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ABSTRACT BOOK

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Construction of a genetic linkage map and QTL analysis for late leaf spot and rust in groundnut (*Arachis hypogaea* L.)

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Late Leaf Spot (*Phaeoisariopsis personata* [(Berk. and Curt.) Deighton] and rust (*Puccinia arachidis* Speg.) are the major foliar diseases of groundnut that often occur together leading to 50-70% yield loss in the crop. Two hundred and sixty eight RILs (TAG 24 × GPBD 4) segregating for late leaf spot (LLS) and rust were used to undertake QTL analysis. Phenotyping of the population was carried out under artificial disease epiphytotics for three seasons. Positive correlations between different stages, high to very high heritability and independent nature of inheritance between both the diseases was observed. Parental genotypes (TAG 24 and GPBD 4) were screened with 1089 SSR markers, of which 67 (6.15%) were found polymorphic. The study yielded partial linkage map with 14 linkage groups integrating 56 SSR markers with 364.40 cM genome coverage and average marker distance of 8.7cM. Composite interval mapping (CIM) showed 12 QTLs for LLS (1.2 to 5.6%) in three different environments. In case of rust, 13 QTLs were detected in three different environments with phenotypic variance ranged upto 54.4%. Furthermore, a major QTL associated with rust was identified by both CIM and single marker analysis (SMA) that contribute 18.4 to 54.4% phenotypic variance. Markers linked with this QTL are being validated using a wide range of resistant / susceptible breeding lines as well as progeny lines of another mapping population (TG 26 × GPBD 4). SSR marker(s) linked with major QTL for rust, once validated, will be the potential marker(s) for undertaking molecular breeding for rust resistance.