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Towards Integrating Genomics in Breeding in Groundnut (*Arachis hypogaea* L.)

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Groundnut is an important oilseed crop grown extensively in the semi-arid tropics of Asia, Africa and Latin America. However, its production is adversely challenged by drought and foliar diseases such as late leaf spot (LLS) and leaf rust (LR). Marker-assisted selection offers an important tool to enhance tolerance/resistance to above stresses which are difficult through conventional breeding. However, a very limited amount of genomic resources were available until recently. As a collaborative effort with several partners, large scale genomic resources such as simple sequence repeat (SSR) and Diversity Array Technology (DArT) markers have been developed recently. For instance, 4,245 SSR markers were screened on parental genotypes of five mapping populations segregating for abiotic / biotic stresses. Genotyping of these mapping populations with polymorphic markers has facilitated development of five genetic maps with 83-191 marker loci. Based on these genetic maps, a consensus genetic map comprising of 362 SSR loci spanning 3,543 cM was constructed. In parallel, mapping populations were phenotyped extensively for drought tolerance traits, LLS and LR. Detailed QTL analyses provided 87 QTLs for drought tolerance traits and 19 QTLs each for LLS and LR. While majority of QTLs for drought tolerance and LLS explained small phenotypic variation, one major QTL, contributing upto 54.4% phenotypic variation was identified for LR. This QTL at present is being introgressed in three elite groundnut varieties namely ICGV 91114, JL 24 and TAG 24 by using marker-assisted backcrossing. Integration of such genomics approaches in breeding programme should enhance crop productivity of groundnut.