

DISCOVERY OF CONSERVED DOMAINS FOR DEVELOPMENT OF FUNCTIONAL MARKERS AND IDENTIFICATION OF microRNAs FROM DROUGHT RESPONSIVE EXPRESSED SEQUENCE TAGS (ESTs) IN CHICKPEA (*Cicer arietinum* L.)

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Domains can be thought of as distinct functional and structural units of protein. We have analyzed 5885 drought responsive expressed sequence tags (ESTs) for the identification of conserved domains and microRNAs in chickpea. The occurrence of conserved domains, super families and multi domains having putative functions like insect pest resistance, improved quality parameters, resistance to abiotic stresses other than drought *viz.*, temperature, salinity, evolutionary functions and physiogenic nature have been identified. Identified conserved domains or gene families from the drought responsive ESTs could be utilized for the identification of gene-targeted markers and for development of functional markers to accelerate marker assisted breeding in chickpea. Based on homology and secondary structure analysis potential miRNA targets have been found for newly identified chickpea conserved miRNAs. These target genes included number of transcription factors that control plant growth, development and metabolic enzymes, as well as other genes involved in stress response.

Methodology

The 5885 chickpea drought responsive ESTs were downloaded from NCBI (<http://www.ncbi.nlm.nih.gov>) was used for conserved domain search. The search for conserved domains within query EST was analyzed using conserved domain search service available online (<http://www.ncbi.nlm.nih.gov>).

The same set of ESTs was used for identification of drought specific miRNAs as shown in Fig:2.

Conclusion

Identified conserved domains or gene families from the ESTs could be utilized for the identification of gene-targeted markers and for development of functional markers to accelerate marker assisted backcross breeding in chickpea.

miRNAs and their target genes can initiate further study on chickpea miRNA regulation mechanisms and can help in knowing more about the important role of miRNAs in chickpea. These findings suggest that computational analysis is a good alternative strategy for identifying new conserved domains, miRNA candidates and their target genes in plants.

Results

Fig:1 Distribution of 5885 hits for CDD search

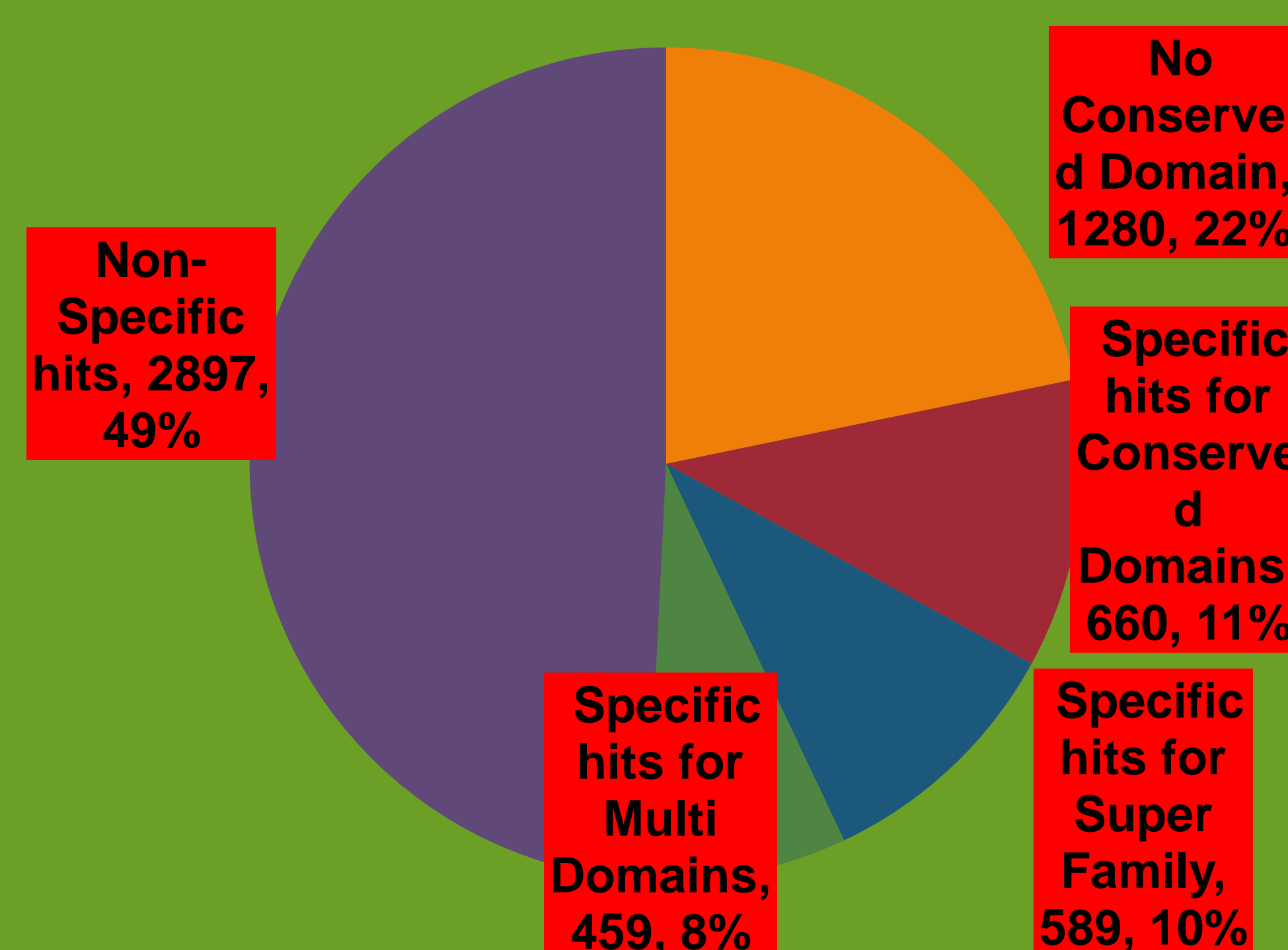


Fig:2 Computational identification of drought specific miRNAs

