

Quantitative Trait Loci (QTL) Mapping of Resistance to Gray Leaf Spot in *Lolium*

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Objectives:

1. To complete the existing partial linkage map of the existing MFA x MFB population, and map QTL for resistance in this population as measured by lesion type and severity of gray leaf spot.
2. To create a new mapping population by crossing resistant progenies from the MFA x MFB population with susceptible perennial genotypes, create a linkage map, and map QTL for lesion type and severity.

Start Date: 2003

Project Duration: three years

Total Funding: \$87,883

Gray leaf spot (GLS) on perennial ryegrass (*Lolium perenne*) caused by *Magnaporthe grisea* is a rapidly spreading, destructive, and unpredictable disease. Improved resistance in perennial ryegrass is desperately needed to improve the utility of this versatile cool-season turf species and reduce dependence on fungicide applications. The identification of resistant ryegrass plants, genes for resistance carried by those plants through linkage analysis and quantitative trait locus (QTL) mapping, and development of molecular DNA markers tightly linked to QTL for resistance genes will allow the tracking and combining of resistance genes during the cultivar development process.

Plant materials used in this study include a segregating population derived from a cross between two annual (*Lolium multiflorum*) and perennial ryegrass hybrid clones (MFA and MFB), the perennial ryegrass grandparents of the segregating population (Manhattan-1 and Manhattan-3), and several plants from annual ryegrass cv. Floregon, the same cultivar used to develop the population.

Greenhouse inoculations of the mapping population were performed using two different *M. grisea* strains, one being



Mapping parent clones MFA (left) showing a resistant reaction to gray leaf spot, and MFB showing susceptible gray leaf spot lesions, leaf twisting, and blighting.

isolated from a diseased ryegrass fairway (GG9) and the other being a lab strain previously used to clone a rice blast resistance gene from rice. After inoculation, plants were incubated in a growth chamber and disease was rated using lesion type. A genetic linkage map was constructed in collaboration with Dr. Reed Barker and Dr. Scott Warnke using several types of DNA markers and the interval mapping method of QTL detection.

The linkage map of the MFA x MFB population is complete with good density and genome coverage. The mapping population is segregating for gray leaf spot resistance and it appears to be partial resistance, as resistant plants show reduced size lesions when inoculated with GG9 (type 2 with occasional small type 3). The perennial grandparents exhibit a susceptible reaction (type 4), the parents MFA and MFB are intermediate (full-sized type 3), and interestingly, plants of 'Floregon' annual ryegrass showed a range of reaction from type 2 to type 4. Reaction to strain 6082 was similar except that the MFA parent was resistant with type 2 lesions, while the MFB parent was susceptible with type 4 lesions.

The two growth chamber inoculations with GG9 showed potential QTL on linkage groups 3 and 6, and these could be localized to a narrow interval around a single DNA marker. For lab strain 6082, a single QTL was detected on linkage group 4, indicating multiple resistance mechanisms in perennial ryegrass to divergent strains of the GLS pathogen. Preliminary inoculations with several ryegrass isolates collected from diseased ryegrass fairways yielded similar disease reactions for selected progeny, which suggests lack of race-specificity. It appears likely that gray leaf spot resistance is controlled by very few genes, which will simplify breeding for GLS resistance.

A new ryegrass mapping popula-



Gray leaf spot evaluation plot at Carbondale, Illinois in collaboration with Dr. Ken Diesburg.

tion has been developed from a cross between a resistant MFA x MFB progeny and a susceptible perennial genotype. A set of 15 randomly selected progeny from this new population has been inoculated with GG9 in the growth chamber. Segregation for resistance was detected, with a higher proportion of the progeny showing resistant reactions than the MFA x MFB population. Resistant plants showed equal resistance as the resistant parent (type 2 lesions), while the susceptible plants were more susceptible than the susceptible parent.

Summary Points

- QTL mapping results of the MFA x MFB population suggest three genomic regions are important for partial resistance to two different isolates.
- These QTLs can be localized to narrow intervals around known DNA markers, which will be very valuable for marker-assisted breeding of GLS resistance.
- Field GLS evaluations of both populations are currently underway in two locations.
- The second ryegrass mapping population, which will be used to confirm the QTL detected in the MFA x MFB population, is also segregating for GLS resistance and greenhouse inoculations are in progress.