COMPARATIVE ANALYSIS OF GRAIN PROTEINS OF MAIZE, SORGHUM, PEARL MILLET, TEOSINTE AND TRIPSACUM

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Gene prospection has been considered a strategic resource of the modern biotechnology for identification of genes, promoters and regulatory sequences of potential use for improvement of biological processes in plants. Although a large amount of information about storage proteins in cereals like maize and wheat is available. many species have not been characterized in this regard. Better knowledge about storage polypeptides and their gene families in other grass species can lead to the identification of gene sequences that can be used for manipulation of grain quality in economically important cereal species. We report results of the first phase of a gene prospection study directed to identification of potentially important endosperm-specific storage protein gene and promoters through comparative analysis of seed proteins of maize, sorghum. pearl millet, teosinte and tripsacum. We show by SDS-PAGE and immunological analysis ("western blotting") with policlonal antibodies raised against maize proteins (alfa-, beta- e gamma-zeins) that there are similarities and divergences amongst polipetides of the several species analyzed. Also, the western blots indicated marked differences in amount of similar polipeptides of the several species. These results will help direct our work on identification, cloning and characterization of genes and regulatory sequences potentially useful in the improvement of cereal grain quality through genetic engineering. Supported by: CNPq, FINEP/PADCT, FAPEMIG and EMBRAPA.