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PHYLOGENETIC RELATIONSHIP BETWEEN 28 TROPICAL MAIZE OPEN POLLINATED VARIETIES OBTAINED WITH RAPDs MARKERS.

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Open pollinated varieties are a important genetic resource for maize breeding programs in the tropics. Pedigree information and genetic relationship between maize tropical varieties do not allow a clear picture of phylogeny among them. The objectives of this study were: a) to compare phylogenetic relationship among maize tropical varieties obtained with RAPDs markers with expectations based on known pedigree data. b) to verify the relationship between genetic distances estimated with RAPDs and specific combining ability (SCA) obtained from 5 and 10 environments. Twenty eight open pollinated varieties were used as parents of a diallel. The parents and their 378 F1's were evaluated in 5 locations and two years in Brazil. SCA was estimated for five locations in one year and for the 10 environments. The SCA from 10 environments were used to obtain two heterotic groups with four and six varieties respectively. A bulk of 100 seedlings was used to obtain DNA from each variety. This DNA was used for RAPD analysis. Phylogenetic data obtained with RAPD markers agreed with the known pedigree data. Flint genotypes tended to be grouped separately from dent germplasm. Genetic distances obtained with RAPDs markers for the whole data set and for the two heterotic groups were correlated with: a)SCA obtained from one year and five locations; and b) SCA obtained from 10 environments. Correlation between genetic distances for each pair of parents and SCA for the 378 F1's in 10 environments was low and positive (r=0.15**). Correlation's between genetic distances and SCA from 10 environments were higher (r=0.61**) when only the two heterotic groups were considered. The conclusions of this study are: a) RAPDs markers could be used to asses phylogenetic relationship among maize open pollinated varieties; b) The quality of the SCA estimators could influence the relationship between SCA and genetic distances.

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STORAGE PROTEIN SYNTHESIS AND ACCUMULATION DURING ENDOSPERM DEVELOPMENT IN DIFFERENT SMALL MILLETS

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Seed proteins from cereals and pulses form an important part of human diet, but are deficient in certain amino acids. The understanding of the synthesis and deposition of the storage proteins could lead to manipulations of their deposition and alteration in the aminoacid composition so that it will be made more nutritious for human diet.
Studies on the changes in the protein fractions during endosperm development in small millets viz., *Echinochloa frumentaceae* (barnyard millet), *Panicum miliaceum* (proso millet), *Panicum miliare* (little millet), *Setaria italica* (foxtail millet) and *Paspalum scrobiculatum* (kodo millet) revealed that dry matter content increased steadily whereas total prolamin and glutelin percentage increased during seed development. SDS-PAGE pattern of prolamin at different stages of seed maturation showed that the prolamin polypeptide synthesis commenced before 10 DAF in proso, little and foxtail millets and 14DAF in barnyard and kodo millets. Immunoblot analysis of total prolamins extracted at different stages of seed development also confirmed the results obtained through SDS-PAGE. Not much variations were found in the protein accumulation pattern among all the small millets except kodo millet. In kodo millet at early stages of seed development 22KD and 20 KD polypeptides showed cross reactivity with the antibody raised against prolamins of kodo millet. During latter stages of maturation only the 20 KD prolamin found to react with the antibody. This indicates perhaps the post translational modification during grain development

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DIFFERENTIALLY EXPRESSED GENES FROM A SUGARCANE STEM CDNA LIBRARY: EXPRESSION PATTERN OF THE TRANSCRIPTS AND PROMOTER RECOVERY.

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Messenger RNAs were isolated from leaf, stem and root tissues of field-grown sugarcane cultivar Pindar (10 month old). A sugarcane stem-specific cDNA library was made in Lambda ZapII (Stratagene) and differentially screened using ^{32}P-labelled root, leaf and stem cDNAs. We isolated 49 cDNA clones and used them for probing Northern and Southern blots. Nine clones proved to be constitutively expressed throughout the different tissues tested. Eight other clones were tissue-specifically expressed, some of them showing different and interesting patterns of expression within the stem tissue. The expression of clones #3 and #19, whose sequences are different, is restrained to the meristematic region of the stem. Clone #18 is more expressed in the younger parts of the stem, with a gradual decrease of expression towards the more mature parts of the stem. There is also a low level of expression in the root system. Clone #35B is root and stem-specific. Clone #51 is fully stem-specific, its expression level peaking in the top and in the mature parts of the stem. Clone #53A shows a low level of stem-specific expression. Clone #57 is also fully stem-specific, with a higher level of expression in the younger parts of the stem. Clone #67 is expressed in the mature parts of the stem and also slightly in the roots. High stringency Southern analysis revealed between three and six hybridising bands in sugarcane genomic DNA samples digested separately with various restriction endonucleases then probed with the various cDNA clones. Most of these clones have been partially or completely sequenced, enabling the identification of a likely functional role for some of them. Based on expression patterns, copy number and gene identity, we have selected some of the cDNAs for the recovery of the corresponding promoters by iPCR. We have already isolated the promoter of #67, made a fusion construct to the GUS reporter gene and transformed sugarcane (by particle bombardment) and tobacco (*via Agrobacterium tumefaciens*).