**Genetic variability and identification of genomic regions associated with stem rot disease resistance in cultivated and interspecific derivatives of peanut (*Arachis hypogaea* L.)**

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Peanut is an important food and oilseed legume crop. Stem rot of peanut is a major soil-borne disease causing pod yield loss of 20-80%. Genetic variability of 160 peanut genotypes including interspecific derivatives was assessed by screening at ICRISAT-Hyderabad and ICAR-DGR-Junagadh. The genotypes showed a variability of 13-80% for percent mortality (PM) at ICRISAT sick field with ten resistant (13-19% PM) and fourty moderately resistant (20-29% PM) genotypes. Fourty four of these, (9 resistant and 35 moderately resistant) were interspecific derivatives from wild *Arachis* species *A.villosa*, *A.correntina*, *A.helodes*, *A.diogoi*, *A.cardenasii*, *A stenosperma*, *A.paraguariensis, A.kempff-mercadoi*, *A.hoehnei* belonging to AA, EE genomes. To identify the genomic regions governing stem rot disease resistance, an RIL population (from the cross, ICGV 02266 x NC 3033) with 192 lines (F9) was studied. Genotyping the RILs using 2.5K *Arachis* mid-density panel revealed the presence of 441 polymorphic markers between the parents, of which 426 high resolution SNPs were mapped across the 20 linkage groups. These SNPs spanned a map-length of 0 to 592.71cM. QTL analysis revealed the presence of one major and several minor QTLs governing disease resistance. We presume that the QTL qIC-3-1, located on chromosome 3, might be a potential stem rot disease resistance QTL, owing to its consistency and highest PVE value (14%) among all the QTLs identified. This study highlights the importance of interspecific derivatives as potential sources of stem rot resistance in peanut, and the identified genomic regions can be utilized to develop diagnostic markers for their use in peanut breeding.

***References:***

*[1]**Cui R. et al, ‘Quantitative trait loci sequencing–derived molecular markers for selection of stem rot resistance in peanut’, Jounal Crop Sci Jul, vol. 60, 2020, p. 2008-18*