

## ACCUMULATION OF DEHYDRIN TRANSCRIPTS IN RESPONSE TO WATER STRESS IN SEEDLINGS OF *VIGNA UNGUICULATA*

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Dehydrins are plant proteins produced on the late stages of embryogenesis or in response to dehydrative forces like freezing, salt or water stress or also in response to ABA application. It has been hypothesized that dehydrins play an important role in preserving the structure of cellular macromolecules in plant tissues subjected to desiccation. With the aim of characterizing and studying accumulation of dehydrin transcripts in different organs of *Vigna unguiculata* seedlings, we isolated by PCR a fragment of dehydrin gene in two ecotypes with different provenience (cultivated and wild ecotypes). The dehydrin fragments were then cloned: positive clones were selected following differences on the molecular weight and sequenced. Expression of dehydrins in different organs, under normal conditions of irrigation and different levels of water stress imposition was evaluated by semi-quantitative RT-PCR. Database search using aminoacidic sequences revealed that inside the cowpea genome there are at least seven members of the multigenic dehydrin family. These members presented a high identity with cowpea clones responsive to dehydration which were correlated to different dehydration stresses. Semi-quantitative RT-PCR revealed that dehydrin transcripts accumulate in all organs except in mature leaves. The accumulation of dehydrin transcripts was significantly different in the two ecotypes at level of roots and hypocotyls. Cultivated ecotypes showed levels of dehydrin transcript accumulation lower than the wild ecotype. Significant differences were not observed on the first leaves.