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Modelling the population history using population genomics: the tomato domestication as a case of study

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A bottleneck is commonly associated to the study of crop domestication, in which a population experiences a drastic reduction in size and nucleotide diversity. The population genomic era offers new opportunities to document this scenario through the study of the site frequency spectrum (SFS), a powerful method for summarizing genomic data at the genome-wide level. Using a diffusion approximation approach (Gutenkunst et al., 2009) to model SFS, we estimated the demographical history of a major crop, the cultivated tomato (Solanum lycopersicum) and its wild relative (S. pimpinellifolium). We compared the observed 2 dimensional SFS, obtained from 20 individuals and ~84,500 SNPs markers, to the modelled ones, obtained from four different scenarios. Variants were polarized to ancestral and derived alleles based on the eggplant outgroup sequences. Assuming a mutation rate of 3×10⁻⁹ and a generation time of 1 year, our results suggest that in the best fitting model, population split occurred ~3750 years ago (95%CI: 2985-4552 yrs), wild tomatoes experienced a dramatic bottleneck (effective population size: -87%; reduction of nucleotide diversity: -63%) that occurred ~420 years ago (95%CI: 337-541 yrs). After this bottleneck, migration rate, from cultivated to wild population, was estimated to less than ~1 migrant per generation. Although, 3.1% of the genes derived from neutral expectations suggesting evolutionary forces acting on. These results demonstrate the power of the approach and provide estimates of demographical parameters that fit previous studies of the tomato domestication (Blanca et al., 2015).

Potato germplasm collection in the Czech Republic

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In the Czech Republic bank of potato (Solanum ssp.) genetic resources works in the Potato Research Institute Havlíčkův Brod. The institute is in charge of this activity in the framework of the National Programme of Conservation and Utilization of Plant Genetic Resources and Agro-biodiversity and it is the only organization in the Czech Republic with the long-term engagement in this objective. The bank’s mission is an assembly, evaluation, documentation, maintenance and delivery of potato genetic resource accessions. The collection involves 2.497 accessions maintained in an in vitro culture and divided into six sub-collections (Solanum tuberosum varieties, Solanum tuberosum tetraploid hybrids, dihaploids and diploids, cultivated Solanum species, wild Solanum species, interspecific Solanum hybrids). Derived information is a part of the genetic resource database maintained in the Czech Republic, which could be found on the website http://www.genbank.cz/genetic/resources and from June 2015 also on https://grinczech.vurv.cz/gringlobal/search.aspx. The data are also accessible on the website http://europotato.org. The long-term maintenance is based on slow-growth culture and in vitro tuberization. Microtubers are induced using appropriate media and modified culture conditions. Chitting microtubers after dormancy period or surviving stem segments are subjected to the regeneration passage onto new media in 14-18 months. A revitalization and valorization program is running in the gene bank with the focus on virus infection eradication and screening of maintained material for presence of quarantine viruses, viroids and bacteria, complying with the EU directives.