

Project code & Title: PIG06005SI-Molecular characterization of mulberry genetic resources for the identification of duplicates and effective utilization.

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Introduction: Mulberry is an important economical crop plant in sericulture. Its foliage is the sole food for domestic silkworm (*Bombyx mori* L.) which produces natural silk. In mulberry, vegetative propagation is the only means to maintain the cultivars identity. Long history of cultivation for sericulture and recent efforts by traditional breeding methods for mulberry improvement has resulted in number of varieties grown in different regions. Conservation efforts by countries involved in sericulture have resulted in the accumulation of approximately 5000 accessions in the field gene banks all over the world. According to a rough estimate based on passport information, a large portion of these collection are suspected to be duplicates or redundant. Accessions might have been collected from common or identical collection areas. Sometimes expeditions may have been carried out without prior knowledge about the distribution of genetic variation across the areas. The diversity in the germplasm collections is a prerequisite for the effective utilization of genetic resources. Molecular markers are useful complements to morphological and phenological characters because they are plentiful, independent of tissue or environmental effects and allow accession identification in the early stages of development. Such techniques reveal polymorphisms at the DNA level and are very powerful tool for characterization and genetic diversity estimation. In this study, SSR markers have been used to characterize the mulberry genetic resources available in the germplasm bank and to utilize the information to demarcate duplicates from mulberry germplasm.

Objective: Identification of duplicates and their demarcation using morphological descriptors and molecular markers.

Outcome: In the present study, both morphological descriptors and SSR markers were utilized for the identification of duplicates. The results of the study highlighted that out of 84 suspected duplicates, 14 accessions were confirmed as true duplicates. Among 86 SSR primers screened, 12 are found to be polymorphic. These polymorphic markers can be used to screen mulberry germplasm. Moreover, most of the accessions collected from Gujarat, Rajasthan, Assam, Arunachal Pradesh and South Indian states like Tamil Nadu, Karnataka and Kerala are found to be duplicates. It is evident that both morphological and molecular characterization with highly informative markers is important to determine duplications if any and gives valuable trait information for future researchers and breeders.

Recommendations/Utilization:

After the identification of duplicates using molecular characterization of mulberry germplasm several utilities and benefits can be derived as below:

- 1. Resource optimization:** By eliminating the duplicate accessions, resources such as land, labor and maintenance costs can be redirected towards the conservation and utilization of unique and diverse germplasm. This optimizes the efficiency of mulberry collections and ensures that resources are utilized effectively.
- 2. Genetic diversity preservation:** The identification of duplicates allows more accurate assessment of the genetic diversity present in the mulberry germplasm collection. Preserving the diverse set of mulberry genetic resources is crucial for crop improvement. Also unique accessions can be prioritized for conservation and further research.
- 3. Breeding and trait improvement:** Molecular characterization helps to identify unique accessions with desirable traits. These accessions can serve as valuable genetic resources for breeding programs aimed at developing improved mulberry cultivars with enhanced traits.
- 4. Exchange and collaboration:** Accurate identification of duplicates using molecular markers facilitates effective exchange and collaboration between institutions, researchers and gene banks. This allows for sharing of unique accessions and the avoidance of redundant efforts, promoting greater collaboration and efficiency in mulberry research and breeding programs.
- 5. Conservation and germplasm security:** Molecular characterization using SSR markers aids in maintaining the integrity of mulberry germplasm collections. By accurately identifying the duplicates, the risk of losing the valuable germplasm due to mislabeling or accidental loss is minimized. This ensures the long-term conservation of diverse mulberry germplasm for future generations.

Therefore, the utility of the mulberry germplasm lies in optimizing resource allocation, preserving genetic diversity, facilitating breeding and crop improvement, supporting research endeavours and ensuring long-term conservation of valuable resources.