

GENOME-WIDE ASSOCIATIONS OF SALINITY TOLERANCE TRAITS IN COMMON BEAN (PHASEOLUS VULGARIS L.)

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Salinity is one of the major environmental stresses that limits crop productivity worldwide, it has been estimated that about 20% of cultivated and 33% of irrigated farmland is affected by high salinity levels globally (Munns and Tester, 2008). Salinity can impair plant development and metabolism, producing a variety of physio-morphological alterations (Parihar et al. 2015 and references therein). Common bean (*Phaseolus vulgaris* L.), a member of the legume family, is a widely cultivated food crop representing about half of the produced and consumed pulses in the world. Being a glycophyte, this species is particularly sensitive to salt which can significantly reduce yield as well as dry matter gain in both roots and shoots (Taïbi et al. 2016). Different studies explored the genetic variability of cultivated bean cultivars exposed to salinity at germination stage and seedling (Kouam et al., 2017).

The aim of this study is to screen a common bean diversity panel for salinity tolerance and apply GWAS to identify putative genetic determinants involved in early salt stress tolerance. The effect of salt treatment was measured at germination as well as on ten days-old seedling grown in hydroponic. For GWAS, salt stress tolerance ability was described by the reciprocal, normalized difference between shoot and root dry weight under controlled and stressed conditions (NaCl 75 mM), respectively. 130 genotypes were successfully characterised; shoot (SDW) and root dry weight (RDW) under control and salt stress conditions showed quite high degrees of

variation. After Bonferroni correction, GWAS found no significant association for salt tolerance related to RDW; however, significant associations with the observed variation of SDW were detected in 7 regions located on 6 different common bean chromosomes. Candidate genes, identified by proximity to the signal, are involved, among others, in the vesicular trafficking machinery, plant developmental processes as well as abiotic stress responses.

Bibliography

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