Ryegrass, Rust and Resistance

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ABSTRACT

This project aims to investigate crown rust resistance in perennial ryegrass (*Lolium perenne* L.) through extensive phenotypic and genotypic analysis of mapping populations. Mapping populations have been established and phenotypic analysis of one F_1 family indicates that there is sufficient variation for genetic analysis in this generation. Transgressive segregation for latency period, pustule number and size, and extent of chlorosis and sporulation has been observed. Preliminary genetic analysis has begun and will continue in conjunction with further phenotypic analysis. Quantitative trait loci will be mapped for crown rust resistance to allow marker assisted selection to be used to breed perennial ryegrass cultivars with enhanced resistance to this pathogen.

KEY WORDS

Crown rust, resistance, perennial ryegrass, quantitative trait loci, marker assisted selection.

INTRODUCTION

Perennial ryegrass (*Lolium perenne* L.) is an important temperate pasture species worldwide. In Australia alone it is estimated that at least 6 million hectares are sown to perennial ryegrass based pasture. Crown rust, caused by the fungus *Puccinia coronata* f. sp. *lolii* (Corda) is widely regarded as the most serious disease of perennial ryegrass. Infection may lead to significant economic losses from reductions in yield, nutritional quality and palatability. Susceptibility to crown rust is common among existing cultivars however, resistant cultivars are known (1). The genetic control of resistance to this pathogen is poorly understood.

We are investigating crown rust resistance in perennial ryegrass, the host-pathogen interaction and variation within pathogen populations through extensive phenotypic and genotypic analysis of mapping populations. Quantitative trait loci (QTL) for components of crown rust resistance will be mapped in perennial ryegrass using a range of molecular markers. The results from these experiments will be used to develop a comprehensive strategy for marker assisted selection of crown rust resistance as part of the Australian National Perennial Ryegrass Improvement Program, with the ultimate aim of producing cultivars with enhanced crown rust resistance.

MATERIALS AND METHODS

A set of parental ryegrass genotypes was established to generate mapping families segregating for rust resistance. Parental genotypes were selected from a range of Australian and New Zealand cultivars. Selection was based on reaction to artificial infection with a composite crown rust inoculum consisting of spores from geographic isolates from across Australia. In addition, parental genotypes were evaluated for their reaction to two individual geographic crown rust isolates, one from Gatton (Qld.) and the other from Hamilton (Vic.). These individual isolates were field collections. All inoculations were carried out under controlled conditions and evaluation of resistance was based purely on pustule number per unit leaf length.

Parental genotypes were pair crossed to produce a number of F_1 populations. Based on the parental individual isolate data, one F_1 family (L88 x L89) was selected for preliminary resistance screening with

the Hamilton crown rust isolate. The L88 x L89 family was screened twice under controlled conditions with this isolate; three replicates of each genotype were included in each screen. Phenotypic variation assessed in the F_1 family included pustule size, and extent of chlorosis and sporulation, in addition to number of pustules per unit leaf length.

RESULTS AND DISCUSSION

Phenotypic analysis of 60 F_1 genotypes from the L88 x L89 family indicated that there is sufficient variation for genetic analysis. The results of the preliminary analyses showed a high degree of transgressive segregation; the F_1 population had a much wider distribution than the two parental genotypes and a large number of F_1s were highly resistant (Fig. 1).

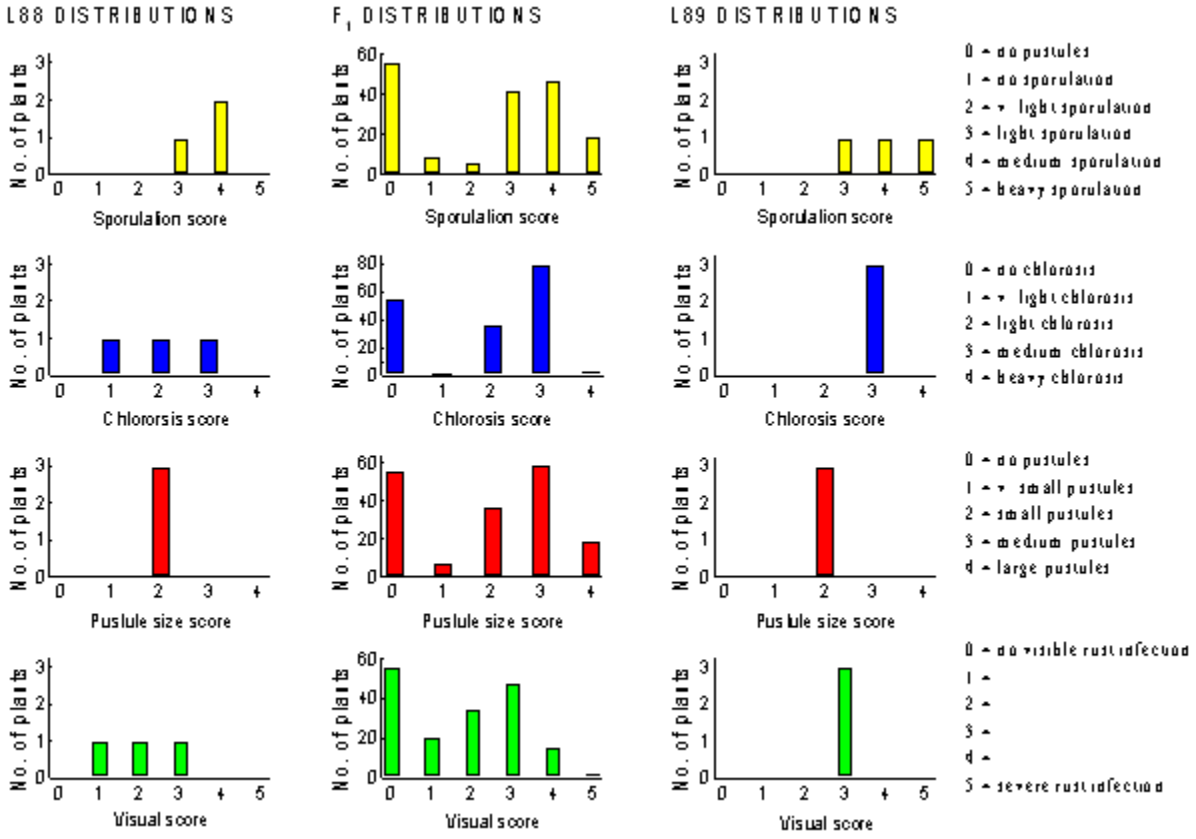

Figure 1. Variation in rust resistance in L88, L89 and L88 x L89 F_1 distribution graphs for sporulation, chlorosis, pustule size and visual score for the first of the crown rust resistance screens using the Hamilton isolate (3 replicates of each genotype).

CONCLUSION

Populations have been developed and are being screened for rust resistance. Future work will include genotyping the L88 x L89 family with a range of molecular markers such as RFLP, AFLP and SSRP and identification of QTL. Phenotypic analysis will extend to screening new F_1 families for rust resistance, inoculating with a number of rust isolates to evaluate the specificity of resistance QTL and evaluating rust resistance under field conditions. Investigations will also be carried out using single-spore isolates to examine within-pathogen population variability.

The successful completion of this project would allow marker assisted selection to be utilised in the breeding program to speed up the development of cultivars with enhanced crown rust resistance.

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REFERENCES

1. 1. Clarke, R.G., Villalta, O.N. and Hepworth, G. 1997. *Aust. J. Agric. Res.*, **48**, 191-8.