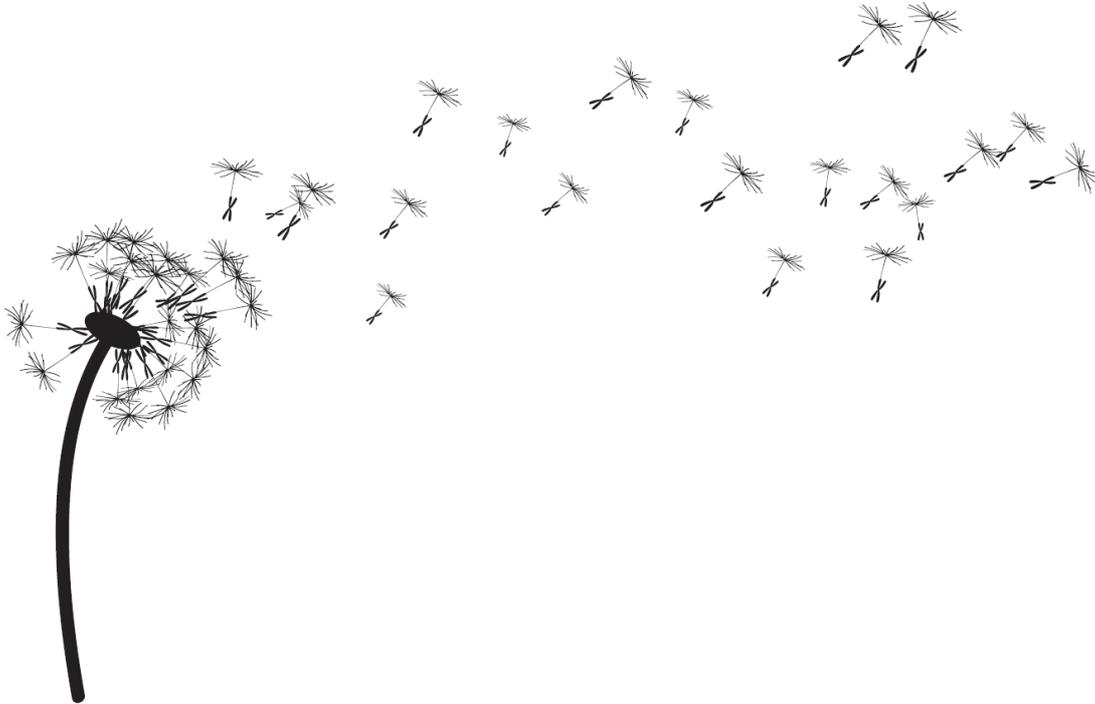


# Population genetics of polyploids, from theory to practice

Olivier Hardy, Filip Kolář, Patrick Meirmans, Patrick Monnahan, Polina Novikova, Marc Stift

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*Objectives:* Polyploidy is widespread and frequent in plants (including many crops), but also occurs in animals such as fish and amphibians. However, our understanding of the genetics of polyploid populations and populations of mixed ploidy is still poor. This is mainly because population genetics theory was originally developed for diploids. Moreover, there is often a gap between theory developed for polyploids and its practical implementation. This practically-oriented course will attempt to bridge this gap. Simulation-based exercises (among others using R) will elucidate theoretical foundations of both diploid and polyploid population genetics. Additionally, analyses of real or realistic example datasets (microsatellite and SNP markers) will give participants hands-on training in several available methods for the population genetic analysis of polyploids.

The exact topics will include clustering methods with specific attention to the problem of mixed ploidy, analysis of population genetic/genomic structure in polyploid complexes, effect of mating system variation and analysis of selection in polyploid genomes. Participants will also devote time to a group project focused on application of gathered knowledge in further modelling or on analyses of empirical datasets with discussion of further prospects and methods limitations. Materials from the previous course run can be found at <https://botany.natur.cuni.cz/ecolgen/node/30>.

*Prerequisites:* Basic knowledge of R programming language and general knowledge of population genetic foundations of diploid populations (diversity, differentiation). Experience in scripting in R is useful, but for the beginners there will be an extra R-introductory day before the workshop start.

*Costs:* course participation is free and includes food and accommodation, but travel arrangements are at own cost except for ForBio members.

*How to apply:* Please submit a ca 200-500 word summary of your research and motivation and the CV, merged in a single PDF file, no later than November 1<sup>st</sup> 2020. Later applications will be considered until the course is fully booked. In case the participant is willing to provide their own data for the project work (not obligatory), please also attach a short description of the data set (organism, type of markers, analyses done/in progress) and the scientific questions that could be addressed. There is a maximum of 16 participants. If needed, we will select participants based on topical relevance and motivation. Members of ForBio and PhD students will be prioritized (but MSc students and postdocs will also be considered). For non-ForBio members we require registration as ForBio associates (free of charge).

Tentative schedule:

Date	Time slot	Activity
Sat 20.2.	9-12	Mental preparation and travel
	14-17	Arrival
	19-...	Arrival
Sun 21.2.	9-12	Arrival
	14-17	Arrival (ideally no later than 17.00)  [optional for those not yet comfortable with R simulations] <b>Introduction to scripting and simulations in R</b> (Patrick Meirmans)
	19-...	Participant presentations, Welcome reception
Mon 22.2.	9-12	<b>A. Introduction to autopolyploid population genetics theory, calculating diversity and differentiation</b> (Patrick Meirmans, Marc Stift, Filip Kolář)
	14-17	<b>B. Clustering methods</b> (Patrick Meirmans, Filip Kolář)
	19-...	Participant presentations, selection of group project
Tue 23.2.	9-10	B. continued
	10-12	<b>C. Impact of mixed-mating on autopolyploid populations and the estimation of selfing rate</b> (Olivier Hardy)
	14-17	C. continued
	19-...	Work on group project
Wed 24.2.	9-12	<b>D. Analysis of genome-wide variation in populations of varying ploidy</b> (Polina Novikova)
	14-17	D. continued
	19-...	Work on group project
Thu 25.2.	9-12	<b>E. Selection analyses in autopolyploids and challenges in cross-ploidy comparisons</b> (Patrick Monnahan)
	14-17	E. continued
	19-...	Work on group project
Fri 26.2.	9-12	<b>Practical data evaluation - data workflow, problems &amp; applications</b> (Patrick Meirmans, Olivier Hardy, Filip Kolář, Marc Stift, Polina Novikova)
	14-17	<b>Group project presentations</b> (participants) Concluding discussion & evaluation
	19-...	Farewell social event
Sat 27.2.	9-12	Leaving
	14-17	Travel and sleep
	19-...	More sleep