DNA MARKERS FOR DISEASE RESISTANCE BREEDING IN PEAS (*PISUM SATIVUM* L.)

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ABSTRACT

Introducing resistance genes through plant breeding remains an important and effective means of protecting plants from diseases. Plant species commonly carry genes for disease resistance within their collective germplasm base. Disease resistance can either be monogenic (ie. encoded by a single gene) or quantitative (ie. encoded by a number of genes). The first step in disease resistance breeding is to identify accessions carrying the resistance phenotype. The conventional process of breeding for resistance involves making controlled crosses and selecting sexual progeny for improved disease resistance. While relatively straight-forward for dominantly-inherited single gene resistance, this process becomes progressively more difficult and time-comsuming for resistance encoded by single genes with recessive inheritance and for quantitatively inherited resistance.

Through the process of genetic linkage mapping, molecular markers which are linked to disease resistance genes can be identified, and these can then be applied in plant breeding programmes to assist in resistance gene introgression. Our research group has identified DNA tags for a number of genes for resistance to diseases affecting peas (*Pisum sativum* L.). For example, DNA markers linked to recessive genes for resistance to pea seed-borne mosaic virus (PSbMV) pathotype P-1 (Timmerman *et al.* 1993) and to powdery mildew fungus (Timmerman*et al.* 1994) have been identified. These genes are termed *sbm-1* and *er-1*, respectively. In more recent research, we have identified markers linked to the dominantly inherited gene for resistance to pea enation mosaic virus (PEMV). This gene is termed *En.*

The molecular markers linked to these three monogenic disease resistance genes have been applied in a field pea breeding programme to develop germplasm containing multiple disease resistance phenotypes. DNA tags linked to *sbm-1* and *er-1* have been used in conjunction with limited direct testing for disease resistance. Although widely distributed throughout the world, PEMV does not occur in New Zealand; therefore breeding for resistance to PEMV requires the use of overseas disease testing or DNA tags. The DNA tags linked to *En* have been used in the early stages of cultivar development without direct testing for disease resistance.

The genes contributing to quantitatively inherited disease resistance can also be characterised using linkage maps and DNA markers and DNA tags can be developed (Michelmore 1995). Experiments to map the genes for resistance to Ascochyta blight of peas are currently underway, using a QTL mapping experimental design. Similar experiments have been carried out by our research group to map genes for two other quantitatively inherited traits, seed weight (Timmerman-Vaughan*et al*. 1996) and green seed colour (McCallum*et al*. 1997). Ascochyta blight is a serious disease of peas which is caused by a trio of fungal pathogens: *Mycosphaerella pinodes*, *Ascochyta pisi* and *Phoma medicaginis*. Accessions with improved resistance to Ascochyta blight have been identified among peas bred by the Crop & Food Research field pea breeding programme. Using these accessions as the resistant parents, large populations of F_2 progeny and their descendants have been developed. The genotypes of these segregating

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progeny are currently being determined using DNA markers from our linkage map of the pea genome and field trials to measure disease resistance are underway in Western Australia.

Keywords: *Pisum sativum* L., DNA markers, linkage mapping, disease resistance, quantitative trait loci

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