

GENOME-WIDE ASSOCIATION STUDY REVEALS CANDIDATE GENES FOR FLOWERING TIME VARIATION IN COMMON BEAN (*PHASEOLUS VULGARIS* L.)

CAPRONI L.*, RAGGI L.*, CARBONI A.***, NEGRI V.*

*) Dipartimento di Scienze Agrarie, Alimentari e Ambientali, Università degli Studi di Perugia

**) Consiglio per la Ricerca in Agricoltura e l'analisi dell'economia agraria. Centro di Ricerca Cerealicoltura e Colture Industriali (CREA-CI)

The common bean is one of the most important staples in many areas of the world. Extensive phenotypic and genetic characterisation of unexplored bean germplasm are still needed to unlock the breeding potential of this crop. Dissecting genetic control of flowering time is of pivotal importance to foster common bean breeding and to develop new varieties able to adapt to changing climatic conditions. Indeed, flowering time strongly affects yield and plant adaptation ability. The aim of this study was to investigate the genetic control of days to flowering using a whole genome association approach on a panel of 192 highly homozygous common bean genotypes purposely developed from landraces using Single-Seed Descent. The phenotypic characterisation was carried out at two experimental sites throughout two growing seasons, using a randomised partially replicated experimental design. The same plant material was genotyped using double digest Restriction-site Associated DNA sequencing producing, after a strict quality control, a dataset of about 50 k SNPs. The Genome-Wide Association Study revealed significant and meaningful associations between days to flowering and several SNP markers; seven genes are proposed as the best candidates to explain the detected associations.