

Mapping Iron Deficiency Chlorosis Tolerance in Peanut

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Iron deficiency chlorosis (IDC) under calcareous and alkaline soils is a significant abiotic stress affecting the growth and yield of peanut. We have mapped the genomic regions governing IDC tolerance using a recombinant inbred line (RIL) population derived from TMV 2 (susceptible to IDC) and TMV 2-NLM (tolerant to IDC), which was phenotyped during the rainy seasons of 2019 and 2020 in the iron-deficient calcareous plots. The best linear unbiased prediction (BLUP) values for IDC tolerance traits like visual chlorotic rating (VCR), and SPAD chlorophyll meter reading (SCMR) were used for QTL analysis along with a genetic map carrying 700 GBS-derived SNP, AhTE and SSR markers. In total, 11 and 12 main-effect QTLs were identified for VCR and SCMR, respectively. Among them three QTLs were major with the phenotypic variance explained (PVE) of 10.3–34.4% for VCR, and two QTL were major for SCMR with PVE of 11.5–11.7%. A region (159.3–178.3 cM) on chromosome Ah13 carrying two QTLs (one each for VCR and SCMR) was consistent with the previous report. A SNP marker, Ah14_138037990 identified from single marker analysis for VCR was located in the intronic region of the gene *Arahy.QA0C1*, which is important for protein binding. Overall, this study identified new QTLs and also validated QTL for IDC tolerance. These genomic resources could be useful for genomics-assisted breeding of peanut for IDC tolerance.