**Genomic and nutritional analyses of bitter vetch, a traditional grain legume adapted to marginal semi-arid regions**

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Bitter vetch (*Vicia ervilia*, 2n=14), is a traditional Mediterranean/west Asian forage and grain legume with no economic significance to industrial economies. Despite being listed among the Neolithic Near Eastern 'founder crops'1, it is still understudied. Due to its adaptation to drought and shallow soils bitter-vetch is cultivated in semi-arid steppe regions and given climate-change scenarios may be considered as a climate-resilient forage and alternative protein source. A germplasm collection of wild and domesticated genotypes was assembled and is being evaluated for agronomic and nutritional-quality traits. Pod-shattering and hardseededness are typical of wild forms while non-shattering and free germination characterize the domestic genepool2. The range of seed protein and of amino acids levels in the various genotypes was tested. Likewise, metabolomics based analysis shows consistent separation based on grain metabolic features. Pollen fertility of domesticated x wild F1 hybrids were above 90% in certain combinations, and 50% in others, indicative of chromosome order variation among the wild genepool. QTL and GWAS analyses of agronomic, grain quality and domestication traits will be based on a high-quality chromosome level (96.34% completeness; BUSCO) reference genome of 3.6 Gb. RAD-seq genotyping of ~1300 accessions comprised of the entire germplasm array and hybrid progeny populations will expose the structure of both domestic and wild genepools and identify selective domestication associated sweeps. Understanding the evolutionary trajectory of bitter vetch in the wild and under domestication may help discover the genetic basis of its adaptation profile and provide clues for future breeding and yield and quality improvement.

***References:***

[1] Abbo S, Gopher A (2022) Plant Domestication and the Origins of Agriculture in the Near East. Cambridge University Press.

[2] Ladizinsky G, van Oss H (1984) Genetic relationships between wild and cultivated Vicia ervilia (L.) Willd. Bot J Linn Soc 89: 97-100.