A DNA marker correlated with tolerance to *Aphanomyces* root rot is tightly linked to *Er-1*.

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Common root rot, caused by *Aphanomyces euteiches* Drechs., is a serious disease on pea in many parts of the world including the United States, northern Europe, Tasmania and New Zealand (1). Several sources of tolerance to root rot have been identified, and breeders are attempting to combine these various sources in commercial varieties. Unfortunately, the transfer and pyramiding of genes conferring tolerance has proven very difficult because the trait appears to be polygenic and its expression is influenced by many environmental factors.

In the breeding program at Wisconsin, 12 pea lines (five with some degree of tolerance and seven susceptible) were intercrossed and subjected to seven cycles of selection for tolerance to root rot as well as other horticultural characters (2). Several pea lines have been produced from this experiment with increased levels of tolerance. We used the original parents and selected lines to search for genetic markers linked to the genes in the original parents responsible for tolerance to common root rot

DNA was extracted from four of the original lines (MN 494-A11, MN 108, CSC 8221, and B275-191) displaying some tolerance to root rot as well as from all seven of the susceptible lines (Badger, a backcross derived line of 'Dark Skin Perfection', L1073, L1532, WIS 7101, 8615, and 8617) and seven of the derived lines with enhanced tolerance. RAPD phenotypes for 318 primers were determined on each of the extracts. We identified 21 primers (Table 1) that generated fragments present in one or more of the tolerant parents and most or all of the selected lines, but rare or lacking in the susceptible lines.

At present, most of these RAPDs have been shown only to be correlated with the inheritance of tolerance to root rot, and we do not know if any will be particularly useful for selecting tolerant genotypes in other crosses. However, one of the RAPDs, $OPA5_{680}$ also was segregating in the set of recombinant inbred lines derived from the cross JI1794 x Slow, which has been used to help develop the pea linkage map. The RAPD mapped to a position on linkage group VI very close to *Er-1,* a locus controlling resistance to powdery mildew. Indeed, $OPA5_{680}$ is our closest marker to *Er-1,* with no recombinants found among the 45 recombinant inbred lines analysed.

The linkage to *Er-1* complicates our analysis slightly because powdery mildew resistance was screened for in the early cycles of selection and two of the root rot susceptible parents possessed the marker and also displayed resistance to powdery mildew. Hence, the high incidence of $OPA5_{680}$ in the derived lines could be attributed to selection of powdery mildew resistance rather than enhanced root rot tolerance. However, despite the early screening for powdery mildew resistance, most of the derived lines (5 out of 7) with enhanced tolerance to root rot are susceptible to powdery mildew. Thus, in at least these five derived lines, the $OPA5_{680}$ marker did not come from those parents carrying *er-1,* but instead must have come from the root rot tolerant parents. At present, we can not determine if the remaining two lines with enhanced resistance possess a marker derived from a powdery mildew resistant parent.

Table 1. Primers generating amplified fragments that occur in at least one of the root rot tolerant parents, few or none of the susceptible parents, and most or all of the derived lines.

Primer	Sequence (5' to 3')	Fragment size
OPA4	AAT CGG GCG T	300 bp
OPA5	AGG GGT CTT G	680 bp
OPA15	TTC CGA ACC C	1200 bp
OPD7	TTG GCA CGG G	710 bp
OPD20	ACC CGG TCA C	1240 bp
B192	GCA AGT CAC T	820 bp
B301	CGG TGG CGA A	520 bp
B314	ACT TCC TCC A	1240 bp
B344	TGT TAG GCA C	1090 bp
B384	TGC GCC GCT A	1800 bp
B409	TAG GCG GCG G	1400 bp
B411	GAG GCC CGT T	750 bp
B414	AAG GCA CCA G	2100 bp
B422	CAC CTG CGG G	2200 bp
B429	AAA CCT GGA C	1000 bp
B451	CTA ATC TCG C	1200 bp
B474	AGG CGG GAA C	800 bp
B493	CCG AAT CAC T	1000 bp
B499	GGC CGA TGA T	850 bp
GT06	ATG TGG TGG T	580 bp
S34	GAT AGC CGA C	820 bp

We do not know if the other RAPDs we have identified map to the same region because they were not polymorphic in the JI1794 x Slow RILs and have to be mapped in other populations. However, several of the RAPDs gave slightly different patterns of distribution among the original parents and derived lines, and it is probable that several regions of the genome are tagged by these RAPDs.

1. Hagedorn, D.J. 1985. *In* The Pea Crop, Eds. P.D. Hebblethwaite, M.C. Heath and T.C.K. Dawkins, Butterworths, London, pp. 205-213.
2. Lewis, M.E. and Gritton, E.T. 1992. J. Am. Soc. Hort. Sci. 117:638-642.