

IDENTIFICATION OF MOLECULAR MARKERS FOR BLOTCH DISEASES IN THE NORTH

Merrill Fordyce¹ and Greg Platz¹

¹Hermitage Research Station, M/S 508, Yangan Road, Warwick, Queensland. 4370

Abstract

The barley variety Kaputar carries resistance to the net blotch pathotype NB50 that is effective both at the seedling and adult plant stages. Crosses to the susceptible parent Klaxon were made and F₁s selfed to produce an F₂ population. Two hundred seeds were screened for reaction to NB50 and DNA collected from each seedling prior to inoculation. After infection scores were recorded, plants were transplanted to the field for verification on F₃ material.

Bulk segregant analysis was employed to find markers associated with the resistance. AFLPs were used as the preferred marker system and silver staining used to visualise polymorphisms. Bulks were made from 10 resistant and 10 susceptible plants. The following primer sequences were used to identify differences between bulks.

Selective Nucleotides and Restriction Enzymes used

MseI	PstI
CAA	AG
CTC	AG
CAT	AG
CTG	AG
CAA	AT
CTC	AT
CAT	AT
CTG	AT

Sets in bold identified polymorphisms between the two bulks and screening of individuals within each bulk also confirmed these. Screenings across the remaining 180 F₂ plants of the

population have yet to be completed. The experiment was repeated with a second F₂ population for the spot form of net blotch resistance conferred by the cultivar Tilga. Franklin was used as the susceptible parent and the spot form of net blotch pathotype used in screening was NB74S. Confirmations of polymorphism on the remaining 180 F₂ plants have yet to be completed.

Once verification is completed, conversion of these markers to simpler PCR primer based tests will aid in screening large breeding populations and pyramiding of multiple blotch resistance genes.

This paper will be available during the Symposium.