

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

Total Funding: \$87,883

Gray leaf spot on 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.

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 devel-



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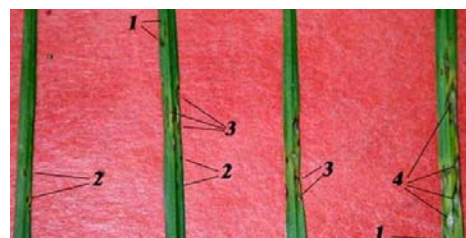
op the population.

Greenhouse inoculations of the mapping population were performed using a single *M. grisea* isolate with both a mist chamber and a growth chamber method, and disease was rated using lesion number and severity (mist chamber) and lesion type (growth chamber). A genetic linkage map was constructed using several types of DNA markers, and the interval mapping method of QTL detection has been used.

The linkage map of the MFA x MFB population is nearing completion, with good density and genome coverage. Also, inoculation results show that the mapping population is segregating for gray leaf spot resistance. The resistance appears to be partial resistance, as resistant plants show smaller lesions. The perennial grandparents exhibit a susceptible reaction, the parents MFA and MFB are intermediate (full-sized type 3), and plants of Floregon annual ryegrass showed a range of reaction from type 2 to type 4.

QTL analysis using data from four inoculation experiments has begun. The first two mist chamber inoculations revealed potential QTL on linkage group 2 of the ryegrass map, for lesion severity, and on linkage group 4 for lesion number. The second two growth chamber inoculations, rated for lesion type, showed potential QTL on linkage groups 3 and 6, and these appeared more significant than the QTL from the first two experiments. It is worth noting that potential QTL had also been indicated on linkage group 3 in the earlier experiments, though these were less consistent. Thus it appears likely that gray leaf spot resistance is controlled by as few as two genes.

These QTL will be tested further in several ways. Under cooperation with Dr. Andy Hamblin at Univ. of Illinois, field tests of the MFA x MFB population are now in progress. Also, additional isolates will be used for greenhouse inoculations of



Gray leaf spot resistance is being rated on ryegrass progeny based on the severity of leaf lesions.

the MFA x MFB population. These experiments will provide information on potential race-specificity of the resistance. Preliminary inoculations with several ryegrass isolates 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.

Finally, the new ryegrass mapping population, derived from a cross between a resistant MFA x MFB progeny and a susceptible perennial genotype, will allow further testing of the QTL numbers, effects, and positions on the linkage map. Thus using this population will provide further evidence to support what we find from the current population. This will be important for marker-assisted selection by detecting useful associations between DNA markers and gray leaf spot resistance.

Summary Points

- An annual x perennial ryegrass mapping population is segregating for partial resistance to gray leaf spot, and the resistance appears to be derived from the annual ryegrass parents of the population.
- QTL mapping results so far suggest two genomic regions are important for partial resistance.
- Field GLS evaluations of the population are currently underway.
- The second ryegrass mapping population, which will be used to confirm the QTL detected in the MFA x MFB population, is nearly ready for DNA-marker mapping and gray leaf spot inoculations.