

SALIENT ACHIEVEMENTS

MOLECULAR BIOLOGY / BIOTECHNOLOGY / BREEDING / DISTANT HYBRIDIZATION

1. Using a next generation sequencing platform (ion torrent PGM™) with Microsatellite enrichment methodology, 249 simple sequence repeats (SSRs) for *Plantago ovata* were generated very first and markers were used for molecular characterization of cultivated and wild species of *Plantago*.
2. Candidate genes responsible for downy mildew resistance in pearl millet have been successfully identified using next generation transcriptome sequencing. Transcriptome produced a total of 2419 EST-SSRs markers of which 230 markers based on their function in downy mildew-pearl millet interaction were validated.
3. Nine hundred and thirty-six accessions of *Jatropha* were collected and 43 elite genotypes were submitted to ICAR-NBPGR, New Delhi and IC number were allotted.
4. In rice, regeneration and genetic transformation protocol has been developed and transformation for drought tolerance was successfully done.
5. Flowering induced successfully in saffron under control environmental condition in glasshouse
6. Identified low ricin castor genotypes (JI379, ANDCM-2, ANDCH-11-3, JI355) through ELISA immunological technique
7. Generated DNA fingerprinting profiles for 190 released varieties of University and other private intenders.
8. Isolated and identified drought resistance ESTs in pearl millet (*Pennisetum glaucum*)
9. In cotton a total of 200 novel EST-SSR markers associated with fibre traits were developed through *In silico* study which can be used for linkage mapping and association study in cotton for identification of genes associated with fibre quality.
10. Transcriptome study was carried out to get insight of the genes associated with fibre quality of *Gossypium herbaceum*.
11. Diversity was captured in okra using SSR markers on 125 genotypes including wild relatives.
12. Using next generation sequencing platform, a set of 6421 SSR primers were generated from genomic sequences of cumin.
13. In cumin, a protocol is established for isolation of high quality RNA for RNA-seq and RT-PCR study.
14. A set of 100 EST-SSR markers has been developed in cluster bean (*Cyamopsis tetragonoloba*)
15. Genome wide association study has been carried out for the first time in rice using 6K SNP chip to identify the SNP controlling the expression of secondary metabolites in grain.
16. LC/MSMS method has been successfully developed for identification and quantification of 80 secondary metabolites including phenols, carotenoids, alkaloids etc.
17. Validation of aroma allele specific marker in Rice germplasm.
18. For the first time DNA content and ploidy analysis carried out in cumin.
19. *In vitro* genetic transformation and regeneration protocol has been developed in tomato cultivar SL 120.

20. Transcriptome analysis of tomato cultivars (AT-3 susceptible and SL-120 Resistance) has been carried out for identification of root knot resistance genes.
21. Transcriptome analysis of saffron stigmas has been successfully carried out for identification of genes responsible for colour and fragrance principles.
22. Transcriptome analysis of leaf of teak has been carried out for identification of drought responsive genes.
23. Root Knot resistance *Mi* gene has been successfully isolated and cloned into plant specific binary vector.
24. Successful isolation of *CCD-2* and *GLT-2* genes responsible for colour and fragrance principle in saffron stigmas has been done.
25. The different wild germplasm of Okra have been screened on the basis of naturally infection, net house and DNA based study against YVMV. The result revealed that two accessions *A. moschatus subsp. tuberosus* (IC 470750) and *A. moschatus subsp. tuberosus* (IC 413569) are highly resistance against YVMV.
26. The seed material of 17 different wild and introgressed cultivated species of tomato have been imported from TGRC, California. The material has been evaluated against TLCV, nematode and drought in tomato. A line *S. arcanum* (LA-2157) was found highly resistant for both *M. incognita* and *M. javanica*.
27. There are 24 lines developed through inter-specific hybridization in Cotton (*G. herbaceum* × *G. arboreum*) having fibre length >28 mm.
28. Different species of cotton i.e. *G. raimondii*, *G. herbaceum*, *G. arboretum*, *G. stockii*, *G. nelsonii*, *G. capitata-viridis*, *G. barbadense*, *G. triphyllum*, *G. robinsoni*, *G. thurberi*, *G. tomentosum*, *G. sturtianum*, *G. brasiliense* and *G. trilobum*, have been successfully established in the field for evaluation and germplasm maintenance.
29. Development of cholchiploid in desi cotton has been done through the Seed soaking treatment and Cotton swabbing method. 28 new cholchicine treated plants have been established in the farm. During the cytology and cytometry study the results have been found mixoploid.
30. Development of distant hybrids / wide crosses in custard Apple has been carried out. There are 25 interspecific hybrids established in the field. Interspecific hybrids were subjected to PCR amplification for confirmation of hybrids purity and DNA banding pattern supported the hybrid purity of 17 hybrids.
31. The 28 lines of mustard including 20 lines derived through interspecific hybridization using *B. napus*, *B. carinata* and *B. rapa*, 5 private hybrids, along with 3 local checks GM-2, GM-3 and GM-4 raised and have been evaluated against aphid. Top five interspecific inbred lines of mustard with lowest aphid score have been found as GM 3 × *B. carinata* (Kiran) (1.58), GM 3 × *B. napus* (GSL-1) (1.62), GM 3 × *B. napus* (GSL-1) (1.77), GM 3 × *B. napus* (GSL-1) (1.83) and GM 3 × *B. napus* (GSL-1) (1.87).
32. About 48 Interspecific lines of cucumber have been developed and evaluated against fruit fly and leaf minor. Out of 48 lines, top 3 lines from BC₁F₇ generation are being evaluated under PET trial.