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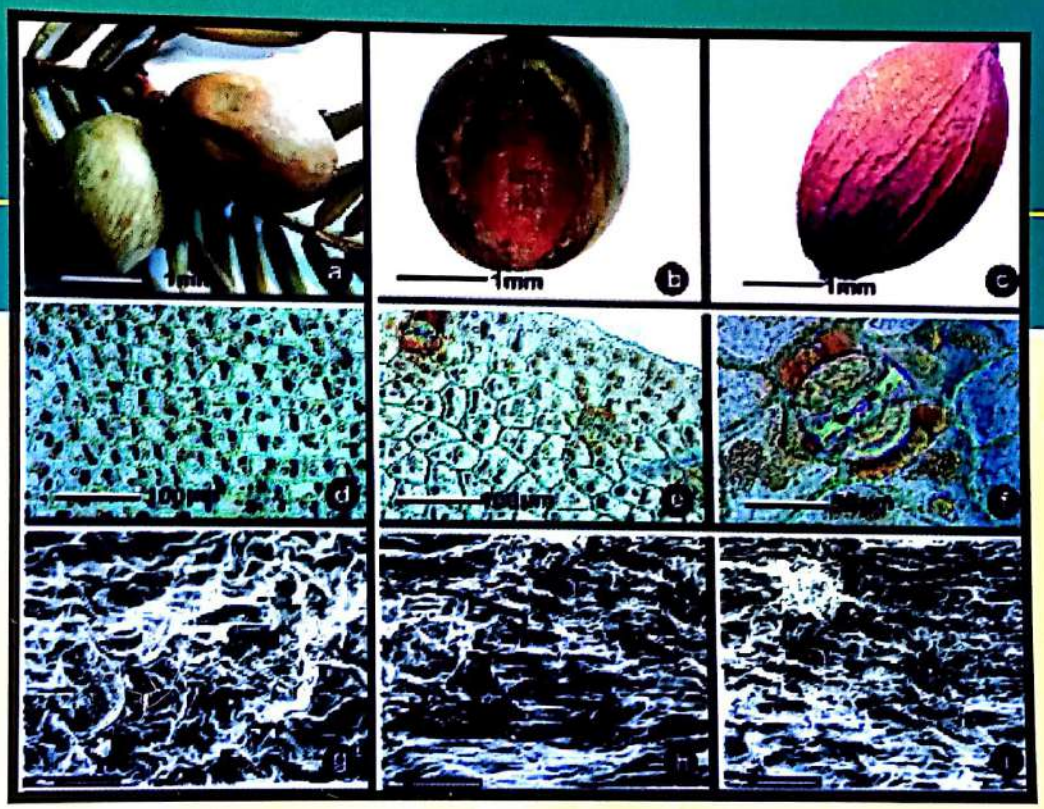

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Department of Botany, University of Calcutta,
Taraknath Palit Siksha Prangan,
35, Ballygunge Circular Road, Kolkata 700 019, India

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Editorial

On the relevance of morphological and molecular data in Taxonomy

Plant Taxonomy has entered a new phase in recent years. This subject with the invention of sophisticated instruments and techniques has been enriched greatly like some other disciplines of plant science. Plant taxonomy had its journey starting with observations by naked eyes, subsequently with hand lens, simple microscope, and compound light microscope. Through this phase of microscopy, a huge amount of data on morphological features of plants are obtained and used in systematic studies. These morphological features include a vast array of characters of flowers, fruits, seeds, leaves, stems and roots. With the invention of scanning electron microscope (SEM), transmission electron microscope (TEM), scanning force microscope (SFM) and atomic force microscope (AFM), there has been a revolution in plant taxonomy in recent years with availability and derivation of intricate micro- and ultra-characters in the domain of plant science including morphology. These microscopes being highly expensive have not been made possible to be available to great number of workers (scientists). But the sophisticated data obtained are much more reliable and species-specific in most of the cases which provide support in the phylogenetic and cladistic analyses.

Since the early 1990's molecular systematics has made a changed approach in the classification of plants which is based upon the analysis of DNA sequence data. In this regard an international collaboration by the Angiosperm Phylogeny Group has provided a new and reliable framework of classification. Premolecular classifications primarily based on traditional morphological characters together with palynological, embryological, anatomical, and phytochemical data include those of Cronquist (1981, 1988), Thorne (1992, 2007), Takhtajan (1997, 2009) and Dahlgren (1975, 1983). These classifications were widely accepted in different parts of the world. Prior to these classifications, Bentham and Hooker (1862-1883), Engler and Prantl (1887-1915), Bessey (1915), Hutchinson (1934, 1959), Sporne (1956), and some others were the proponents of classification systems mainly based on morphology. These were highly satisfactory and as such accepted for use quite for a long time.

Remarkably, four major milestones in the name of Angiosperm Phylogeny Group (APG I, 1998; APG II, 2003; APG III, 2009; APG IV, 2016) have contributed stability to the classification system supported by a wide range of genes. However, molecular data may be more valuable and convincing in the study of phylogeny and creating perfected classificatory systems of plant groups, but these are also riddled with problems and constraints. For evaluating the importance of molecular data in taxonomy, one has to rely on the morphological characters for their justification. Morphological characters belong to the most versatile category of phylogenetically useful information.

Several authors have argued that morphological data should not be combined with molecular data because they exhibit greater convergence and homoplasy than do molecular data. Morphology is regarded as being more susceptible to directional selection pressures that may cause a functional complex of characters to evolve several times within a lineage. In some cases, molecular data had a significantly higher consistency index than morphology. Hence, morphological data are of little value in recognizing species and their relationships in sharp contrast to molecular data used in the interpretation of phylogenetic relationships. The actual difference in homoplasy between DNA sequence data and morphology has not been supported by other studies. Their analysis compared consistency indices for studies based exclusively on one type of data, but an examination of

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some studies that combined molecules and morphology for the same sets of taxa revealed higher consistency than molecules.

If morphological data do generally exhibit greater homoplasy than molecular data, this is not justified for disregarding their importance. Only characters with the highest consistency be included in an analysis. Therefore, many molecular characters would have to be removed from an analysis along with all of the morphological evidence. Many morphological data sets have high consistency, and even in relatively homoplasious data sets there will be both consistent and inconsistent characters that are highly informative.

We know that morphological data have several advantages over molecular data. For example, the collection of morphological characters is easy and less expensive than generating the molecular data. The fossils are studied and characterized mainly by morphological features. If morphological evidence is ignored, the phylogeny of a large number of life will be ignored. Further, the combined morphological characters have great predictive value and should be considered in classification with molecular data depending on the taxa under consideration.

Prof. N. D. Paria

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