

**EXPRESSION OF THE SEMIGAMY MUTATION IN PIMA COTTON: A CYTOLOGICAL EVALUATION**

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**Abstract**

Haploids have long been used in breeding programs to accelerate the development of improved lines. Doubled haploids aid in producing homozygous lines, allow for easier selection of desired characteristics, and permit the fixation of segregating populations. The *Semigamy* mutation of Pima cotton (*Gossypium barbadense*) was reported in 1963 and has occasionally been used to produce cotton haploids, doubled haploids, cytoplasmic substitutions, and somatic chimeras for experimental purposes. We are interested in studying the biology and genetics of this mutant and expanding its usefulness.

Previous analyses of the *semigamy* mutation (*Se*) documented that the seeds are monoembryonic and that seedling haploids, chimeras, and tri-chimeras occur at frequencies that are largely dependent on the parental genotype combinations. These findings led to the inferences that *semigamy* is incompletely dominant and that the mutation disturbs the normal sexual reproductive process. However, these efforts were largely based on phenotypic scoring of seedling families from controlled crosses. To further analyze the inheritance and developmental biology of this mutant, we used a much different approach, one based on direct cytological analyses that would help define the timing and mode of *semigamy* action. Here we report cytological observations regarding the phenotypic expression and genetics of this unusual mutation.

Our examination of optically cleared ovule nucelli from *Se* mutants revealed that they undergo normal egg/sperm cellular fusion (syngamy) but forgo karyogamy, the natural fusion of sperm and egg nuclei. The nuclei enlarge and undergo separate but simultaneous divisions. This process can result in a variety of different outcomes, including diploid, haploid, or chimeric embryos, all of which can develop normally. Homozygous *Se* mutants, heterozygotes, and wild-type *G. barbadense* plants were reciprocally crossed in a 3x3 factorial design and the resulting ovules were evaluated cytologically for semigamous reproduction versus normal karyogamy. The frequency data indicate that the pattern of *semigamy* expression most closely resembles either a recessive mutation active in the zygote or one that is gametophytically regulated. A chi-squared analysis failed to reject these models. Additionally, we showed there is a maternal effect present which allows homozygous females to produce semigametic offspring when crossed to wild-type males. However, this effect was recessive, as the differences in frequencies of semigamous ovules were nonsignificant between heterozygote females and heterozygote males when crossed to homozygous mutants.

Our future efforts will be directed at identifying the underling gene(s) and protein(s) involved in this process, mapping the genetic locus through linkage mapping and aneuploid transmission analysis, and development of semigamous lines useful for research and breeding.