

Comprehensive RNAseq analysis for identification of genes expressed under terminal heat stress in lentil

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November 9, 2020

Abstract

Lentil crop is highly sensitive to abrupt increase in temperature during mid to late reproductive stage leading to severe reduction of biomass and seed yield. Therefore, in the present investigation, RNAseq analysis was carried out between IG4258 (heat tolerant) and IG3973 (heat sensitive) lentil genotypes at reproductive stage under both normal and heat stress conditions in the field. It resulted in a total of 2,09,549 assembled transcripts and among these 1,61,809 transcripts had coding regions of which 94,437 transcripts were annotated. The differential gene expression analysis showed up-regulation of 678 transcripts and down regulation of 680 transcripts between tolerant and susceptible genotypes at early reproductive stage. While 76 transcripts were up-regulated and 47 transcripts were down-regulated at late reproductive stage under heat stress conditions. The validation of 12 up- or down transcripts through RT-PCR corresponded well with expression analysis data of RNAseq with a correlation of $R^2=0.89$. KEGG pathways enrichment analysis identified transcripts associated with genes encoding proteins/regulating factors related to different metabolic pathways including signal transduction, fatty acid biosynthesis, rRNA processing, ribosome biogenesis, gibberellin (GA) biosynthesis and riboflavin biosynthesis. This analysis also identified 21,487 genic-SSRs that can be used in molecular mapping of heat tolerant genes in lentil.

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