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EVOLUTIONARY HISTORY OF CROP LEGUMES: NEW INSIGHTS FROM RUNNER BEAN (*PHASEOLUS COCCINEUS* L.) DOMESTICATION

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The introduction of next generation sequencing technologies has revolutionised genetic analysis, creating new opportunities for plant research that can also be applied to non-model species. We used RNA sequencing (RNA-Seq) technology to investigate the whole runner bean (*Phaseolus coccineus* L.) transcriptome of 29 wild and domesticated accessions; we added further 19 accessions as controls, including wild and domesticated accessions of *P. dumosus*, *P. acutifolius*, *P. lunatus* crop species and *P. microcarpus*, *P. angustissimus* and *P. leptostachyus* wild species. The materials were chosen on the basis of previous molecular analyses carried out using multilocus molecular markers, as well as passport information in order to have a set of accessions representative of the genetic diversity of the species. A total of 27.197 genes were investigated at 657,260 SNPs in all accessions, and 182,725 SNPs considering only the *P. coccineus* ones. Population structure and genetic diversity analysis allowed us to identify a single domestication event for runner bean, likely occurred in Mexico; a relative high loss of genetic diversity of domesticated compared to the wild forms at coding regions was detected. We investigated genes/ genomic regions responsible for the phenotypic variation related to domestication syndrome and made comparisons with data obtained in previous studies for the sister species *P. vulgaris* to investigate different evolutionary scenarios such as convergent (same genomic regions selected) or functional (functionally convergent phenotype coded by completely different genes) evolution.