Project code & Title: PIG06004SI-Studies on cytological status of mulberry genetic resources.

Period: 01-03-2020 to 31-03-2023 (Three years)

Investigators: Mr. Raju Mondal (PI) & Dr. M.C. Thriveni (CI)

Introduction: Mulberry (*Morus* spp.) is an economically important crop plant in sericulture since its foliage is the only source of food for the domesticated silkworm which produces natural silk. The long history of cultivation for sericulture and recent efforts by traditional breeding for mulberry improvement has resulted in a number of varieties grown in different regions. Polyploidy has played a major role in the evolution of its various species. Higher production of foliage must increase the volume of rearing and in turn the production of silk per unit area. Cytological confirmation of ploidy and chromosome behavior during meiosis of genotypes is very much essential in polyploidy breeding. The present study attempted to understand the chromosome number and variation of ploidy among the mulberry germplasm.

Objective: Identification of chromosome number and ploidy level of mulberry genetic resources.

Outcome:

1. An economically feasible protocol was developed using shoot tips for metaphase plate preparation and chromosome number estimation (Bio-Protocol; DOI: 10.21769/BioProtoc.4643).
2. In the present study, the chromosome number and ploidy level of 200 accessions have been studied. Among these, 154 accessions are diploid, 03 accessions are aneuploid, 23 accessions are triploid, 15 accessions are tetraploid, 05 accessions are hexaploid and one accession is decasoploid.
3. The species-level distribution reveals that *M. alba*, *M. indica*, *M. laevigata* and *M. macroura* comprise three types of cytotypes viz., diploid, triploid, and tetraploid. *M. serrata* and *M. tiliaefolia* are hexaploid and *M. nigra* decasoploid. The remaining species are diploid.
4. The genome size of all the cytotypes was estimated using flow cytometry data (Plos One; DOI: 10.1371/journal.pone.0289766).

Recommendations/Utilization:

1. Developed protocol using shoot tips can help to optimize the cytological study (pre-treatment, fixation, enzymatic treatment, staining, and squashing were carried out) of other tree species.

2. The chromosome and genome size data will help to correlate and identify ploidy-associated characters. Generated information can also be useful in selecting the superior parental breeding lines.
3. The ploidy information can be complemented to understand the gene-to-phenotype network modelling as well as to develop future polyploidy conservation strategies concerning climate change.