

## Enhancing drought tolerance in chickpea using genomics approaches

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Terminal drought is one of the major constraints in chickpea (*Cicer arietinum* L.) leading to more than 50% production losses. To overcome these production losses due to drought, a range of translational genomics approaches are being used in chickpea breeding to develop improved chickpea varieties for enhancing food and nutritional security in developing countries in the context of climate change. For understanding the complex nature of drought tolerance, precise phenotypic data (20 drought component traits evaluated in one to seven seasons at one to five locations in India on two intra-specific mapping populations - ICC 4958 × ICC 1882 and ICC 283 × ICC 8261) together with extensive genotyping data was analyzed. As a result, nine QTL clusters containing QTLs for several drought

tolerance traits have been identified, which can be targeted for molecular breeding. Among these clusters, one cluster harbouring 48% robust M-QTLs for 12 traits and explaining about 58.20% phenotypic variation present on CaLG04 has been referred as "QTL-hotspot". This genomic region contains seven SSR markers (ICCM0249, NCPGR127, TAA170, NCPGR21, TR11, GA24 and STMS11). This QTL region has been introgressed in several leading varieties (e.g. JG 11, Chefe, KAK2) by using marker-assisted backcrossing (MABC) approach. Multi-location evaluation of these MABC lines provided several lines that have up to 24% higher yield than the recurrent parents. Introgression of this region into other elite cultivars will enhance production and productivity in chickpea.

## Trait introgression to evolve rice cultivars suitable for the water saving aerobic cultivation: evidence for physiological breeding.

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Evolving suitable rice cultivars is crucial for harnessing the water-saving advantage of semi-irrigated aerobic cultivation practice. Though several drought adaptive traits have been identified and validated, introgressing several of these onto the same genetic background alone can enhance crop performance under semi-irrigated aerobic conditions. We developed novel phenotyping approaches based on stable isotopes of carbon and oxygen to capture the genetic variability, water use efficiency and water use; and also developed strategies to assess root traits using specially designed root structures. A temperature induction response technique was developed to screen for variability in acquired tolerance traits. Using these phenotyping approaches, we screened a set of diverse *indica* rice germplasm for trait diversity. Around 300 genome wide SSR markers revealed significant molecular diversity and a population structure segregating the

population into six subgroups. Association mapping revealed several robust QTL governing the variability in these drought adaptive traits which were validated using bi-parental mapping populations.

The best root, WUE and acquired tolerance trait donor genotypes, AC39020 and IET16348, were identified and crossed separately with a mega rice variety, IR64. The F1 plants were inter-mated and the resultant double-cross F1 was backcrossed with IR64 till BC3F1. At each generation, QTL-markers were used for foreground selection and a set of 120 genome wide SSRs for background selection, and phenotyped for yield and  $\Delta^{13}C$ . This marker assisted-phenotypic selection led to the identification of superior lines with trait improvement with more than 97% of IR64 genome recovered demonstrating the power of physiological breeding.