

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.

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Project Duration: three years

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Gray leaf spot (GLS) of perennial ryegrass (*Lolium perenne*) caused by *Magnaporthe grisea* is a rapidly spreading, destructive, and unpredictable disease. The lack of resistance in current cultivars adds to the importance of the disease, as well as recent reports of *M. grisea* strains resistant to azoxystrobin (Heritage®), one of the major fungicides used to control it. 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.

Previous results from QTL mapping using the annual x perennial ryegrass MFA x MFB population revealed several important results. The two inoculations with ryegrass isolate GG9 showed potential QTL on linkage groups 3 and 6, and these could be localized to a narrow interval around a single DNA marker, which will be very important in future marker-assisted breeding for GLS resistance in turf-type perennial ryegrass. Also, preliminary inoculations with several *M. grisea* isolates collected from diseased ryegrass fairways yielded similar disease reactions for selected progeny, which suggests lack of race-specificity. This means the resistance is likely to be effective against a wide range of *M. grisea* isolates that the plants may be exposed to in a turf planting. Thus, it appears likely that gray leaf spot resist-



Collaborative gray leaf spot evaluations are at underway at Carbondale, Illinois in collaboration with Dr. Ken Diesburg and at Lexington, Kentucky with Dr. Dave Williams.

ance in this population is controlled by a few genes, which will simplify breeding for GLS resistance. These results will be even more useful in breeding if they can be confirmed by testing if the marker-GLS resistance associations are stable across ryegrass populations.

Plant materials used in this study include a segregating population derived from a cross between a resistant individual, MF-8 from the original MFA x MFB population, and an unrelated susceptible individual, L4B-5. These two genotypes were induced to flower and crossed in the greenhouse. Gray leaf spot inoculations of the mapping population, along with the parents, were performed using two different *M. grisea* strains isolated from diseased ryegrass, GG9 and LexF2A. After inoculation using aqueous conidial suspensions, plants were incubated in a growth chamber, and disease severity was rated using lesion type. Two separate inoculations were performed for each isolate. A genetic linkage map was constructed using several types of DNA markers, and the interval mapping method of QTL detection has been used so far.

The linkage map of the L4B-5 x MF-8 population has adequate marker density and genome coverage for QTL mapping. Also, inoculation results show that

the mapping population is segregating for gray leaf spot resistance, and that more of the plants are GLS-resistant in this population than in the first population. QTL analysis using data from four inoculation experiments revealed several important results. The four inoculations showed a potential QTL on linkage group 3, which had been the most important QTL in experiments with the MFA x MFB population. While the weaker QTL on linkage group 6 from the first population was not detected in the current phase of this study, the result from linkage group 3 shows that the markers associated with resistance are likely to be easily transferred to different populations. This result, along with the increase in resistance levels in the current population relative to the first one, will be very important in future marker-assisted breeding for GLS resistance in turf-type perennial ryegrass.

Finally, field tests of the both mapping populations are now in progress, in collaboration with Drs. Ken Diesburg at Southern Illinois University, Carbondale, and Dave Williams at University of Kentucky, Lexington.

Summary Points

- QTL mapping results of the MFA x MFB population suggested two genomic regions are important for partial resistance to gray leaf spot.
- The second ryegrass mapping population has been inoculated twice with two different ryegrass field isolates (four experiments), and shows a higher proportion of resistant individuals than the MFA x MFB population.
- QTL mapping in the new population suggests that the most important genomic region for GLS resistance in the MFA x MFB population, on linkage group 3, is still associated with GLS resistance.
- Field GLS evaluations are currently underway in two locations.