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ASSOCIATION MAPPING TO INVESTIGATE THE GENETIC BASIS OF ADAPTATION IN *PHASEOLUS VULGARIS*

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The common bean (*Phaseolus vulgaris* L.) is widely cultivated in and out of its centre of domestication (America) making this species highly useful to investigate the genetic basis of adaptation to different agro-ecolocial conditions.

In the context of the BEAN_ADAPT project, funded through the 2ndERA-CAPS call, ERA-NET for Coordinating Action in Plant Sciences, we re-sequences 200 American and European common bean accessions and we phenotyped these lines to investigate the association between different phenotypic traits (including phenology, plant traits and metabolites) and SNPs that are polymorphic in European and American accessions.

The panel of common bean accessions (100 from Europe and 100 from the Mesoamerican and Andean centres of domestication) were cultivated both in controlled conditions (temperate/long-day and short-day conditions in a greenhouse) and in field trials in Potenza (Southern Italy), Golm and Gatersleben (Germany).

Here we present the results of a genome wide association analysis that allowed to identify different genomic regions underpinning the expression of phenotypic trais of interest in the process of adaptation of common bean to the European agroecosystems.