

PIE-3451: DNA MARKER AIDED ANALYSIS OF MULBERRY GENE BANK TOWARDS A CORE ASSEMBLY FOR SUSTAINABLE CONSERVATION AND ENHANCED UTILIZATION IN CROP IMPROVEMENT (DBT sponsored collaborative project with CSRTI, Mysore)

Period: September, 2010 - December, 2013

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Introduction:

The vast collection and maintenance of 1269 mulberry genotypes at CSGRC, Hosur and many breeders' collections maintained at other Institutes of CSB such as CSR&TI, Mysore. Large collection and redundant genotypes are of matter of concern of its effective utilization and conservation. Identification of core-subset / panel of germplasm are important requirement for effective utilization of mulberry genetic resources in breeding /crop improvement programmes. Accordingly, an attempt was made to develop a core set of mulberry germplasm using phenotypic and SSRs & AFLPs molecular markers so as to get maximum diversity representation.

Objectives

- Identification of a panel of diverse mulberry germplasm amenable to association mapping by marker (by genomic and EST SSRs) aided analysis
- Evaluation of panel of diverse mulberry germplasm for important traits viz., sprouting, senescence, rooting, leaf quality, yield contributing traits and key morphological characters
- Construction of a core sub-set of mulberry germplasm by molecular marker (SSRs and AFLPs) and phenotypic analysis

Outcome:

- ❖ Highest coefficient of variability (59.27%) was observed for stem yield followed by leaf yield/plant (51.12%) and weight of 100 leaves (50.29%).
- ❖ Number of branches ranged from 1 to 25 with mean of 10 branches. Higher number of branches in the range of 7-13.
- ❖ Leaf yield ranged from 930 - 1938 g/plant with mean yield of 1492.8g. Most of the accessions were in the range of 205-805 g/plant.
- ❖ Though harvest index ranged from 28.34 - 89.92%, most of the accessions were in the range of 50-60%.
- ❖ Days to sprouting in exotic accessions ranged from 9 to 32 days with mean 23 days and coefficient of variation 22% while in indigenous accessions, days to sprouting varied from 7-35 with mean of 19 days and coefficient of variation 19.86%.

Recommendations/ Utilization:

- ✓ A panel of diverse germplasm (300 entries) and core sub set (150 entries) with maximum genetic and phenotypic diversity were sampled for use in linkage disequilibrium (LD) mapping and mulberry crop improvement programme.
- ✓ A total of 36 mandatory accessions were included in the core collection, which have been the integral part of Indian mulberry breeding programme over last four to five decades.
- ✓ By assessment of total diversity available in mulberry germplasm and construction of a core subset helps for effective utilization of natural gene pool in crop improvement.



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