

PROGRAM*

NGS WORKSHOP: BIOM SPRING CAMP

17. 4. – 21. 4. 2016

Organizer: Institute of vertebrate biology, AS CR, v.v.i.

Venue and lectures: Research facility Studenec, IVB AS CR, v.v.i.

Student accommodation: Field station Mohelský mill

Sunday 17. 4. 2016

11:00 – 12:00	Arrival of participants to Studenec
12:00 – 13:00	Lunch
13:00 – 13:15	Introduction to the workshop (A. Fornůsková)
13:15 – 15:00	Introduction to NGS (D. Čížková)
15:30 – 17:00	Introduction to RADseq (L. Piálek)
17:30 – 19:00	Introduction to Metabarcoding dietary analysis (J. Kreisinger)
19:30	Bus departure to Mohelský mill
20:00 – ????	Dinner and welcome party

Monday 18. 4. 2016

7:00 – 8:00	Breakfast
8:15	Bus departure to Studenec
9:00 – 12:00	Metabarcoding dietary analysis (J. Kreisinger)
12:00 – 13:00	Lunch
13:00 – 19:00	Metabarcoding dietary analysis (J. Kreisinger)
19:30	Bus departure to Mohelský mill
20:00 – 21:00	Dinner

Tuesday 19. 4. 2016

7:00 – 8:00	Breakfast
8:15	Bus departure to Studenec

9:00 – 12:00	Introduction into population genetic concepts of speciation genomics (R. Burri)
12:00 – 13:00	Lunch
13:00 – 17:00	Introduction to genomic parasites: transposable elements (TEs) and endogenous viruses (EVEs) (A. Suh)
17:30 – 19:30	More than SNPs, other things RADseq can be useful for (E. Trucchi)
19:30	Bus departure to Mohelský mill
20:00 – 20:30	Dinner

Wednesday 20. 4. 2016

7:00 – 8:00	Breakfast
8:15	Bus departure to Studenec
9:00 – 12:00	Phylogenomic tests for introgression (M. Matschiner)
12:00 – 13:00	Lunch
13:00 – 14:30	Phylogenomic tests for introgression (M. Matschiner)
14:30 – 15:30	Using NGS to characterize RNA virus genomes directly from infected animal tissue (S. Gryseels)
15:30 – 19:30	Environmental DNA and its application in conservation biology (P. Taberlet)
19:30	Bus departure to Mohelský mill
20:00 – 21:00	Dinner

Thursday 21. 4. 2016

7:00 – 8:00	Breakfast
8:15	Bus departure to Studenec
9:00 – 12:00	CopperMap how to analyse NGS data & applications on MHC & MCMV (S. Baird)
12:00 – 13:00	Lunch
13:00 – 13:30	Next-generation of DNA barcoding (T. Aghová)
13:30 – 15:30	Orthologue finding and the Lohse&Barton approach of estimating genome-wide coalescence (B. Nurnberger)
16:00 – 21:00	Refreshment, final discussion and departure (Maruska´s pub)

*The organizer reserves the right to make changes to the event program

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