

Strain Genotypes of *Gibberella fujikuroi* mating population A (*Fusarium moniliforme*) Mapping Population

Jin-rong Xu and John F. Leslie- Department of Plant Pathology, 4002 Throckmorton Plant Sciences Center, Kansas State University, Manhattan, Kansas 66506-5502. Present address of first author: Department of Biological Sciences, Purdue University, West Lafayette, Indiana 47907-1392.

Genetic maps are useful for researchers outside the originating laboratory only if the strains and markers used in the analysis of the mapping population and the genotypes of the strains composing the mapping population are available for analysis. This brief communication gives the genotypes for the strains that compose a recently constructed mapping population of *G. fujikuroi*. Strains and probes are available from FGSC.

We have recently constructed a recombination-based genetic map of *Gibberella fujikuroi* mating population A (asexual stage *Fusarium moniliforme*). This fungus is an important pathogen of maize and produces the fumonisin class of mycotoxins. A detailed map and a description of its features has been published elsewhere (Xu and Leslie 1996 *Genetics* **143**:175-189). In this communication we report the genotypes of the 121 strains in the mapping population that was used to construct the map. The parental strains, the progeny, and the probes are all available from the Fungal Genetics Stock Center.

Twelve linkage groups have been identified that correspond with the 12 chromosomes identified using CHEF gel electrophoresis (Xu *et al.* 1995 *Molecular Plant-Microbe Interactions* **8**:74-84). Linkage groups are numbered based on the physical size of the corresponding chromosome. Except as noted, RFLP markers were localized to the same linkage group/chromosome using both recombination frequencies and Southern hybridizations of the probe to CHEF gel blots.

Contribution 95-627-A from the Kansas Agricultural Experiment Station, Manhattan.

Figure 1. RFLP mapping data for the *Gibberella fujikuroi* mating population A mapping population.

From left to right: Progeny 1 to 121 from cross 1006G (FGSC nos 7950-8070). Progeny from perithecium A-1-19, B-20-36, C-37-54, D-55-74, E- 75-91, F- 92-115 and G- 116-121.

From top to bottom: Markers arranged by position on linkage groups as determined by a mapping program (Xu and Leslie 1993 *Fungal Genet Newsletter* **40**:80-82).

- [Linkage group 1](#)
- [Linkage group 2](#)
- [Linkage group 3](#)
- [Linkage group 4](#)
- [Linkage group 5](#)

- [Linkage group 6](#)
- [Linkage group 7](#)
- [Linkage group 8](#)
- [Linkage group 9](#)
- [Linkage group 10](#)
- [Linkage group 11](#)
- [Linkage group 12](#)
- [Unlinked probes](#)

N: Female parental phenotype (Nepal), from A-04643 (FGSC 8078).

C: Male parental phenotype (California), from A-00015 (FGSC 7607).

-:No data or equivocal data.

All probes were assigned to linkage groups on the basis of segregation data and confirmed by hybridization to Southern blots and CHEF gels. Probes marked with an * are included with the linkage group on the basis of hybridization data; linkage to other markers in this linkage group not detected. The physical location of markers marked with a [[section]] was not confirmed by CHEF gel hybridization. Probes in the unlinked section were not linked to any of the other probes and either were not hybridized to determine location or hybridized to a doublet or triplet band that precluded unambiguous assignment of a probe to a chromosome/linkage group.

1 This probe is linked via recombination to marker 6E67, but not to any of the other markers on this linkage group. No hybridization data are available to confirm this placement.

2These two probes are linked to each other but not to any other marker on this linkage group.

Last modified 7/25/96 KMC