

GENOTYPING-BY-SEQUENCING OF TWO EX SITU COLLECTIONS PROVIDES INSIGHTS ON THE PEA EVOLUTIONARY HISTORY

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Pea (*Pisum sativum* L. subsp. *sativum*) is one of the oldest domesticated species and a widely cultivated legume. In this study, we combined data from two genotyping-by-sequencing (GBS) libraries, each referring to a different *Pisum* germplasm collection. The selection of loci covered by both libraries caused some loss of sequencing information; however, this did not prevent the obtainment of one of the largest datasets ever used to explore pea biodiversity, consisting of 652 accessions and 22,127 SNPs. The analysis of genetic structure allowed to define a spatio-temporal model for the expansion of pea cultivation from the domestication centre to other regions of the world. Average decay of linkage disequilibrium (LD) in distinct pea genetic clusters ranged from a few bases to hundreds of kilobases, thus indicating different histories in terms of genetic drift and selection. Genome-wide scan resulted in the identification of putative selective sweeps associated with pea domestication and breeding, including genes known to regulate shoot branching, cotyledon colour and resistance to lodging. In addition to providing information of major interest for fundamental and applied research on pea, our work describes the first successful example of integration of different GBS datasets generated from ex situ collections – a process of potential interest for a variety of purposes, including conservation genetics, genome-wide association studies, and breeding.