

Analysis of genotype x environment interactions for needle damage caused by *Dothistroma* needle blight in radiata pine

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Summary

Dothistroma needle blight is a serious fungal disease that causes productivity losses in planted radiata pine in New Zealand. Delivering improved tolerance to this disease that is consistent across environments is critical in the Central North Island where significant outbreaks often occur.

This paper presents the results of a preliminary analysis modelling the needle damage caused by *Dothistroma* needle blight across 19 sites in the Central North Island using a factor analytic approach. Genetic correlations in the majority of trials show strong and positive relationships. The modelled correlation matrix indicates that genetic responses among all environments tested will be consistent and predictable, good news for breeding and deployment of selections in areas exposed to this needle disease.

Keywords: dothistroma septosporum, genetic correlation, factor analytic, pinus radiata

Introduction

Dothistroma band needle blight is a serious needle pathogen of planted forests of *Pinus radiata* D. Don in New Zealand (Bulman et al. 2013). The disease is caused by *Dothistroma septosporum* (Dorog.) M. Morelet and was first detected in New Zealand, near Rotorua in 1962. The pathogen causes premature needle cast, significantly reducing growth and stand productivity. Infection of *Pinus radiata* (radiata pine) by this pathogen is highly dependent on climatic conditions. High levels of infection follow periods where both warm temperatures and long periods when needles remain wet are present (Bulman et al. 2013). *Dothistroma* needle blight has a significant economic impact on the forest growing industry, with estimated costs of \$19.8 million per year in lost revenue and chemical control (Watt et al. 2011).

Genetic improvement is one of the tools available for management of *Dothistroma* needle blight (Bulman et al. 2013). Tolerance to this needle blight has been shown to be heritable (Carson 1989, Ivković et al. 2010). There is limited information on genetic correlations of this needle disease across sites. This study is an initial analysis across 19 sites to investigate how important genotype-by-environment interaction is for this disease and how best a breeding strategy might be implemented to mitigate the effects of this disease.

Material and methods

Data from 19 experimental sites was used from across the Central North Island of New Zealand.

Damage caused to needles from *Dothistroma septosporum* was assessed using three methods:

1. Needle loss due to damage caused by *Dothistroma* needle blight, assessed as a percentage infection/needle loss of the crown (DOI), measured in 5 percent increments (van der Pas et al. 1984).
2. Needle retention in the crown after needle damage due to *Dothistroma*, measured in 5 percent increments Subjective score of needle damage due to *Dothistroma* on a 1-9 scale, where 1 = healthy and no needle damage and 9 = 90 percent infection /needle damage due to *Dothistroma* needle blight. Needle retention scores were made equivalent by reversing the subjective scores to match the scale of foliage infection percentage.

Statistical analysis followed implementation of factor analytic modelling methods outlined in Cullis et al. (2014), implemented in ASReml (Butler et al. 2009).

Results

Genetic correlations were remarkably high and consistent across the majority of sites, but ranged between 0.3 and 1.0 with a mean of 0.8 (Figure 1). Among the trials analysed, only two were not well correlated with the other sites. These lower correlations are able to be explained by biology. One of these trials was assessed at age 8, when damage levels are usually assessed between year 3 and 4 after planting, and may have also unintentionally incorporated needle loss due to increasing competition among trees prior to canopy closure. The other trial was assessed at an earlier age, at only 2 years after planting and with an observed low disease load.

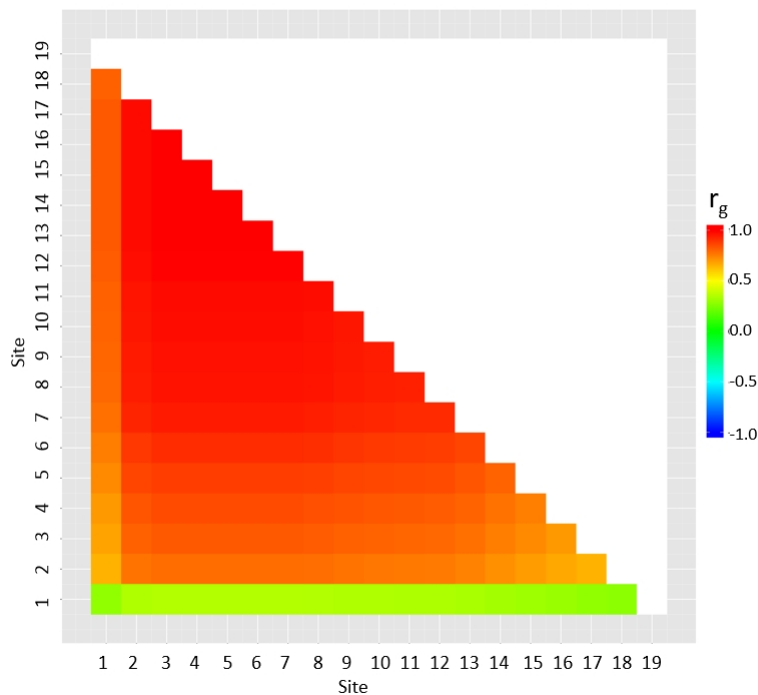


Figure 1. Genetic correlations among sites 1-19. Key shows genetic correlations from 1.0 to -1.0 where genetic correlations close to 1.0 are favourable.

Delivery of genetic gain into the forest is the ultimate aim of tree breeding programmes. Estimates of genetic gain (without inbreeding restriction, data not shown) indicate at least 27% genetic gain in improved needle retention could be possible. All sites analysed here had an average of 35%.

Conclusions

Genetic correlations across sites have indicated that genotype x environment interaction is low for needle damage caused by *Dothistroma* needle blight on radiata pine. Genetic gain will be able to be delivered consistently across sites. The impact of breeding resistance to this needle disease could be considerable. It appears that genetic improvement achievable should be sufficient to bring the average needle damage to below the ~15% threshold for chemical control (Watt et al. 2011). A multi-trait analysis is now needed to understand the impact of selection for needle retention on the key breeding traits: growth and wood quality.

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