SNP-BASED INFERENCES ON EXPRESSION, REPRODUCTIVE RAMIFICATIONS AND INHERITANCE OF THE SEMIGAMY GENE OF COTTON (GOSSYPIUM BARBADENSE L.), A RARE ANGIOSPERM MUTANT AFFECTING KARYOGAMY Andrea B. V. Maeda David. M. Stelly Department of Soil and Crop Sciences, Texas A&M University College Station, TX

<u>Abstract</u>

The Semigamy (Se) mutant of Pima cotton (Gossypium barbadense L. 2n=4x=52) was first reported in 1963, for its remarkable production of monoembryonic haploids at high frequencies. Our lab has established its cytological mechanism, akaryogamy, responsible for this bizarre form of quasi-apomictic (asexual) reproduction that leads to the production of haploids and chimeras composed of sectors of maternal and paternal origin. In terms of seed production, levels of Se expression are less than 100% i.e. normal, tetraploid progeny occur even on homozygous mutants. More knowledge about the mode of gene action and expression of Semigamy could be very valuable for breeders and geneticists such as for mass production of doubled haploids, rapid synthesis of true-breeding genetic stocks and haploid/doubled haploid populations for genetic mapping. To extend previous studies of Semigamy, I analyzed crosses and reciprocal crosses between a semigamous line (SeSe) and heterozygous plants (Sese) to detect and investigate differences between male and female Se expression according to allelic inheritance from maternal and paternal heterozygous (Sese) parents. Phenotypic seedling markers were used to differentiate parental origins of chimeric haploid sectors, and SNP markers linked to Semigamy were used to analyze the allelic inheritance in each sectorial tissue to characterize the behavior of Se allele in male and female Sese parents. The genotypic results of maternal and paternal haploid sectors differ markedly from each other. This finding strengthens our suspicion that the mutant gene Semigamy behaves differently according to parent of origin and that a detailed molecular characterization is desirable.