

## IDT7-075 | Qtl mapping for drought resistant in cowpea

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Wide crosses were made between drought tolerant (IT98K-205-8) parent and the susceptible parent (NG/SA/01/09/004) with a view to raising mapping population for Linkage and QTL mapping in cowpea. The drought tolerant seeds were white while the susceptible parents were all brown seeds. Parental lines were screened to ascertain their tolerance level using the method of Singh with little modifications. The drought tolerant parent (IT98K-205-8) was confirmed to have retained its drought tolerant level. Sixteen crosses out of 227 attempts were successful only when IT98K-205-8 was used

as the female plant. The F2 plants were raised from the sixteen successful F1 seeds using single seed decent method. It was observed that some seeds from F1 generation were not viable and did not germinate. The F2 plants were selfed and raised to F3 for mapping population. Phenotyping was carried out on the mapping population and the two parental lines using ten characters traits. Seventy five SSR markers were developed and screened for polymorphism. Forty polymorphic markers were identified and used for bulk segregant analysis for marker development and linkage analysis.

## IDT7-076 | Breeding tropical legume crops for resilient cropping systems in Sub-Saharan Africa

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Legume crops are important components of sustainable agricultural production, household income and dietary systems. However, legume production in the tropics is challenged by a number of biotic (diseases and pests) and abiotic (heat, and drought) stresses. With support from bilateral projects such as Tropical Legumes (TL1, TL2 and TL3), CGIAR centers together with national research partners devoted resources and time to address these challenges. Genetic resources such as reference sets, pre-breeding, magic and intraspecific mapping populations, as well as genomic resources such as comprehensive genetic maps, whole genome sequences, QTLs and trait-specific markers have been developed for tropical legume crops such as chickpea, groundnut, common bean, pigeonpea, soybean and cowpea. Besides, integrated breeding approaches including high throughput genotyping and phenotyping platforms, marker-assisted selection (MAS) in pedigree breeding schemes, marker-assisted

backcrossing (MABC) and marker-assisted recurrent selection (MARS) have contributed to accelerated development of breeding lines and varieties. Improved varieties have been released and disseminated together with integrated crop management practices. Innovative seed and associated technology dissemination systems including public-private sector partnerships, community seed production initiatives, quality declared seed, mini seed packs, contractual seed production, and revolving seed fund, among others, were used to popularize these varieties. This has resulted in enhanced adoption and subsequent improvement in productivity. More efforts are needed to enhance genetic gain by reducing time required for cultivar development through application of genomic and phenomic tools, enhancing selection intensity through automation, mechanization and digitization, and increasing the crossing scale and number of cycles per year.