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**Project Title: Construction of a genetic linkage map and identification of molecular markers associated with resistance to TSWV, leafspots and other important traits**

Construction and improvement of a genetic map for peanut continues to be an important task in order to facilitate quantitative trait locus (QTL) analysis and the development of tools for marker-assisted breeding. The objective of this study was to develop a comparative integrated map from two cultivated x cultivated recombinant inbred line (RIL) mapping populations and to apply in mapping TSWV resistance and high oleic traits in peanut. A total of 4576 simple sequence repeat (SSR) markers from three sources: published SSR markers, newly developed SSR markers from expressed sequence tags (EST) and from bacterial artificial chromosome (BAC) end-sequences were used for screening polymorphisms. Two CAPS (cleaved amplified polymorphic sequence) markers were also included to differentiate *ahFAD2A* alleles and *ahFAD2B* alleles. A total of 324 markers were anchored on this integrated map covering 1,352.1 cM with 21 linkage groups (LGs). Combining information from duplicated loci between LGs and comparing with published diploid maps, 7 homoeologous groups were defined and 17 LGs were aligned to corresponding A-subgenome or B-subgenome of diploid progenitors. One reciprocal translocation was confirmed in the tetraploid cultivated peanut genome. Several chromosomal rearrangements were observed by comparing to published cultivated peanut maps. High consistence with cultivated peanut maps derived from different populations may support this integrated map as a reliable reference map for peanut whole genome sequencing assembling. Further two major QTLs for TSWV resistance were identified for each RILs, which illustrated the application of this map.