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# The macro- and microevolutionary processes driving allopolyploid evolution in *Dactylorhiza* (Orchidaceae)

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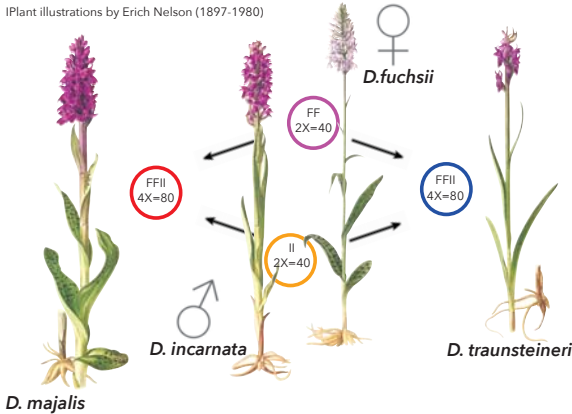
plantgenomics.univie.ac.at

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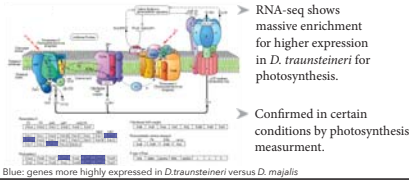


## DACTYLORHIZA POLYPOID COMPLEX

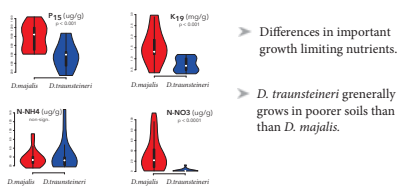
!Plant illustrations by Erich Nelson (1897-1980)



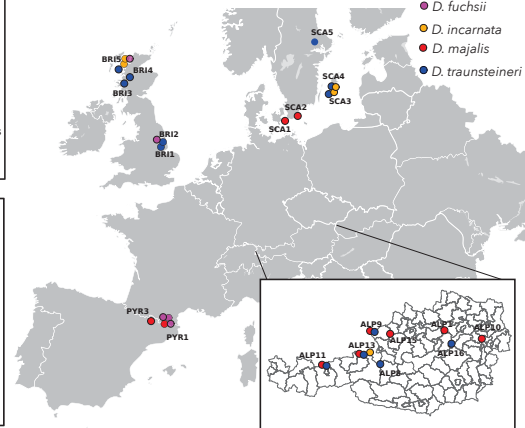
### PHOTOSYNTHESIS DIFFERENCES



### SOIL DIFFERENCES



### SAMPLING



## INTRODUCTION

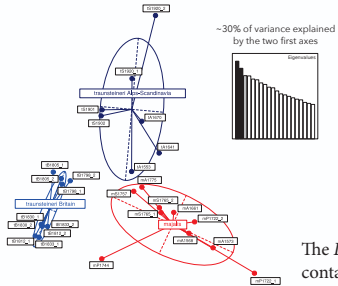
Recurrent origins are widespread among polyploids. These can produce a multitude of genetically and ecologically distinct populations. As their multiple origins provide natural replicates, sibling allopolyploids are excellent models to uncover mechanisms of adaptation to divergent environments, which are assumed to lead to diversification and biodiversity increase.

## METHODS

With powerful transcriptomic (RNA-seq) approaches we are screening the genome-wide natural diversity among ecologically-divergent, sibling allopolyploids. Individuals were grown in common gardens for two years in order to remove any environmental factors due to the collection season.



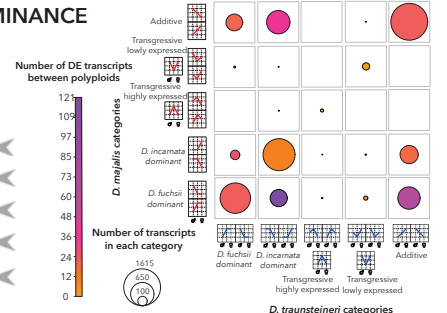
## GENETIC DIFFERENTIATION



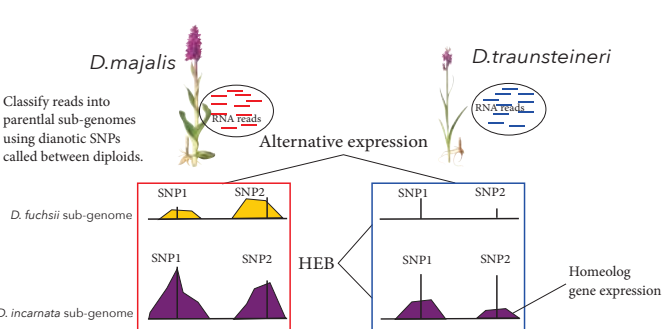
- *D.traunsteineri* is divided into two distinct British and continental genetic groups.
- There is hybridization between sympatric Alpine populations.

- There are more *D.fuchsii* dominant genes in *D.majalis* than *D.incarnata* dominant genes.
- There are more *D.incarnata* dominant genes in *D.traunsteineri* than *D.fuchsii* dominant genes.
- Transgressivity seems mainly due to down regulation from parental expression levels.
- The *D.majalis*, *D.fuchsii*-dominant and *D.traunsteineri*, *D.incarnata*-dominant category (purple circle) contains the most differentially expressed genes between polyploids.

## EXPRESSION LEVEL DOMINANCE



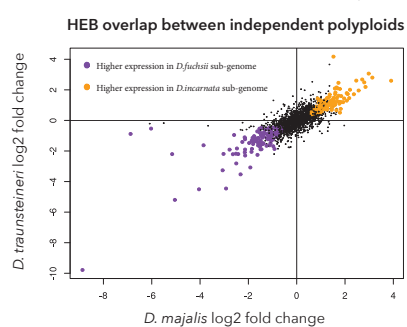
## APPROACH FOR READ CLASSIFICATION



## CONCLUSION

- Hybridization is observed in sympatry and *D.traunsteineri* forms two distinct genetic groups.
- *D.traunsteineri* grows in poorer soils than *D.majalis* and is massively enriched in photosynthesis related functions.
- Constraints are observed in the patterns of dominance between sister polyploids.
- Similar selective forces are shaping both sub-genomes in both sister polyploids.
- General patterns of parental dominance are in opposite directions between sister polyploids and shape their ecological divergence.

## HOMOELOG EXPRESSION BIAS (HEB)



- Constrained homoeolog expression.
- No opposite homoeolog expression.
- Sub-genomes from the same parent in both polyploids have similar distributions.
- There are less low frequency non-synonymous SNPs in the *D. incarnata* (paternal) sub-genome of *D. traunsteineri* than in *D. majalis*.

## SITE FREQUENCY SPECTRUMS (SFS) OF SUB-GENOMES

