

## Cowpea Improvement in the Genomic Era: A conceptual framework



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Cowpea (*Vigna unguiculata* L. Walp.) is protein rich, and supplies grain, edible leaves and immature pods, and forage in the semi-arid tropics, mostly for subsistence farmers. Conventional breeding continues to play important role in cowpea varietal development, however, the breeding process is slow. Presented here is a conceptual design for cowpea breeding, targeting the stacking of multiple traits of agronomic significance including tolerance to drought, insect pests, diseases, parasitic weeds and low soil fertility. The design integrates genomics from germplasm characterization through population development and elite-line selection. This strategy should lead to more rapid and cost-efficient development of higher-yielding, stress-resilient, farmer and consumer-preferred cowpea varieties.

We have assembled a diverse germplasm collections of over 250 cowpea lines from different countries including local collections from various regions of Uganda (Fig. 1)



Fig.1. Geographical distribution of the cowpea breeding germplasm collection. The germplasm consists of cowpea lines with both erect and semi-erect growth habits, multiple traits sources including drought tolerance, disease resistance and yield

Collections are being phenotyped for various agronomic traits across three locations in Uganda. GGE-biplot analysis of 2016 A IYT depicted both stable and environmentally sensitive lines (Fig. 3)



Fig.3. Clustering of cowpea genotypes in intermediate yield trials (IYT) to reflect their sensitivity and stability across three locations in Uganda: SERERE (NaSARRI), ARUA (Abi ZARDI), KAB (MUARIK). Panel (a) display a genotype with high yield potential in IYT at KAB. Panel (b) depicts stability, genotypes close to the average environment coordination axis (AECA) are stable.

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To initiate the genomic integration platform, 25 cowpea lines were SNP genotyped. Cluster analysis displayed high diversity among the genotyped cowpea lines (Fig.2)



Fig.2. Diversity among the 25 cowpea lines genotyped at UCR using iSelect SNP genotyping platform. This information is being utilized to select distant parents to include in hybridization schemes



Fig.4. Cowpea genomic integrated breeding pipeline. Assemble, phenotype and genotype germplasm; combine phenotype and marker information to create unique breeding/mapping populations, discover/validate markers/develop GS models for use in marker aided selection and Distinctness Uniformity and Stability (DUS) testing.





A conceptual breeding frame work that integrates genomic information into the conventional breeding scheme is being developed. The scheme is deemed to enhance cowpea genetic improvement (Fig. 4).