

G6007.04 -Improved chickpea productivity for marginal environments in sub-Saharan Africa

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- University of Frankfurt, Frankfurt am Main, Germany: Peter Winter, Guenter Kahl
- University of California-Davis, USA: Doug Cook
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Research highlights:

Chickpea (*Cicer arietinum L.*) is an important grain legume in South Asia and SSA, especially in eastern and southern Africa. Drought, globally the number one constraint to chickpea production, occurs during the terminal growth stages as the crop is largely grown rainfed during the post-rainy season on residual soil moisture. Pod borer (*Helicoverpa armigera* Hubner) is a highly devastating insect pest of chickpea worldwide. It feeds on various plant parts such as leaves, tender shoots, flower buds, and immature seeds. The major goal of this project is to improve incomes and livelihoods by establishing the capacity to improve the insect (pod borer) resistance and drought tolerance in farmer-preferred chickpea varieties using modern molecular tools. This goal will be achieved by: (1) screening a large collection of novel chickpea germplasm to identify important new sources of resistance to the above insect pests and drought component traits; (2) developing a greatly enhanced set of molecular tools for use in chickpea; (3) determining the genes involved in insect pest resistance; (4) determining the genes involved in specific root traits contributing to drought; and (5) introgressing resistance/tolerance into farmer varieties.

Reference collection, developed based on earlier GCP-SP1 sponsored chickpea genotyping project, has been phenotyped for root traits, insect resistance and harvest index (HI) in Patancheru. A higher level of phenotypic variation for all three traits has been observed in the reference collection. These data will be used to develop new genetic populations for root traits and insect resistance for Africa and Asia. Towards developing genomic resources in chickpea, a total of 1,655 novel SSRs have been isolated from a SSR-enriched library (311) and BAC-end sequences (1,344) in collaboration with

University of Frankfurt and University of California-Davis, respectively (Nayak et al. 2008). These SSRs are being used to genotype one interspecific reference population (*C. arietinum* ICC4958 x *C. reticulatum* PI 489777) with an objective to integrate newly developed markers to the reference genetic map (Varshney et al. 2008). In order to enhance the density of chickpea genetic map, it is planned to develop either DArT or SNP markers.

The reference population segregates for insect resistance and therefore it has been phenotyped under natural field infestation conditions as well as green house conditions using detached leaf assays. A quantitative variation for different parameters conferring insect resistance was observed. Phenotyping of the population for insect resistance for the second year is in progress. Two intraspecific (*C. arietinum*) mapping populations (ICC 4958 x ICC 1882, ICC 8261 x ICC 283), developed before the start of the TLI project, segregate for root traits and harvest index. These populations have been phenotyped for root traits using PVC Cylinder approach (Kashiwagi et al. 2006) and also for harvest index. For both, root traits as well as harvest index, normal distribution has observed in the mapping populations. While phenotyping of these populations is in progress for the second year, marker genotyping data are being generated on these populations by using newly developed as well as already existing SSR markers in public domain. Marker genotyping data together with the phenotyping data will provide QTLs for insect resistance and root traits for their deployment in chickpea breeding.

As a major root trait QTL was identified before starting TLI project, efforts are being made to introgress this QTL in some drought sensitive chickpea lines of Africa and Asia through marker-assisted back crossing (MABC). In this direction, BC1F1s have already been generated for three crosses. In parallel, marker-assisted recurrent selection (MARS) approach has been initiated and three sets of crosses using good x good genotypes from Africa and Asia have been developed.

References/Publications

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3. Varshney RK, Penmetsa RV, Varghese N, Farmer A, Reddy P S, Sarma B, Nayak Spurthi, Carrasquilla Garcia N, Lekha P, Gao J, Jayashree B, Steiner S, Gaur PM, Srinivasan R, Hoisington D, Winter P, Bruening G, May G, Cook DR (2008). A genomics platform for molecular breeding and comparative genomics in chickpea (*Cicer arietinum* L.). Oral presentation at Cool season legume workshops at Plant and Animal Genome (PAG) conference XVI, San Diego, USA, 12-16 January, 2008.