). A species tree was then generated in ASTRAL, measuring branch support as posterior probability. To explore gene tree discordance we calculated overall quartet support for the main, alternative and second alternative topologies, calculated the number of concordant and discordant bipartitions on each node using phyparts (Smith et al. 2015) with a cutoff of ten for informative bootstrap values (-s 10) and visualised gene tree discordance using the script phypartspiecharts.py (available from https://github.com/mossmatters/MJPythonNotebooks). A claudogram of all gene trees was visualised using ggdensitree from the R package ggtree v.3.4.0 (Yu 2020). Trees were modified using r packages phytool v.1.0-3 (Revell 2012) and treeio v.1.20.0 (Wang et al. 2020), with branch lengths forced into ultrametric structure for visualisation purposes only.

To explore the sources of inconsistency between phylogenies inferred with different methods and the clade relationships that differed from out expectations based on previous research (e.g., Barfuss et al. 2016), we also generated maximum-likelihood trees for subsets of the data, excluding different clades: a species tree was constructed (i) containing exclusively K clades, (ii) excluding clade K.2.1, (iii) excluding the species *T. mima* and *T. marnier-lapostollei*, which shared a branch showing inconsistent placement between inference methods.

Investigating monophyly and deviations from tree structure

To further explore the relationships within and among clades and deviations from tree structure by employing several variations of the D-statistic, we performed D-statistic tests.

Admixture between groups was inferred by exploiting asymmetries in the frequencies of nonconcordant gene trees in a three-population tree ordered (((P1,P2,),P3),O) (Durand et al. 2011; Green et al. 2010). The statistic is based on the frequencies of different patterns of allele sharing where the outgroup O carries the ancestral allele A and the derived allele is denoted as B. Following this, ABBA sites are those where P2 and P3 share a derived allele while P1 has the ancestral allele, and BABA represents sites at which P1 and P3 share the derived allele while P2 has the ancestral allele. Under a null hypothesis assuming no gene flow, ABBA and BABA patterns are assumed to be equally likely due to incomplete lineage sorting, while excess gene flow between any two groups should result in significant deviations from that expectation. The deviation from the expected ratio is termed the D statistic, calculated as the differences in the count of ABBA and BABA patterns across the genome, divided by their sum: $D = [\Sigma(ABBA) - \Sigma(BABA)] / [\Sigma(ABBA) + \Sigma(BABA)]$. D would equal 0 under the null hypothesis, a positive D indicates an excess of ABBA patterns and accordingly, D < 0 indicates an excess of BABA patterns (Martin et al. 2015). Specifically, the D-statistic we implemented uses allele frequency estimates which allows to include several individuals per taxon and does not require the implicit assumption that the outgroup is fixed for the ancestral allele (Malinsky et al. 2021).

We first examined the consistency of assigning individuals to a clade by testing whether individuals assigned to the same clade always share more derived alleles with eachother than with any individual from another clade by implementing a variation on the Dstatistic (henceforth referred to as D_G). Following Malinsky et al., (2018) we calculated $D(A,G_1;G_2,O)$ for all possible combinations of individuals, where G_1 and G_2 are assigned to the same clade and A is assigned to a different clade. *Tillandsia complanata* was used as the outgroup for all comparisons. For this comparison and all related D-statistics hereafter, significance was assessed using a jackknife procedure with 200kb window size, and familywise error rate (FWER) was calculated and corrected for multiple comparisons following the Holm–Bonferroni method with the p.adjust function in R (R Core Team 2020).

To further characterise the relationship among clades, we examined the consistency of monophyly of several clades within our set of window-based trees using the check_monophyly function in the ETE Toolkit v.3 (Huerta-Cepas et al. 2016). We next performed a principal components analysis (PCA) with SNPRelate v.1.20.1 (Zheng et al. 2012) on a set of biallelic SNPs, pruned to be at least 10kb apart and filtered to allow a

maximum of 10% missing data. We then used D_{min} , another variation of the D-statistic (Malinsky et al. 2018), to infer if allele-sharing among clades is consistent with a tree-like structure. Assuming no known topology, D_{min} provides the minimum absolute value of D across all possible arrangements of a trio. This provides a 'lower bound' estimate of the amount of gene flow within each trio, so that a significantly positive D_{min} score signifies the sharing of derived alleles between the species in the trio is inconsistent with a single species tree relating them, even in the presence of incomplete lineage sorting.

Finally, to quantify and visualise the relationship among clades along the genome we used topology weighting by iterative sampling of subtrees with Twisst v.0.2 (Martin and Van Belleghem 2017). This method focuses on the relationships among taxa or groups and quantifies the contribution of each individual taxon topology to the full tree, enabling to locate genomic regions that are associated with certain topologies. Since large genomic windows may lead to reduced accuracy due to overestimation of the most prevalent topology and small genomic windows may lead to underestimation of the most prevalent topology, we chose windows of 50 SNPs following the strategy of Martin and Van Belleghem (2017). We focused on the three largest clades and reduced the number of possible topologies by including only the Peruvian South American, K.2.1 and K.2.3 clades. To produce subtrees, the VCF file was partitioned using the biostar497922 script from Jvarkit (Lindenbaum 2015) and maximum-likelihood trees were inferred for each window as described above. Visualisation of the summary of weighted topologies was produced using the plot_twisst.R script from Twisst and visualisation of topologies along genomic coordinates was performed using a modified version of plot twisst. R to avoid averaging the obtained signal over regions with high rates of missing data.

Characterising hybridization and introgression

To assess the rates of hybridization among all species in our data-set, we used the original implementation of the D-statistic and estimates of admixture fraction f (henceforth: f_4 -ratio) in Dsuite v.0.5r45 (Malinsky et al. 2021), obtaining a genome-wide signal of introgression between species. We additionally computed D-statistic for each reference chromosome, using a jackknife procedure with windows of 150 SNPs to obtain a sufficient number of blocks for computing p-values. Given a certain level of uncertainty regarding the true relationship among species, we specified no input tree to focus on estimates where

Dsuite orders each trio so that the BBAA pattern is more common than the discordant patterns, instead using a priori knowledge of taxon relationships.

Gene flow events between groups are not independent. Instead, groups that are involved in hybridization may share branches on a phylogenomic tree and a single gene-flow event can present multiple correlated instances of significantly elevated D-statistic. This is especially expected when introgression events involve ancestral lineages, hence affecting internal branches of a phylogenetic tree. With Dsuite, we estimated the *f*-branch metric (Malinsky et al. 2021; henceforth: $f_b(C)$), another estimator of allele sharing that was developed to create a less correlated summary. Using all *f*-scores on a given tree, $f_b(C)$ captures excess allele sharing involving branches and by utilising multiple *f*4-ratio calculations, provides additional information about the timing of introgression events. We next focused on hypotheses regarding hybridization events between Mexican species by inferring a species network under a maximum pseudo-likelihood approach using PhyloNet v.3.8.0 (Cao et al. 2019; Than et al. 2008; Y. Yu and Nakhleh 2015). For this analysis, we produced a reduced 16-taxon set excluding the branch containing *T. marnier-lapostollei* and *T. mima* and sampled 1,000 trees at random, inferred as previously described from non-overlapping windows of 100kb.

To investigate the signature of introgression on specific loci and to locate highly admixed loci in regions of interest (see results), we used the Dinvestigate function implemented in Dsuite, which calculates several statistics suitable for analysis in sliding genomic windows. Our analysis was performed on windows of 50 SNPs with a step size of ten SNPs. The D-statistic itself shows large variance when applied to genomic windows (Martin et al. 2015), hence we used the statistic f_{dM} , which was designed to investigate introgression in small genomic windows (Malinsky et al. 2015). While the different statistics offer different advantages, their limitations and benefits across different evolutionary scenarios have yet to be thoroughly understood (Malinsky et al. 2015; Martin et al. 2015). We chose to focus on results using the f_{dM} statistic due to its ability to better account for allele sharing between P1 and P3 - nonetheless, we found in our analysis that the different statistics were correlated and offered consistent patterns. We further used *Twisst* as previously described to explore and visualise topologies along the genome. To investigate loci on chromosome 18, where we recognized high values of f_{dM} involved in hybridization with *T. achyrostachys*, we chose to investigate patterns of hybridization between *T. punctulata*, *T.*

butzii and *T. achyrostachys* (P1, P2 and P3). Shared variation is quantified as positive values of f_{dM} when shared between P2 and P3 and as negative values when shared between P3 and P1. Finally, to gain insight into the possible functional basis of genes that were involved in ancient hybridization, we identified regions which exhibited D-statistic values exceeding the 95% quantile of the D-statistic distribution.

Results

Read mapping and variant calling

After removing samples with low coverage, high inbreeding coefficient and species with unclear circumscription, we retained for our analyses 64 accessions. The average number of reads retained per accession ranged between 22.6M and 254.5M. The average mapping rates were 89.8%, ranging between 69.4% and 97.5%, resulting in an average sequence coverage of 11.3x. Mapping rates were slightly higher for clade K.2.3 and slightly lower for the SA clade (97.5% and 92.9% on average), however the differences in mapping rates between clades were not significant (Kruskal–Wallis test, P = 0.22), suggesting limited biases towards the used reference genome. After variant calling and filtering we retained 2,162,143 high-quality SNPs.

Phylogenomic inference recovers several topologies

IQ-TREE determined TVMe+ASC+R2 as the best-fit substitution model - a transversion model with equal base frequencies, two substitution rates and ascertainment bias correction, which was used for maximum likelihood estimations hereafter. Coalescence-based analyses were performed on 3,785 genomic windows of 100kb.

The concatenated maximum-likelihood (ML) tree and the species tree (Supporting figure S1 and Figure 1, respectively) recovered different back-bone phylogenies for *Tillandsia* and both contradicted previously inferred phylogenies (Barfuss et al. 2016; Granados Mendoza et al. 2017; Rivera 2019). Within species clustering in both trees agreed with previously obtained assignments (Barfuss et al. 2016; Rivera 2019), however neither the South American species nor the Mexican clades formed monophyletic groups. Instead, the South American species were separated into a clade consisting of the endemic Peruvian species together with the widespread species *T. adpressiflora*, and a second clade containing

T. marnier-lapostollei and *T. mima*, with clade K.2.1 placed as sister to the first South American clade (Supporting figure S1; Figure 1). The species tree recovered an overall similar phylogeny to the concatenated tree, but placed the branch containing *T. marnier-lapostollei* and *T. mima* as sister to the other South American and the K.2.1 clades. Several other differences between the trees inferred with different methods concerned relationships among species within clade K.2.3: for example, in the ML tree (Supporting figure S1), a clade consisting of *T. bulbosa* and *T. ionantha* was a sister to a clade containing *T. caput-medusae* and *T. concolor*; however in the species tree the latter was sister to a different clade, containing *T. festucoides*, *T. schiedeana* and *T. juncea*. These differences were coupled with overall poor resolution of the relationships between currently recognized taxa within clade K.2.3, reflected in low bootstrap values in the concatenated tree and high levels of gene tree incongruence in the species tree (see below), suggesting substantial allele sharing and high rates of gene flow within the clade.

Gene tree discordance was widespread within the data-set, especially on internal nodes with inconsistent placement in trees inferred with different methods. Such was the case of the node representing the common ancestor of K.2.1 and all South American clades, as well as the majority of internal nodes within clade K.2.3 (Figure 1). The relationships between South American species and clade K.2.1 were characterised by many alternative topologies and often more than half of the gene tree topologies were discordant with a main topology. High levels of discordance were also found within the intermediate CAM clade K.1.

Maximum likelihood trees constructed separately for concatenated matrices of each reference chromosome retrieved many different topologies: solely considering relationships between clades, we recognized nine different topologies among the 25 different trees (see Supporting file 1). The signal from eight chromosomes recovered within-clade relationships similar to those in the concatenated whole-genome tree while several other trees presented different placements of basal branches, and while the South American species formed a monophyly in six trees, in four of them a monophyletic South American clade was placed as a sister clade to K.2.1. While each chromosome tree likely contains high amounts of gene tree discordance, the abundance of different topologies imply that several evolutionary histories can be traced along the genome in *Tillandsia* and that several genomic processes muddy the relationship between gene trees and the true species tree. Maximum-likelihood trees

constructed for subsets of the data recovered similar topologies in the first and third subset (Mexican *Tillandsia* only and excluding the branch containing *T. marnier-lapostollei* and *T. mima*), however when excluding clade K.2.1, the South American species were recovered as monophyletic (Supporting file 1).



Figure 1. Coalescent-based species trees generated on 3,785 genomic windows with ASTRAL-III for 64 individuals representing 32 species of Tillandsia subgenus Tillandsia, plus two outgroups. Branch lengths are given in coalescent units. Node values represent local posterior probabilities for the main topology and are equal to one unless noted otherwise. Pie charts at the nodes show levels of gene tree discordance: the percentages of concordant gene trees (blue), the top alternative bipartition (green), other conflicting topologies (red) and uninformative gene trees (grey).

Lack of monophyly and deviations from tree-like structure

Patterns of allele sharing as tested with D_G fully supported clade assignment for all species, indicating that individual species assigned to the same clade always shared more alleles with other species within the clade than with species from other clades. Patterns of clade monophyly across the 3,785 genomic windows generally indicated consistent clade monophyly but varying relationships among clades: each of the Mexican clades were monophyletic in the majority of the windows tested with the exception of clade K.1, which was monophyletic in fewer than 40% of the window. Clades K.2.1, K.2.2, K.2.3 and K.1 were monophyletic in 3,485, 3,007, 2,537 and 1,501 trees, respectively. All the South American species in our data-set formed a monophyletic clade in a basal position in 646 trees, while the Peruvian South American group was monophyletic in 1,354 trees. Applying the same strategy to investigate relationships among clades, we recovered a group clustering all South American species and clade K.2.1 (similar to the topology of the species tree) in 587 trees, while a topology similar to that obtained in the ML tree was found in 542 trees. Finally, all K clades were together monophyletic in just 622 trees. After distance-pruning and allowing for maximum 10% missing data we retained 16,204 SNPs for the PCA analysis. The analysis provided evidence for consistent interspecific genetic structure, separating the South American group, clade K.2.1 and the remainder of the K clades. Clades K.1, K.2.2 and K.2.3 clustered closely together (Supporting figure S2).

Patterns of allele sharing indicated widespread deviations from tree-like structure, driven mostly by allele sharing between Mexican taxa. We computed the D_{min} statistic for a total of 7,141 trios (i.e., plus the outgroup) and found 3,650 comparisons with a significantly elevated value (P<0.05) with more than 95% of those being highly significant (P<0.01), indicating that patterns of allele sharing in 51.5% of the trios tested did not conform with a tree-like structure. The rate of elevated D_{min} values was highest for comparisons involving accessions from clade K.2.1 with 58.7% of the trios showing significant D_{min} values, followed by K.2.2 with 56.1%, K.1 with 57.9% and K.2.3 with 51.4%, respectively (Supporting figure S2). Fewer significantly elevated values included South American groups, with 42% of comparisons and 10.4% of comparisons including the South Peruvian group and the group of *T. marnier-lapostollei* and *T. mima*, respectively. In general, the majority of deviations from tree-like structure were found in trios containing species from different clades, rather than within a clade (Supporting figure S2).

We considered three distinct tree topologies for topology weighting: the most frequent topology was congruent with the one recovered in phylogenomic inference, which placed the Peruvian South American clade as sister to K.2.1 in 42% of the windows. The second topology, placing the Mexican clades as sister clades, was recovered from 35% of the genome, while a third topology placing K.2.3 as sister to the Peruvian South American clade appeared in 23% of the genome (Figure 2). The three topologies were broadly equally distributed along the genome – however, in few chromosomes the first topology frequented the centromeric regions, characterized by low recombination rates and reduced genic density (Gill et al. 2008; Yan and Jiang 2007). Topology weighing is a descriptive method which does not explicitly test for introgression or ILS, hence, it does not allow to discern the reason for a specific phylogenetic signal. Regardless, these findings suggest that the common topology represents the phylogeny's backbone (Figure 2).

Correlated and widespread gene-flow events

We performed a total of 7,141 tests with the D-statistic measure, of which 4,331 were significantly elevated values with D values ranging between 0.021 and 0.581 (after Holm-Bonferroni correction; Figure 3). All species were involved in potential hybridizations. A prominent signal revealed introgression between species in clade K.2.1 and all other Mexican clades. Other notable signals for hybridization were indicated within clade K.2.3 and within the South American clade. f4-ratio scores ranged between 0.0017 and 0.357 and indicated that in most hybridization events, the proportion of the genome involved was smaller than 10% (Supporting figure S3). A few exceptions where larger parts of the genome were admixed were found in events within clades: for example, T. caput-medusae was involved in two hybridization events with T. butzii and T. fasciculata involving 31.7% of the genome (see Supporting figure S3). D-statistic signal affected all chromosomes and widespread signals inferred in the whole-genome analysis generally were not located to a specific chromosome – for example, a significant D-statistic signal between clade K.2.1 and the other Mexican clades appeared on all 25 chromosomes (Supporting file 2). Notably, a significantly elevated D-statistic was found on chromosome 18 involving T. achyrostachys and the majority of species in the CAM clade K.2.3 (Supporting file 2). Tillandsia achyrostachys is a member of clade K.1, a group of generally intermediate C3-CAM species which exhibit small to intermediate tank structures and intermediary values of stable carbon isotope ratios (δ^{13} C:



Figure 2. Variation along the genome in relationships between the major Tillandsia clades. Visualization was produced using topology weighting by iterative sampling of subtrees in genomic windows of 50 SNPs. Colours represent the frequency of each topology along chromosomal position in each chromosome: grey lines indicate regions excluded due to high levels of missing data, including highly repetitive regions. Two chromosome are presented: chromosome 4, to depict typical distribution of the main topologies, and chromosome 18, to contrast.

see Supporting Table S3, but see also Messerschmid et al. 2021). Within our sampling, *T. achyrostachys* exhibits the strongest CAM phenotype and δ^{13} C values (-14.7; Crayn et al. 2015).



Figure 3 Heatmap summarizing 7,141 four-taxon D-statistic tests. Tillandsia complanata was used as the outgroup in all tests. The four taxa in each test have been rearranged to always obtain positive D values, and P2 and P3 are shown on the axes. Colour indicates the value of D and log value of p-value, the latter estimated using a block jackknife procedure with a 200kb window size and corrected for family wise error rate. Colours on the bars correspond to the clades in Figure 1.



Figure 4 Heatmap summarising the statistic $f_b(C)$, where excess sharing of derived alleles is inferred between the branch of the tree on the Y axis and the species C on the X axis. The ASTRAL species tree was used as input topology for the branch statistic. The matrix is colored according to the legend of the $f_b(C)$ values and grey squares correspond to tests that are inconsistent with the ASTRAL phylogeny. Dots within the matrix denote a significant pvalue, estimated using a block jackknife procedure and corrected for family wise error rate. Colours correspond to the clades in Figure 1.

The f-branch metric calculated 2,520 $f_b(C)$ scores of which 428 were significantly elevated (P < 0.05). 48 out of a total 70 branches showed significant excess allele sharing with at least one other species. The highest $f_b(C)$ estimate was 36.6% between T. makoyana and T. albida. Other high values were inferred especially within clades, for example between T. gymnobotrya and T. cossonii in clade K.1, and between T. fuchsii and three closely related species in clade K.2.1 (Figure 4). $f_b(C)$ values supported the identification of a cryptic T. tricolor hybrid sample (T.tricolor.hybrid) as a hybrid between T. tricolor and T. fasciculata. Significantly elevated scores were also inferred between the ancestor of clade K.2.1 and an ancestor of all other sampled Mexican clades with an average score of 5.9% (Figure 4). Other species that exhibited a signal of hybridization with the hypothesised ancestor of the Mexican clades are T. filifolia and T. adpressiflora, the latter being the only species within its sampled clade which is not endemic to Peru, but instead is distributed across South America from Bolivia to Northern Brazil and Colombia. Networks inferred in PhyloNet with varying numbers of reticulation events repeatedly indicated the involvement of clade K.2.1 in hybridization with the South American and Mexican clades, with higher weights assigned to the former (Figure 5). Additional reticulation events were assigned within clade K.2.3. Overall, these findings confirm the extensive violations of a tree-like structure revealed in the previous part of the analysis and suggest that these patterns are the result of many gene-flow events throughout the evolutionary history of the radiation, with high rates of gene flow between Mexican clades.

 f_d and f_{dM} statistics were calculated on a total of 9,185 windows and ranged between -4.14 and 3.8 for f_d and -0.78 and 0.83 for f_{dM} . Across all chromosomes, mean values were negative at -0.19 and -0.043, respectively, fitting the expectation for higher rates of gene flow between closely related species (Supporting figure S4). Chromosome 18 was however characterized by two regions of high positive values, which were also evident when using topology weighting and coincide with regions of low genic density (Supporting figure S4). The loci exhibiting high D-statistic values contained 194 genes. Surveying the genes, we found they were associated with a variety of functions. For example, serine/threonine-protein kinase prpf4B is known to have a role in pre-mRNA splicing in yeast and humans (Eckert et al. 2016), and it is associated with stress response in millet (Parvathi et al. 2019). We also recognized S-adenosyl-L-methionine-dependent methyltransferase superfamily protein (SAM-Mtase), a key enzyme in plant metabolic pathways like the phenylpropanoid and flavonoid pathway (Joshi and Chiang, 1998; Sistla and Rao 2004; Supporting figure S4).



Figure 5 Best maximum pseudo-likelihood species networks inferred with PhyloNet for zero to four reticulation events. Curved branches indicate reticulation events. Numbers next to curved branches indicate inheritance probabilities for each event. Colours correspond to the clades in Figure 1.

Discussion

The generic and sub-generic classification of subfamily Tillandsioideae in general and of the genus *Tillandsia* in particular remained fluid through decades of phylogenetic research, first inferred based on morphological characters and later on a limited number of genomic markers. Our whole-genome resequencing of *Tillandsia* subgenus *Tillandsia* provides peculiar additions to our understanding of the complex evolutionary history of *Tillandsia* and offers intriguing hypotheses on the processes that accompanied diversification in this group.

The use of a large number of genomic regions spread across the genome increases the statistical confidence in resolving phylogenies while potentially revealing phylogenomic discordance (Davey et al. 2011; de La Harpe et al. 2017; Pease et al. 2018). The latter can be produced by uninformative 'noise' (see below) or reflect the genomic signature of cardinal molecular processes. The large amount of sequences used in the concatenated alignment and in the coalescent-based method generated high branch support for almost all nodes (Pease et al. 2016; Salichos and Rokas 2013), yet no single phylogenomic tree gave us a complete picture of the relationships between species. The branch clustering *T. mima* and *T. marnier-lapostollei* showed the most inconsistent placement between analyses. Maximum-likelihood methods perform poorly in the presence of incomplete lineage sorting (Degnan et al. 2009; Solís-Lemus et al. 2016), and the generally short internode distance coupled with high rates of discordance suggests the inconsistencies are an effect of high levels of ILS during rapid speciation (Suh et al. 2015). Regardless, ILS and hybridization can be mutually inclusive and multiple processes likely contributed to the inconsistencies along the phylogeny (Hibbins et al. 2020; Morales-Briones et al. 2021).

In stark contrast to previously inferred phylogenies, our inference retrieved the Mexican clade K as polyphyletic. Pinzón et al. (2016) sampled 108 species of *Tillandsia* with a focus on subgenus *Tillandsia* and performed analysis of plastid DNA and the external transcribed spacer (ETS) of the nuclear ribosomal DNA. In their work that also included the species *T. mima* and *T. marnier-lapostollei*, both the Mexican and South American species formed well-supported and monophyletic clades. However, they found incongruences between the plastid and ETS phylogenies and hypothesised these could be caused by plastid capture and homoplasy, in line with our main hypothesis for the incongruence between

previous studies and our phylogeny. In a phylogeny of the subfamily constructed from plastid loci and several nuclear regions, both clade K and the genus as a whole were monophyletic but poorly supported (Barfuss et al. 2016). Finally, Granados Mendoza et al. (2017) increased the sampling to represent 30% of the recognized species in the genus and constructed a phylogeny from the matK–trnK plastid region. They found a monophyletic and wellsupported clade K, however the backbone of the phylogeny remained generally unresolved. Overall, phylogenies based on plastid and relatively few nuclear genomic regions offered little resolution for shallow phylogenetic in this young genus, particularly within clade K (Granados Mendoza et al. 2017).

Despite the extensive number of different topologies, a summary of the allele-sharing patterns over 3,785 genomic windows provided several points of consensus, further supported by network inference. The assignment of species to clades was highly supported as was the polyphyly of clade K, with topology weighting demonstrating that clade K.2.1 is genetically differentiated from the other K clades. Interestingly, despite their high morphological diversity, species within clades K.1, K.2.1 and K.2.2 are genetically closely related (Supporting figure S2). Each K clade formed a well supported monophyletic group and the high rates of allele sharing did not compromise clade boundaries. Departures from tree structure were recurrent and encompassed all Mexican clades and species, probably owing to the radiation's young age. Givnish et al. (2014) placed the crown age of Tillandsioideae (15.2 \pm 0.42 Mya) and "core tillandsioids" (9.6 \pm 0.67 Mya) in the middle or late Miocene and Barfuss et al. (2005) suggested that *Tillandsia* are phylogenetically young, based on low genetic divergence. Apart from hybridization, various molecular processes can contribute to violations of a strictly bifurcating species tree, such as ILS, paralogy and gene duplication and loss (Edwards 2009; Galtier and Daubin 2008; Smith et al. 2015). We suggest there is strong evidence for ancestral hybridization as the source of discordance between K.2.1 and other K clades: f-statistic and D-statistic tests are robust to the presence of ILS, as is PhyloNet (Malinsky et al. 2021; Martin et al. 2015; Wen et al. 2018) and ancestral population structure is unlikely to segregate through the demographic events that accompanied Tillandsia's dispersal into central America (see below). fb(C) indicated that gene flow was bi-directional and involved in addition to species also internal branches or, in other words, ancestral lineages. Ancestral introgression is generally congruent with the current distribution of species in clade K.2.1, which includes several narrow endemics, likely

limiting current opportunities for extensive gene flow. The high occurrence of endemism in this clade prompts us to reject an alternative hypothesis: While the close relationship of K.2.1 and the South American clades may, in principle, be the product of recent gene flow, the clades currently share a minimal distribution. In contrast to ancestral introgression, the exceptionally high gene tree discordance within clades and specifically within the predominantly CAM clade K.2.3 probably resulted from several non-mutually exclusive processes. ILS is peculiarly associated with short inter-nodes due to rapid diversification (Galtier and Daubin 2008; Morales-Briones et al. 2021) and previous studies on *Tillandsia* subgenus *Tillandsia* found evidence for changes in population sizes and elevated rates of gene duplication and loss, specifically associated with photosynthetic syndrome shifts (de La Harpe et al. 2020; Yardeni et al. 2022).

Regardless, we present evidence that hybridization played a central role in the evolution of Mexican Tillandsia. Our use of D-statistics revealed prevalent recent and ancient gene flow. Notably, the obtained $f_b(C)$ ranges were in general far higher than those previously inferred for ancestral introgressions between species of Malawi cichlids (Malinsky et al. 2018) and hares (Ferreira et al. 2021), but comparable to other rapid radiations (De-Kayne et al. 2022; Suvorov et al. 2022). Networks inferred with PhyloNet repeatedly supported the hypothesis of gene flow between K.2.1 and other K clades. While the timing of the events cannot be inferred from the networks, the placement of reticulation events suggests these involve ancestral lineages. Tillandsia subgenus Tillandsia bear seeds adapted to wind dispersal and usually exhibit ornithophilous pollination syndromes, both which may facilitate high rates of inter- and intra-specific gene flow (Kessler et al. 2020; Wessinger 2021). Interestingly, the strongest $f_b(C)$ was indicated between T. albida and T. makoyana and affected an estimated 30% of the genome (Supporting figure S3), despite morphological differences and dissimilar distributions of the two species, most notably different flower colours (Espejo-Serna et al. 2004). Notable high rates of introgression with other species were also indicated for T. filifolia, a species with a unique flower morphology. Exhibiting small, pale lavender, non tubular flowers, this species is probably entomophilous. The generality of the obtained signal could be affected by our sampling; a wider sampling would allow us to infer if introgression involved related or ancient lineages.

Our analyses produce novel insights regarding cryptic species and the relationships between them: for example, our inference suggests that *T. mima* and *T. mima var. chiletensis*

are not only separate species, but also not that closely related, despite morphological similarities. Similarly, *T. fuchsii* and *T. fuchsii* var. *stephanii* did not form a monophyletic clade, raising a need to revise their species status. Interestingly, samples identified as *T. cossonii* formed a paraphyletic clade. Although both were collected at the same site in Jalisco and only 10km apart (Supporting Table S2), the samples may represent different sub-species or ecotypes, perhaps partially reproductively isolated due to differences in elevation.

Hybridization is an important factor in plant speciation and evolution, and Tillandsia presents an excellent opportunity to study its role in rapid diversification. Speciation in Tillandsia seems to have been reticulated and advanced in the presence of recurrent gene flow, rather than by refined reproductive barriers. This study therefore provides another example to the mounting evidence of the generality of diversification with gene flow (Arnold et al. 2016; Filiault et al. 2018; Keller et al. 2013; Nosil 2008; Seehausen et al. 2014; Stankowski et al. 2019; D. Zhang et al. 2021). While genetic variation introduced through hybridization can be maladaptive or neutral, the potential adaptive role of hybridization had been demonstrated in numerous animal and plant taxa (Arnold et al. 2016; Dasmahapatra et al. 2012; Lamichhaney et al. 2015; Taylor and Larson 2019). The high rates of accumulation of morphological and physiological disparity suggest that radiation in *Tillandsia* may have been adaptive: furthermore, since adaptive syndromes require the accumulation of mutations in different genic regions, hybridization through porous species boundaries may drive adaptation by continuously introducing novel alleles into populations. The current study was conducted with an incomplete taxon sampling, hence we cannot yet draw observations about adaptive introgression in *Tillandsia*. Future studies in *Tillandsia*, especially those employing wider sampling and deeper coverage, will gain by considering the role of hybridization. Intriguingly, the introgressed region we reported on chromosome 18 occurred in a region of low genic density and at a chromosome edge. Theory suggests that introgression may avoid the immediate consequences of natural selection and 'go under the radar' when alleles with mildly deleterious effect introgress into regions of low gene density and that barriers to introgression may be weaker towards chromosome ends (Barton and Bengtsson, 1986; Martin and Jiggins 2017; Sankararaman et al. 2014).

Our results portray a Neotropical plant radiation that proceeded in several episodes of dispersal, diversification and gene flow. The characteristic phenotypic syndrome which allowed *Tillandsia* to expand into humid and xeric habitats had been gained and lost

repeatedly, possibly involving recurrent gene flow between closely related taxa, a likely scenario especially in the light of our results. Previous studies proposed that the ancestor of *Tillandsia* subgenus *Tillandsia* may have been South American (Barfuss et al. 2016; Granados Mendoza et al. 2017), and we complement the tale by suggesting that different Mexican taxa may have had different geographical origins. It's possible that several migration events into Central America proceeded with strong population bottlenecks and episodes of gene-flow, resulting in relatively long internal branches. In summary, whole-genome resequencing data provided clear advantages over the use of few highly conserved markers yet ultimately, the complex evolutionary history of *Tillandsia* remains elusive. Future phylogenomic investigations will require a combination of analytical approaches and deeper taxonomical sampling to uncover the interplay of processes that drove this rapid diversification.

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Supporting Information, including Supporting Figures, Supporting note, Supporting files and Supporting Tables



Supporting figure S1. Maximum-likelihood (ML) phylogenomic tree inferred on a dataset of concatenated SNPs with IQ-TREE, using substitution model TVMe+R2 with ascertainment bias correction. Branch lengths were calculated by number of substitutions per site and branch support was assessed using ultra-fast bootstrap estimation with 1,000 replicates. Colours follow the clades in Figure 1.



Supporting Figure S2 Widespread deviations from tree-like structure in Tillandsia phylogeny. Colours follow the legend and Figure 1. A, Claudogram of 3,785 ML phylogenetic trees inferred from non-overlapping 100kb genomic windows. Windows were forced to an ultrametric shape for visualisation purposes. B, Derived allele conveys deviations from tree structure affecting the K clades. The Euler diagram represents the proportion of significantly elevated Dmin scores for comparisons in trios including species from within or between clades. Numbers indicate the total number of significantly elevated Dmin for each overlap. C, PCA analysis for all clades on bi-allelic, distance-pruned 16,204 SNPs, including maximum 10% missing data.



Supporting Figure S3 Heatmap summarising 7,141 f4-ratio tests. Tillandsia complanata was used as the outgroup for all tests. Colour indicates the value of f4 and log value of p-value, the latter estimated using a block jackknife procedure with a 200kb window size and corrected for family wise error rate. Colours correspond to the clades in Figure 1.



Supporting Figure S4 Signature of introgression and topology weighting on chromosome 18 between T. punctulata, T. butzii and T. achyrostachys (P1, P2 and P3; T. complanata was used as the outgroup). A, f_{dM} statistic (green dots and smoothed with a green line, with the scale on the right side Y axis) on genomic windows. Analysis was performed on windows of 50 SNPs with a step size of ten SNPs. Shared variation is quantified as positive values when shared between P2 and P3 and as negative values when shared between P3 and P1. Gene content is shown with lavender shape, scale on the right side. B, values of f_{dM} statistic for each chromosome for T. punctulata, T. butzii and T. achyrostachys. C, Topology weighting by iterative sampling of subtrees in genomic windows of 50 SNPs, using Twisst. Colours represent the frequency of each topology in D along chromosomal position in each chromosome: grey lines indicate regions excluded due to high levels of missing data.

Supplementary note – in a phylogenomic tree constructed with IQ-Tree (see methods; figure below), *Tillandsia zoquensis* was inferred as monophyletic with *T. fasciculata*, suggesting a need to revise its species status. For sample collection details, see Supporting Table S2.



Supporting file 1 – maximum likelihood trees constructed for each of the 25 chromosomes and for subsets of the data, excluding different clades: a species tree was constructed (i) containing exclusively K clades (ii) excluding clade K.2.1. (iii) excluding the species *T. mima* and *T. marnier- lapostollei*.
























































Supporting file 2 Heatmaps summarizing 7,141 four-taxon D-statistic tests for each of the 25 reference chromosomes, indicate on each figure. *Tillandsia complanata* was used as the outgroup in all tests. The four taxa in each test have been rearranged to always obtain positive D values, and P2 and P3 are shown on the axes. Colour indicates the value of D and log value of p-value, as appears in legend (bottom right).



























rature	1 endemic/ widespread	Endemic [1] [6]	widespread[1 5]	Endemic [6]	widespread	widespread	widespread	Endemic [6]	Endemic [6]	Endemic [25]	Endemic to N. penu[25]	widespread[6]	widespread	widespread	widespread	widespread; Endemic [BS]	Endemic [15]	Widespread [25]	Endemic [6]	Endemic [25]	widespread	Widespread [25]
ng lite	Conservation status	vulnerable		LC	LC			ΓC		LC		LC				endangered [BS]	vulnerable		vulnerable	ΓC		
orrespondir	Other	occur on 35·1 % of B. copallifera trees[2]		xerophytic [17]	Myrmecophyte [16]	Myrmecophyte [22]	Myrmecophyte [22]					xeromorphic [3], occurs in juniper forests[3], mature forests[10]		non-tubular flowers						xerophyte	semi-xeric [5]	increase in abundance in disturbed forests, isolated trees in pastures,coffee plamations
ences to co	reproductive system	ornithophilous, SI[7], outcrossing[3]	ornithophilous	ornithophilous	ornithophilous	ornithophilous	omithophilous; SI[7]	ornithophilous	ornithophilous	ornithophilous	ornithophilous	ornithophilous	ornithophilous	entomophilous	ornithophilous	ornithophilous	ornithophilous	ornithophilous/ entomophilous	ornithophilous/ entomophilous	ornithophilous	ornithophilous; outcrossing[5] or mixed, exserted genitalia[5]	omithophilous; Self & cross. hummingbird pollinated[34]
wn). Ketei	elevation [meters]	330-2350 [6]	0-1000[14]	1380-2150[6]	0-1030[6]	800-2810[6]	0-2300[6]	0-1090 [6]	1500-2600[6], 3900[24]	300-700 [25]	500-700[13], 2500 m[25]	0-1860[6]	25-1400[6]	0-1750[6]	380-1500[6]	400-2016[6]	200	900-2800[6]	100-2800[6]	1000-1100[25]	0-1750[6]	0-2500[6]
logy (it kno	Ecology (if known)	oak forests[3]/ desert scrub[3]/ palm grove[3], xeric [4]	epiphyte lower montane forest	xerophytic [17]	Myrmecophyte [16], xeromorphic [20]			exposed habitats, coastal[23]		dry forest[25]	xerophytic [25]	juniper forests[3]/palm grove[3]mature forests[10]	decidious, evergreen and semi-evergreen				deciduous-leaf shrubland			dry forest[25], dry valleys[BS]	desert scrubs[3] xeromorphic [20]	juniper forest[3]/ oak forest[3]
phenotype and eco	distribution	Mexico[1]	Bolivia, Venezuela, Colombia, Ecuador, Peru, French Guiana, northern Brazil[15]	Mexico[15]	Belize, Brazil, Caribben, Colombia, Costa Rica, Ecuador, El Salvador, French Guiana, Guetanala, Cuyana, Honduras, Mexico, Nicaragus, Panama, Suriname, US, Venezuela	Mexico, Panama, Honduras, Guatamala, Nicaragua, El Salvador, Costa Rica, Belize	Belize, Costa Rica, El Salvador, Guatemala, Honduras, Mexico, Nicaragua, Panama	El Salvador, Mexico [6]	Mexico[24]	Peru[15]	Penu[25]	Mexico, Central America, West Indies, N. South America.[15]	Belize, Caribbean, Costa Rica, Guatemala, Honduras, Mexico, Nicaragua, Panama [15]	Belize, Costa Rica, Guatemala, Honduras, Mexico, Nicaragua[15]	Mexico, Guatemala, El Salvador, Honduras, Nicaragua [15]	Mexico, Guatemala[15]	Mexico[15]	Costa Rica, El Salvador, Guatemala, Honduras, Mexico Northeast, Mexico Southeast, Mexico Southwest, Nicaragua, Panamá[15]	Mexico - Cosa Rica [15]	Peru[25]	central Mexico to Nicaragua[5]	Bolivia, Brazil, Caribbean, Colombia, Costa Rtee, Ecuador, El Salvador, Guatamala, Honduras, Mexico, Nicargua, Panama, Peru, US, Venezuela[4]]
gnment, J	petals/flower colors	green (citron)[2]	purple[19]	cream[IN]	purple (li1a) [20]	purple (lila)[IN}	purple (lila)[11]	red pink[GY]	yellow-green (citron)[IN]	blue-violet	dark violet[25]	purple (lila)[9]	purple (lila)[IN]	pale lavender, white[29]	purple (lila)[IN]	purple[BS]	purple[BS]	purple (iila)[IN]	purple[15]	blue-violet[BS]	purple[12]	purple (lilà)[3] [12], pink
de assig	bract colors	Pink[2]	red/yellow[19]	yellow[IN]	green[20]	red/green[IN]	pink[11]	green red [GY]	pink[IN]	par	green/red[25]	red/yellow[3]	[N]]par	green[29]	red[IN]	red[BS]	red[BS]	red[BS]	pink[15]	green[BS]	red[12]	green red[3]
<i>w</i> ith cla	water tank	maybe[WT], small[4]	yes[19]	ntermediate [18]	no[20]	no[22]	no[7][22]	small, ntermediate [18]	yes[GY]/ ntermediate[WT]	Yes [IN]	yes[IN]	no[12]	no[BS]	no[BS]	intermediate	оп	ou	yes[31]	maybe		no[12]	no[12]
study v	trichome	yes[4]	no?[19]	yes[18] I	yes[21]	yes[22]	yes[22]	yes [18] ii	yes _{ir}	no [IN]	NA	yes[12]	NA	yes [BS]	NA	yes	yes	no[BS]	NA	NA	yes[12]	yes[34]
ed for this s	leaf	dark green, short and thick[4]	green thin leaves 10-15 cm wide[19]	white, smooth leaf surfaces [18]	thick, green, hard, crooked[16]	thin, hard[22]	thick, twisting, bulbous[22]	chick, greyish green, red in sun[GY], white, smooth leaf surfaces[18]	Green-grey, wide and long	green, wide, shiny[IN]	iin, wide, green. develop purple foliage[25]	öreyish thin leaves, thick cuticle[12]	light green, thin and grassy[BS]	many thin green leaves, filiform[29]	green, hard	many thin and greyish	many thin and greyish	reen, wide and long[BS]	wide, thin, light green greyish	white cross-banded leaves[BS]	yes[33]	thick, narrow, grassy, bluish green
sampl	Isotope ratio 813C (‰)	- 14.7[13]	-26.2[13]	-21.9[13]	-12.4[13]	-13.1[13]	-15.4[13]	-18.6[13]	-22.7[13]	NA	-18.8[13] ^{tl}	-16.1[12], - 0 19.9[13]	-14.6[13]	-27.2[13]	-15.1[13]	-21.1[13]	NA	-25.3[13] g	-23.9[13]	NA	-13.9[12]	-15.3[12]
ecies	Photosynthis (CAM / C3)	CAM[13]	C3[13][14]	C3[13]	CAM[13]	CAM[13]	CAM[13]	CAM[13]	C3[13]	C3?[IN]	CAM[13]	CAM[8][12] [13]	CAM[13]	C3[13]	CAM[13]	33[13]/ CAM	CAM	C3[13]	C3[13]	prob. CAM	CAM[12]	CAM[12]
st of s _f	leaf succulence/ tydroderma	rather no	9	yes	yes	yes[22]	yes[22]	yes	maybe	0E	yes	yes[12]	rathes yes	No [BS]	Q	somewhat [BS]	somewhat	no[BS]	Q	yes	yes[12]	yes[12]
ible S1 lis sheet 2.	habit (epiphyte, terrestrial, saxicolous) h	Epiphytic [1]	Epiphytic [14]	Epiphytic [19]	epiphytic [20]	Epiphytic [22] in mostly dry open habitats	epiphytic [7]	Epiphytic [23]	ephiphytic	lithophytic [25]	saxicolous[25]	Epiphytic [3]	epiphytic [3]	epiphytic [28]	epiphytic [IN]	epiphytic [BS]	epiphytic [BS]	epiphytic [30]	Saxicolous and epiphytic, cliffs and forest	Saxicolous[25]	epiphytic, occasionally saxicolous[5] or terrestrial [12]	Epiphytic and terrestrial[12]
ing ta led in	dade	K.1	SA	K.2.1	K.2.3	K.2.3	K.2.3	K.2.3	K.1	SA	SA	K.2.3	K.2.3	K.2.1	K.2.3	K.2.1	K.2.1	K.2.2	K.1	SA	K.2.3	K.2.3
Support are detail	species	T. achyrostachys	T. adpressiflora	T. albida	T. bulbosa	T. butzii	T. caput-medusae	T. concolor	T. cossonii	T. ecarinata	T. extensa	T. fasciculata	T. festucoides	T. filifolia	T. flabellata	T. fuchsii	T. fuchsii. var. steph	T. guatemalensis	T. gymnobotrya	T. hildae	T. ionantha	T. juncea

endemic/ widespread	Endemic [6]	widespread	Endemic [6]	Endemic [6]	Endemic	Endemic	Endemic [25]	widespread	Endemic [6]	Endemic [25]	widespread	widespread	Endemic	widespread			
Conservation status			ΓC		LC	LC	LC			ΓC		Threatened	LC	widespread	LC - Least concern		
Other	increase in abundance in disturbed forests, isolated trees in pastures,coffee plantations						xyrophyte	increase in abundance in disturbed forests, isolated trees in pastures,coffee plantations						non-terminal blooming bromeliad, axillary inflorescences.			
reproductive system	ornithophilous	omithophilous/? entomophilous	ornithophilous; mixed[38]	monocarpic, Sc [, hummingbird pollinated26]	ornithophilous	ornithophilous	ornithophilous	ornithophilous; pref. Outcrosser	ornithophilous and SC, high-selfing[7]	ornithophilous	ornithophilous	omithophilous; possibly deistogamous[29]	ornithophilous	ornithophilous/ entomophilous	SI - self incompitable	SC - self compitable	
elevation [meters]	1000-2100[6]	800-1900[6]	1800-3300[6]	50-2320[6]	500-1880[13]	650-1900 [BS]	800m[25]	200-2200[6]	0-2230[6]	1700[25]	250-1820[6]	550-1170[6]	3000	750-3000 [IN]			
Ecology (if known)	mesic [BS]		<pre>ak forest[3], pine forest, oak-pine forest[37]</pre>	oak forest[3]	saxicolous	saxicolous	terrestrial in dry valley	doud forest[40]	juniper forest[3]/ oak orest[3] desert scrub[3]/ palm grove [3]	dry forest[25]		amazon forest, Premontane Humid Forest[25]	lithophyte				
distribution	Mexico[15]	Belize, Costa Rica, El Salvador, Guatemala, Honduras, Mexico Central, Mexico Gulf, Mexico Southeast, Mexico Southwest, Nicaragua, Panamá[15]	Mexico[37]	Costa Rica, El Salvador, Guatemala, Honduras, Mexico, Nicaragua[15]	Ecuador?[25]	Colombia, Ecuador, Peru[15]	Peru[25]	Belize, Costa Rica, El Salvador, Guatemala, Honduras, Mecico, Nicarague, Panama[15]	Belize, Caribbean, Colombia, Costa Rica, El Salvador, Guatemala, Honduras, Mexico, Nicaragua, Venezuela[15]	Peru[25]	3elize, Costa Rica, Guatemala, Honduras, Mexico, Nicaragua, Panama[15]	Belize, Bolivia, Colombia, Costa Rica, Cuba, Dominican Republic, Florida, Custenala, Hati, Honduras, Jamaca, Mexico Central-Southwes, Nicanagua, Panamá, Puerto Rico, Venezuela[15]	Bolivia[15]	Bolivia, Peru, northern Brazil, Colombia, Guyana, Costa Rica, Panama, Cuba, Jamaica, Trinidad, Venezuela, Ecuador [15]			
petals/ flower colors	purple (lila)[3]	purple[12]	purple[3]	purple (lila)[3], citron stamens[3]	blue-violet	violet	dark-violet[25]	dark purple, black, white apex[BS]	yellow/green[3]	purple[IN]	purple[BS]	lavender to blue[BS]	blue-violet	blue (and purple- red)			
bract colors	green red[3]	red[12]	pink[3]	green red[3]	green	carmine-red	carmine-red	green[BS]	red[3]	green[IN]	red yellow green[BS]	green red[BS]	green	red or green			
water tank	intermediate[36]	yes[12]	intermediate	yes[26]	yes	yes	intermediate	intermediate[32]	no[7]	intermediate	ы	yes[42]	yes[42]	yes[42]			
trichome	[N]]ou	no[12]	yes[37]	yes[IN}	NA	yes[BS]	yes	maybe	yes[35]	NA	yes[BS]	no[BS]	NA	QL			
leaf	Green sheets, long filiform. [36]	soft, green, wide[IN]	semi-fleshy, ashen-green	greyish, glaucous-grey	large, green-greysh, wide	large, hard, greyish- green[BS]		thick, narrow, grassy, bluish green	thin, hard, greyish[BS]	thin, wide, greyish	narrow, green or red, greyish[BS]	soft	thick, green	thin, green			
Isotope ratio δ13C (‱)	-22.9[13]	-31.3[12]	-20.8[13]	- 13.9[13]	-14.6[13]]	-15[13]	NA	-24.5[13]	-12.1[13]	NA	- 15.2[13]	-12.7[13]	NA	NA			
Photosynthis (CAM / C3)	C3[13]	C3[12]	C3?[13]	CAM[13]	CAM[13]	CAM[13]	CAM	C3[13]	CAM[13]	CAM	CAM[13]	CAM[13]	IJ	Ü			
leaf succulence/ 1ydroderma	OU	no[12]	no[39]	rather yes	rather yes	yes[BS]	yes	<u>e</u>	yes[41]	rather no	yes[BS]	01	8	9			
habit (epiphyte, terrestrial, saxicolous)	epiphytic [GY]	Epiphytic and terrestrial [12]	epiphytic [37]	epiphytic [26]	lithophyte	lithophyte or epiphyte[BS]	Saxicolous[25]	Epiphytic [40]	epiphytic [41]	Saxicolous [25]	epiphytic	epiphytic [15]	lithophytic [25]	epyphitic, lithophytic			
dade	K.1	K.2.2	K.1	K.2.1	SA	SA	SA	КЛ	K.2.3	SA	K.2.3	K.2.3	outgroup	outgroup			
species	T. kirchhoffiana	T. leiboldiana	T. macdougallii	T. makoyana	T. marnier- lapostollei	T. mima	T. mima var. chilensis	T. punctulata	T. schiedeana	T. spiraliflora	T. tricolor	T. variabilis	T. carnosa var. boliviensis	T. complanata			

Corresponding literature for supporting table S1.

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- IN blog/forum
- bromeliad society website and articles BS
- GY field observations. G. Yardeni
- Walter Till, private correspondence none

Supporting table S2 sampled accessions in this study with collection, locality and voucher information. samples marked grey were removed from analysis (see table 3)

					-					_															_		
	səţou	Camino Viejo a Corralitos	Camino Viejo a Corralitos					Hromadnik: HR18 (Blass: s. n.)	Senderos Costa, Prusia		Camino Viejo a Corralitos	Camino Viejo a Corralitos		putative hybrid			Las Joyas	Tepehuaje, camino viejo a Corralitos					disturbed forest				
	Coordinates	19°39'20.17" N, 104°19'45.86" W	19°39'20.17" N, 104°19'45.86" W				10.43375,- 84.0124444		15°38'07.3" N, 92°48'14.3" W		19°39'20.17" N, 104°19'45.86" W	19°39'20.17" N, 104°19'45.86" W			-4.112886,- 78.968189	19°35'58.0" N, 096°22'49.1" W	19°35'11.9" N, 104°15'57.9" W	19°39'05.2" N, 104°20'06" W									
	(m) notisvəl∃	1400	1400			no data	17	no data	1800		1400	1400			1200		2000	1500	1100	2000	no data	2000		no data	1200	1200	750
	Γοςαίζελ	Reserva de la Biósfera Sierra de Manantlán, Jalisco	Reserva de la Biósfera Sierra de Manantlán, Jalisco			Venados Valley	La Selva Biological Station	no data	Reserva de la Biósfera El Triunfo, Chiapas	Al O de Teopisca	Reserva de la Biósfera Sierra de Manantlán, Jalisco	Reserva de la Biósfera Sierra de Manantlán, Jalisco	Mecapca	Cerro Macuilteptl	Bombuscaro	La Mancha biological station	Reserva de la Biósfera Sierra de Manantlán, Jalisco	Reserva de la Biósfera Sierra de Manantlán, Jalisco	Rock wall above Pucara	Abra Chanchillo - Balsas	no data	Abra Chanchillo - Balsas	Agüita Fría	Lago de Atitlán	Barva north of Heredia	Sumidero Canon at Tuxtla Gutierrez, El Mirador km 17	SW declivities of Cordillera de Tilaran, along the road from Sta. Elena to Rancho Grande, at Guaria
	State	Jalisco	Jalisco			Hidalgo		no data	Chiapas	Chiapas	Jalisco	Jalisco	La Paz	Veracruz		Veracruz	Jalisco	Jalisco	Cajamarca	Amazonas	no data	Amazonas	Veracruz	Sololá	Heredia	Chiapas	Puntarenas
	Country	Mexico	Mexico	Brazil	Mexico	Mexico	Costa Rica	Colombia	Mexico	Mexico	Mexico	Mexico	Bolivia	Mexico	Ecuador	Mexico	Mexico	Mexico	Peru	Peru	Peru	Peru	Mexico	Guatemala	Costa Rica	Mexico	Costa Rica
	Collector	L. Silva-Mijangos	L. Silva-Mijangos	na	R. & F. Wolf	R. & F. Wolf	na	no data	L. Silva-Mijangos	J.P. Pinzón	L. Silva-Mijangos	L. Silva-Mijangos	A. Seringer	G. Yardeni	I. Olivares	G. Yardeni	L. Silva-Mijangos	L. Silva-Mijangos	H. & L. Hromadnik HR 23020	H. & L. Hromadnik HR 4198	no data	H. & L. Hromadnik HR 4198	G. Yardeni	G. Noller 9106	W. & S. Till WT 7004	R. Ehlers EM 890701	W. ଋ S. Till WT 7116
	.JəŪ	L. Silva-Mijangos, Jun. 2017	L. Silva-Mijangos, Jun. 2017	na	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss	na	L. Hromadnik	L. Silva-Mijangos, Jun. 2017	J.P. Pinzón	L. Silva-Mijangos, Jun. 2017	L. Silva-Mijangos, Jun. 2017	A. Seringer, W. Till, M.H.J. Barfuss	W. Till, Jul 2017	I. Olivares	G. Yardeni	L. Silva-Mijangos, Jun. 2017	L. Silva-Mijangos, Jun. 2017	L. Hromadnik	L. Hromadnik	no data	L. Hromadnik	G. Yardeni	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss
	өроо_пөртед	e e	na	na	BG Wien (HBV) 0000271 ([B12/87)	BG Wien (HBV) 0000269 (B2/91)	na	Hromadnik HR18	na	(field collection)	na	na	BG Wien (HBV) 0029144	na	na	na	Па	Па	Hromadnik HR23020	Hromadnik HR4198 (2)	BG Wien (HBV) 0024653 (B223/91)	Hromadnik HR4198 (1)	na	BG Wien (HBV) 0026950 (B103/94)	BG Wien (HBV) 0024655 (B99/91)	BG Wien (HBV) 0024656 (B108/94)	BG Wien (HBV) 0024657 (B179/91)
	DAA_code in M. Barfus collection	ра	ра	na	71	MHJB-B370	na	MHJB-B1222	na	MHJB-B833	ра	па	MHJB-B1865	na	na	na	na	na	MHJB-B1871	MHJB-B1870	MHJB-B1878	MHJB-B1882	na	MHJB-B1839	MHJB-B1841	MHJB-B360	MHJB-B1840
	əmsn_nottoəlloD	LSM_370B	LSM_370A	BR3.2015 (8951)	0000071[B12/8]	0000269[B2/91]	oL010_f	HBVSN/B1222	LSM_132C	B833	LSM_369C	LSM_369E	UD10002	GY084	IO041	GY133	LSM_381C	LSM_365C	UD10006	UD10005	UD10007	UD10010	GY004	HBV26950	HBV24655	HBV24656	HBV24657
(c	əpelə	K.1	K.1	SA	K.2.1	K.2.1	K.2.3	K.2.3	K.2.3	K.2.3	K.2.3	K.2.3	SA	K.2.3	outgroup	K.2.3	K.1	K.1	SA	SA	SA	SA	K.2.3	K.2.3	K.2.3	K.2.3	K.2.3
אוחשו אשלו אופע	Species	T. achyrostachys	T. achyrostachys	T. adpressiflora	T. albida	T. albida	T. bulbosa	T. bulbosa	T. butzii	T. butzii	T. caput-medusae	T. caput-medusae	T. carnosa var. boliviensis :	T. cf. Tricolor.fasciculata	T. complanata	T. concolor	T. cossonii	T. cossonii	T. ecarinata	T. extensa	T. extensa	T. extensa	T. fasciculata	T. fasciculata	T. fasciculata	T. fasciculata	T. fasciculata
	name_in_project	ach 58	ach 9	adp50	alb59	alb269	bul16	bul29	but3	but87	cap32	cap 61	car92	cat27	com90	con 14	cos38	cos39	eca88	ext89	ext90	ext91	fas 26	fas 30	fas24655	fas24656	fas 24657

səton	_				-	2				UTRECHT: E.J. Gouda (BG. U, Staff), 3Z						BG Linz				Tepehuaje, camino viejo a Corralitos		disturbed forest						
Coordinates			10.433750, - 84.012444	10.433750, - 7 84.012444) 17.824333, -96.243) 17.824333, -96.243	15°42'55" N,) 92°51'21.3" W	15°42'55" N,) 92°51'21.3" W	15°37'49.7" N,) 92°48'12.1" W		19°39'20.17" N, 104°19'45.86" W	15°39'32.4" N,) 92°48'28.5" W	15°39'32.4" N,) 92°48'28.5" W	19.498694, -) 96.97147) 17.68052,-96.5533	_			_	19°39'05.2" N, 104°20'06" W		19 °31'14.9", 096°59'23.4"			19°33'20.4" N, 104°09'00.8" W	19°33'20.4" N, 104°09'00.8" W	19°39'05.2" N, 104°20'06" W	19°39'05.2" N, 104°20'06" W
(m) notheval3	no data	no data	1	1	300	300	1250	1250	1600		1400	2000	2000	2040	2210	no data	o no data	100	no data	1500	1200		1030		2800	2800	1500	1500
Locality	no data	Sta. Teresa Esquintla	La Selva Biological Station	La Selva Biological Station	San Juan Bautista Valle Nacional	San Juan Bautista Valle Nacional	Reserva de la Biósfera El Triunfo, Chiapas	Reserva de la Biósfera El Triunfo, Chiapas	Reserva de la Biósfera El Triunfo, Chiapas		Reserva de la Biósfera Sierra de Manantlán, Jalisco	Reserva de la Biósfera El Triunfo, Chiapas	Reserva de la Biósfera El Triunfo, Chiapas	Coatepec	San Felipe Usila	no data	100 km befor Altamiran	Near the town of Tehuantepec, Rio Huamelula near San Pedro Huamelula, epilithic	Rio Grijalva	Reserva de la Biósfera Sierra de Manantlán, Jalisco	Xicotepec de Juárez - La Union	Agüita Fría	2 km N San Ranion	Tunapaz	Reserva de la Biósfera Sierra de Manantlán, Jalisco			
State	no data	Escuintla	Heredia	Heredia	Oaxaca	Oaxaca	Chiapas	Chiapas	Chiapas		Jalisco	Chiapas	Chiapas	Veracruz	Оахаса	Cajamarca	no data	Oaxaca	Chiapas	Jalisco	Puebla	Veracruz	Alajuela	Chiapas	Jalisco	Jalisco	Jalisco	Jalisco
Сопиц.А	Honduras	Guatemala	Costa Rica	Costa Rica	Mexico	Mexico	Mexico	Mexico	Mexico	Mexico	Mexico	Mexico	Mexico	Mexico	Mexico	Peru	Mexico	Mexico	Mexico	Mexico	Mexico	Mexico	Costa Rica	Mexico	Mexico	Mexico	Mexico	Mexico
Collector	Kamm	W. Welz 3132	O. Loiseau	O. Loiseau	M. de la Harpe	M. de la Harpe	K. Silva-Mijangos	K. Silva-Mijangos	L. Silva-Mijangos	U: 1997GR00709	L. Silva-Mijangos	L. Silva-Mijangos	L. Silva-Mijangos	M. de la Harpe	M. de la Harpe	no data	R. Ehlers EM 911306	J. Lautner	no data	L. Silva-Mijangos	KD. & R. Ehlers EM942601	G. Yardeni	W. & S. Till 7112	J.P. Pinzón & al. 120	L. Silva-Mijangos	L. Silva-Mijangos	L. Silva-Mijangos	L. Silva-Mijangos
Det.	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss	O. Loiseau	O. Loiseau	M. de la Harpe	M. de la Harpe	E. Espejo-Serna, Jan. 2017	E. Espejo-Serna, Jan. 2017	E. Espejo-Serna, Jan. 2017		L. Silva-Mijangos, Jun. 2017	E. Espejo-Serna, Jan. 2017	E. Espejo-Serna, Jan. 2017	M. de la Harpe	M. de la Harpe	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss	W. Till, M.H.J. Barfuss	L. Silva-Mijangos, Jun. 2017	W. Till, M.H.J. Barfuss	V. Guzman	W. Till	J.P. Pinzón	L. Silva-Mijangos, Jun. 2017	L. Silva-Mijangos, Jun. 2017	L. Silva-Mijangos, Jun. 2017	L. Silva-Mijangos, Jun. 2017
Garden_code	BG Wien (HBV) 0025334 (B99B53-1)	BG Wien (HBV) 0025390 (B97/94)	na	na	na	na	na	na	na	BG Utrecht 1997GR00709	na	na	na	na	na	BG Wien (HBV) 0027606	BG Wien (HBV) 0030230 (B219/91)	BG Wien (HBV) 0024697 (B279/95)	BG Wien (HBV) 0025358 (437/82)	na	BG Wien (HBV) 0026412 (B95/9)	na	BG Wien (HBV) 0024715 (B82/91)	(field collection)	na	na	ша	na
DAA_code in M. Barfuss collection	MHJB-B1838	MHJB-B1837	na	na	na	na	na	na	na	MHJB-B1726	па	na	na	na	na	MHJB-B1880	MHJB-B1845	MHJB-B1844	MHJB-B439	па	MHJB-B1308	na	MHJB-B1842	MHJB-B843	ра	na	na	na
oniection_name	HBV25334	HBV25390	OL009c	OL009e	MH080b	MH080a	LSM_273c	LSM_273a	LSM_170A	B1726	LSM_368F	LSM_15D	LSM_15C	MH027C	MH124c	UD1009	HBV219	HBV24697/B279	HBV437	LSM366D	B1308	GY25	HBV24715	B843	LSM385A	LSM385B	LSM374B	LSM374C
əpelə	K.2.3	K.2.3	K.2.3	K.2.3	K.2.1	K.2.1	×.	Ŀ.	K.2.1	K.2.1	K.2.1	K.2.2	K.2.2	K.1	K.1	SA	K.2.3	K.2.3	g K.2.3	K.2.3	K.1	K.1	K.2.2	K.2.2	K.1	K.1	K.2.1	K.2.1
Secies	T. fasciculata	T. fasciculata	T. festucoides	T. festucoides	T. filifolia	T. filifolia	T. flabelata	T. flabelata	T. fuchsii	T. fuchsii	T. fuchsii var. stephanii	T. guatemalensis	T. guatemalensis	T. gymnobotrya	T. gymnobotrya	T. hildae	T. ionantha	T. ionantha var. maxima	T. ionantha var. van-hyni	T. juncea	T. kirchoffiana	T. kirchoffiana	T. leiboldiana	T. leiboldiana	T. macdougallii	T. macdougallii	T. makoyana	T. makoyana
name_in_project	fas25334	fas 25390	fes15	fes64	fil49	fil65	fla51	fla94	fuc24	fuc53	fus4	gua19	gua95	gym17	gym18	hil98	ion219	iom24697	iov437	juné	kir28	kir56	lei31	lei57	mac78	mac79	mak 22	mak 80

səton															
coordinates				5 18.54803, -95.15098	15°38'08.1" N, 0 92°48'14" W	17.824333, - 0 96.24375	19°39'05.2" N, 0 104°20'06" W	19°39'05.2" N, 0 104°20'06" W			8.7934722, - 4 82.97138	8.7934722, - 1 82.97138		15°36'50" N,) 92°49'21"W	15°36'50" N,) 92°49'21"W
(m) notisvel3	600 800	2500	1000	1105	1800	300	1500	1500	1700	1700	1134	1134		1200	1200
لمcality	at Río Chancay, between km 6 & km 15 at road to Santa Cruz, E Río Chancay bridge	Gualaceo - Remigio Crespo	Magdalena District, Huaquillas, valley of Río Magdalena	San Andres Tuxtla	Reserva de la Biósfera El Triunfo, Chiapas	San Juan Bautista Valle Nacional	Reserva de la Biósfera Sierra de Manantlán, Jalisco	Reserva de la Biósfera Sierra de Manantlán, Jalisco	km 355, E Balsas	km 355, E Balsas	Estación Biológica Las Cruces	Estación Biológica Las Cruces		Reserva de la Biósfera El Triunfo, Chiapas	Reserva de la Biósfera El Triunfo, Chiapas
State	Cajamarca	Azuay	Cajamarca	Veracruz	Chiapas	Оахаса	Jalisco	Jalisco	Amazonas	Amazonas				Chiapas	Chiapas
Сопиди	Peru	Ecuador	Peru	Mexico	Mexico	Mexico	Mexico	Mexico	Peru	Peru	Costa Rica	Costa Rica		Mexico	Mexico
Collector	W. Rauh R 35345	H. & L. Hromadnik HR 17078	W. Rauh R 69103	M. de la Harpe	L. Silva-Mijangos	M. de la Harpe	L. Silva-Mijangos	L. Silva-Mijangos	H. & L. Hromadnik HR 4203	H. & L. Hromadnik HR 4203	O. Loiseau	O. Loiseau	I. M. Ramírez M. 1798	L. Silva-Mijangos	L. Silva-Mijangos
Det.	W. Till, M.H.J. Barfuss	L. Hromadnik	W. Rauh	M. de la Harpe	A. Hernández-Rojas, Dec 2016	M. de la Harpe	L. Silva-Mijangos, Jun. 2017	L. Silva-Mijangos, Jun. 2017	L. Hromadnik	L. Hromadnik	O. Loiseau	O. Loiseau	J.P. Pinzón	E. Espejo-Serna, Jan. 2017	E. Espejo-Serna, Jan. 2017
Garden_code	BG Wien (HBV) 0024729 (B98B87-1)	Hromadnik HR17078 (1)	BG Wien (HBV) 0020417	na	ра	na	na	па	Hromadnik HR4203 (1)	Hromadnik HR4203 (2)	ра	na	(field collection)	na	na
DNA_code in M. Barfuss collection	MHJB-B1879	MHJB-B1864	MHJB-B1438	na	na	na	па	па	MHJB-B1866	MHJB-B1867	na	na	MHJB-B1181	na	па
Sollection_name	UD1008	UD1001		MH016_h	LSM_147C	MH076_B1	PSM373d	LSM373c	UD1003	UD1004	OL053C	OL053_A	B1181	LSM188A	LSM188C
ချာဗျာ	SA	SA	SA	K.1	K.1	K.2.3	K.2.3	K.2.3	SA	SA	K.2.3	K.2.3	K.2.3	K.2.3	K.2.3
Species	T. marnier-lapostollei	T. mima	T. mima var. chiletensis	T. punctulata	T. punctulata	T. schiedeana	T. schiedeana	T. schiedeana	T. spiraliflora	T. spiraliflora	T. tricolor	T. tricolor	T. variabilis	T. zoquensis	T. zoquensis
name_in_project	mar21	mim11	mim20417	pun2	pun5	sch12	sch41	sch83	spi67	spi68	tri42	tri8	var43	zoq45	zoq46

Supporting table S3 samples accessions with information about sequence read number, alignment rates and number of sequences after filtering. samples marked grey were removed from analysis

Number in project	Species	clade	read (total)	Coverage sam	read (bowtie reports)	Alignment rate [bowtie,%]	reads_High Q reads_High Q_%	ecoverage_ Hoplication rate[picar notes
ach58	T. achyrostachys	K.1	52788378	6.90072	26295156	80.09	29026704 0.5499	4.9 0.12
ach9	T. achyrostachys	K.1	80291160	9.67788	39292670	89.36	46563014 0.5925	6.54 0.02
adp50	T. adpressiflora	SA	254468532	26.581	127234266	79.76	114344720 0.4493	14.4 0.14
alb269	T. albida	K.2.1	111574508	13.3495	55627601	90.09	71520128 0.6428	9.75 0.04
alb59	T. albida	K.2.1	30988234	4.55497	15346023		19696207 0.6356	3.29 4.55 Removed - kinship
bul16	T. bulbosa	K.2.3	84840706	9.88809	NA	NA	45316108 0.5341	6.44L5719
bul29	T. bulbosa	K.2.3	38074934	4.77021	18364059	92.08	23750445 0.6467	3.37 0.02
but3	T. butzii	K.2.3	111336080	6.4598	NA	NA	61116328 0.5489	8.73 0.01
but87	T. butzii	K.2.3	114263320	17.4267	56988347	90.69	76935744 0.675	13.1 0.18
cap32	T. caput-medusae	K.2.3	35151386	4.18141	15605180	95.49	20163869 0.5736	2.85 0.01
cap61	T. caput-medusae	K.2.3	27891184	6.42161	22621489	84.65	27891184 0.6165	4.74 0.15
car92	T. carnosa var. boliviensis	outgroup	74302808	9.54226	36866422	84.99	36571892 0.496	5.96 0.14
cat27	T. cf. tricolor (fasciculata	K.2.3	22654846	2.62	10781334	85.82	4711113 0.2185	1.91 0.01
com90	T. complanata	outgroup	138144334	14.4118	69072167	78.72	22448508 0.1625	1.32 0.12
con14	T. concolor	K.2.3	43808582	6.14989	NA	NA	27640577 0.6309	12.9)5013
cos38	T. cossonii	K.1	50458014	6.06038913	22947865	85.90	29486934 0.6425	4.18 0.02
cos39	T. cossonii	K.1	65645928	7.92850913	30234425	88.38	38758323 0.641	5.49 0.03
eca88	T. ecarinata	SA	82002040	11.5218	40297289	90.66	48138176 0.5973	8 0.14
ext89	T. extensa	SA	98455094	13.7545	48372944	90.52	57308431 0.5924	9.5 0.14
ext90	T. extensa	SA	67806390	9.54891	33538475	90.37	39655139 0.5912	6.59 0.14
ext91	T. extensa	SA	94123032	13.0489	46140271	90.05	54138476 0.5867	8.98 0.15
fas24655	T. fasciculata	K.2.3	111924314	14.7251	55775701	91.60	73296850 0.6571	10.6 0.02
fas24656	T. fasciculata	K.2.3	119276338	15.9522	59439920	94.33	80802242 0.6797	11.5 0.02
fas24657	T. fasciculata	K.2.3	99528422	13.5494	49598337	94.39	69184879 0.6975	10 0.02
fas25334	T. fasciculata	K.2.3	116009950	14.64	57852756	88.98	74013253 0.6397	10.6 0.03
fas25390	T. fasciculata	K.2.3	118874624	15.9264	59254274	93.95	80811228 0.6819	11.6 0.02
fas26	T. fasciculata	K.2.3	50581700	10.61466	40331611	96.55	56465112 0.7	8.06 0.01
fas30	T. fasciculata	K.2.3	113808178	15.266	56724350	94.59	76324527 0.6728	10.9 0.02
fes15	T. festucoides	K.2.3	137091043	20.5653	NA	NA	24503411 0.1787	12.910377
fes64	T. festucoides	K.2.3	34387048	4.87198	16854289	85.74	21227094 0.6297	3.62 0.12
fil49	T. filifolia	K.2.1	48655424	5.53092	23756120	73.21	21235876 0.4365	3.56 0.15
fil65	T. filifolia	K.2.1	41312422	6.00225	20323674	93.29	23202264 0.5708	3.87 0.12
fla51	T. flabelata	K.2.3	66866856	7.70898	32909030	69.43	33282888 0.4977	5.7 0.14
fla94	T. flabelata	K.2.3	110010160	17.4969	54861404	94.90	75017296 0.6837	12.8 0.17
fuc24	T. fuchsii	K.2.1	79838208	9.61418	NA	NA	41364101 0.5181	5.9412125
fuc53	T. fuchsii	K.2.1	64787956	7.76007	31729566	77.11	30814205 0.4756	5.13 0.13
fus4	T. fuchsii var. stephanii	K.2.1	62087942	7.06142	28021332	93.35	34019031 0.5479	4.76 0.02
gua19	T. guatemalensis	K.2.2	172102484	20.52466	81411367	91.80	113288052 0.6583	15.8 0.05
gua95	T. quatemalensis	K.2.2	87904454	13.6799	43767379	96.57	64734545 0.7395	10.7 0.17
gym17	T. gymnobotrya	K.1	93638542	11.7848	NA	NA	57063301 0.6094	8.07 0.03
gym18	T. gymnobotrya	K.1	101435088	14.9781	NA	NA	70412561 0.6942	9.9 0.01
hil98	T. hildae	SA	70949240	9.99907	34997243	90.68	41740743 0.5963	6.93 0.14
iom24697	T. ionantha var. maxima	K.2.3	132065572	15.0519	65855931	82.73	80799847 0.6135	11.3 0.03
ion219	T. ionantha	K.2.3	124883972	13.1334	57556828	82.48	68984356 0.5993	9.67 0.03
iov437	T. ionantha var. van-hyniaii	K.2.3	109934468	13.5141	54682124	88.95	72554789 0.66	10.2 0.03
jun6	T. juncea	K.2.3	110743706	16.5723	NA	NA	22571180 0.2038	11.2)6804
kir28	T. kirchoffiana	K.1	53096276	5.19772	NA	NA	36782664 0.6928	5.23)9556
kir56	T. kirchoffiana	K.1	81479690	12.4275	39963671	94.07	55756859 0.6843	9.45 0.17

lei31	T. leiboldiana	K.2.2	150161252	18.8141	NA	NA	118514539 0.7892	15.6 0.04
lei57	T. leiboldiana	K.2.2	42676818	6.45938	20975923	94.77	29498334 0.6912	4.93 0.13
mac78	T. macdougallii	K.1	39408152	6.15202	19643666	96.22	27741194 0.7061	4.64 0.12
mac79	T. macdougallii	K.1	10078600	1.57143	5023495		7091601 0.7058	1.19 0.12 Removed – low coverage
mak22	T. makoyana	K.2.1	106064342	14.4793	NA	NA	21372571 0.2015	9.02)1177
mak80	T. makoyana	K.2.1	72766412	11.0298	36053208	94.89	45989576 0.6378	7.73 0.16
mar21	T. marnier-lapostollei	SA	75255838	10.9557	37299312	92.62	46113479 0.6182	7.67 0.14
mim11	T. mima	SA	125250164	18.1102	62170380	92.85	78647362 0.6325	12.9 0.11
mim20417	T. mima var. chiletensis	SA	117572260	13.5333	58627406	87.38	70473252 0.601	9.67 0.04
pun2	T. punctulata	K.1	97971356	9.41656	NA	NA	45184568 0.4612	6.3817001
pun5	T. punctulata	K.1	63141784	5.65639	NA	NA	26733658 0.4234	3.85 0.13
sch12	T. schiedeana	K.2.3	25957066	3.30669	12437299	94.09	16146387 0.6491	2.29 0.01
sch41	T. schiedeana	K.2.3	80657614	13.208	39910790	97.50	56261863 0.7048	9.64 0.13
sch83	T. schiedeana	K.2.3	71166278	11.2028	35168539		47982660 0.6822	8.23 0.14 Removed – kinship
spi67	T. spiraliflora	SA	91525124	12.9233	45379698	90.50	54596826 0.6016	9.06 0.15
spi68	T. spiraliflora	SA	93990912	13.141	46266543	90.32	55228655 0.5969	9.16 0.16
tri42	T. tricolor	K.2.3	101139726	16.1895	49526526	96.74	68878107 0.6954	11.8 0.2
tri8	T. tricolor	K.2.3	65988912	8.85426	32215167	96.87	42448855 0.6588	6.06 0.01
var43	T. variabilis	K.2.3	127220668	20.2525	NA	NA	88987802 0.6995	15.1 0.15
zoq45	T. zoquensis	K.2.3	12345936	1.90631	6039269	93.11	8049613 0.652	1.38 0.14 removed from analysis
zoq46	T. zuquensis	K.2.3	37574672	5.87874	18465772	93.72	25076729 0.6674	4.31 0.16 removed from analysis

Conclusions and outlook

Recently and rapidly radiating lineages are fascinating to study as they showcase divergence at the intersection of evolution, ecology and adaptation. Their young age provides a glimpse into an early point of the 'speciation continuum', when the footprint of genomic processes is still fresh. Nevertheless they remain one of the biggest challenges in the study of the tree of life, posing obstacles that are seldom simply resolved by 'applying more data'.

The use of NGS provided unprecedented resolution for Tillandsia phylogenomics and was especially successful in species delimitation and inference of subgeneric relationships. Tillandsia is a textbook example of rapid radiation: their phylogeny is characterized by short internal nodes with high rates of gene tree discordance which coincides with morphological innovation (Kandziora et al., 2022; Parins-Fukuchi et al., 2021). While gene tree discordance most likely resulted from several entangled genomic processes, chapter 2 of this thesis provided evidence for the extensive role of both ancient and recent hybridization in gene-tree conflict. However, species of Tillandsia exhibited genetic cohesiveness, both in assignment to species and to clades, evident in the population genomics analysis section of chapter 1 and in tests for monophyly in chapter 2. We found rather weak evidence for population structure in chapter 1, as is typical for species that experience high rates of ongoing gene-flow and species exhibiting ornithophilous pollination - however, our rather limited sampling restricted our ability to draw clear conclusions. Finally, chapter 2 offered a re-telling of the evolutionary history of the clade. Whole-genome sequences and a phylogenetic network approach surprisingly provided evidence that Tillandsia subgenus Tillandsia may have expanded into Central America through several independent dispersal events.

Beyond questions aimed at the lineage's history, this work provided findings on species delimitation and systematics. For example, we noted observations on the clade assignment of *T. zoquensis* and on the relationship between *T. mima* and *T. mima. var. chiletensis* in **chapter 2**. *Tillandsia* phylogeny and systematics will very likely remain a topic for lively scientific discussion, as these intriguing species are not easily delimited by morphological traits nor do they adhere to traditional species concepts. Numerous cryptic species complexes in this lineage await 'entanglement' and resolution, which is complicated by recurrent gene-flow.

Abundant data requires an abundance of technical and conceptual considerations. Chapter 1 explicitly examined the performance of different bait sets for target capture in the context of studying recent, rapid radiations. Contrary to our early expectations, we found that a highly-curated bait-set did not necessarily offer crucial advantages. These results suggest that studies aiming at macro-evolutionary inference can evade the investment required in the design and development of home-made baits without risking satisfactory phylogenetic resolution. These are exciting findings in the context of collaborative and inclusive science: cost-effective and highly efficient genomic tools can provide comparable data-sets that can be readily integrated, encourage collaborative investigations and pose fewer financial barriers to research groups. Conversely, a specifically-designed bait set is beneficial for a number of investigative and technical aspects. As chapter 1 details, we obtained more information on gene tree incongruence and had greater confidence in testing population genomic structure with Bromeliad1776. During analysis we observed technical advantages that were beyond the scope of the manuscript. Utilizing pipelines based on sequence assembly was difficult for the universal bait-set, especially when we attempted to include regions that were not directly targeted (i.e., 'flanking'). In the universal set, those sequences exhibited high rates of mapping and assembly error; filtering the data-set proved complex and time-consuming, a property also reported by colleagues (Viruel, J., private correspondence). When using an alternative method of calling variants, we had less confidence in the universal data-set in terms of biologically-meaningful values. For these reasons, we ultimately estimated population genomic parameters using only the taxon-specific set.

The field of genomics advances with a quickly-changing selection of technologies and tools. Two types of data were utilized in this dissertation, each providing different advantages. While whole-genome re-sequencing is less laborious in terms of molecular work and offers a broad view of a species' genome, it requires a reference genome and may provide data-sets infused with analytical 'noise' and challenging to filter. On the contrary, target capture provided the author with 'simpler' and 'cleaner' data-sets and with valuable knowledge of the regions targeted. A biased choice of loci may amplify error as discussed in the supporting information of **chapter 1**. The scientific questions at hand ultimately drive the choice of genomic tools, however it's interesting to note that large genomic data-sets are not only costly to produce, but are also costly to store, analyze, document and maintain. To that

end, I believe that classical phylogenetic 'small-data' tools should not be underestimated for their reliability and elegant performance.

Tillandsia offers an intriguing model group for studying rapid radiations in general and Neotropical biota in particular. The observed quick accumulation of morphological traits, especially in a correlated manner, invites questions regarding the interplay of genomics and selection in the formation of adaptive syndromes. This dissertation provides early evidence for genomic processes resembling those reported in other fascinating and well-studied evolutionary radiations, like cichlid fish and *Heliconius* butterflies (Brawand et al., 2014; Malinsky et al., 2018; Martin et al., 2013). Key genomic resources are now available to study *Tillandsia*, including a reference genome and a bait set fit for studies spanning population genomics and genomic processes, from novel mutations to copy-number variation. The current work and existing tools will hopefully inspire other evolutionary biologists to do so.

Hybridization in *Tillandsia* had been observed and its role speculated by earlier researchers. In her publication from 1984, Gardner (1984) highlighted the prevalence of interspecific hybridization in *Tillandsia*, writing that "natural hybridization appear [sic] to be responsible for some portion of the phenetic variation expressed by these species". **Chapter 2** provides evidence for the extent and timing of hybridization in *Tillandsia*, a process that is in no sense unique to this lineage. The role of hybridization in species radiations and the prevalence of speciation with gene-flow have both received growing attention in the last decades. Hybridization may increase adaptive potential by enhancing variation (Grant & Grant, 2019) and adaptive introgression was found to play a role in adaptation to climate (Leroy et al., 2020), disease (Bechsgaard et al., 2017) and photosynthetic shifts (Tefarikis et al., 2022), among others (Suarez-Gonzalez et al., 2018; Taylor & Larson, 2019). Furthermore, the observation of deviations from a bifurcating tree structure and the use of phylogenetic networks to describe species' diversification are both becoming ubiquitous, if not necessary, to phylogenomic inference.

It is then clear that bifurcating trees do not reliably describe the evolutionary history of many lineages and that numerous assumptions on species behaving like discrete and isolated entities are insufficient to understand speciation (Mallet et al., 2016). These notions seem common within the scientific community (Appendix 1) and are inspiring new analytical models and tools, as well as new forms of thinking. I find interest in observing which modes of speciation and which hypotheses were emphasized by evolutionary biologists of the modern synthesis, in comparison. Divergence was often described as a process driven by forces of 'colonization' and 'competition' and was completed in 'isolation'. The vast evidence for the prevalence of hybridization in species' radiations suggests a parallel narrative, one in which diversity and survival are driven by subtle 'sharing' of genomic resources and allelic 'cooperation' between closely-related lineages, rather than competition alone. As a new evolutionary synthesis materializes, so do the manifold stories about evolution. The author and botanist Robin Kimmerer wrote on the topic of sharing knowledge, "[language] ... is a prism through which we see the world." (Kimmerer, 2013). As scientists, we design many such 'prisms' when we communicate ideas and findings. We also have the opportunity to be mindful of their meanings when we tell the story of how species appear, survive and prosper in nature.

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Appendix 1



Twitter meme on the topic of phylogenomic inference (December 2021). The meme received 144 likes and 18 retweets, reaching a total of 11,765 people and indicating certain community interest in the concepts presented

Appendix 2 – conference contributions

Monocots IV, October 2018, Natal, Brazil

Towards understanding the genomic substrate of diversification in *Tillandsia* subgenus *Tillandsia*

<u>Gil Yardeni</u>¹, Jaqueline Hess¹, Michael H. J. Barfuss¹, Margot Paris², Thorsten Krömer³, Michael Kessler⁴, Walter Till¹ & Christian Lexer¹

¹Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria; ²Department of Biology, University of Fribourg, Fribourg, Switzerland; ³Centro de Investigaciones Tropicales, Universidad Veracruzana, Xalapa, Veracruz, Mexico; ⁴Institute of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland

Corresponding author: gil.yardeni@univie.ac.at

Abstract

The species-rich and ecologically diverse Bromeliaceae family provides an excellent system for studying adaptive radiation in neotropical plants. The genus *Tillandsia* is the largest and most diverse within the family with over 600 species, extensive geographical range and a variety of ecological adaptations to different habitats such as epiphytism and various photosynthetic syndromes. Our research goal is to identify the genomic variability that provided the substrate for adaptive radiation within the enigmatic subgenus *Tillandsia* of genus *Tillandsia* using tree-, network, and coalescent-based approaches. To that end, we used whole-genome sequencing data from selected species within a taxonomic clade (Core Group I, also known as 'The Mexican clade') to construct phylogenomic trees and networks and infer species delimitation. To shed light on the genomic processes that gave rise to diversity within the clade, we performed tests for reticulation, introgression and post-speciation gene flow. We will present our first results, describe the genomic tools used for inference and outline future prospects towards understanding of genomic processes at micro- and macroscales. This research project provides a unique case study for emerging research on the evolutionary genomic underpinnings of plant species radiations in the neotropics.

Keywords: Tillandsia, adaptive radiation, introgression, reticulation, phylogenomics.
PopGroup53, The 53rd Population Genetics Group Meeting, January 2020, Leicester, UK.

A target capture approach for exploring the drivers and constraints of adaptive radiation in tillandsioid bromeliads (Tillandsia spp), a highly diverse neotropical plant group

<u>Gil Yardeni</u>¹, Jaqueline Hess¹, Marylaure de La Harpe¹, Michael H. J. Barfuss¹, Juan Viruel², Margot Paris³, Clara Groot Crego¹, Walter Till¹, Thibault Leroy¹, Ovidiu Paun¹, Christian Lexer¹

¹Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria; ²Royal Botanic Gardens, Kew, Richmond, UK; ³Department of Biology, University of Fribourg, Fribourg, Switzerland

Abstract

The study of adaptive radiation calls for a synthesis between macro-evolutionary and population genetic approaches to uncover the genomic substrate and mechanisms of biological diversification at different time scales. The species-rich and ecologically diverse Bromeliaceae family of flowering plants provides an excellent system for studying the drivers and constraints of adaptive radiation. The genus *Tillandsia* is the largest and most diverse within the family with over 600 species, extensive geographical ranges and a variety of key adaptations such as epiphytism and divergent photosynthetic syndromes. Here, we present a roadmap to the development of a taxon-specific target sequence capture set, specifically created to address hypotheses on neutral processes (tracked via demographic modeling) and the dynamics of adaptive and deleterious variation during a textbook adaptive radiation. To assess the utility of the approach, we compare it to a 'universal' capture approach based on a widely used Angiosperm probe set (Angiosperm-353), examining the power of both sets in resolving the phylogenomic relationships within recent radiations and in common population genetics inference of admixture and introgression. We will discuss the benefits and limitations of the approach.

Botany 2020, July 2020, virtual

Custom-made or universal? The use of target capture to bridge macro- and microevolutionary processes in tillandsioid bromeliads (Tillandsia spp), a Neotropical rapid radiation

<u>Gil Yardeni</u>¹, Jaqueline Hess¹, Marylaure de La Harpe¹, Michael H. J. Barfuss¹, Juan Viruel², Margot Paris³, Clara Groot Crego¹, Walter Till¹, Christian Lexer¹, Thibault Leroy¹, Ovidiu Paun¹

¹Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria; ²Royal Botanic Gardens, Kew, Richmond, UK; ³Department of Biology, University of Fribourg, Fribourg, Switzerland

The study of rapid radiations calls for integrative approaches, bridging phylogenetics and population genetics to uncover the genomic substrate of diversification at different time scales. Target capture approaches emerged as an important tool to study evolutionary radiations in non-model taxa, enabling researchers to retrieve large data sets with few genomic resources. While developing taxon-specific target capture kits requires sustained effort, universal kits are readily available but may offer comparatively shallower insights, especially at short evolutionary timescales. The species-rich and ecologically diverse Bromeliaceae family provides an excellent system for studying the drivers and constraints of rapid, adaptive radiations. We focus on Tillandsia, a young subgenus (~6 Mya), yet the largest and most diverse within bromeliads with over 600 species, extensive geographical ranges and a variety of key adaptations such as epiphytism and divergent photosynthetic and pollination syndromes. We present a taxon-specific target sequence capture set for bromeliads, designed to address a wide range of evolutionary hypotheses and to assess the dynamics of adaptive and neutral variation by targeting 1,776 coding regions, including also genes putatively involved in several key traits. We compare our bait set to the 'universal' Angiosperms353 probe set, examining their power to resolve phylogenomic relationships using concatenation and species tree methods, estimate population genetic statistics and infer admixture with a focus on Tillandsia subgenus Tillandisa. The taxon-specific set results in high enrichment success across the entire family, yet both kits offer abundant information. The taxon-specific set outperforms the universal set with respect to gene tree concordance and inferred population structure, and provides reliable data for inference of admixture and population structure. Importantly, the performance of both kits is comparable for phylogenomic analysis, highlighting the vast potential of universal kits in research at different evolutionary scales. We further discuss methodological aspects and limitations of the approach.

Society for Molecular Biology & Evolution meeting, July 2021, virtual

Taxon-specific or universal? Using target capture to study the evolutionary history of a rapid radiation

G. Yardeni¹, J. Viruel², M. Paris³, J. Hess^{1,4}, C. Groot Crego¹, M. de La Harpe¹, N. Rivera¹, M. H. J. Barfuss¹, W. Till¹, V. Guzmán–Jacob⁵, T. Krömer⁶, C. Lexer¹, O. Paun¹, T. Leroy¹ University of Vienna. Austria. ²Roval Botanic Gardens Kew, UK. ³University of Friburo. Switzeland, ⁴UFZ Helmholtz, Germany, ⁴University of Gertingen, Germany, ⁴University of Vienna, Austria.

niversity of Vienna, Austria, 'Royal Botanic Gardens Kew, UK, 'University of Fribourg, Switzerland, 'UFZ Helmholtz, Germany, 'University of Goettinge



Young Systematists' Forum 2021,

November 2021, virtual

Taxon-specific or universal? Using target capture to study the evolutionary history of a rapid radiation

Gil Yardeni^{1,*}, Juan Viruel², Margot Paris³, Jaqueline Hess^{1,4}, Clara Groot Crego^{1,5}, Marylaure de La Harpe¹, Norma Rivera¹, Michael H. J. Barfuss¹, Walter Till¹, Valeria Guzmán-Jacob⁶, Thorsten Krömer⁷, Christian Lexer¹, Ovidiu Paun¹, Thibault Leroy¹

¹ Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria ² Royal Botanic Gardens, Kew, Richmond, UK

³ Unit of Ecology & Evolution, Department of Biology, University of Fribourg, Fribourg, Switzerland

⁴ Department of Soil Ecology, Helmholtz Centre for Environmental Research, UFZ, Halle (Saale), Germany

⁵ Vienna Graduate School of Population Genetics, Vienna, Austria

⁶ Biodiversity, Macroecology and Biogeography, University of Goettingen, Göttingen, Germany

⁷ Centro de Investigaciones Tropicales, Universidad Veracruzana, Xalapa, Mexico

*Corresponding author: gil.c.yardeni@gmail.com

Target capture has emerged as an important tool for phylogenetics and population genetics in nonmodel taxa. We present a newly developed target capture set for Bromeliaceae, a large and ecologically diverse plant family with highly variable diversification rates. The set targets 1776 coding regions, including genes putatively involved in key innovations, with the aim to empower testing of a wide range of evolutionary hypotheses. We compare the relative power of this taxon-specific set to a universal kit designed for all Angiosperms, the Angiosperms353 set, focusing on the rapid radiation of *Tillandsia* subgenus *Tillandsia*. We highlight differences in kit performance for constructing phylogenies, exploring gene tree discordance and investigating nucleotide diversity and population structure. While the overall performance of both kits is comparable, the taxon-specific kit offers benefits in more detailed phylogenetic or population genetic analyses. The comparative study provides potential lessons for future investigations, in particular for rapidly radiating clades.

Upcoming: Congress of the European Society for Evolutionary Biology, August 2022, Prague, Czech Republic

Rapid radiation characterized by prevalent hybridization in the Neotropical genus *Tillandsia*

Yardeni, G.¹, Barfuss, M. J. H.¹, Till, W.¹, Lexer, C¹, Leroy, T¹, Paun, O.¹

The recent rapid radiation of Tillandsia subgenus Tillandsia (family Bromeliaceae) is a highly diverse Neotropical Monocot group which provides an attractive system for studying the drivers and limitations of species diversification. This subgenus, which consists of predominantly epiphytic plants, is thought to have diversified within the last 3 million years during its expansion from South into Central America, following the closing of the Isthmus of Panama. We inferred phylogenomic relationships among 32 species of Tillandsia using whole-genome data and employed a tree-based approach to explore the evolutionary history of the clade. We report a lack of monophyly and deviations from a tree-like structure coupled with rampant gene tree discordance. High rates of hybridization within and between clades suggest that the expansion of the subgenus into Central America proceeded in several migration events, followed by episodes of diversification and gene flow. Focusing on hybridization, Patterson's D (ABBA-BABA) and related statistics were used to describe the rates and timing of introgression events and to assign introgression events to tree branches rather than species. Finally, we discusse the possible contribution of intraspecific gene flow to adaptive trait shifts. Our work provide an example of how hybridization and introgression, rather than problems to overcome in phylogenomic inference, can be investigated to deepen our understanding of complex processes that accompany species radiation.