

Identification of Allelic Variation in Drought Responsive Dehydrin Gene Based on Sequence Similarity in Chickpea (*Cicer Arietinum* L.)

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Chickpea (*Cicer arietinum* L.) is a food legume of economic importance. It is cultivated in arid and semi-arid soil and in a variety of conditions like rainfall, residual moisture, and restricted irrigation. This makes it susceptible to drought stress.

Knowledge of candidate genes for stress resilience is limiting in chickpea. Modernization and cost-effectiveness of sequencing technology provides a rapid method for the generation of remarkable sequence data, which helps to identify the genes responsible for various stress tolerances.

A recent study by Kumar et al., 2020 elucidates the association between candidate gene and morpho-physiological traits for the screening of drought tolerance in chickpea.

Abiotic stress-responsive gene *Dehydrin* (DHN) was identified in some of the chickpea genotypes based on the sequence similarity approach to play a major role in drought tolerance. Higher readings of Relative water content (RWC), membrane stability index (MSI) played a significant role in osmotic regulations leading to drought tolerance resulting in yield stability under drought. The genotypes

Pusa1103, Pusa362, and ICC4958 were found most promising genotypes for drought tolerance (Figure 1). The results were further supported by a sequence similarity approach for the *DHN* gene when analysed for the presence of single nucleotide polymorphisms (SNPs) and InDels.

The presence of homozygous InDels and SNPs in the *DHN* gene in Pusa1103 and Pusa362 genotypes suggests that such changes can be highly associated with drought tolerance response. The strong correlation of the *DHN* gene suggests that it helps in keeping the original cell volume, preventing cellular collapse. *DHN* genes can thus be explored in developing superior chickpea varieties with improved yield under abiotic stress conditions (Figure 1).

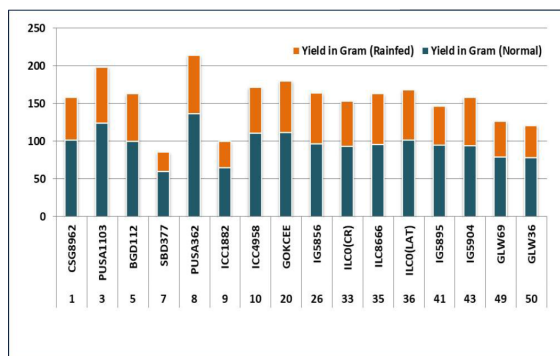
This study (Kumar et al., 2020) will help us identify and characterize the drought-tolerant genotypes by utilizing the morphological traits and allelic variation of the *DHN* gene by sequencing techniques and also to discover the allelic variation of the gene. Data from the coding regions are regularly in use for the identification of genes responsible for

stress tolerance from different plant species like *Arabidopsis thaliana*, *Medicago truncatula*, and many more. Identification of allelic variations in the drought-responsive candidate genes from diverse genotypes can provide genomic resources with different alleles to develop improved genotypes for drought tolerance.

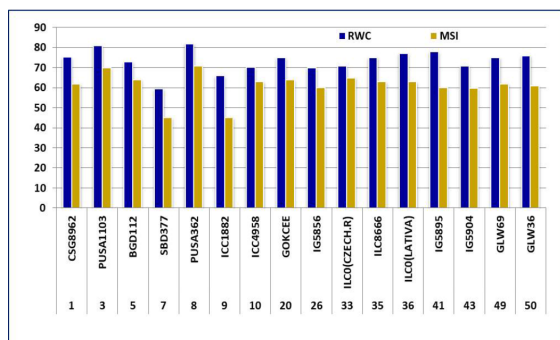
The present study (Kumar et al., 2020) provides a comparative study of the candidate gene and morphological

traits for drought tolerance in chickpea, which can be used in improving drought tolerance in chickpea.

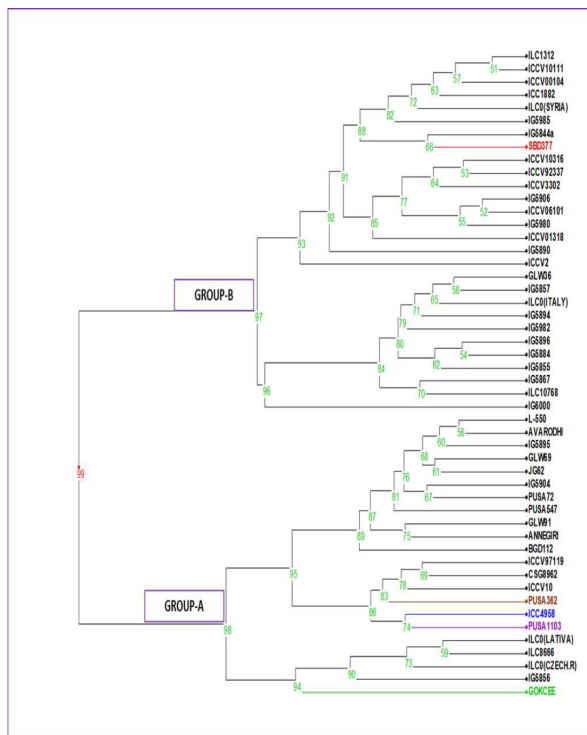
Reference: Kumar T, Tiwari N, Bharadwaj C, Sarker A, Pappula SPR, Singh S and Singh M (2020) Identification of Allelic Variation in Drought Responsive *Dehydrin* Gene Based on Sequence Similarity in Chickpea (*Cicer arietinum* L.). *Front. Genet.* 11:584527.



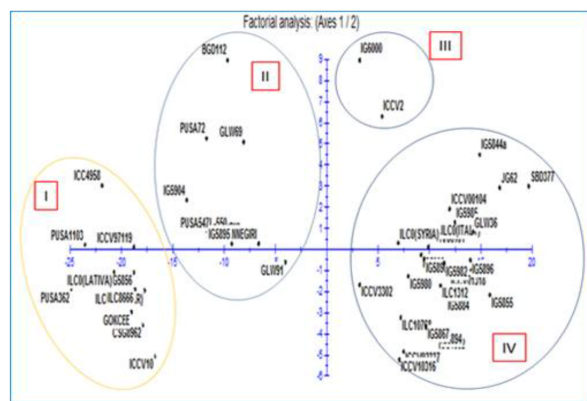
(A) Comparison of the yield of selected genotypes under rainfed and normal conditions.



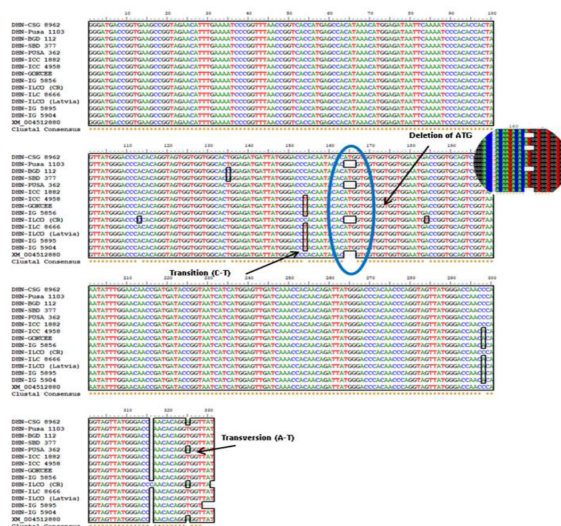
(B) Comparison of the RWC and MSI of selected genotypes.



(C) Dendrogram generated from an unweighted pair group method analysis (UPGMA) cluster analysis based on all the stressed morphological characters for drought. The first two clusters form Group A showing all tolerant to moderate tolerant genotypes.



(D) Representation of the 1–2 plane of factorial analysis based on drought stress morphological traits for fifty chickpea genotypes.



(E) Multiple alignments of nucleotide sequences of the DHN gene from different chickpea genotypes were done by using the BioEdit version 7.0.9. The presence of SNP in the DHN gene is been indicated.

Figure 1. Selected figures on analysis by Kumar et al., 2020. Please visit DOI for more details.