



The University of Adelaide  
Faculty of Agricultural and Natural Resource Science

## **Resistance of faba beans to Ascochyta blight**

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Master of Agricultural Science

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## **STATEMENT**

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This thesis contains no material which has been accepted for the award of any other degree or diploma in any other university or other tertiary institution. To the best of my knowledge and belief, this thesis contains no material previously published or written by another person, except where due reference is made in the text.

I give consent for this thesis being made available for photocopying and loan.

Uyek Malik Yakop

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## SUMMARY

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Ascochyta blight, caused by *Ascochyta fabae*, is one of the most destructive diseases on faba bean and it is widely distributed in all states in Australia, particularly in the southeastern region. Cultivation of resistant cultivars may reduce the damage. The present study was conducted to investigate various aspects of genetic resistance to Ascochyta blight of several accessions with the objective of providing the information to implement an efficient breeding strategy for the long-term control of Ascochyta blight.

There was variation among putatively resistant accessions in their response to Australian isolates of *A. fabae*. Several accessions were resistant to all isolates, while the remainders were resistant to several isolates and susceptible to the others. The variance within several accessions was reduced when lines produced by single plant selection were tested, rather than bulk samples. The average reaction of accessions that were homogenous resistant did not differ between single plant selections and the bulk populations. Variability for virulence was also evident and some isolates produced symptoms on all accessions, while others infected only several accessions.

The genetic resistance of Acc 622, one of the components of the Australian cultivar Ascot was investigated. Ascot was crossed to the *A. fabae* susceptible Australian cultivar Icarus and the reactions of reciprocal F<sub>1</sub> hybrids and the F<sub>2</sub> and F<sub>3</sub> generations were tested for reaction isolate 331/91. Reactions of the three generations indicated that a single co-dominant, or partially recessive, gene conferred resistance to isolate 331/91, relative to the susceptible Icarus.



The specific resistance of resistant accessions, most of which were obtained from ICARDA, was compared with Acc 622. The resistant lines were crossed to Acc 622 and the F<sub>2</sub> generation of each cross was tested for reaction to isolate 331/91. The alternative parent was considered to carry the same resistance gene as Acc 622 when all F<sub>2</sub> progeny produced a resistant reaction. Transgressive segregation, indicated by the presence of susceptible F<sub>2</sub> plants, was observed in several crosses and it was concluded that the *A. fabae* resistance of the alternative parent was conferred by a different gene to that present in Acc 622. Eight accessions (Acc 295, 297, 303, 484, 496, 668, 680 and 975, derived from BPL460, BPL465, BPL472, BPL74, BPL365, L83120, BPL2485 and L83125, respectively) were identified to carry the same resistance gene as Acc 622 and six accessions (Acc 299, 674, 712, 948, 970 and 1046, derived from BPL471, L83124, L82003, Quasar, ILB752 and BPL646, respectively) were different. The relationship between these alternative sources of resistance was not determined. Results for four populations were inconclusive due to a high variance of one of the parents.

AFLP analysis was utilised to identify the genetic distance among 20 resistant and 2 susceptible accessions. Three primer combinations (*Pst*ACA-*Mse*CAG, *Pst*ACA-*Mse*CCA and *Pst*ACA-*Mse*CGA) revealed a high level of polymorphisms. The average of genetic distance over all accessions was 0.34 with the pair-wise range from 0.09 to 0.53. The phylogenetic tree divided the 22 accessions into two major groups and several groups of two and three. The analysis was inconclusive when the genetic control of resistance to *A. fabae*, the region of origin and the source population were compared to the genetic distances among the accessions.

Resistance to *A. fabae* in the well adapted Australian cultivar Ascot is under simple genetic control therefore it should be relatively straightforward to transfer this resistance to other high yielding, but susceptible, lines either through simple crossing or backcrossing. As resistance is either partially recessive or co-dominant selection would be effective in the early generations. Identification of alternative resistance genes to the one in use in Australian agriculture should enable a long-term strategy for the development and deployment of resistant cultivars to be implemented.