

Publishable Summary of SEX-NGS: Sex-linked loci, sexual specialization and local adaptation in *Mercurialis annua* complex

The sexual system of a plant species directly regulate how genes are transmitted across generations and together with environment determine population patterns of local adaptation. Plants that have expanded their geographic ranges, such as *Mercurialis annua*, tend to show lower genetic diversity at their new range margins, and thus may have lost their adaptive potential as a result of the repeated genetic bottlenecks that occur during colonisation. In outcrossing species, however, range-edge populations might maintain sufficient genetic variation for continued responses to selection, either because colonisation bottlenecks are less severe for outcrossers, or because outcrossing facilitates continued gene flow into range-edge populations from elsewhere. However, the genetic and molecular mechanisms underlying local adaptation in the context of range expansions are not well understood yet. How will plant populations adapt to a rapidly changing world? Why and how separate sexes evolve and are maintained in plants? What are the consequences of antagonistic sexual selection for plant survival at different spatial scales (local, widerange)? SEX-NGS examined these questions by studying the impact of range expansions and natural selection on the genome of the European plant *Mercurialis annua*, a wind-

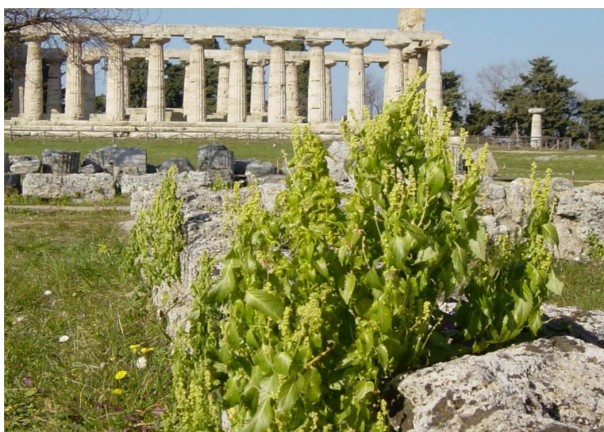


Figure 1 *M. annua* ancestral population in Turkey

pollinated dioecious (and thus outcrossing) annual plant that currently occupies a wide environmental range in Europe following range expansion from an eastern Mediterranean refugium (Figure 1). This information is critical to assess whether (and how) plant populations will respond to challenges from abiotic and biotic stressors brought about by climate change in the European context.

SEX-NGS has developed an exome capture experiment that allowed us to sequence ca. 7% of *Mercurialis annua* genome, including the 103,743 exons over 30 bp found in the current genome draft of the species and 436 sex-linked regions, in 48 specimens collected from eastern ancestral populations in Greece and Turkey and in colonisation-front populations from Catalonia, France and UK. Levels of nucleotide diversity (based on over 4 million Single Nucleotide Polymorphisms) were lower (0.0026 vs. 0.0033) and inbreeding higher (0.12 vs. -0.04) in the colonisation-front, but substantial genetic diversity remained and we did not find an excess of fixation of deleterious polymorphisms in colonization-front populations, suggesting that range expansions did not substantially reduce evolutionary potential in the species. Moreover, genetic processes at the local scale appeared to be as relevant as long-range expansions, with some ancestral eastern populations characterized by low effective population size having as low genetic diversity as populations from the western colonization-front (e.g. Trabzon, in the Black Sea coast, with nucleotide diversity of 0.0026). High levels of genetic differentiation between Mediterranean and Atlantic

expanded regions (about 15%, as high as those between these regions and the ancestral populations in the eastern Mediterranean) suggest that multiple waves of colonization may have taken place.

By using Bayesian outlier detection of highly-differentiated loci and standard neutrality tests, we were able to identify 109 candidate loci for antagonistic sexual selection (Figure 2). Forty-seven (i.e. about half) of these markers are located in sex-linked regions and may help to pin up the elusive *Mercurialis annua* sex chromosomes.

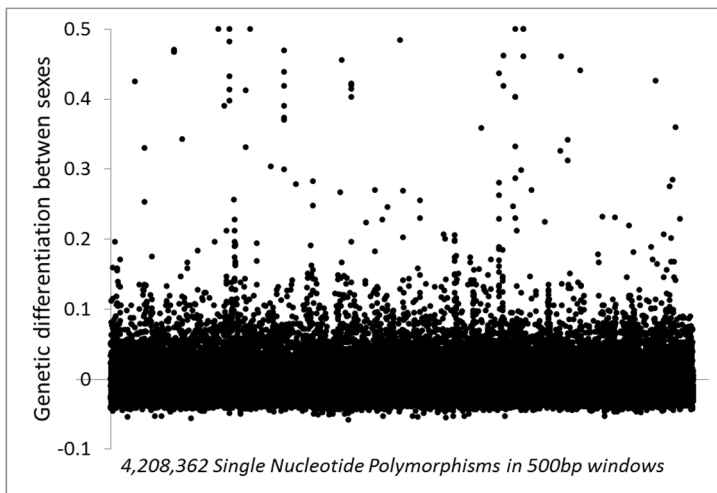


Figure 2 Genetic differentiation between males and females in a rangewide sample covering both eastern and western populations of *Mercurialis annua*

The exome capture assay has also been successfully applied to a wide sample of commercial species of the Euphorbiaceae family, including manioc, a main staple food, *Jatropha curcas*, used to produce biofuels, and *Ricinus communis*, the castor oil plant. Comparative genomic analyses across this species will provide valuable insights on genes associated with responses to biotic and abiotic stressors under impending climate change.

SEX-NGS Marie Curie project has strengthened collaborative research in plant sciences within the European Research Area, being instrumental to create the *Mercurialis* Genomics Network (www.unil.ch/mergen). The Network is currently formed by 12 teams from eight European and Near East countries and it has recently submitted a collaborative research proposal to the ERA-CAPs that will continue and extend current efforts to understand the genomic changes brought about by plant range expansions in Europe and their impact on the capacity of plant species and populations to respond to new selection pressures. Outreach activities of this project have targeted the general public through its webpage. In addition, a science workshop for school children (Figure 3) has presented concepts of plant sexual systems and adaptation, and the links with nature conservation in a context of climate change.



Figure 3 The Marie Curie fellow holding a male (left) and female (right) *Mercurialis annua* specimen before starting a science workshop at Vignettaz B primary school in Switzerland, May 2014