

## IDT9-073 | Comparison of expression and sequence of SnfK and DREB2A transcript in heat tolerant lentil genotypes

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To identify the heat tolerance lentil genotype, 190 genotypes were screened for consecutive two years following augmented design. They were sown in 18th November (normal sowing, NS) and also in 11th December (late sowing LS) with three popular cultivars as check in. Most of the late sown (LS) plants showed reduced vegetative phase than those of NS by four days. But eleven genotypes showed delayed flowering in LS condition and several of them also exhibited terminal heat tolerance ability. Mean seed weight/plant (g) varied from 1.04 to

6.5 in NS whereas it varied from 0.04 to 3.78 in LS. Three lines showed only 20-30% reduction in yield as compared to 60% reduction in average. Degenerate primer pairs from known genes like DREB2A and SnfK from *M. truncatula* were used for amplification and relative quantification of the transcript. Sequence of the analogous Genes from lentil were compared among the contrasting genotypes to identify SNPs. Part of a gene showed complete similarity with stress responsive ORF of chickpea.

## IDT9-074 | Constructing improved chickpea genome assemblies using skimGBS

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Chickpea (*Cicer arietinum* L.) is the second most important grain legume after soybean and plays an important role in food security. The application of genomics provides the potential to increase the productivity and resilience of this important crop. We have developed a novel strategy to assess and improve the chickpea reference genomes. The quality of both chickpea *desi* and *kabuli* draft genomes were assessed using sequence data from flow cytometry isolated chromosomes to identify misplaced contigs. Using SNPs derived from whole genome sequence data of ICC 4958 x PI 489777, and skim sequence-based genotyping of this popula-

tion, we could validate and correct the draft assembly. In addition to placing the misplaced sequence regions into corresponding chromosome positions, most of the previously unplaced contig sequences have now been incorporated into the pseudomolecules of the improved version. The total chromosome sequence length has increased from 124.38 Mb and 347.24 Mb to 375.06 Mb and 423.28 Mb for the *desi* and *kabuli* genomes respectively. Both genomes have been re-annotated. A total of 33,473 genes from *kabuli* and 31,419 genes from *desi* were predicted. Both improved genomes are available at <http://cicer.info>.