

WHAT IS THE WRITER OF A FLORA TO DO? EVOLUTIONARY TAXONOMY OR PHYLOGENETIC SYSTEMATICS?

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ABSTRACT

Plant classification and nomenclature are in a continuing state of flux and heated debate between two opposing schools—**1**) traditional taxonomists supporting “evolutionary” or “Linnaean taxonomy”; and **2**) cladists supporting “phylogenetic systematics” or “cladonomy.” While it is a multifaceted controversy that has spanned several decades, relatively little attention has been focused specifically on the ramifications for floristics. The two goals of this paper are **1**) to give special emphasis to the implications of the controversy for the writers of floras, and **2**) to provide an overview of some of the arguments in a format accessible to a diverse audience of botanists interested in floristics. We examine some of the issues we have confronted in our floristic work, discuss how we are attempting to balance the strengths and weaknesses of both approaches, and indicate what we believe is the best, albeit imperfect, approach to the writing of floras at the present time. We argue that, for both practical and theoretical reasons, a modified traditional system (binomial nomenclature, ranked hierarchies) be used in floras (allowing paraphyletic groups but eliminating all polyphyletic groups despite some nomenclatural instability). Further, these floras should incorporate information on newly discovered phylogenetic relationships (even if too preliminary, tentative, or inappropriate for nomenclatural change) and discuss these in appropriate family and generic treatments in order to facilitate as complete an understanding of plant evolution as possible.

RESUMEN

La clasificación y nomenclatura de las plantas está en un flujo continuo y debate ardiente entre dos escuelas opuestas—**1**) taxónomos tradicionales que apoyan la “taxonomía Linneana” o la “evolutiva”; y **2**) cladistas que apoyan la “sistemática filogenética” o “cladonomía.” Mientras esta controversia se ha extendido durante varias décadas, se ha prestado relativamente poca atención a las ramificaciones de la florística. Las dos metas de este artículo son **1**) dar un énfasis especial a las implicaciones de la controversia para los autores de floras, y **2**) ofrecer una visión general de algunos de los argumentos en un formato accesible a una audiencia diversa de botánicos interesados en la florística. Examinamos algunos de los resultados que hemos confrontado en nuestro trabajo florístico, discutimos como hemos intentado equilibrar las bondades y debilidades de ambos métodos, e indicamos lo que creemos que es el mejor, aunque imperfecto, método de escribir floras en la actualidad. Argumentamos que, tanto por razones teóricas como prácticas, se use en las floras un sistema tradicional modificado (nomenclatura binomial, sistema jerarquizado) (que permita grupos parafiléticos pero eliminando todos los grupos polifiléticos aunque causen inestabilidad nomenclatural). Además, estas floras deberían incorporar información sobre las relaciones filogenéticas recién descubiertas (incluso si son demasiado preliminares, tentativas, o inapropiadas para cambios nomenclaturales) y discutir éstas en la familia apropiada y tratamientos genéricos para facilitar una comprensión lo mas completa posible de la evolución de las plantas.

INTRODUCTION

Plant taxonomy is the science that deals with the *identification, nomenclature, and classification* of plants. The term plant systematics (or systematic botany) is often used synonymously with plant taxonomy (as is done here), but sometimes has the connotation of mainly using recently developed techniques or approaches such as chromosomal studies, electron microscopy, molecular biology, or cladistics to answer questions about plant relationships. From the definition of plant taxonomy it follows that the primary goals of the discipline are to:

- 1) identify and describe all the various kinds of plants;
- 2) develop a system of naming plants [e.g., International Code of Botanical Nomenclature (Greuter et al. 2000) or potentially a future version of the PhyloCode (2002)];
- 3) arrange plants with common characteristics into groups that reflect their evolutionary relationships (Lawrence 1951; Porter 1967; Radford et al. 1974; Jones & Luchsinger 1986; Judd et al. 1999, 2002).

In terms of nomenclature, the goal of plant taxonomy has been to develop a uniform, practical, and stable system of naming plants—one that can be used by both plant taxonomists and others needing a way to communicate precisely and retrieve information about plants. In the words of Stevens (2002), “The value of any naming system is how effectively it establishes conventions that allow people to communicate and to develop their ideas. ...”

Regarding classification, the goal has been to arrange plants with common characteristics into groups that reflect their relationships—in other words, to develop a scheme of classification that is useful—that conveys maximum information and has predictive value. Since the time of Darwin, a primary goal of plant taxonomists has been to reflect phylogeny or evolutionary history in their systems of classification. There are several reasons for this. One is that taxonomists want their classification system to reflect the reality of the evolutionary history of life on earth. Second, a system that reflects evolution should have maximum predictive value and usefulness (since related species should share similarities due to common descent). While this basic evolutionary approach is agreed on by virtually all botanists, in recent years there has been heated debate between two main schools of taxonomists:

1) traditional taxonomists practicing what is sometimes referred to as “Linnaean classification” (Brummitt 1997) or “evolutionary taxonomy.” Traditional or evolutionary taxonomists, while attempting to have a classification system based on evolutionary relationships, also try to reflect the amount of evolutionary change undergone by groups. In addition, they try to incorporate other goals, including practicality and stability, into the classification system (see Brummitt

1997 for a detailed discussion of traditional classification). The names Linnaean classification or Linnaean taxonomy (Stuessy 2000; Forey 2001, 2002; Nicolson 2002), are perhaps inappropriate since the system is very different from that established by Linnaeus. In its more recent version it is perhaps better called “evolutionary taxonomy” (Sanders & Judd 2000) or “evolutionary systematics” (Grant 2001b) signifying the attempt to reflect evolutionary relationships. Grant (2001b) uses the acronym TTES “to include the two subschools of traditional taxonomy and evolutionary systematics.” When considered from the standpoint of nomenclature, this is a system that incorporates binomial nomenclature (two-part scientific names consisting of a genus name and specific epithet) and a hierarchy of formal ranks (e.g., family, genus, etc.). The nomenclatural application of this viewpoint has been referred to as the “L-code” and its principles are embodied in the International Code of Botanical Nomenclature (Greuter et al. 2000).

2) cladists, whose method of constructing phylogenies is derived from the ideas of the German entomologist Willi Hennig, practicing “phylogenetic systematics” or “cladistic classification” (referred to as “cladonomy” by Brummitt 1997) based explicitly and solely on phylogenetic relationships. In other words, the overriding goal is that classification should reflect the branching patterns of evolution. It should be noted that in a clade-based classification and resulting nomenclature system, there are no formal ranks, including family or genus, and no formal binomial nomenclature (de Queiroz & Gauthier 1992; Lidén et al. 1997; Cantino 1998; Brummitt 2002). The nomenclatural application of this viewpoint has sometimes been referred to as the “P-code” and its ideas are embodied in the PhyloCode (2002).

Currently, classification and nomenclatural systems are in a state of flux between these two main opposing camps—both of which attempt to reflect evolutionary relationships. Those practicing cladistic systematics have made major contributions to our understanding of plant evolution, and have brought about some long overdue changes. In fact, some of their methodology has contributed to a well-recognized revival in taxonomy/systematics. Some of the most evident examples of this are the incredible breakthroughs in knowledge of plant relationships resulting from molecular phylogenetics. It should also be noted that there is significant variation in the extent to which various “phylogenetic” systematists follow all of the implications of the cladistic approach—most, for example, still use binomial nomenclature even though they may disagree with it on theoretical grounds. At the same time, the system of nomenclature (binomial, etc.) and hierarchical classification that has developed over the past 250 years has served and continues to serve the botanical and broader communities well. There are thus positive aspects to both of these approaches.

Because of major differences in philosophy and methodology, the classifi-

cation systems produced by proponents of evolutionary taxonomy and cladistics are often quite different. It is not unexpected then that the two conflicting viewpoints have produced a vigorous and heated debate (e.g., Nixon & Carpenter 2000), which has even been referred to as a “maelstrom” (Benton 2000). The proposed approach of phylogenetic classification has certainly not “mostly been politely accepted by the systematic community” as stated by Schander (1998). In fact, the tone of a few of the articles and discussions (on both sides of the argument) has been surprisingly impolite by the standards of modern scientific discourse, with Webster (2002) referring to the arguments as “an ideological cacophony of bombast and invective.” There is a voluminous literature on the subject, including numerous recent articles about the different taxonomic and nomenclatural approaches (e.g., Moore 1998; Stevens 1998; Diggs et al. 1999 (Appendix 6); Mishler 1999; Benton 2000; Cantino 2000; de Queiroz 2000; McNeill 2000; Nixon & Carpenter 2000; Sanders & Judd 2000; Stevens 2000; Stuessy 2000, 2001; Withgott 2000; de Queiroz & Cantino 2001; Grant 2001a, 2001b; Langer 2001; Lee 2001; Pennisi 2001; Berry 2002; Brummitt 2002; Forey 2002; Kress & DePriest 2002; Nicolson 2002; Stevens 2002; Webster 2002). Symposia and workshops have also been held (XVI International Botanical Congress—August 1999; Smithsonian’s National Museum of Natural History—March 2001; Hunt Institute for Botanical Documentation—June 2002), and a new system of nomenclature has been proposed (PhyloCode 2002). However, few authors or discussions have specifically addressed the special problems faced by writers of floras (but see Stevens 1998, Sanders & Judd 2000, and Berry 2002). This controversy is actually multifaceted, with many quite different aspects (e.g., are taxon names defined?—Stuessy 2000, 2001, de Queiroz 2000, de Queiroz & Cantino 2001; which system will ultimately be more stable?—Forey 2002) that are beyond the scope of the discussion here. In this paper we are focusing on the implications for floristics.

IMPLICATIONS FOR FLORISTICS

As writers of a flora (the *Illustrated Flora of East Texas* project—Diggs et al. in prep.; www.easttexasflora.org), we and our co-authors are faced with the question of *what type of classification and nomenclatural concepts should be followed in a large regional flora* (ca. 3,300 species or roughly 1/6 the species in North America north of Mexico). We are acutely interested in this question, because as floristicians we must translate and synthesize a variety of types of botanical research, both practical and theoretical, into a form usable by a very diverse audience—one that ranges from professional taxonomists and other scientists to lay botanists, students, and interested amateurs, many of whom are unacquainted with taxonomic methods. In fact, we believe that addressing the needs of diverse users is one of the most important tasks of floristicians. Further, developing a “general-purpose system” that effectively addresses the needs of

multiple users is often considered to be the “historical and continuing function” of taxonomy as a whole (Cronquist 1987). The answer to the question of what type of concepts should be followed varies greatly depending on who one asks. The most conservative voices would say that the traditional system of nomenclature, a ranked hierarchical system of classification, traditional families, etc., should be used due to both theoretical and practical considerations. Some would even argue that clearly polyphyletic traditional families (e.g., Liliaceae in the broad sense) should continue to be used in floras since this is a very useful and practical approach. The most extreme voices on the other side (i.e. extreme cladists) would say that no set categories should be recognized (e.g., no families, no genera; instead, only supportable clades), only monophyletic groups (= a common ancestor and **all** its descendants; Fig. 1) should be given taxonomic recognition (i.e., no paraphyletic groups should be allowed—currently many genera and families are paraphyletic; paraphyletic groups are defined as those containing a common ancestor and some, but not all, of its descendants). Further, the extreme cladists argue that binomial nomenclature should be replaced (since genera have no objective reality, there can be no generic names and hence no binomials; only clade-based names should be used). Interestingly, our previous flora (*Shinners & Mahler's Illustrated Flora of North Central Texas*—Diggs et al. 1999) was criticized by individuals from both extremes. Despite having more information on cladistics (lengthy appendix discussing the issue, discussions in numerous family synopses) than any other regional or state flora we know of (e.g., Hickman 1993; Yatskievych 1999; Rhodes & Block 2000; Wunderlin & Hansen 2000), we were criticized for not applying the cladistic approach throughout the flora. Likewise, some conservative botanists were disturbed by decisions such as lumping some groups (e.g., *Najas* into the Hydrocharitaceae), splitting others (e.g., *Senecio* into *Senecio* and *Packera*), and following an alphabetical rather than a traditional sequence (showing supposed relationships) of families and genera (a logical impossibility since a written flora is linear and evolution is a branching process). One thing to keep in mind when discussing this clash of viewpoints is the realization that any system of classification, nomenclature, and written presentation will be an imperfect reflection of the complexity represented by the evolutionary history of life on earth. In the words of Benton (2000), “phylogeny is real, classification is not.” While we now have access to increasingly sophisticated and diverse sources of data, factors such as extinction, an incomplete fossil record, and the complexity of evolutionary processes (e.g., reticulate evolution—Wagner 1954; see discussion below) will prevent us from producing completely accurate phylogenetic reconstructions. Despite these limitations, as floristicians attempting to produce a useful flora, we have to use approaches to classification and nomenclature that best reflect a diverse and complex set of needs.

It is generally agreed that the primary goal of a flora is to allow identifica-

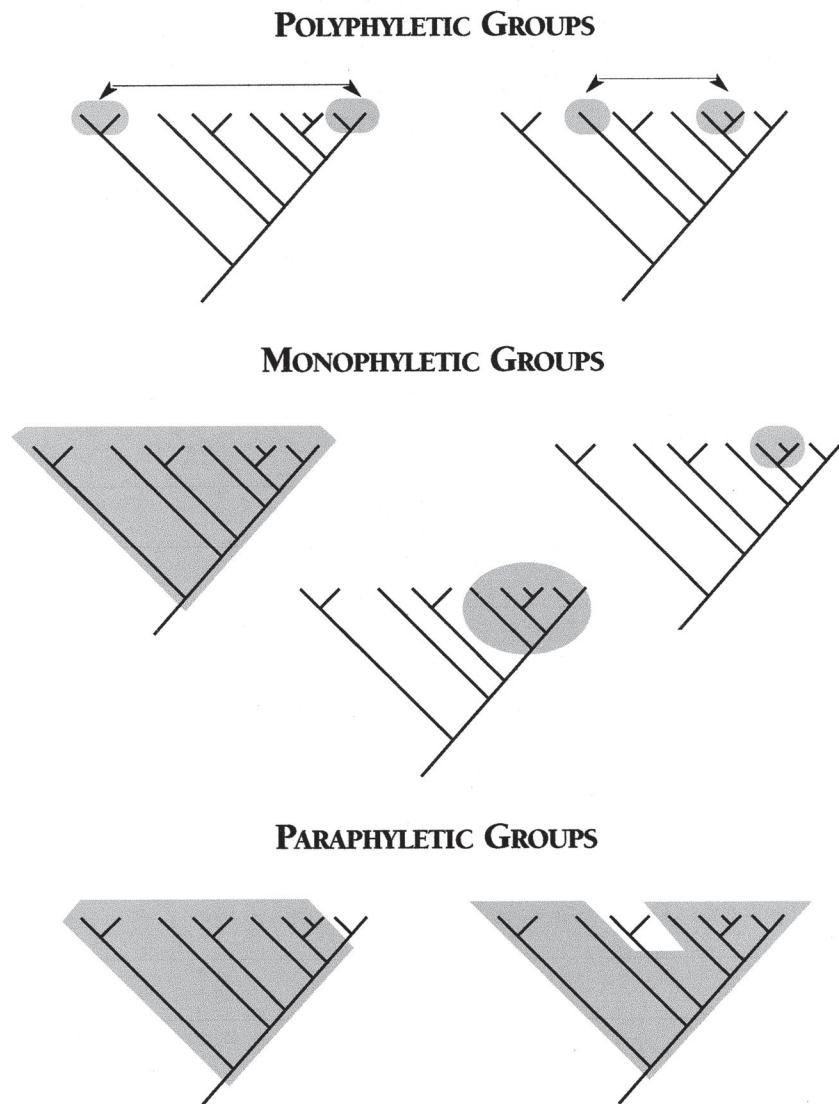


FIG. 1. Diagrammatic representation of polyphyletic, monophyletic, and paraphyletic groups (from Diggs et al. 1999).

tion of the plants treated. However, there are a number of secondary goals. According to Sanders and Judd (2000), these are: **1)** to provide entry into the systematic literature; **2)** to provide thumbnail summaries of the current state of

our knowledge (including systematic, ecological, ethnobotanical, etc.); **3**) to serve as a reference for other professionals; and **4**) to fix the concepts of taxa, especially families and genera, in the minds of users. Generally we agree with these secondary goals, and expended considerable thought and effort in applying them in our previous floristic effort (Diggs et al. 1999). We also agree with Sanders and Judd (2000) that there is a critical need for the collaboration (and probably more importantly cross-training) of floristic, monographic, and phylogenetic researchers. However, we disagree with Sanders and Judd (2000) in *how* to accomplish the fourth of their stated goals. They argue that the methods of phylogenetic classification should be applied consistently in floras (e.g., only monophyletic groups allowed, hence precluding paraphyletic families). We believe that this approach, if inflexibly applied, would hinder the primary goal (of a flora) of allowing effective identification. Further, if all aspects of the cladistic approach are followed (e.g., elimination of ranks and binomial nomenclature) in a flora, we envision significant erosion of this primary goal. The loss of many morphologically coherent and easily recognizable paraphyletic families, the discontinuity in information retrieval due to a radical change in nomenclature, the lack of effective mnemonic devices to replace such widely recognized and practically important ranks as family and genus, and instability in nomenclature (and hence identification) associated with rapidly changing cladograms are a few of the reasons for this concern.

In some cases, floristicians, for practical or historical reasons, are unable to apply even the most important recent phylogenetic discoveries in their floras. For example, the critically important Flora of North America Project, because of the long time span necessary for such a massive multi-volume work, had to adopt a standard years ago (Cronquist system of families)—hence, the Liliaceae (in the broad sense), now known to be clearly polyphyletic, is still being recognized in a forthcoming volume (with an extensive discussion of phylogeny). While we strongly agree with cladists that polyphyletic groups should be eliminated (whenever possible), we disagree with the advisability of eliminating the numerous useful and meaningful paraphyletic groups, particularly at the levels of family and genus (see further discussion below). We would add three other goals to the four (Sanders & Judd 2000) enumerated above: **5**) to address specifically the needs of diverse users (discussed above); **6**) to connect the work of monographers and other researchers to the “consumers of botanical information” (T. Barkley, pers. comm.; Barkley 2000) who need to use these discoveries; and **7**) to use systems of classification and nomenclature that allow meaningful comparisons with other floristic works. In other words, for conservation, biogeographical, ecological, etc. purposes, it should be easy to compare data such as the total number of species, the number of endemics, or the number of introduced species from flora to flora (with the realization that the comparisons will be far from perfect, but useful nonetheless). Ultimately, we somehow

hope to combine several important but not necessarily compatible approaches. We not only want to produce a useful, informative, and user-friendly flora, but also one that accurately reflects evolutionary history (i.e., be phylogenetically informative) and incorporates recent discoveries in botany.

APPROACH TAKEN IN THE *ILLUSTRATED FLORA OF EAST TEXAS*

After considerable thought, discussion with a variety of individuals, and a review of the pertinent literature, we are taking what we hope is an intermediate, albeit somewhat conservative, approach in the *Illustrated Flora of East Texas*. Our goal is to provide maximum information while retaining a practical and utilitarian framework.

Cladistic side

On the **cladistic/phylogenetic systematics side** of the argument, a number of our decisions have been influenced by the desire to increase information content and accuracy:

1) We are attempting to provide detailed information on the known evolutionary relationships of various plant groups. A tremendous amount of new information has become available recently (primarily, but not exclusively, as a result of the application of Hennigian principles to molecular data), and as much of this as possible is being included and references provided. For example, in the draft family synopsis of the Lemnaceae (duckweed family), we (Diggs et al. in prep.) have included the following statement.

Lemnaceae are tiny and extremely reduced morphologically making it difficult in the past to determine the phylogenetic relationships of the family. Kvacek (1995) suggested that the fossil genus *Limnobiophyllum* is a fossil link between Araceae and Lemnaceae, and Stockey et al. (1997), using a cladistic approach and material of *Limnobiophyllum*, concluded that *Pistia* (a free-floating member of the Araceae) plus *Limnobiophyllum* and Lemnaceae form a monophyletic group. Indeed, this linkage of Lemnaceae to Araceae goes back over 175 years (Hooker and Brown in Smith 1824; see discussion in Les et al. 2002). In addition, molecular studies have linked *Lemna* with *Pistia* (Araceae) (Duvall et al. 1993b) or more recently to Araceae subfamily Aroideae (French et al. 1995). In fact, the Lemnaceae is considered by many authorities to have evolved from within Araceae (JACK-IN-THE-PULPIT family) by extreme reduction, and it has been suggested that Lemnaceae be reduced to a subgroup within a more inclusive Araceae (Mayo et al. 1995, 1997, 1998; Stockey et al. 1997). From a cladistic standpoint, Araceae (without Lemnaceae) are paraphyletic and inappropriate for formal recognition.

Even where very preliminary information is available, we have included and referenced it in an attempt to foster a better understanding of evolutionary relationships.

2) Also on the cladistic side (and on that of most other plant taxonomists), we are rejecting all clearly polyphyletic groups, even when these are practical and of long-term or wide usage. The best example of this is the Liliaceae (lily family) sensu lato (in the broad sense). Extensive morphological and molecular data

now clearly indicate that as broadly conceived, this family is a heterogeneous mixture based on superficial similarities in flower structure (e.g., Fay et al. 2000; Rudall et al. 2000b). In fact, recent molecular studies (e.g., Chase et al. 2000) have shown that species traditionally treated in the Liliaceae should be placed in at least four different *orders*. As a result, we are recognizing 14 separate families (all previously treated in the Liliaceae) for East Texas. However, from the standpoint of usability, we are incorporating a table in the Liliaceae (narrow sense) family treatment that clearly indicates in what family the genera formerly included in the Liliaceae (broad sense) are now placed. Furthermore, in the main key to families, as many as possible of the liliaceous (broad sense) families will be clustered together and clearly indicated. Likewise, the genus *Nolina* (bear-grass) and its relatives, which have often been included in the Agavaceae (agave family), are now known to not be closely related to that family and we are excluding them. In a draft family synopsis we (Diggs et al. in prep.) say,

In the past, taxa included here in the Nolinaceae were sometimes included in a broadly conceived Liliaceae (e.g., Kartez 1999) or often in the Agavaceae (e.g., Correll & Johnston 1970; Diggs et al. 1999; Verhoek & Hess 2002 following Cronquist 1988) based on certain morphological similarities. However, recent evidence suggests that the Agavaceae and Nolinaceae are not closely related and should be recognized separately (Dahlgren et al. 1985; Eguiarte et al. 1994; Bogler & Simpson 1995, 1996; Kubitzki et al. 1998; Chase et al. 2000). Molecular evidence indicates that Nolinaceae is closely related to Convallariaceae and Ruscaceae, and some studies (e.g., Chase et al. 1995a; Chase et al. 2000; Fay et al. 2000) have suggested that the Nolinaceae should be included in the Convallariaceae. Following such preliminary studies, Judd et al. (1999), lumped the Nolinaceae into the Convallariaceae. On the other hand, Rudall et al. (2000a) and Judd et al. (2002) included the Nolinaceae in a broadly interpreted Ruscaceae. However, there has been disagreement in molecular analyses of the family and its presumed relatives (e.g., Rudall et al. 2000a; Yamashita & Tamura 2000). Since the Nolinaceae appears to be a well-defined monophyletic group (Bogler & Simpson 1995, 1996), and until the phylogeny of this complex is clarified and the nomenclature more stable, we are recognizing it as a distinct family.

Hopefully, such explanations will allow users to see that the understanding of plant relationships is still changing and improving. With such insights, we hope that non-taxonomists will be less resistant to *needed* nomenclatural changes.

3) Again on the cladistic side, when *established useful family concepts are not excessively distorted*, we are lumping small groups whose relationships have now become clear. For example, the monogeneric family Najadaceae (the genus *Najas*) is now known to be derived from within the Hydrocharitaceae (R. Haynes, pers. comm.; Shaffer-Fehre 1991; Les et al. 1993; Les & Haynes 1995; Haynes et al. 1998; Haynes 2000). Including *Najas* in the Hydrocharitaceae more accurately reflects evolutionary history, yet does not substantially modify the concept of the Hydrocharitaceae nor distort it beyond the bounds of usability. We are therefore following several recent floristic treatments (e.g., Thorne 1993; Diggs et al. 1999) in lumping *Najas* into the Hydrocharitaceae.

4) Our families, genera, and species are arranged alphabetically. Some very traditional taxonomists want “related” families placed together in the linear sequence physically required of a book. However, the complex branching pattern of evolution does not follow such a linear form and thus any linear sequence is highly arbitrary and distorts actual evolutionary relationships. An easy to use alphabetical sequence, while not reflecting relationships, at least does not distort them. In addition, an alphabetical arrangement allows quick and easy access to the material so arranged.

Evolutionary taxonomy side

On the **evolutionary taxonomy** side of the argument, a number of our decisions have been influenced by both practical and/or theoretical considerations:

1) We are continuing to use the system of nomenclature that has developed over the past 250 years (International Code of Botanical Nomenclature—Greuter et al. 2000). This (particularly the use of binomials) is an eminently useable system that addresses the needs of an audience far broader than the taxonomic community (“the consumers of botanical information”—T. Barkley, pers. comm.; Barkley 2000). We believe that eliminating it would cause great confusion among the many non-taxonomists who use plant names. In fact, it is likely that if plant taxonomy went to a specialized non-binomial, clade-based system, some separate static system of “accepted plant names” would be developed by the horticultural community or other user groups (e.g. agricultural, ecological, conservation). Such a move would both marginalize plant taxonomy and ultimately result in a nomenclatural system with much less information content than at present. This practical consideration may well be one of the most important reasons for maintaining our current system of classification and nomenclature. In fact, even those developing the PhyloCode (2002), the nomenclatural system being produced by phylogenetic systematists, have not yet come to grips with what to do regarding the naming of “species.” It is interesting to note that Stevens (2002) has argued that binomials have been used so long and so widely (across many cultures and in many contexts) because they are inherent in human perception—in other words, having such a two word nomenclature system may be built into the organization of our nervous systems. Nixon and Carpenter (2000) in a similar vein suggested that, “Our natural form of communication (even as evidenced by the common human binomial system of naming ourselves) is clarified by the use of ranks and binomials.” Likewise, anthropologist Brent Berlin (1992) noted that there are widespread cross-cultural regularities in the classification and naming of living organisms by people in traditional, nonliterate societies—these systems more closely approximate Linnaean binomials than clade-based nomenclature. Further, when the diverse users of a flora are considered, a radical shift in the system of nomenclature used seems particularly ill-advised, especially at a time when the public needs to be brought closer

to, rather than pushed further away from, an appreciation and understanding of botany. Indeed, these ideas raise questions about a “dominant” code (T. Barkley, pers. comm.) of nomenclature. Undoubtedly, a P-code will be used, but it remains to be seen how widely such a system will be accepted by the diverse users of botanical information—the L-code may continue to be used as the primary or dominant code by the user community long after a functioning P-code (presumably the PhyloCode) is finalized.

2) While many taxonomists have long realized that the traditional ranked categories (e.g., family, genus) are not used consistently and are simply human constructs (unlike species which have some biological reality), they do, however, provide important mental pegboards or mnemonic devices to allow a practical way to arrange our thinking. As Stevens (2002) has said, “Hierarchical naming systems pervade our whole language and thought.” We are thus retaining a traditional ranked hierarchical system of classification (in other words, groups of organisms arranged in a hierarchy of categories—genus, family, etc.). While there are evident problems with such a system, the “cornucopia of categories” (Colless 1977) resulting from a cladistic approach does not seem to be an overall improvement in communication, and in fact seems less suited to human mental abilities. In a clade-based system, a particular species is in dozens if not hundreds of successively larger clades—how does one choose which of these clades to use in real-world situations (e.g., floras, textbooks). This point seems to be particularly crucial to writers of floras—unless all genera or even species are to be arranged alphabetically, which would be extremely user unfriendly, some higher level organization must be agreed upon. It seems clear that some *arbitrary convention* to replace the convenience of currently used families would have to be developed for use in a completely clade-based system—in other words, someone would arbitrarily have to decide which of the innumerable clades to recognize. Otherwise, there would be no practical way to group species in floras (now grouped in families and then genera) and no groups to refer consistently to when comparing different floras, etc. In fact, for practical reasons many cladists still use traditional ranks such as family and genus (e.g., Judd et al. 2002), despite stating that “one logical step would be to eliminate ranks altogether.” Currently, only three words (e.g., Fagaceae, *Quercus alba*) are needed to communicate a great deal of information about a particular organism and these are used consistently by botanists. In our flora for example, genera are being arranged alphabetically under alphabetically arranged families. Does this mean that these families are viewed as somehow being equivalent?—of course not. They are, however, effective means of conveying information. As stressed by Stevens (2002), if we are going to be able to effectively communicate, “...conventions will be needed. To paraphrase Linnaeus, without convention, all is chaos.” As Stevens (2002) so clearly pointed out, even early botanists (e.g., Linnaeus, Bentham) were quite concerned about effective communication.

What would be the system of organization under a system of unranked clades and how could consistency (and thus communication, information retrieval, comparability, etc.) be assured in different floras, textbooks, etc.? Ultimately, some arbitrary convention (not unlike our current family system) would seem to be required. To be fair, it should be noted that the PhyloCode (2002) is not yet complete and nomenclatural conventions will have to be worked out in the future. Whatever system is ultimately settled upon, the conventions used should take into consideration a variety of factors (e.g., accuracy of information conveyed, effectiveness of communication to a broad range of users, compatibility with the organization of the human nervous system, etc.).

3) Furthermore, we are *not* rejecting paraphyletic groups (e.g., families). For example, it now seems clear (as stated above) that the Lemnaceae (duckweed family) arose from within the Araceae (arum family), which is thus paraphyletic. It seems more reasonable to us to continue to recognize both easily distinguishable families, and unambiguously state in discussions associated with both what the evolutionary relationships between the two are. Clearly the duckweeds have undergone extraordinary morphological and genetic divergence in adapting to an aquatic environment—so much so that the question of their ancestry was only recently resolved. To lump the two families and have their genera mingled in a taxonomic treatment accomplishes little and seems to result in a loss of clarity and evolutionary information. As currently recognized, both families have significant morphological coherence and thus recognition and predictive value—together, they are a mixture of two very different types of morphology. A similar example can be seen with the Cactaceae. That family has recently been shown to have evolved from within the Portulacaceae (Hershkovitz & Zimmer 1997; Applequist & Wallace 2001). Lumping the two families in a floristic treatment would only obscure the many differences between these useful and easily recognizable groups. This reflects the view of evolutionary taxonomists, who while attempting to have a classification system based on evolutionary relationships, also try to reflect the amount of evolutionary change undergone by groups (Fig. 2). Evolutionary taxonomists argue that classification is “... more than just branching patterns of evolution” (Stuessy 1997). Brummitt (2002) stressed Mayr’s (1995) observation that Darwin indicated evolutionary classification depends on two factors, descent and modification, not descent alone. To use a well known animal example, because birds are so different from other vertebrates (e.g., fly, have feathers, etc.), they are treated as a different class of vertebrate even though they are known to have evolved from within the paraphyletic class known as reptiles (Fig. 3). From the practical standpoint, there are numerous other useful and evolutionary meaningful paraphyletic groups. Examples include the Araceae, Capparaceae, Clusiaceae, Moraceae, Portulacaceae, etc. Radically changing their circumscription (e.g.,

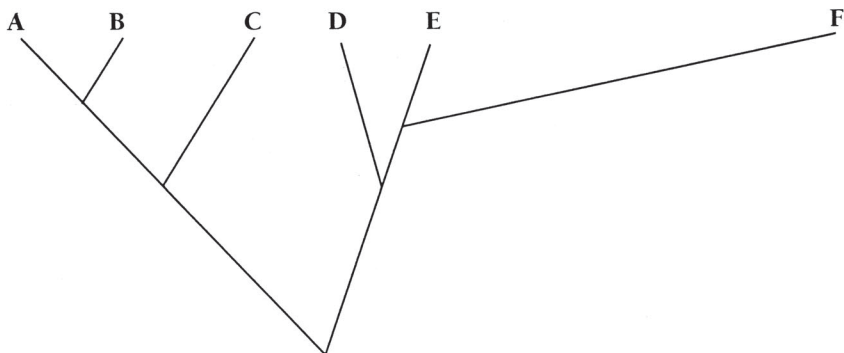


FIG. 2. Phenetic distance diagram; horizontal distance between species indicates phenetic difference. Note that species F, while most closely related phylogenetically to species E, is quite different in terms of phenetics (from Diggs et al. 1999).

adding Cactaceae to Portulacaceae, Podostemaceae to Clusiaceae, or Lemnaceae to Araceae) results in confusion and a loss of information. This risk of confusion is particularly problematic if the same name is variously used to include quite different sets of species (e.g., Portulacaceae in the narrow sense or in the broad sense including Cactaceae). The risk of a nomenclatural “train wreck” (Stevens 2002) is a troubling possibility. Very different uses of the same names “will be decidedly unsettling for society and perhaps damaging for our discipline” (Stevens 2002). Unfortunately, taxonomists have long had the reputation of changing names without regard for the implications, and great care needs to be taken to avoid non-essential changes. Grant (2001b) stressed that splitting up paraphyletic groups (e.g., genera such as *Gilia* or *Linanthus*) obscures relationships and multiplies generic names where one would be sufficient. Does the splitting up of recognizable and well known genera really best serve the broad constituency of users (keeping in mind that professional taxonomists are a small fraction of the users of scientific names)? Changes in classification at the generic level are particularly significant because of the resulting changes in scientific names.

Further, Brummitt (1997, 2002) has argued that paraphyletic groups are inevitable. He goes on to say that any genus “must have originated from a species in another genus, which is thus paraphyletic.” The same logic applies at other levels in the hierarchy, including the species level. Species, unlike other categories in our hierarchical system of classification, have some objective biological reality (e.g., Rieseberg & Burke 2001). However, if a small subgroup of a species differentiates or specializes enough to become a distinct entity, the original species is thus rendered paraphyletic even though it may still be a reproductively isolated or otherwise distinct group. Species can be excluded by defi-

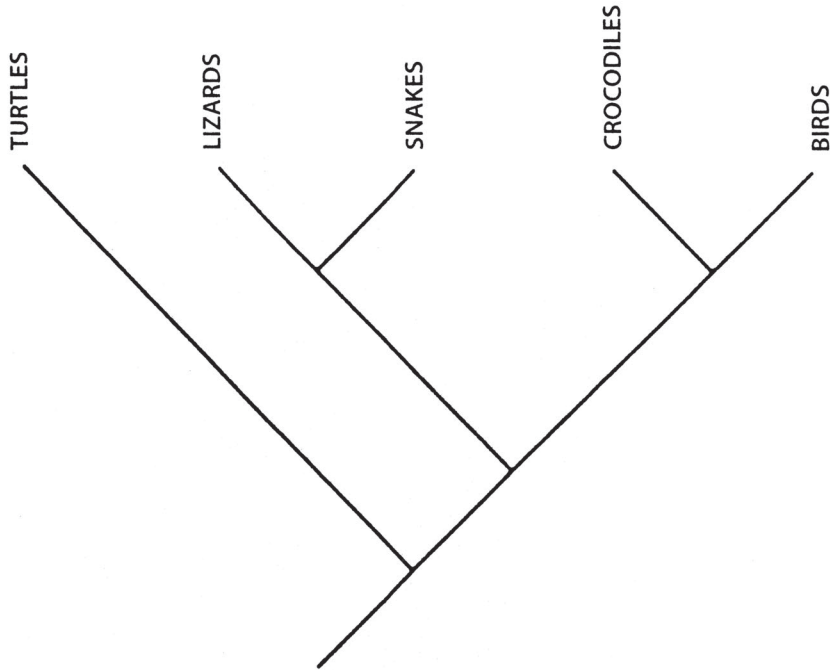


FIG. 3. Dendrogram showing relationships of some vertebrate groups. Note the paraphyletic nature of the "Reptilia" (from Diggs et al. 1999).

tion as not being paraphyletic (Sanders & Judd 2000) as done by some cladists, but in reality, by standard use of the term, they are often paraphyletic (see Mishler 1999, 2000). As Brummitt (2002) noted, the abandonment of species "seems to me to be a necessary logical extension to abandoning all other ranks" (Brummitt 2002). Further, Rieseberg and Brouillet (1994) argued that based on the modes of speciation known to occur in plants, paraphyletic species are common. In the words of Sosef (1997), "When a single diaspore [e.g., seed] accidentally reaches an isolated habitat and its offspring gradually changes (a linear process) and produces a new species, nothing 'happens' to the parent species." The new species thus renders the unchanged previous species paraphyletic. Ultimately, paraphyly thus seems unavoidable. An excellent example of this problem can be seen in the California tarweeds (genus *Raillardiopsis*) and the Hawaiian silverswords (genera *Argyroxiphium*, *Dubautia*, and *Wilkesia*) in the Asteraceae. It now appears (Baldwin et al. 1991) that *Raillardiopsis* (which had previously been considered a "phenotypically conservative genus of two nearly identical species") was the "ancestral genetic source" for the endemic and extremely morphologically divergent Hawaiian silversword alliance. *Raillardiopsis*

is thus clearly paraphyletic, even though its two species are “nearly identical.” When taken to its logical extreme, the failure to recognize paraphyletic groups would require the rejection of many useful groups (e.g. tarweeds). In animal taxonomy, this means the rejection not just of the group Reptilia (which gave rise to birds), but also Amphibia (which gave rise to reptiles), and Pices (which gave rise to Amphibia). Anyone understanding the basics of evolution realizes that fishes gave rise to amphibians. Does that make the class Pices any less useful a concept? Likewise, the capers (Capparaceae) gave rise to the mustards (Brassicaceae)—both families are still useful and meaningful concepts that can help us understand evolution and organize our thinking. Cronquist (1987) stressed the need for paraphyletic groups, indicating that both evolutionary relationships and the amount of evolutionary divergence among taxa is important. He said that “the reasons for this belief are rooted in the historical and continuing function of taxonomy as a general-purpose system of classification that can be used by all who are concerned with similarities and differences among organisms”—in other words, diverse users of botanical information. While we believe it is critically important for paraphyletic groups to be clearly distinguished from monophyletic groups, the usefulness of paraphyletic taxa (e.g., effective communication, recognition of divergence, morphological similarities, etc.) seems to be an important consideration.

4) Additionally, there are many cases where it is not yet clear what should be done cladistically. Thus in these cases we are retaining traditional usage until more information is available. For example, it is very likely that such families as the Lamiaceae (mint family), Verbenaceae (vervain family), and Scrophulariaceae (figwort family), as traditionally conceived, will have to be changed substantially. However, if we had to finalize treatments of these families today for our flora (which fortunately does not have to happen since these dicot groups will be treated in Vol. 2 of the *Illustrated Flora of East Texas* to be published in 2008), we would probably follow the traditional circumscriptions and accompany them with substantial explanations. The reason is that adequate research has not yet been done on these groups to provide answers that are definitive enough to warrant major changes in classification and nomenclature. In the words of Berry (2002), “it will be some time before our sampling of organisms at the molecular level will be good enough that we can get an adequate idea of relationships across the entire span of biological diversity.” Further, it does not seem desirable that classification (and nomenclature) should change with every new cladistic discovery—do we really want nomenclature that “depend[s] rigidly on the particular cladogram favoured at the moment” (Benton 2000)? Indeed, Sanders and Judd (2000) discuss the criteria for accepting revised classifications. Before making major nomenclatural changes, there should be substantial taxonomic evidence, to avoid more of the numerous ex-

amples where initial cladistic hypotheses have proven to be wrong. For example, in the past, some authorities have suggested major changes in family circumscription based on preliminary information (e.g., lumping the Apiaceae (carrot) and Araliaceae (aralia) families—Judd et al. 1994; Zomlefer 1994), only to have more detailed work (Plunkett et al. 1996 [1997]) clarify the situation and indicate that the families should be maintained in nearly their traditional circumscriptions. According to Plunkett et al. (1996 [1997]), the approach taken by Judd et al. (1994) “hides rather than resolves the difficulties in Apiales.” Likewise, Downie et al. (2001) did not lump the Araliaceae. Another example is the genus *Trillium*—it has often been treated in the Liliaceae in the broad sense (e.g., Correll & Johnston 1970) or based on early phylogenetic analyses in the Trilliaceae (e.g., Zomlefer 1996; Tamura 1998d; Judd et al. 1999). However, more recent phylogenetic analyses (e.g., Rudall et al. 2000b) indicate that it belongs in the Melanthiaceae. There are also instances where the best and most recent evidence conflicts. A number of molecular studies have suggested that Burmanniaceae (previously considered to be related to Orchidaceae) is in the Dioscoreales and thus more closely related to such families as Dioscoreaceae and Nartheciaceae than to Orchidaceae (which is in order Asparagales) (Chase et al. 1995b; Caddick et al. 2000, 2002; Chase et al. 2000). In contrast, other recent molecular research including more genera than previously sampled, indicates that the family (minus the superficially similar but unrelated genus *Corsia*) plus Thismiaceae is in a relatively isolated position “not closely aligned with either the Dioscoreales or the Orchidaceae” (Neyland 2002). Writers of floras are thus faced with having to judge which cladistic studies to accept and when there is enough evidence to use the new discoveries in floristic treatments. At the same time, writers of floras must avoid the instability and confusion that would result from changing classification and nomenclature with every new study published. Furthermore, recent tests (Grant 2001a) of the accuracy of cladograms when compared with known phylogenies (e.g., domesticated and experimental plant groups with known pedigrees), raises questions about basing classification and nomenclature solely on cladistic methodology. Grant (2001a) demonstrated that the “cladograms of the four plant groups [tested] all differ in significant details from the known pedigrees.” Particularly important is his following point: “It is also recognized by all evolutionary systematists and most cladists that reconstructed phylogenies are unverified hypotheses. Some cladists, however, seem to regard their cladograms as real phylogenies.” He (Grant 2001b) also indicated that “Molecular cladograms are very good indicators, but we should not lose sight of the fact that the groupings they indicate are molecular clades, not taxa.” A recent paper by Rydin et al. (2002) on Gnetales is particularly telling in this regard. Depending on which molecular analysis was used, the phylogenetic position of Gnetales differed significantly. According to Rydin et al. (2002), “It is becoming increasingly clear that the understanding of

molecular evolution and its impact on phylogenetic studies is poor. Nucleotide data alone might not be able to solve phylogeny and evolution of this ancient, once rapidly evolving group, and attempts to do so should include a comprehensive taxon sampling and several genes. Molecular data can definitely be misleading, and by ignoring that, science will not progress." From the standpoint of a floristician, while recognizing the obviously valuable contributions made by molecular systematists and cladists, careful thought must be given to avoid accepting major, sometimes disruptive (and occasionally incorrect) classification and nomenclature changes prematurely.

5) Finally, we are *not* accepting some aspects of phylogenetic classification (particularly strict monophyly—sometimes and perhaps better referred to as holophyly) since there are **serious theoretical problems** that make it at least partially incompatible with the reality of the natural world (however, see Freudenstein 1998 for an opposing viewpoint). Brummitt (2002, pers. comm.) has stressed the importance of these theoretical considerations, and in terms of the implications for floristics, these are perhaps as important as or even more important than the purely practical considerations. **One of the most serious problems** (referred to as a "fatal one" by Stuessy 1997) is that cladistics uses only branching information in phylogeny. In contrast, evolution is a complex process including such phenomena as asexual reproduction, progenitor-derivative species pairs, lateral gene transfer, polyploidy, and reticulate evolution (the latter resulting from hybridization between species and subsequent speciation in the offspring) (Rieseberg & Brouillet 1994; Sosef 1997; Stuessy 1997). These complexities cannot be accommodated in a classification system requiring only strict monophyletic groups and dichotomous branching. In the words of Stuessy (1997), "... simple dichotomous branching diagrams cannot do justice to the real world of higher plant phylogeny." An excellent example can be seen in the reticulate evolution of the fern genus *Asplenium* as discussed in the classic paper by Wagner (1954). In this case, the hybrids between two parental species become reproductively isolated (and thus constitute a separate new species). Another example can be seen in the Triticeae (*Elymus*, *Hordeum*, *Secale*, *Triticum*, and their relatives; Poaceae). This tribe has an extremely complex evolutionary history involving hybridization, polyploidy, and reticulate evolution (Barkworth 2000; Mason-Gamer & Kellogg 2000). Both of these examples emphasize that some evolutionary relationships are simply impossible to reflect accurately in a system requiring strict monophyly and only dichotomous branching. As Brummitt (1997) indicated, "No matter how much we may long for all our taxa to be monophyletic, if we are considering the whole evolutionary process, it is a logical impossibility." Another way of stating the problem is that simple branching patterns are unable to reveal all significant dimensions of phylogeny (Stuessy 1997).

A second theoretical problem with strict monophyly is that "only the tips

of evolutionary branches can be classified" (Meacham & Duncan 1987) in such a system, and "Species at the interior nodes of the tree must remain unclassified." Not including ancestral species, some of which may well have survived to the present, seems untenable. However, including them leads cladists insisting on strict monophyly (holophyly) down the path of the "telescoping" or "snow-ball" effect (also known as the "taxonomic black hole") where more and more organisms have to be included in a futile attempt to reach the mythical (and impossible to reach) strictly monophyletic group (Sosef 1997; Brummitt 2002; but see Stevens 1998 and Sanders and Judd 2000 for a different viewpoint). Ultimately, the whole Tree of Life (2002) would have to be included in one giant monophyletic group. In the words of Brummitt (2002), "If we are classifying all the products of evolution, i.e., the whole evolutionary tree of life, every taxon we recognise must make another taxon paraphyletic. That is a simple logical fact. It is obvious to most people that if you cannot have paraphyletic taxa, you cannot have a classification showing anything beyond one original species, genus, family, etc." He points out that *if ranks are to be used* (which seems essential from the standpoint of practicality), paraphyly is unavoidable (Webster 2002 referred to this as "Brummitt's Paradox"). Thus, there is a "fundamental incompatibility between Linnaean classification and a system of monophyletic taxa, or clades" (Brummitt 2002). In other words, including all extinct species would mean that no monophyletic groups (or only one huge one) could be recognized. From this standpoint, "extinction [and our lack of knowledge about extinct species] is the saving grace of phylogenetic systematics" (T. Barkley, pers. comm.). *Importantly, "Brummitt's Paradox" means that simply converting cladograms into Linnaean nomenclature is impossible.* Ultimately, this means that in order to have strict monophyly, phylogenetic systematists must develop a rankless system such as the PhyloCode. While some modern phylogenetic systematists continue to recognize families for practical/pedagogical reasons (e.g., Judd et al. 2002), if carried to its logical conclusions, cladistics would mean that these families (particularly if extinct taxa are considered) would be telescoped into ever larger groups.

A third related theoretical problem demonstrates that a strictly monophyletic system *using Linnaean ranks* is incompatible with evolution (Brummitt, pers. comm.). As Brummitt (2002) indicated, "...I think we all understand that evolution has continually been throwing up greater and greater diversification of plants and animals, and yet the cladistic idea of classification requires that all successive descendant groups have to have lower and lower taxonomic rank. Something which has evolved from within one genus must have a rank lower than genus. Is this view of taxonomy really a sensible idea? How can we apply lower and lower ranks when evolution is producing wider and wider variation? In a clade-based classification you can go on extending your clades as evolution progresses *ad infinitum*, but if you are using a traditional taxon-based classification you can't keep on giving them lower ranks." Without paraphyly, the use

of ranks in a monophyletic system therefore is simply not workable (hence the advocacy of a rankless Phylocode by some cladists). This problem seems to clearly indicate the logical impossibility of a rank-based, strictly monophyletic system.

A fourth theoretical problem is that our current methodology of obtaining phylogenetic trees is based on a series of assumptions and indirect evidence (e.g., character polarity, choice of outgroups, etc.) (Stuessy 1997), as well as mathematical algorithms (e.g., parsimony) that result in trees that “are almost always inappropriate as phylogenetic hypotheses in any but the most general sense” (Zander 1998). Zander (1999) further indicated that, “Selecting one phylogenetic hypothesis of several or many reasonable alternatives as ‘best’ and presenting it as a reconstruction cannot provide a probabilistic or dependable basis for action.” Is the pursuit of the shortest tree the ultimate goal of systematics? The answer seems clearly to be no, since there are well-documented non-parsimonious pathways of evolution (Stussey 1997). Thus, totally tying classification and nomenclature to such a system seems problematic. A final concern that follows from this is that the current classification and nomenclature system is independent of a particular approach. As stated by Jørgensen (2000), “A problem inherent with the system proposed by Cantino & de Queiroz (2000) [PhyloCode] is that their nomenclature depends upon a specific way of taxonomic thinking, i.e., nomenclature is ruled by the taxonomic system. This probably reflects that they are as convinced of their taxonomic system as Linnaeus was of his, but, please, at least consider the possibility that new taxonomies may evolve. Should we then change the nomenclatural system each time?”

FURTHER IDEAS AND DISCUSSION

The following ideas and quotes seem to provide substantial insight into the controversy. Because of both philosophical and practical implementation problems, Brummitt (1997) pointed out that while the controversy should be debated, it seems unlikely that “Linnaean classification” will soon be abandoned. Brummitt (1997) suggested that both a “Linnaean classification” system and a clade-based phylogeny are desirable because they have different functions. He argued that both be allowed to exist side by side and that the nomenclature of the two should be easily recognized as different (Brummitt 1997). In summarizing his ideas he stated, “... we should not follow traditional practices just because they are traditional, but neither should we adopt new ideas just because they are new. We need to understand the possibilities and appreciate the different objectives and functions of the different options. In the meantime, it seems to me and to many others that the compromise of maintaining Linnaean classification but trying to eliminate paraphyletic taxa is nonsensical and should be abandoned before any more damage is done to existing classifications and nomenclature.” Lidén et al. (1997) indicated, “If applied consistently, Phyllis [= Lidén et al. term for

nomenclatural application of cladistics] will cause confusion and loss of information content and mnemonic devices, without any substantial scientific or practical advantage.... any attempts to make Phyllis formal would be disastrous. We can find no conclusive, valid arguments against keeping the body of our current system intact." Sosef (1997) stressed the same idea saying, "The quest for monophyletic taxa and the splitting of former paraphyletic ones should halt immediately, as they unnecessarily deteriorate classifications which will often prove to be valid."

An interesting point was also made by Stuessy (1997) when he said, "... in this urgent climate of seeking to inventory the world's biota (Anonymous 1994), and requesting funds from the rest of society to do so, it would be highly counterproductive to simultaneously recommend whole-scale change of names of organisms for any reason." In the words of Paul Ehrlich (2002), who was stressing the need for taxonomists to focus on conservation activities, "Others spend their time trying to replace the functional Linnaean system for general communication about organisms with one based on estimates of times of phylogenetic divergence; a sillier enterprise is hard to imagine. ..."

While recognizing it is not perfect, Wheeler (2001, and quoted in Forey 2002) noted that Linnaean nomenclature "is stable enough to say what we know, flexible enough to accommodate what we learn; independent of specific theory, yet reflective of known empirical data; compatible with phylogenetic theory, but not a slave to it; particular enough for precise communication, general enough to reflect refuted hypotheses."

While strongly supporting a cladistic system, Welzen (1998) also noted that a compromise between the two types of classification is impossible. He also understood that because of practical reasons it is impossible to abandon Linnaean classification "... because too few cladograms are available to replace the existing system with a complete phylogenetic classification. Moreover, quite a few cladograms will not be that trustworthy due to the many homoplasies [result of convergent evolution] that have evolved; they will therefore, provide an unstable classification at best." Welzen (1997) went on to say, "I think, therefore, that the best solution is to choose the second option that Brummitt (1997) provides in his paper, namely, 'retaining Linnaean classification, with paraphyletic taxa, but developing alongside it an independent clade-based dichotomous system with its own separate nomenclature.'" Recently, Brummitt (2002) indicated that, "If people insist on monophyly, the clade-based PhyloCode will provide a logical solution. If they want to use the traditional ranks, the answer is very simple: recognise paraphyletic taxa." Brummitt (1997) made what seems to be a very reasonable suggestion: "Our task is to produce an optimally practical classification, and indicate which genera have evolved from which other genera, which families from which other families, and so on."

Indeed, recently it seems to have become clearer that two separate systems

will be necessary (Cantino 2000; Brummitt 2002). Years ago, Woodger (1952, and quoted by Brummitt 2002) concluded that, "The taxonomic system and the evolutionary phylogenetic scheme are quite different things doing quite different jobs, and only confusion will arise from identifying or mixing them." Similarly, it has been argued more recently that to attempt to apply cladistic rules (e.g., elimination of all paraphyletic groups) on the traditional Linnaean system is a logical impossibility (Brummitt 2002) or at minimum highly detrimental (see discussion above). According to Brummitt (2002), "I believe there is no middle way which will combine universal monophyly with formal Linnaean ranks, and this is now increasingly being realized." However, while it is becoming more widely recognized that the two systems are incompatible (but see Stevens 2002), there is clearly value in having a strictly phylogenetic system of classification. It would thus seem that the most reasonable course for the near term would be to allow the concurrent existence of two separate systems—Linnaean and phylogenetic. The Linnaean system would retain hierarchical ranks, binomial nomenclature, and paraphyletic taxa, while the phylogenetic system (e.g., PhyloCode) would recognize monophyletic clades (but have neither ranks, binomial nomenclature, nor paraphyletic taxa, and possibly not even species). Because of practical considerations, the Linnaean system will probably continue to be the "dominant" system used (nearly exclusively) to communicate information about plants by scientists outside of systematics (e.g., ecologists, horticulturalists, conservationists, etc.) and by the general public. The phylogenetic system will make contributions among systematists and others attempting to further understand the evolutionary history of life on earth.

SUMMARY

Where does all this leave the writers of floras? We would argue that a modified traditional system (binomial nomenclature, ranked hierarchies—L-code) be used in floras (allowing paraphyletic groups but eliminating all polyphyletic groups despite some nomenclatural instability), and that these floras (and this is a critical point) should also incorporate newly discovered information on phylogenetic relationships. In order to facilitate as complete an understanding of plant evolution as possible, this new information should be briefly discussed/summarized in appropriate family and generic treatments even if too preliminary, tentative, or inappropriate for nomenclatural change (e.g., that would result in the loss of meaningful paraphyletic taxa).

In summary, in the *Illustrated Flora of East Texa*, we are thus attempting to reflect some of the many contributions and insights from "phylogenetic systematics," while retaining the practical benefits of an "evolutionary taxonomy" framework. As indicated above, no system will be a totally accurate representation of the complexity of the evolutionary history of life on earth. We believe, however, that by reflecting both evolutionary relationships and the amount of

evolutionary change, while maintaining a flexible approach punctuated with practicality, that a classification and nomenclature system useful to a broad audience, including non-taxonomists, can be achieved. We agree fully with Berry (2002) who said, "there are many users of scientific names—myself included—who are interested in both floristic inventories and evolutionary relationships, and nomenclatural stability as well." Ultimately, writers of floras need to present information accurately (i.e., reflect evolution) *and* in ways that can be used—that allow effective communication and identification, promote information retrieval, and are useful comparatively (e.g., in conservation assessments, to evaluate levels of endemism, to determine levels of introduced exotics, to form the basis of biogeographical studies, to do ecological surveys). All of these uses depend on having a unit (species) that can be meaningfully compared and classification and nomenclatural systems that allows effective communication. Taxonomic botanists are thus faced with the challenge of working toward systems that make such communication and comparisons possible (Berry 2002). Writers of floras, in particular, as the translators of botanical information to a wider audience, are uniquely faced with a difficult task—to apply the evolving concepts of modern systematic botany to floristics in a way that allows modern floras to be both accurate and useful. It is hoped that this article will stimulate discussion among those involved in or interested in the writing of floras.

ACKNOWLEDGMENTS

We would like to thank Ted Barkley for helpful discussions and comments. We also thank Richard Brummitt, Verne Grant, Roger Sanders, and Rudolf Schmid for their extremely constructive reviews which improved this paper.

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