GENE FLOW FROM DETASSELED MAIZE IN A REGULATED PRODUCTION SYSTEM. Gene Stevens, Michael Horak, Sharon Berberich, and Mark Halsey; University of Missouri, Portageville, MO; Monsanto Co., St. Louis, MO; Chlorogen, Inc., St. Louis, MO; and Donald Danforth Plant Science Center, St. Louis, MO. (121)

Genetically modified maize produced for regulated products such as pharmaceutical or industrial proteins will require methods to confine transgenic pollen. In one production system, nontransgenic maize would be used to pollinate detasseled transgenic inbred plants. Resulting hybrid kernels would be used for protein extraction or seed increase. The effect of different female inbred detasseling efficiency levels on gene flow was tested at three locations in Southeast Missouri in 2000 and 2001. Pollen sources were yellow inbred isolines representing transgenic females planted in alternating rows with white inbred maize representing non-transgenic males. During detasseling, female plants were intentionally missed at rates of 0, 730, 1460 and 7300 tassels ha^{-1}. Each detasseling treatment was matched with a maize isoline and traceable marker. White hybrid trap plots were planted on three dates at 200 m and 300 m from pollen sources. Dates that maximized silking synchronization with yellow isoline tasseling were selected for sampling. Gene flow was detected by counting yellow kernels in white maize plots. When no tassels were removed from an isoline, the highest recorded gene flow was 0.03% at the 200 m and 0.02% at the 300 m isolation distances. At greater detasseling levels, gene flow decreased. Gene flow was 0.0013% or less when 730 tassels ha^{-1} remained. When complete detasseling was intended, one positive kernel with a tracer gene was detected at 200 m, and none was detected at 300 m. For effective control of regulated transgenes in pollen by detasseling, complete and timely tassel removal will be necessary.