

FINAL REPORT

Identification of genetic markers associated
with *Meloidogyne Incognita* race 2
resistance in soybean
O18/06

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October 2004

IDENTIFICATION OF GENETIC MARKERS ASSOCIATED WITH *MELOIDOGYNE INCOGNITA* RACE 2 RESISTANCE IN SOYBEAN**Abstract**

Soybean production in South Africa suffers from yield loss caused by two predominantly occurring parasitic root-knot nematodes, *Meloidogyne javanica* and *Meloidogyne incognita* race 2 (*Mi* race 2). The most effective defence against these pathogens is by planting resistant varieties. In order to achieve sustainable resistance, it is necessary to introgress resistance to both these nematodes in a single cultivar. This complicates phenotypic selection and makes it virtually impossible to determine whether all resistance quantitative trait loci (QTLs) are retained in the progeny of a cross between resistant parents.

The use of marker assisted selection (MAS) could simplify the breeding process. Tamulonis et al. (1995) identified three RFLP markers linked to resistance to *M. incognita* race 3 (*Mi* race 3). A major QTL was found on LG-O conditioning 31% of variation in gall number, flanked by Satt492 and Satt358 and a minor QTL on LG-G (14%) flanked by Satt012 and Satt505 (Li et al. 2001). It was, however, unknown whether these markers would be applicable in the South African situation as *Mi* race 2 is predominant in South Africa. It was therefore necessary to test these markers and develop new markers for resistance to *Mi* race 2, if necessary, in order to facilitate selection for both nematode resistance traits, as different genes could control the resistance. The objectives of this study were: (1) To determine whether the same QTL conditioned resistance in our local material, as two different races of the nematode is involved; (2) Identify molecular markers linked to resistance to *Mi* race 2 in a segregating population using microsatellite (SSR) and/or amplified fragment polymorphism (AFLP) analysis for use in marker-assisted selection (MAS) in our local material; (3) Identify new QTL's where applicable; (4) Screening of germplasm for the presence of *M. javanica* and *M. incognita* race 2 marker genes with molecular techniques, and (5) Verification of *Mi* race 2 resistant soybean genotypes in microplot and field trials.

Crosses were made between LS5995 (resistant parent) and Prima2000 (susceptible parent) for the development of a segregating F₂ population for development of markers. The markers identified in PI96354 were evaluated

for linkage in the F_2 population. Microsatellite markers Satt492, Satt012 and Satt505 were not polymorphic in our population. The two markers on LG-G were not polymorphic between LS5995 and Prima2000. Two other SSR markers mapping on LG-G, Satt191 and Satt038 were polymorphic, but no indication of a QTL could be found. The local F_2 population was, therefore, screened with a number of SSR markers evenly distributed throughout the genome. A major QTL was identified on Linkage Group M between markers Satt201 and Satt590 accounting for 62.4% of gall rating values and 80% of eggs / root system variation in the segregating population. A minor QTL, accounting for 31.7% of the gall rating values, was located between markers Satt487 and Satt358 on Linkage Group O in accordance with published results. The frequency distribution of the different phenotypic nematode parameters (gall-indices and egg numbers) measured, as well as the DNA data suggested that resistance to *Mi.* race 2 in the soybean cultivar LS5995 is controlled by a few genes. Genomic DNA was also analyzed with AFLP and bulked segregant analysis. One hundred and twenty seven *EcoRI/MseI* primer combinations were screened against the parents and contrasting bulks, but no linkage could be established in the individuals comprising the bulks.

These *Mi* race 2 resistant markers, together with markers for resistance to *M. javanica* (previously developed) will now be used in the ARC-GCI soybean breeding programme to enhance the development of resistant cultivars.