

Molecular taxonomy and morpho-taxonomists' concerns

Floras are documented accounts of plant species occurring naturally in specific regions with defined or loose boundaries. These documentations are generally accomplished for specific groups and not for all plant groups collectively, although the word 'flora' is indicative of all groups together. They appear either as soft versions (e-floras/PDFs) or in hard copies such as book volumes or books. Taxonomists associated with different herbaria/institutions usually author them. The systematic arrangements/classifications that gets admittance in the organization of these floras are largely those adopted by herbaria/institutions to which they are associated. Since the founding fathers of Indian seed plant taxonomy were primarily the British, many floras published in the late 19th and early 20th centuries for the Indian subcontinent/India/erstwhile provinces had adopted the Bentham and Hooker classification, a system detailed in *Genera Plantarum* (1862–1883). This system is based on morphological vividness and affinities among species. In some instances, evidence drawn from allied fields that account for few minute or internal features perceived in embryology, anatomy, cytology, phytochemistry, palynology, etc. has been used to modify/complement our grasp on various groups explained in this classification. These allied fields remained supportive of classical taxonomy. The Commonwealth of Nations had employed the same classification in the initial phases of flora writings. Although students were taught artificial, natural and phylogenetic systems of classification, emphasis was given to the Bentham and Hooker classification as it was adopted in flora writings. With a few exceptions, majority of the herbaria adopted this classification in specimen arrangement. The floras usually provide diagnostic keys to families, genera and species, and those with basic botanical knowledge can effectively utilize them in identifying unfamiliar species. In summary, floras help in identifying the plant wealth of a region by botanical names, sustainably using diverse species based on their virtues, looking for endemic species, and to monitor and protect overexploited and threatened species. Knowledge of the flora of a specific region enhances our appreciation of varied expressions of nature, diverse ecosystems, their components and functions. These expressions are showcased differently and uniquely in different phytogeographic regions of India. The Western Ghats (Sholas: montane grasslands interspersed with evergreen trees), Eastern Himalaya including North East India (evergreen rainforests, conifer–rhododendron forests,

alpine flora), Western Himalaya (cold deserts, conifer forests, alluvial grasslands and alpine meadows), and Andaman and Nicobar Islands (mangroves and commonalities with Southeast Asian floral elements) present some notable and unique ecosystems. The potential utility of floras gradually fades as new knowledge gets accumulated in different groups, conceivably calling for modification/shift in the placement of these groups. New additions through explorations require inclusions and then, floras desirably undergo updating or revisions. This innate fluidity in the floras do not undermine the essentiality of having a national flora. Plant inventories published in the form of national flora serve as a reference to the state-of-the-art on floral wealth at the time of publication of the work.

Classificatory systems based on phylogeny are founded on the theory of descent and evolution. These systems were prompted by wider acceptance of Darwin's theory of Evolution, when he published his book on the *Origin of Species* in 1859. By the end of the 20th century and with progress in genetics, there was a realization that traditional natural systems in floras had failed in projecting monophyletic groups (those that include all the descendants of a common ancestor). Taxonomists started believing in the significance of molecular evidence in building true evolutionary relationships, with monophyly being the core focus in deriving true clades (a clade is a taxonomic group comprising a single common ancestor and all its descendants). Such relationships could be attained among individuals/populations/species/higher taxa using a combination of molecular data (nuclear/mitochondrial/chloroplast DNA, protein sequences, and presence or absence of compatible elements) and appropriate application of statistical techniques. The subject had gained more appeal, and taxonomists began to pursue molecular taxonomy in the presentation of their work. This was further accelerated with the introduction of the Angiosperm Phylogeny Group (APG) system of classification in 1998. Also, many countries have now adopted or have shown an inclination to adopt the APG classification. The APG group tries to establish a consensus on orders/families/genera of angiosperms that would reflect new knowledge about their relationships based on phylogenetic studies. Four incremental versions of this system of classification were published in succession between 1998 and 2016, and the latest one which appeared in 2016 with 64 angiosperm orders and 416 families is considered closer to phylogeny.

Despite gaining wide acceptance, the approaches in molecular taxonomy have several limitations, if not lapses. The invisibility of molecule segments taken into account in this approach is never addressed as a grave issue in the practical application of assigning/authenticating taxa by names and in delimiting species. During all these years plant recognition and identification were done visually by their morphological features. Now with molecular taxonomy, a set of DNA sequences assumes primacy in place of morphological features in the final identification of any taxon. The DNA approach focuses on the similarity or dissimilarity of a chosen sequence and monophyly. It is a fact that taxa named through natural systems with cognitive diagnostics display no bearing whether the taxa under reference are monophyletic (a group that consists of the most recent common ancestor and all of its descendants), paraphyletic (consists of the most recent common ancestor and some of its descendants) or polyphyletic (consists of unrelated organisms that lack a most recent common ancestor). The purpose of taxonomy was never to look for true evolutionary frames in the classification, but to know every visually recognizable taxon by a universally accepted scientific name. There are instances where molecular approaches go against more apparent and convincing diagnostics derived through classical approaches. For example, Malvaceae, as projected in APG II and subsequent versions, consists of 243 genera and at least 4225 species. It now includes several former segregate families such as Sterculiaceae, Tiliaceae and Bombacaceae. These families have characteristic identities which distinguish them from Malvaceae, but have now lost their identity in this molecular shower. Similarly, Cochlospermaceae is now subsumed in Bixaceae. Molecular taxonomy has not created a base on its own, but depends on the foundations generated through the classical approach. Further, the diagnostic features used in classical taxonomy have no worthwhile relevance and connectivity with the genetic sequence similarities used in the empirical evaluation of species and their placement in the cladograms. Moreover, DNA as a tool, especially in species delimitation, is not standardized and people use different markers for different families/groups. The most common types of markers used today are RFLP, RAPD and isozymes. In all probability, researchers may arrive at different results based on selected markers or the entire genome they choose to use in the analysis. This could result in different diagnoses, depending on whether one uses a sequence from the nuclear genome or the mitochondrial or chloroplast genome. The Earth Bio-Genome Project aims to sequence, characterize and create a database of genomes of all of the Earth's eukaryotic biodiversity in about 10 years. The results or the then drawn conclusions on phylogeny possibly will be different when the full genome sequence of all known plants is made available. Classical taxonomists know what they mean when they refer to a taxon, unlike molecular taxonomists who have no such objective impressions or subjective bias on any taxon they deal with, since their conclusions are machine-dependent/dictated.

One argument that often comes forth in favour of molecular taxonomy is its ability to recognize novelties at a

much faster pace. Taxonomists are alleged to be describing new species at a painstakingly slow pace. Only about 1.8 million species had received formal descriptions in comparison to the far higher expected estimated figures. It is argued that we are losing species faster than they are being discovered. The procedure of recognizing known and unknown species through molecular taxonomy is mechanical and straight forward. DNA is extracted from the type specimen of a known species which serves as the reference sample for the said species. From this DNA sample, one or several gene regions are amplified by PCR and sequenced. The resulting sequences serve as an identification tag/standard for future reference for the species from which the sample was derived. This sequence is made available through appropriate databases, together with the type specimen and its details. DNA is thus used alongside morphology to authenticate species distinctiveness from others. Once a significant sequence database has been developed, new samples can be checked against these existing sequences to assist species authentication or in new species description. The International Barcode of Life (IBOL/BIOSCAN) started building reference libraries of known species with their identifying sequences. However, the real task is to provide specific DNA sequences for all the known and named species. For example, the Botanical Survey of India herbaria possess about 27,000 type specimens, and to attach a DNA tag to each one of them is practically difficult for several reasons. Let us assume a situation that different identification tags get generated even for the types of synonyms. Then can we afford to revive these synonyms as good species? In doing so, what could be the predictable disturbance to the existing literature? With such instability of names, it would not be surprising that even specialists turn unfamiliar to the group they are known to be experts for years. What about the status of commoners in the entire process of knowing plants by botanical names, as it subverts the central concept of keeping the floras user-friendly? With these changed procedures and perceptions in the delimitations of different taxonomic groups, there might be typification and name issues affecting the International Code of Nomenclature for algae, fungi and plants (ICN). All these years, taxonomists were attempting to stabilize the nomenclature of plants and amending the rules of ICN as and when required through the publication of proposals in *Taxon*, the official journal of IAPT. It is uncertain whether such an established framework continues to regulate the proliferation of names resulting from molecular taxonomy.

P. Venu¹
M. Sanjappa^{2,*}

¹Flat# 803, Jade Block, My Home Jewel,
Hyderabad 500 049, India

²Mahatma Gandhi Botanical Garden,
University of Agricultural Sciences, GKVK,
Bengaluru 560 064, India

*e-mail: sanjappam@ymail.com