

SSR-based genetic linkage map for cultivated groundnut (*Arachis hypogaea* L.) for QTL analysis and comparative mapping

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Molecular markers and genetic linkage maps are pre-requisites for molecular breeding in any crop species. In order to develop first genetic linkage map for tetraploid cultivated groundnut, a total of 1145 microsatellite or simple sequence repeat (SSR) markers available in public domain and unpublished markers from several sources were screened on two genotypes, TAG 24 and ICGV 86031 that are parents of a recombinant inbred line (RIL) mapping population. As a result, 144 (12.6%) polymorphic markers were identified and these amplified a total of 150 loci. A total of 135 SSR loci could be mapped into 22 linkage groups (LGs). While six LGs had only two SSR loci, the other LGs contained 3 (LG_AhXV) to 15 (LG_AhVIII) loci. Phenotyping data obtained for drought tolerance related traits such as transpiration (T), transpiration efficiency (TE), specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) for two years were used for QTL analysis. Although, 2-5 QTLs for each trait mentioned above were identified, the phenotypic variation explained by these QTLs was in the range of 3.5-14.1%. In addition, alignment of two linkage groups (LG_AhIII and LG_AhVI) of the developed genetic map was shown with available genetic maps of AA diploid genome of groundnut and *Lotus* and *Medicago*. The present study reports the construction of the first genetic map for cultivated groundnut and demonstrates its utility for molecular mapping of QTLs controlling drought tolerance related traits as well as establishing relationships with diploid AA genome of groundnut and model legume genome species.