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THE CHANGING PARADIGM OF ANGIOSPERM SYSTEMATICS: SYMBIOSIS OF MORPHOLOGY AND MOLECULES*

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The past half-century has witnessed impressive advances in floristics, incorporation of new comparative data, and methods of phylogeny reconstruction and classification. Innovations in use of molecular data, tree-building algorithms, and statistical evaluations have changed the field of systematics. Rapidly accumulating DNA sequences from chloroplast, nuclear and mitochondrial genomes have provided new informative sets of data. The most significant developments of the last two decades have been the introduction of a truly evolutionary approach through use of cladistic methods, determination of new relationships based on molecular data, and the application of systematics to the problems of biodiversity conservation. In addition to the employment of new DNA data, there has been integration of data from morphology, anatomy, embryology, palynology, reproductive biology, cytology and phytochemistry. DNA barcodes hold the promise to facilitate rapid assessments of species richness in particular geographic regions or taxonomic groups, aid species delimitation, and speed up identification of cryptic species. But there is a continued need for carefully curated DNA databases from specimens correctly identified by specialist taxonomists. The future has been envisioned to be an interactive "cybertaxonomy" with dynamic online description and publication of new species. With the rich biological resources in India and the many excellent taxonomists who are intimately familiar with the regional floras and interesting systematic questions, more molecular systematic studies by the Indian taxonomists should advance our understanding of the tree of life at the global scale and offer opportunities to address many new evolutionary questions.

Keywords: Angiosperm systematics, biological classification, molecular phylogeny

Systematics is the science of organismal diversity. It entails the discovery, description, and interpretation of biological diversity, as well as the synthesis of information on diversity in the form of predictive classification systems. The fundamental aim of systematics is to discover all the branches of the evolutionary tree of life, to document all the changes that have occurred during the evolution of these branches, and to describe all species – the tips of these branches. Systematics is therefore the study of the biological diversity that exists on earth today and its evolutionary history. Systematics provides the framework, or classification, by which other biologists communicate information about organisms.

The basic activities of systematics – classification and naming – are ancient human methods of dealing with information about the natural world. This information has helped early in human cultural evolution and has led to remarkably sophisticated classifications of important organisms. We depend on many species for food, shelter, fiber for clothing and paper, medicines, tools, dyes, and for other products for life and livelihoods. Knowledge of systematics guides in discovery of resources with potential commercial importance. It focuses on mechanisms of the evolution and phylogenetic trees provide the basis of evolutionary interpretation.

Systematics provides a reference system for the whole of biology and therefore can be seen as both the most basic and the comprehensive area of biology. Systematics is basic because organisms cannot be discussed in a scientific way until some classification has been achieved to recognize them and give them names. Systematics is most wide-ranging because it gathers together and summarizes everything that is known about the characteristics of organisms, whether geographical, morphological, physiological, genetic, ecological or molecular.

1. The progressive nature of plant systematics

Current taxonomy represents a body of work that has accumulated over the past ~300 years, since the introduction of the binomial naming system by Linnaeus in the 1750s. Since the advent of Linnaean nomenclature, taxonomists have been describing and naming thousands of species every year due to the incorporation of

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new tools for discovery and exploration of lesser known areas of the planet. It is extremely modern, constantly changing and adapting, yet it has strong historical roots that always keep it connected to its past (Stuessy 2006).

Our knowledge of the biological world has changed greatly since Linnaeus, who first published his artificial sexual system in the Systema Naturae (1735). Since then, several attempts have been made to classify flowering plants. Large scale structural comparisons of plant groups led to elaborate macro-systematic classifications. Such classifications were initiated in the 1950s and were continuously refined (Stuessy 2009a).

In addition to inventorying during the past half-century, new types of comparative data of utility for plant systematics have been developed. In the 1950s, cytological data, especially chromosome number and basic karyotype, were emphasized. In the 1960s, secondary plant products (especially flavonoids), numerical taxonomy or phenetics reigned supreme. The 1970s and 1980s had focus on population-level questions with use of isozymes, that still provide good answers for solving particular types of systematic problems (e.g., hybridization). The application of computer techniques, which allowed more flexibility to handling data, were introduced in the early 1980s. A crucial change in the way biologists practice taxonomy occurred with the development of the cladistic theory and reconstruction of phylogenies, using cladograms, to infer the evolutionary history of taxa. But the exciting new data came with analyses of DNA sequences and fragments in the 1990s and that has led to change in the field.

Phenetics and cladistics stressed quantitative observations and descriptions, the latter also emphasized evolutionary relationships. Phenetic approach emphasized the use of many unweighted characters based on overall similarity, all done objectively, explicitly, and quantitatively. Numerical pheneticists developed methods for objectively grouping organisms by overall similarity in all descriptors. The availability of new electronic computing machines at the same time greatly facilitated the quantitative data comparisons. Phenetics rejected evolutionary interpretations in classification on the ground that there were too difficult and subjective (Sokal and Sneath 1963, Sneath and Sokal 1973). Hennig (1966) provided a basis for reconstructing phylogeny by manual quantitative means and used it as a basis for classification. Cladistics stressed on the use of a selected number of shared derived character states (synapomorphies) that are indicators of shared ancestry at some level in the tree of life, and shared primitive similarities (symplesiomorphic) that are not indicators of shared ancestry (Mishler 2000).

The past half-century has also witnessed impressive advances in floristic inventorying, incorporation of new types of comparative data, and methods of phylogeny reconstruction and classification. New types of data have been added to evaluate phylogenetic relationships and new methods have been employed for the assessment of data using computer softwares. Innovations in use of molecular data, tree-building algorithms, and statistical evaluations have changed the field of systematics (Stuessy *et al.* 2014). The systematists have added different data sources to evaluate relationships, and have forged off beat methods for their assessment using advanced computer softwares. When molecular systematics began its successful ascent, computer softwares were rapidly refined because much larger data sets had to be processed. The new programmes were then used in morphology with more efficiency than before. Thus, morphological cladistics too has benefited from molecular cladistics.

Over the past half-century, plant systematics has made much progress on many fronts. Despite of the frequent complaints by many taxonomists about the diminishing interest in taxonomy, there has been considerable progress and many new and exciting developments have taken place. In the past few decades, there has been a focus on discovery of new phytodiversity, publication of checklists

(Renner and Pandey 2013), revisions, monographs and Floras. More floristic and inventory activities have been initiated than at any point in the history of taxonomy. Many collaborative research programs have been developed and training programs have been organized. The greatest contribution of taxonomy to science and humanity is that taxonomists have discovered, described and classified nearly two million species.

In recent years, substantial progress has been made in observation, description, ordering and interpretation of data. The most significant developments of the last two decades have been the introduction of a truly evolutionary approach through use of cladistic methods, determination of new relationships based on molecular data and the application of systematics to the problems of biodiversity conservation.

The introduction of DNA sequence data has been era-splitting for plant taxonomy, offering access to numerous characters and statistical approaches. Thus, at the turn of the 21st century, the use of molecular data and new tree building algorithms into probabilistic approaches, led the Angiosperm Phylogeny Group (APG) to circumscribe afresh all orders and families of flowering plants and to improve to a great extent over understanding of the classification based on evolutionary relationships (Rouhan and Gaudeul 2014).

2. Taxonomy relies on data from other fields

Plant systematics is an unusual science that uses all sorts of comparative available data from organisms, yet it has no data of its own. The basis of evaluating relationships among taxa comes from comparative data. Hence, it becomes important that all types of data which have been used successfully in plant systematics be re-examined and further evaluation of their potential for future use properly assessed. Data comes in many forms and any piece of information about a taxon is potentially useful in determining and understanding systematic relationships. Based on source, Stuessy (2009b) categorized different kinds of data in to three basic types: (1) those that come from the organism itself (e.g., morphology, cytology, genetics and chemistry; (2) those that result from organism-organism interactions such as cytogenetic crossing data, reproductive biology data (e.g., pollination, animal-mediated dispersal); (3) those that come from organism-organism interactions (e.g., distribution and ecology). Without specific characters and their states, comparisons among taxa become meaningless. Hence, it becomes important that data from different disciplines are gathered, analyzed and evaluated for their taxonomic potential.

The comparative study of plant structure and morphology has always been the backbone of plant systematics. Morphology forms the basis of taxonomic descriptions and generally constitutes the most important procedure in delimiting and circumscribing taxa. In most of the classifications, both macro– and micro–morphological characters have been used and are also most commonly used in the taxonomic keys because of ease and speed of observation, documentation, and subsequent recognition and identification. Out of all the morphological features, floral traits have been utilized most (Leite *et al.* 2014). Other morphological features of taxonomic significance include stomata, trichomes, seed and fruit.

Anatomical data, both from vegetative and reproductive structures, have been employed in taxonomic studies (Carlquist 2001). In contrast to vegetative morphological features, anatomical characters have been regularly used by the systematic anatomists (Metcalfe and Chalk 1979). Anatomical characters of leaves, stems and roots could potentially provide informative data despite their usual ecological adaptations. Plant anatomy can provide valuable characteristics in phylogenetic analyses. Anatomical features, whether used directly to generate a cladogram or merely traced on an existing cladogram, can give insight into major adaptive shifts. Physiology and anatomy are closely correlated, as cell and tissue structure has changed with respect to the evolution of novel functional mechanisms, e.g., Kranz anatomy. One of the most interesting taxonomic features of stem is the variation in sieve-tube element plastids.

Embryological data have been used at different levels of hierarchy and are very valuable in delimiting or aiding in phylogenetic inference. When external morphological characters become inconclusive and misleading in plant systematics, embryological characters emerge out as relatively stable and more reliable parameters, being less prone to the adaptive stress (Davis 1966, Kapil and Bhatnagar 1991, Johri *et al.* 1992, Pandey *et al.* 2014a). Embryological data have been of immense use in resolving systematic problems when combined with other characters (Pandey 1997).

Pollen morphological features provide a wealth of characters that are important in inferring phylogenetic relationships among plants. The features of pollen grains can often be used to identify a particular taxon (Erdtman 1966). Comparative features of exine ornamentation, apertures, pollen wall structure, aggregation of pollen grains and pollen nucleus number, have provided data for systematic considerations (Walker and Doyle 1975).

Another important data source is plant reproductive biology which deals with the mechanisms and processes of sexual and asexual reproduction in plants. Many reproductive traits such as floral mechanisms, UV patterns, floral nectars, pollination syndromes, gene flow, genetic variation and breeding systems have been used in plant systematics. Knowledge of the reproductive phenomenon in plants can help in assessing the adaptive significance and homology of descriptive characters (Simpson 2010).

The period from 1965 to 1985 could be regarded as the golden age of plant chemosystematics. Both micromolecules (flavonoids, terpenoids, alkaloids, betalains, glucosinolates) and macromolecules (proteins and nucleic acids) have been employed in inferring relationships. All phytochemical characters are valuable data source and help in solving different kinds of taxonomic problems (Crawford 1990). Information on the distribution and variation in secondary metabolites in plants may indirectly indicate the functional importance of individual metabolites.

The number, structure and behavior of chromosomes are of great value in taxonomy. Chromosome data relevant to plant systematics and evolution range from simply the number of chromosomes to details of molecular cytogenetics that are at the frontiers of current research. Fluorochrome banding and fluorescence in situ hybridization (FISH) are excellent tools for chromosome identification in studies of chromosome evolution and genome organization and also to reveal the relationships between different taxa (Siljak-Yakovlev *et al.* 2013, Sousa *et al.* 2013, 2014).

Ecological data (e.g., distribution, adaptations) can be useful at different levels of hierarchy but is more useful at specific and infraspecific levels. Distributional data can provide information of patterns of spatial isolating mechanisms and can help indicate the ecological basis for this isolation.

Beginning in the early 1980s and continuing to the present, the applications of DNA studies have represented the “cutting edge” within the entire field of plant systematics. Molecular systematics provides an independent source with which to test hypothesis on the evolution of different taxa. Molecular systematic studies have led to a new and more robust supportive framework of angiosperm phylogeny. Of all the different sources of comparative data being currently used in plant systematics, the data from macromolecules, e.g., DNA sequences, DNA restriction sites (RFLPs), allozymes, microsatellites, RAPDs and AFLPs provide very informative and useful data for inferring phylogenetic relationships (Goulao and Oliveira 2013). DNA-based methods have the potential to provide the much-needed quantum leap in the speed and precision of taxonomic procedures, offering a deeper insight into the heredity material than we have ever had before.

Thus, there are rich sources of comparative data, but we must learn to evaluate it in a modern biological context.

3. Molecular data reveal much about phylogenetic relationships

Molecular systematics and the development of methods in phylogenetic analysis have revolutionized our current understanding of relationships among plants and their patterns of diversification across time, space and form. Molecular markers have opened exciting new windows to view the natural biological world. Since the dawn of the molecular revolution, studies have mainly used DNA sequence data for several applications including systematics, population genetics, and numerous other areas of ecology and evolutionary biology (Tripp and Hoagland 2013).

Plant molecular systematics has relied primarily on the chloroplast genome. This is currently changing as investigators turn to nuclear gene sequences, often to compare nuclear topologies with existing chloroplast-based topologies. At present most of the characters are from the chloroplast genes or regions (e.g., *rbc*L, *mat*K, *trn*L-*trn*F, *trn*C-*trn*D, *ndh*F, *psb*A-*trn*H, *rp*l16, *rp*s16, *trn*D-*trn*T, *trn*S-*trn*M, *psb*M-*trn*D, *trn*T-*trn*L) and nuclear ribosomal genes or regions (e.g. 18S, 26S, 5.8S and the ITS regions). The relative rate of evolution of chloroplast and nuclear genes may vary greatly among groups. For example, ndhF provides more parsimony-informative characters as compared to *rbc*L. The *rbc*L sequence data are typically used at higher taxonomic levels (family and above) in angiosperms. The *atp*B gene has a rate of evolution virtually identical to that of *rbc*L. The utility of the *atp*B-*rbc*L intergenic region has been explored primarily in angiosperms. This noncoding region may be particularly useful within and between genera. Among protein-coding regions in the chloroplast genome, *mat*K is one of the most rapidly evolving. The gene *ndh*F is located in the small single-copy region of the chloroplast genome close to the junction with the inverted repeat. The advantages of the chloroplast genome for phylogeny reconstruction include the fact that the chloroplast genome is small (typically between 120 to 200 kb), making it relatively easy to examine the entire genome. Most genes in the chloroplast genome are essentially single-copy. The conservative evolution of the chloroplast genome has also been considered one disadvantage of this molecule for inferring phylogeny, limiting its applicability among closely related species and at the populational level. A second disadvantage of cp DNA for phylogeny estimation at lower taxonomic levels involves the potential occurrence of chloroplast transfer: the movement of a chloroplast genome from one species to another by introgression. Internal transcribed spacer is called 'workhorse' of plant molecular systematics. Total length of ITS regions plus intervening 5.8S gene is fairly short and relatively uniform (600-700 bp). Mitochondrial DNA (mtDNA) analysis has had a major impact on the study of phylogeny and population genetics in animals rather than plants. Digital image-based morphometrics is being used in evolutionary biology and systematics with special emphasis on taxa with porous genome.

In recent years, DNA data has revolutionized the field of angiosperm systematics. Rapidly accumulating DNA sequences from chloroplast, nuclear and mitochondrial genomes have provided new informative sets of data. In many cases the new knowledge of phylogeny revealed relationships in conflict with the then widely used modern classifications (Cronquist 1981, Thorne 1992, Takhtajan 1997), which were based on selected similarities and differences in morphology rather than cladistic analysis of larger data sets involving DNA sequences. To alleviate this problem, a group of flowering plant systematists proposed a new classification for flowering plants, APG III (Angiosperm Phylogeny Group 2009). The APG represents a refinement and improvement of the previous systems, and not a marked departure.

Phylogenetic utility of several single- or lowcopy nuclear genes has been explored. Highly conserved coding regions (18S, 26S rDNA) are useful primarily at the family level and above, whereas rapidly evolving regions such as ITS are often best suited for comparing species and closely related genera. The mitochondrial genome has been little used in studies of plant phylogeny because it rearranges itself frequently, so that many rearranged forms can occur in the same cell. Comparing trees based on nuclear and chloroplast markers can be particularly valuable at lower taxonomic levels, providing a window into evolutionary processes that could not be achieved with either genome alone.

Molecular data have revolutionized systematics and phylogenetic research. It often focuses on mechanisms of the evolutionary process, yet its greatest challenges lie in providing broad syntheses of relationships among plants in a predictive framework. The challenge before systematists is not the generation of data but interpretation of huge quantities of genomic data that are being generated through New Generation Sequencing (NGS) methods.

Phylogenomics, the study of evolutionary relationships based on comparative analysis of genome-scale data, is indispensible in assessing diverse biological hypotheses. It has developed as an industrial-scale molecular phylogenetics, proceeding in the two classical steps: multiple alignment of homologous sequences, followed by inference of a tree (or multiple trees). Next-generation sequencing technologies are yielding genome-scale data in immense quantities. Genome sequences are now being generated at breadth (e.g. across environments) and depth (thousands of closely related strains, individuals or samples) unimaginable even a few years ago. Next-generation data offer particular promise in the study of population genomics and variation, and of the genetic mechanisms underlying how organisms respond to their environments (Chan and Ragan 2013). Relationships among taxa are inferred based on homology (inheritance from a common ancestor, commonly observed as patterns of sequence similarity) across entire genomes, whether in a comparative gene-by-gene (Chan et al. 2009), concatenated multi-gene or whole-genome approach (Rannala and Yang 2008). However, next-generation data are often incomplete and error-prone, and analysis may be further complicated by genome rearrangement, gene fusion and deletion, lateral genetic transfer, and transcript variation. It can be argued that next-generation data require next-generation phylogenomics, including so-called alignment-free approaches (Chan and Ragan 2013). In recent years, the studies adopting conventional phylogenomic approaches have yielded unprecedented insight into physiology and evolution, and have generated novel hypotheses for future exploration.

4. Morphological data- key to understanding adaptations

Morphology plays a central role in taxonomy. Morphology is broad in concept and there exist different types of morphology, e.g., developmental morphology, process morphology, biomechanics, theoretical morphology, morphometrics and adaptational (or functional) morphology (Stuessy 2003). The Linnean system, based largely on morphological features, has served biology extremely well for almost 300 years. Morphological features are largely used in discrimination of species in almost all plants. Cryptic species are exception, as they are morphologically similar but reproductively isolated. So in most of the cases morphology is the primary tool in taxonomy, but nowadays some other tools are also used in addition to morphology. There are some limitations in morphology-based taxonomy. For example, phenotypic plasticity in the characters employed for species recognition lead to incorrect identifications. Morphologically cryptic species are often overlooked. There is a lack of taxonomic keys to identify immature specimens of many species; and traditional taxonomy requires high level of expertise in any given group and is therefore restricted to specialists.

The search strategy of morphological systematics in the pre-cladistics era was either (1) to search for shared unique, homologous characters (mostly synapomorphies) or (2) to compare a large number of features and then to evaluate different likely possibilities for the systematic position of a group (Endress et al. 2000). When molecular systematics began its successful ascent, computer software was rapidly refined, because much larger data sets had to be processed. The new programmes were then again used in morphology with more efficiency than before. Thus, morphological cladistics has profited much from molecular cladistics. In early 1990s when molecular systematics developed explosively, morphology in systematics suffered. However, awareness of the necessity of comparative morphological study is growing again (Pandey *et al.* 2014b).

There should be more precise delimitation of states in characters showing quantitative variation or positional and developmental effects. Morphology is a rich source of comparative data, but we must learn to evaluate it in a modern biological context. Deep morphology, or structural plant biology in a wider sense, offers a modern program of understanding organismic shape and form (Stuessy 2006). Ecological dimensions of morphology help give real meaning of phenotypic characters (Givinish 2003). We have to know the ecological dimensions of morphology which helps give real meaning of phenotypic characters. As image archives grow, incorporating both digitized publications and images of specimens, it will be possible to harvest and analyze such visual information to understand phenotypic variation in relation to environmental conditions, population structure, morphoclines, and other factors.

Evaluation of structural evolution at all levels of systematic hierarchy, from the lowest to the highest, will be important. This should also include linkage with field studies to elucidate the interdependence of ecological and organizational constraints on plant form. This is the interface between organism and environment, and this is the site of action of natural selection.

5. Understanding phylogeny and evolution requires both morphology and molecules

The breakthrough in molecular systematics towards the end of 20th century, and its contribution to better-supported phylogenetic framework throughout the plant kingdom, is a tremendous stimulus for comparative morphology and anatomy. DNA data are extremely important for revealing phylogenetic history, but external form is what the organism uses to interact with the environment and allows survival and reproduction. The vast majority of studies in systematic biology that have used DNA sequence data have done so in combination with data from other sources (e.g., morphology, anatomy, ecology, biochemistry, behavior) as a means of answering research questions via reciprocal illumination (Tripp and Lendemer 2014). Both morphology and molecules thus need to be combined to provide a fuller view of the evolutionary processes and the resultant phylogenetic relationships.

Herbarium collections are a valuable source of genetic information. Even though the DNA obtained from the specimens is often highly fragmented and present in small quantities, it has been successfully used particularly for DNA sequencing and microsatellite analysis. Difficult and reticent taxa will be best distinguished using molecular methods in addition to morphological data, but molecular methods cannot realistically be the first or only appropriate method (Tautz *et al.* 2003). So a new approach, i.e., integrative taxonomy is needed. Integrative taxonomy has yielded a better biodiversity inventory, without in any way replacing traditional taxonomy. In addition to the employment of new DNA data, there is need to integrate data from morphology, anatomy, embryology, palynology, cytology and phytochemistry. Using multiple disciplines to solve taxonomic problems helps in avoiding failure inherent to single disciplines and increases the rigor in species delimitation (Schlick-Steiner *et al.* 2010).

Although phenetics failed to deliver at the higher levels of hierarchy, it is presently making a strong come back in providing tools for analysis of population-level DNA data such as AFLPs, microsatellites and haplotypes. The integration of morphological data (both macro and micro) with molecular data has led to an increasingly robust phylogeny of the flowering plants.

In order to understand the phylogeny and evolution, a further desirable step is to do combined analysis of morphological and molecular data (Subramaniam *et al.* 2013, Chauhan and Pandey 2014). Although in general, molecular analyses provide better resolution than morphological analyses due to availability of larger data set, a combination of morphological and molecular analyses may furnish a better understanding of taxa as compared to molecular analyses alone. Hence, the two approaches have become greatly intertwined. Morphological cladistic analyses are of prime importance if fossils are included in the search, which is indispensable for comprehensive phylogenetic studies (Endress *et al.* 2000).

All structures from DNA to the external phenotype might be considered morphology and information at all levels of the ontogenetical hierarchy tells us something about evolutionary relationships (Stuessy 2003). This large-scale application of molecular data is clearly bound to revolutionize taxonomy, but the validity and practicalities of molecular approaches to taxonomy have been subject to a variety of criticisms (Vogler and Monaghan 2006). Most recent studies can be grouped into two general approaches that are referred to as DNA taxonomy and DNA barcoding. A major distinction should be made between species identification, generally associated with the idea of 'molecular barcodes', and species circumscription and delineation, broadly referred to as 'DNA taxonomy'. Mallet and Willmott (2003) have expressed doubt that DNA taxonomy will catch on as a mandatory step for species description in all organisms, and believe that most biologists will prefer to see DNA sequence information as a supplement rather than a replacement for morphological data. We need to understand all these different levels.

The continued development of DNA taxonomy will lead to more refined sampling strategies and data analyses than those that are presently used. Based on sequence similarity, sophisticated statistical methods of grouping have already been developed and the units defined in this way have largely unknown evolutionary relevance. In future, a standard DNA taxonomic analysis will include broad sampling of the target taxa across their geographic range, followed by large-scale sequencing of representative samples for a DNA profile of the group, and algorithmic procedures for delineating species limits.

6. DNA Barcoding- key for identification of species?

The concept of DNA barcoding was proposed to rapidly and accurately identify species by using short, standardized DNA markers (Hebert *et al.* 2003). Universal key for identification of a species by running unknown DNA sequences through a DNA barcode database has gained momentum in recent years (Babbar *et al.* 2012, Ali *et al*. 2014). However, the progress has been hampered by three factors. First, it is difficult to design universal primers for the targeted homologous markers for all plants. Second, the proposed DNA markers can be easily amplified and sequenced in some families or genera but not in others. Finally, for a given DNA barcoding marker, the genetic gaps between species are distinct in some plant groups but are lacking in others. Despite these problems, DNA barcoding is applicable in plants by combining two or three DNA markers (*rbc*L, *mat*K, ITS, *trn*H-*psb*A) to make a standardized plant barcode (Hollingsworth *et al.* 2009; Gao *et al.* 2009, 2010). But there is a continued need for carefully curated DNA databases from specimens correctly identified by specialist taxonomists. DNA barcoding is limited in its potential, as it requires a near complete database of vouchers against which individuals can be placed (Moritz and Cicero 2004). It has been further argued that short piece of sequence is insufficient to represent the complexities of species level differences, while morphology is an amalgam of many evolutionary differences and is more informative (Will and Rubinoff 2004). DNA barcodes hold the promise to facilitate rapid assessments of species richness in particular geographic regions or taxonomic groups, aid species delimitation, and speed up identification of cryptic species.

DNA barcoding can provide a routine identification service for cryptic species or difficult to identify pieces of plants such as leaves, seeds, pollen, roots, rhizomes, invasive species propagules in quarantine at the border, unknown plant material in herbal products and forensic identification of plant fragments. It can relieve taxonomists of routine identification work. The ability to quickly put a name to an unknown specimen benefits not only conservationists, but also ecologists and biotechnologists involved in regulatory procedures. Consortium for the Barcode of Life (CBOL) is an international collaboration of natural history museums, herbaria, biological repositories, and biodiversity inventory sites, together with academic and commercial experts in genomics, taxonomy, electronics, and computer science.

DNA barcodes for species-level identification may, at first glance, seem to represent an appropriate use of new technology to solve an old problem of identifying and classifying the world's biodiversity. However, there are serious flaws in the rationale, methodology, and interpretation of results involved in abandoning morphological studies in favor of a narrow and wholly molecular identification system. Tripp and Lendemer (2014) advocated that the diagnoses and descriptions of taxa based solely on molecular characters should be undertaken only as a last resort, i.e., after detailed study has shown that non-molecular characters are unavailable or uninformative.

7. Taxonomy and Biodiversity

Taxonomists are well aware that time is running out to describe and document life on earth. Information gathered by the taxonomists is essential for any solution to the biodiversity crisis. The Global Taxonomy Initiative (GTI) hopes to revive taxonomy by highlighting its importance in the conservation of biodiversity. Planetary biodiversity inventories (PBIs) are global inventories of large clades of organisms predicted to contain many undescribed species, or otherwise requiring major revisions to complete their taxonomy. The time has come for taxonomists to pull together and demand the support that they need for research, education, collections and cyber infrastructure in order to meet the biodiversity challenge. The increasing demand for conservation and sustainable use of biodiversity has also added to the appetite and excitement for doing research in the field of taxonomy. These opportunities have been utilized by many in the developed world, and the results are visible in the form of reinventing the descriptive as well as the phylogenetic taxonomy. The former is being revamped through efforts involving description of all living species through launching a number of projects, and the latter involves activities like APG (Angiosperm Phylogeny Group, 2009) Phylogenomics, DNA barcoding, and Phylo Code for evolutionary classification of flowering plants (Stuessy *et al*. 2014). An ever increasing number of biodiversity databases and softwares have also been developed for collection, storage and retrieval of taxonomic information.

Taxonomists identify species in the wild, notice the risk of extinction or the arrival of invasive species, and follow the changes in biodiversity over time. They undertake inventories to survey the flora and fauna of various areas and provide advice for their protection. Managing and delivering biodiversity data has acquired great significance. Taxonomic information is being increasingly digitized and made available through several global initiatives. The importance of ecological services provided by the biodiversity are now being fully appreciated, strengthening the resolve for conservation of all species in their natural habitats.

CONCLUDING REMARKS

Plant systematics is witnessing a radical change in terms of methodologies and strategies. Due to biodiversity crisis looming large, we must make the exploration of earth's species an urgent and one of the top priorities of science. We must retain the best of traditional taxonomic theory and practice and fuse it with appropriate new technologies from DNA sequencing to cyber infrastructure. One of the side effects of incorporating molecular data into systematic studies that has become particularly pronounced during the past decade of intensified DNA sequencing is the development of a narrower view of the field of plant systematics, and this has translated into narrower training of students. There is a shift from field and greenhouse studies to the laboratory. In some cases, nearly all DNA sources are from herbaria, botanical gardens, or material collected from natural populations by others.

DNA-based studies frequently result in changes in the delimitation of well-established genera, although such changes may be inconvenient. Massive transfers of well-known, widely used, and floristically or phytogeographically significant genera resulting in their 'disappearance' should be done only with a sound phylogeny that provides convincing reasons to accept the new changes. The new or novel can only be fully appreciated or properly interpreted if viewed from the perspective of prior data or ideas (Crawford and Mort 2003).

Plant systematics is at the threshold of a major revolution in the current age of genomics and information technology (Renner and Bellot 2012). The temptation and demand to utilize massive data on nucleic acids available in databases world over through available tools of information technology is irresistible. The revolutionary advances in genetics and information management are enabling the vast amount of data generated from biological specimens to be organized, managed, and converted into useful biological knowledge. Next-generation phylogenomics could allow the use of multiple data types (e.g. genome, transcriptome, proteome and/or metabolome) in a one-stop inference of evolutionary relationships, hybrid approaches (e.g. applying k-mer- and model-based methods for more and less similar sequences respectively), or functional inference based on k-mer spectra. Like molecular phylogenetics in the 1970s, alignment-free phylogenomics has just entered a period of development, refinement and application (Chan and Ragan 2013).

We are entering into a new and exciting era in plant phylogenetics. Plastid phylogenomics will continue to be a fast and inexpensive way to flesh out the green plant clade, but the next wave is to explore the uncharted terrain of the nuclear genome. It is already on the way, as evidenced by large-scale comparative transcriptome projects and the growing number of genome sequencing projects focused on phylogenetically key species (Davis *et al.* 2014).

The future has been envisioned to be an interactive "cybertaxonomy" with dynamic online description and publication of new species. A stronger focus on publishing systematic revisions, monographs and species descriptions should be part of a strategy to alleviate the taxonomic impediment. Although traditional procedures will remain useful in many cases, taxonomy needs to be pluralistic and integrate new approaches for species delimitation. In addition to the employment of new DNA data, there is need to integrate data from morphology, anatomy, embryology, palynology, cytology and phytochemistry. E-taxonomy is another interesting field that will grow and will, therefore, make taxonomists work on the internet not only for making taxonomic information available on-line, but also for describing and naming new species, and for regular revisions on the basis of new information that becomes available. We should realize that we cannot refuse to make use of massive genomics data for taxonomy for too long, since it represents the blueprint of life.

Molecular systematics requires more equipment for data collection and analysis but now affordable in many developing countries. With rich biological resources in developing countries and taxonomists familiar with the regional floras, it will greatly advance the field of systematics and related sub-disciplines if more scientists and students in developing countries are involved in molecular systematic studies. Those interested in molecular work may consider collaborating with an established laboratory within or outside their country for getting trained in molecular techniques.

It is enigmatic but true that while much of the world's plant (or animal) diversity exists in the tropical countries, most of the modern taxonomists work in the developed, temperate countries. Developing countries like India need to, but have failed to invest sufficiently in taxonomy and biodiversity studies. This is largely because we have not been able to appreciate and explain the role of a taxonomist in developmental and economic activities, including biological conservation, management of protected areas, bioprospecting, crop improvement, mitigation of climate change, and biotechnology. India needs a major thrust in taxonomy, both in terms of infrastructure and expertise. To meet the urgent requirement, institutes and centers of excellence in taxonomy should be set up in biodiversity-rich areas such as the North-East, Western Ghats, Eastern Ghats, Himalaya and the Andaman & Nicobar islands. Taxonomy should be a more important part of educational curriculum at school, college and university levels. Critical documentation of flora that can help in monitoring the changes in future due to climate change and other anthropogenic factors is urgently needed. The Biodiversity Act should be suitably amended to facilitate and encourage taxonomic research. Finally, a network of herbaria, parks, museums, and botanical gardens should be set up in different eco-climatic zones for research and conservation.

There is tremendous amount of unfinished taxonomy, especially on some groups of organisms and in some parts of the world, that needs to be done if we want to best manage biodiversity and provide useful documents for the identification of organisms.

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