

Preface to this Volume

In the preceding volume (1B) of this series, emphasis was laid on phylogeny, biodiversity and evolution as analyzed through molecular and other genomic tools specially in plantation crops like coconut, coffee, ginger and papaya and plants of agri-horticultural importance like wheat relatives and grasses. Most articles dealt with monocotyledonous families and a few dicotyledons. The present treatise on the other hand, has concentrated mainly on the dicotyledons, covering legumes like *Cicer*, *Vigna* and *Vicia*, several fruit plants like species of *Prunus* including cherry, peach and apricots, as well as grapes, oranges, olive and pistachio. All groups were subjected to molecular analysis of genome. Solutions of some basic problems of phylogeny, evolution and biodiversity in several taxonomic groups such as Caryophyllales, through chromosomal and molecular data, have been presented.

In legumes, along with other parameters in the study of diversity and phylogeny, the non-specific markers like RAPD/RFLP and those developed in other related crops, as well as SSR have been taken advantage of. While dealing with chromosome dynamics in *Arabidopsis*, a phylogenetic tree has been presented of kinase domains of Aurora kinase on the basis of synteny and colinearity of gene sequences. The similarity of *Arabidopsis* with other groups and selective values of these proteins are emphasized.

In Caryophyllales, the core eudicots, the genomic data, both molecular and organellar, have demarcated boundaries of the order and relationship with non-core groups such as Polygonales and some of the carnivorous genera. In Cardamines, molecular data has indicated highly reticulate evolution at the diploid level, speciation being affected principally through polyploidy and hybridization. In *Sisymbrium*, molecular studies have traced its polyphyletic ancestry and the restriction of the genus only to old world. Similarly, in Besleriaceae, ITS sequences have aided in assessing phylogeny of several genera, simultaneously indicating that all Caribbean taxa originated in North-East part of South America. In the mangrove family Rhizophoraceae, molecular and other methods of genome analysis indicate a wide genetic distance between four genera. However, organellar genome analysis suggests separation of the genera into distinct mitotypes and chlorotypes. The approach through organellar and nuclear genome analysis has also aided taxonomic subdivisions in *Gunnera* of Myrtales from biogeographical aspect confirming the accepted taxonomic state. In *Fagopyrum*, the Buckweeds, different parameters involving chemical, biochemical and genetic characters have been used in assessment of genetic variability and clustering, as well as determination of relationship in Chinese taxa. In Cactaceae, the monophyletic nature of the family has been indicated through molecular studies as also the interrelationships of taxa at the intrafamilial level.

The fruit family Vitaceae including *Leea* has been subjected to molecular analysis utilizing both nuclear and organellar sequences. The comparative status in evolution of the different genera, their affinities and finally the origin of endemic clades in Australia following separation from Antarctica have been discussed. In a separate article on Grape, the relationship through DNA fingerprinting in different cultivars, and the origin of ssp. *sativa* from ssp. *sylvestris* have been confirmed. The status of the orange family Rutaceae as a monophyletic clade of Sapindales is vindicated through genomic analysis simultaneously emphasizing the need for a reorientation of the internal classification of the genus *Citrus*. In the genus *Olea*, tandem repeated sequence families have been utilized as aids in diversification. The present state of family clustering and cultivars could not be correlated through molecular data. The molecular markers and genes applicable to *Prunus* are stated to be on the increase and trait specific sequences are available. A state of the art on this aspect including almond, apricot, cherry, peach and plum has been presented indicating high potential for the future specially through

ESTS, microarray and *in situ* hybridization. Apricots form a separate chapter where diversity studies based on genomic molecular markers including *cp* DNA and ribosomal genes support recent classification.

The last article deals with *Pistacia*, one of the most important genera of Anacardiaceae. Along with other parameters, studies on chromosomes and molecular sequences have been utilized in the determination of phylogeny, evolution and distribution as well as sex determination. The sex associated RAPD markers and sex differentiation are of significance. The occasional presence of monoecism in otherwise dioecious species as observed may provide key to the evolution of sex.

The present treatise along with the preceding one (1B) would be of use to those interested in molecular genomics, plant biodiversity and evolution of higher plants in general and plantation crops, pulses and fruit plants in particular.

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