

SEQUENCE ANALYSIS FROM DIFFERENTIAL CDNA FRAGMENTS OBTAINED FROM SEXUAL AND APOMICTIC PLANTS OF *BRACHIARIA BRIZANTHA*.

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Forage grasses from the genera *Brachiaria* are important for beef and milk production in Brazil. Particularly, *Brachiaria brizantha* has shown to be well adapted to soil, climate conditions and resistance to spittlebug disease, hence its widespread distribution in Brazil. *B.brizantha* can reproduce both sexually and asexually through seed in a process named apomixis. Tetraploid accessions ($2n=4x=36$) are always associated with aposporic apomictic reproduction, while diploid accessions ($2n=4x=18$) reproduce sexually. Ovaries from sexual plants have embryo sacs of the Polygonum-type while apomicts have Panicum-type embryo sacs. In a previous report (Rodrigues et al, 2001), a differential display strategy was used to visualize differences between gene expression of ovaries from apomictic and sexual varieties. The differential fragments were isolated, cloned, sequenced and analyzed using BLASTX software. From **60** differential cDNA fragments, **40** from apomicts and **20** from sexual, 38% (23/60) of the sequences showed no significant homology to data base, while 20% (12/60) showed homology to hypothetical proteins. Ten of these sequences showed homology to proteins involved in RNA metabolism, such as transcription factors, ribosomal proteins and RNA processing proteins. Six sequences showed homology to membrane proteins and another 9 clones showed homology to proteins involved in a variety of cellular processes. Expression profile of all clones was analyzed by reverse northern, using cDNA from early and late stage development ovaries of apomictic and sexual plants as probes. Clones with differential expression were detected. Northern analysis and *in situ* hybridization are now being conducted to compare mRNA distribution during apomictic and sexual ovule development.