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## Genetics of flowering and maturity in Brassica juncea (L.)

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Genome wide association studies (GWAS) were conducted to understand genetics of flowering time and maturity related traits in Indian mustard. The diversity panel comprised 92 Indian, exotic, resynthesized and introgressed genotypes of *B. juncea*. Phenotyping was carried out at three levels of Nitrogen (N) application, over two crop seasons. These were: low dose (N75, with added N @ 75kg/ha), recommended dose (N100, with added N @100kg/ha), and high dose (N125, with added N@125kg/ha)]. Extensive variation was recorded for flowering time (DFI - initiation of flowering, DFL - days to 50% flowering and DCF - days to complete flowering), and days to maturity. Genotyping was performed using the genotyping-by-sequencing method. GWAS was conducted using a mixed linear model that involved both relative kinship and population structure / principle component analysis as covariates to reduce the impact of population structure. GWAS allowed prediction of 18 flowering related candidates genes for their association with SNPs that were consistent across the treatments, years as well as the algorithms used. Of these, KHZ1, KHZ2, FLOR1, FLR1, SOC1, AGL20, ATBPC2, AGL72, GID1b and HULK3 flowering time candidate genes were predicted on chromosomes A02, A05, A09, B05, B06 and B08 for flowering traits. SPL15 located on chromosome B06 was identified for strong association with maturity. Many of these genes could be validated through their expression profiling in transcriptome sequences.

Keywords: Genome wide association studies, Diversity panel, Genotyping-by-sequencing, Population structure, Candidate genes

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