**Identification of QTLs associated with drought avoidance root traits in lentil: towards confirmation of constitutive and adaptive QTLs genomics-assisted breeding for drought tolerance**

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**Abstract**

Lentil (*Lens culinaris* Medik.) is an important crop and staple food in several developing countries. Its seeds are rich source of protein, carbohydrates, vitamins, and minerals. Drought stress is one of major constraints limiting lentil production worldwide. The development of drought-tolerant lentil varieties could help in improving lentil production in drought-prone regions. However, drought tolerance is a complex trait under quantitative control, making it difficult to improve drought-adapted genotypes using conventional breeding approaches. Drought avoidance root traits can be targeted to improve lentil production drought-prone region; however, the screening of these traits is challenging which limits their integration in breeding programs. Thus, genomics-assisted breeding could be a promising way for efficient development of superior drought lentil varieties. In this study, a lentil recombinant inbred line (RIL) population consisting of 126 F7-derived RILs from the cross ILL6002 / ILL5688 was extensively phenotyped for root and shoot traits associated with drought tolerance using both conventional phenotyping methods and an advanced automated high‐throughput phenotyping platform. In addition, Genotyping-by-Sequencing (GBS) derived high-density linkage map consisting of 1373 single nucleotide polymorphisms (SNPs) markers, distributed on 7 linkage groups and spanning total length of 2391.4 cM, was constructed for this population. Analysis of genotypic and phenotypic data allowed the identification of QTLs controlling drought avoidance root traits which could be used in lentil breeding programs targeting drought tolerance as an efficient alternative to labor-intensive and time-consuming conventional breeding methods.

Keywords: lentil, drought tolerance, QTL, genomics-assisted breeding.