

## IDT6-011 | Super early pigeonpea varieties and hybrids: New intervenor for maximized, time specific dry land production

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A neglected crop of yester-years, pigeonpea (*Cajanus cajan*[L.] Millspaugh) is a multi-purpose, versatile food legume, which has seen greater evolution in its plant architecture, duration and yield pattern as time passed. In rainfed ecologies across the globe, pigeonpea fits in as a remunerative option to the farmers. Frequent droughts in recent past have resulted in losses to crops such as cereals, millets and oil seeds, but pigeonpea in the same cropping niche provided at least minimum assurance to small and marginal farmers, owing to its drought tolerance and ability to withstand harsh environments. The enormous variability and plasticity of the crop provided an opportunity to breeders to develop super early maturity group with the life span of less than 100 days. The existing maturity duration -- early (less

than 140 days) and medium (180 to 200 days) -- imposes restrictions on adaptation to drought. The super early genotypes provide the foundation for future pigeonpea breeding because of their earliness, photo insensitive nature, impressive per day productivity, adaptability across the varying range of altitudes, stress escape mechanism and niche to fit well in various agro-ecologist and cropping systems. Rapid generation turnover is a boon to breeders for faster introgression of traits of interest, to carry out studies on genetics of biotic and abiotic stress by developing mapping population within very short duration. In the above context, "super early varieties and hybrids, is a wonderful breeding material to secure future sustainable dry land pigeonpea production".

## IDT6-012 | Fine mapping of QTL for grain yield under drought using rice lines adapted to target populations of environment

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Drought is one of the most serious challenges in rice production worldwide, especially in rainfed ecosystems. Developing high-yielding rice varieties combined with drought resistance will help to increase productivity in drought-prone areas. Conventional breeding for drought tolerance is slow due to difficulty in phenotyping of large progenies. Mapping quantitative trait loci for yield and its components under drought stress predominant in target populations of environment will help to overcome this limitation. A consistent QTL for yield under drought on chromosome 1 between RM8085 - RM3825 (1.6 Mb) was identified in

this laboratory using a recombinant inbred (RI) lines of IR20 x *Nootripathu* and was used for fine-mapping in this study. A set of 67 SSR markers were selected within the QTL region and 12 markers polymorphic among the parents were used in genotyping of the 220 RI lines. The linkage map of chromosome 1 was reconstructed with these additional markers to a length of 251.6 cM and average marker interval of 11.4 cM. The grain yield QTL was fine-mapped to a smaller segment (42.8 kb). The same region was found to be linked to total biomass and plant height under drought in TPE.