

ASSESSMENT OF THE POTENTIAL FOR GENE FLOW BETWEEN TRANSGENIC COTTON AND THE ENDEMIC HAWAIIAN COTTON. John M. Pleasants and Jonathan F. Wendel, Adjunct Assistant Professor and Professor, Ecology, Evolution and Organismic Biology Department, Iowa State University, Ames, IA 50011

We investigated the potential for gene flow via pollen dispersal between transgenic varieties of commercial cotton (*Gossypium hirsutum* and *G. barbadense*) and the Hawaiian endemic cotton species *G. tomentosum*. Because these species are inter-fertile and because artificial crosses lead to viable progeny, interspecific gene flow is possible when: 1) there is spatial proximity between *G. tomentosum* populations and transgenic cotton fields; 2) there is overlap in flowering between *G. tomentosum* populations and transgenic cotton plantings; and 3) there is overlap in pollinators between *G. tomentosum* populations and transgenic cotton. A previous report in the literature documented hybrid populations, substantiating the possibility of gene flow.

1) Evidence in the literature indicates that *G. tomentosum* is present on all of the main Hawaiian Islands except Hawaii and Kauai. Populations of *G. tomentosum* are located on the drier, leeward coastal plains of the islands at low elevations. These are also the parts of the islands that are used for agriculture. The locations of all natural populations of *G. tomentosum* are not known so an evaluation of proximity to plantings of transgenic cotton would have to be made on a case-by-case basis.

2) We monitored flowering phenology for *G. tomentosum* over 2003-4. There was a distinct flowering period that began around the end of January and peaked in April and May. In 2004, when there was a higher than normal precipitation during the wet season, the flowering period extended into August. Thus, any transgenic cotton that was blooming between January and August could potentially overlap temporally with *G. tomentosum*.

3) We observed both honeybees and carpenter bees visiting and pollinating *G. tomentosum* flowers. These same pollinators are known to be pollinators of commercial cotton. Therefore, there is complete overlap in pollinator fauna. In addition, these pollinators are long-distance foragers; honeybees may forage up to 6 miles from their nest. Consequently, to reduce the chances of interspecific pollen transfer to near zero, transgenic cotton fields would have to be placed more than 6 miles from a *G. tomentosum* population.