

**WIDE-CROSS RADIATION HYBRIDS (WRH):
A TOOL FOR PHYSICAL MAPPING OF PLANT GENOMES?**
Wenxiang Gao, Wayne Raska , Z. Jeffrey Chen, and David M. Stelly
Department of Soil and Crop Sciences
Texas A&M University
College Station, TX
John Yu and Russell J. Kohel
Crop Germplasm Research Unit
USDA-ARS
College Station, TX

Abstract

Genome maps are important to genome analysis and genetic manipulation. Radiation hybrid (RH) mapping has been highly effective for high-resolution physical mapping of genomes from humans, mammals and certain other animals. However, RH mapping has been used very little in plants. Resolution of RH maps is often higher and regionally complementary to resolution offered by meiotic crossing-over. Herein, we describe a simple approach that uses a wide cross in combination with whole-genome radiation to produce whole-genome radiation hybrids that can be used for construction of a map. We report preliminary test results from cotton, where the genome of one species, *Gossypium barbadense*, was used to rescue radiation-segmented chromosomes of another species, *G. hirsutum*. Mature pollen grains from *G. hirsutum* were gamma-irradiated and used to pollinate emasculated *G. barbadense* flowers to generate nonchimeric WRHs between those two species. A 5-Krad gamma-ray WRH mapping population was constructed. Tests with eight microsatellite markers spanning 65 cM of a single linkage group revealed that the average retention frequency ranged from 87-94%. Two SSR markers that co-segregated in the reference linkage map population were separated by WRH mapping. The results indicate that WRH mapping complements traditional linkage mapping, and will be useful for genomic analysis of cotton and other plant species. We gratefully acknowledge continued support from TAES and the Texas Advanced Technology Program.