

IDT9-063 | Improvement of Brinjal germplasm for root knot - nematode resistance using molecular markers

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Institute of Biotechnology, PJTSAU, Rajendranagar, Hyderabad – 500030; *Principal Scientist, NBPGR Regional Station, Rajendranagar, Hyderabad – 500030; #Principal Scientist, Biotechnology Unit, ARI, Rajendranagar, Hyderabad - 500030 Brinjal or eggplant (*Solanum melangena* L.) being a poorman's vegetable has been affected with many biotic stresses. In the present study we have identified the root knot-nematode race prevalent in major vegetable growing areas of Telangana in India as *Meloidogyne incognita* race 2 using host differentials and 60 germplasm accessions including different varieties of brinjal were screened against the *Meloidogyne incognita* race 2. However, none of the accessions/varieties which were reported to be moderately resistant were proved so in the present study indicating that there

was a probable escape in previous investigations. Further we also cloned resistant gene homologs from brinjal using degenerate primers designed based on the conserved NBS motifs. Out of 46 recombinant clones, five NBS sequences had high similarity with the known resistant genes namely, Chilli CaMi and Tobacco N gene. Further identification of these resistant gene homologs is underway. Cluster analysis using the deduced amino acid sequences of brinjal with the other reported analogous domains of known R- genes, classified brinjal sequences into two major groups. Isolation of full length genes from these resistant gene homologs would help in improving the genetic resistance of the available superior germplasm against root knot-nematodes. Plant disease resistance (R) genes are abundant in every plant species.

IDT9-064 | Next generation sequencing approaches for understanding genetic mechanism of drought tolerance in Valencia Peanut

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Valencia peanuts are highly susceptible to drought stress. The yield reduction due to stress can result in more than 50% reduction resulting in high aflatoxin contamination. In our present study we have compared Valencia-C genotype with a highly drought tolerant runner type peanut C76-16 using transcriptome sequencing to investigate tissue-specific gene expression and response to abiotic stress. We evaluated the two genotypes under field conditions under irrigated and stress plots in 4 replications. We found that genotype C76-16 outperformed yield compared to Valencia-C under drought stress conditions with only a 30 % reduction in yield while Valencia-C showed a higher loss of up to 70%. Each year the yield varied widely due to the environmental factors but C76-16 was con-

sistently ranked among the top and suffered a minimal loss of yield suggesting that it is best suited for the erratic climatic conditions of southwest U.S. Leave samples were harvested from the control and stress conditions and used for RNA isolation and sequencing. A total of 340 million paired-end reads were generated and were used to find differentially expressed genes and transcripts between tolerant and susceptible genotypes. The pathways and candidate genes involved in drought tolerance will provide basic information and expression markers for drought tolerance in peanut. We will present our findings on genic content and tissue-specific gene expression and discuss the challenges and opportunities of unifying transcript sequence data for the peanut community.