

**MICROARRAY ANALYSIS OF CYTOPLASMIC MALE STERILITY AND RESTORATION IN COTTON****Hideaki Suzuki****Laura Rodriguez-Uribe****New Mexico State University****Las Cruces, NM****James Stewart****University Of Arkansas****Fayetteville, AR****Jinfa Zhang****New Mexico State University****Las Cruces, NM****Abstract**

Cytoplasmic male sterility (CMS) is a maternally inherited phenotype of pollen sterility in >150 higher plants, resulting in the inability to produce functional pollen and is often associated with a novel chimeric open reading frame (orf) found in mitochondrial genomes. It is highly possible that those gene products interfere with the function or assembly of the mitochondrial F<sub>0</sub>F<sub>1</sub>-ATP synthase, resulting in failure of pollen development. Pollen fertility is recovered in the presence of nucleus encoded fertility restorer genes (Rf gene). CMS/Rf system can be exploited to produce F<sub>1</sub>hybrid seeds for the utilization of heterosis. In the present study, microarray analysis was employed to identify differentially expressed genes between fertile and sterile isogenic lines. Sequences for the mitochondrial genes, atp1, atp4, atp6, atp8, atp9, cox1, cox2, and cox3 were also obtained for polymorphism identification between CMS-D8 cytoplasm and normal Upland cotton cytoplasm.