

HD-zip classification in *Vigna unguiculata* and comparative syntenic analysis with *Phaseolus vulgaris*

Artemisa Nazaré Costa Borges, Bruna Piereck, Caroline de Jesús Pires, Flávia Tadeu de Araújo, José Ribamar Costa Ferreira-Neto, Ana Christina Brasileiro-Vidal & Ana Maria Benko-Iseppon

Universidade Federal de Pernambuco – PPGG/LGBV

Vigna unguiculata (cowpea) is an edible legume, with economic importance especially in Africa and South America. The productivity of this legume has been affected by drought, despite its higher adaptability to this stress type. Thus, it is imperative to identify stress-responsive genes associated with drought tolerance, such as the HD-zip transcription factor (TF) family that includes four subfamilies. In this study, the transcriptomes of two contrasting varieties of cowpea were analysed under water deficit (tolerant and sensitive to drought stress). TFs were identified with the iTAK program, followed by ORF-finder translation and Batch-CD-search annotation. Complete conserved domains were aligned using MEGA7 and a phenogram was built with *Neighbor-Joining* method (*bootstrap* 1000 replications). The identified HD-zip candidates were anchored at *Phaseolus vulgaris* genome through a BLASTn (*cut-off* = $1e^{-90}$), and their positions were visualized using Circos program. The iTAK program identified 88 candidates. After annotation with CD-Search, 46 were complete and employed in further analyses. As expected, the phenogram revealed four groups separating the four subfamilies of HD-zip (I - IV) indicating a conservation between subfamilies. Subfamily I (drought stress responsive) was the most abundant with 29 sequences, followed by II, III, and IV with nine, six and two sequences, respectively. The higher amount of subfamily I was expected since the transcriptome analysed was generated under water deficit. Subfamilies III and IV were more closely related, sharing the START motif close to the N-terminal region. After filtering redundancy, the anchoring in *P. vulgaris* genome reported 50 *loci* corresponding to the tolerant plant (*Pingo de Ouro* - PO) and 67 to the sensitive (*Santo Inácio* - SI) displaying a higher microsynteny (gene conservation) with the drought sensitive variety. All chromosomes presented HD-zip representatives, mostly close to terminal regions, being more abundant in *Pv03* and *Pv04*, and less abundant in *Pv01* and *Pv07*. Chromosomes *Pv02*, *Pv05*, and *Pv10* exhibited sequences also in the pericentromeric region, whereas *Pv09* presented sequences in the interstitial region. The minor part of the sequences was in the centromeric region (*Pv02* and *Pv03*). HD-zip sequences were displayed in clusters, with superposition and tandem duplication, indicating evolutionary divergence from a common ancestor by tandem duplications, as reported to other gene families in legumes. The identified HD-zip candidates represent valuable genetic resources and potential targets for genetic transformation of cowpea and related species.

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