



**Second Meeting of the International Society for  
Phylogenetic Nomenclature  
Yale University  
New Haven, June 28 – July 2, 2006**

**PROGRAM AND ABSTRACTS**

**ORGANIZING COMMITTEE**

**Nico Cellinese**, Co-Chair, Yale University  
**Walter Joyce**, Co-Chair, Program Officer, Yale University  
**Michael Donoghue**, Co-Host, Yale University  
**Jacques Gauthier**, Co-Host, Yale University  
**David Baum**, University of Wisconsin, Madison  
**Philip Cantino**, Ohio University  
**Michel Laurin**, CNRS, Paris  
**Kevin de Queiroz**, Smithsonian Institution

**CONTACT INFORMATION AT THE MEETING**

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### **OFFICIAL CONFERENCE VENUE**

On site registration, regular sessions, symposia, and the ISPN business meeting will be held in **Linsly-Chittenden Hall** at 63 High Street, New Haven. This beautifully restored venue is situated on Yale University's Old Campus and thus easy walking distance from all downtown accommodations recommended by the ISPN Program Committee (see map for directions).

### **ICEBREAKER**

The icebreaker will be held on June 28, 2006 starting at 7:00pm at **BAR** on 254 Crown Street, New Haven (see map for directions).

### **TOUR OF THE PEABODY COLLECTIONS**

Conference attendants will have the opportunity to follow behind the scenes tours to a number of Peabody Collections during the late afternoon on July 1, 2006. Highlights include O.C. Marsh's historic dinosaur collections and modern storage rooms in the new Environmental Science Facility. The Peabody Museum is located at the northern end of Yale's Campus at 170 Whitney Avenue, a 20 to 30 minute walk from all downtown localities. As an alternative to walking, buses will be provided to transport attendants from the conference venue to the museum.

### **BANQUET DINNER**

Following the tours to the Peabody collections, an informal banquet dinner will be held under the dinosaurs in the Great Hall of Evolution at the **Peabody Museum** on the evening of July 1, 2006. **Jacques Gauthier** (Yale University) will give an informal speech for the occasion.

## WEDNESDAY JUNE 28, 2006

5:00 – 7:00 **LINSLEY-CHITTENDEN HALL:** REGISTRATION  
7:00 ICEBREAKER

## THURSDAY, JUNE 29, 2006

8:15 – 12:30 REGISTRATION  
8:15 – 9:00 BREAKFAST

### OPENING SESSION

9:00 M. DONOGHUE: Welcome  
9:15 K. DEQUEIROZ: Developments since the First ISPN Conference  
9:30 D. HILLIS: INTRODUCTORY LECTURE: Why is taxonomy lagging behind the rest of biology in the phylogenetic revolution?  
10:30 COFFEE BREAK

### GENERAL SESSION

**CONVENER: WALTER JOYCE**

11:00 M. LAURIN: Representation of the ISPN and the success of the PhyloCode  
11:30 J. GAUTHIER & T. TSUIHIJI: Phylogenetic names and morphological characters: Tetrapoda and necks  
12:00 T. M. KEESEY: A mathematical approach to clade definitions, using order relations on sets of organisms  
12:30 LUNCH BREAK  
2:00 I. N. SARKAR & D. P. REMSEN: Enabling biological knowledge integration through scientific nomenclature  
2:30 S. L. RICHARDSON: Asexual species in limbo: can the PhyloCode accommodate the naming of asexual organisms?  
3:00 J. REVEAL: Suprageneric names: difficult under any code  
3:30 COFFEE BREAK  
4:00 W. JOYCE & J. PARHAM: Experiences from organizing a committee for the naming of turtle clade names  
4:15 DISCUSSION

## FRIDAY JUNE 30, 2006

8:15– 10:00 REGISTRATION

8:15 – 9:00 BREAKFAST

### **SPECIES SYMPOSIUM**

**Conveners: David Baum & Benoit Dayrat**

9:00 M. HABER: The virtue of dual ambiguity in species names.

9:30 Y. BERTRAND: Species names: The best of all possible words?

10:00 D. A. BAUM: Nomenclatural implications of treating species as ranked clades

10:30 COFFEE BREAK

11:00 J. CLARKE, P. CANTINO, B. DAYRAT, & K. DEQUEIROZ: Species in a system of phylogenetic nomenclature: A new solution. Part I.

11:15 B. DAYRAT, P. CANTINO, J. CLARKE, & K. DEQUEIROZ: Species in a system of phylogenetic nomenclature: A new solution. Part II.

11:30 DISCUSSION

12:30 LUNCH BREAK

### **BUSINESS MEETING**

**Convener: Philip Cantino**

2:00 BUSINESS MEETING

3:30 COFFEE BREAK

### **SPECIES SYMPOSIUM**

**Conveners: David Baum & Benoit Dayrat**

4:00 DISCUSSION

## **SATURDAY JULY 1, 2006**

8:15 – 10:00 REGISTRATION

8:15 – 9:00 BREAKFAST

### **IMPLEMENTING PHYLOGENETIC NOMENCLATURE SYMPOSIUM**

**Convener: Philip Cantino**

9:00 P. E. BERRY: Phylogenetic nomenclature through consensus rather than codification: Setting the keel for stormy seas ahead

9:40 C. P. SERENO: Unitary taxonomy considered

10:20 COFFEE BREAK

10:50 P. D. CANTINO AND K. DE QUEIROZ: Precedence, emendations, and recent additions to the PhyloCode

11:30 D. MARJANOVIC: The ivory tower: How can we win the necessary acceptance for phylogenetic nomenclature?

12:10 DISCUSSION

12:30 LUNCH BREAK

### **DISCUSSION SESSION**

**Convener: Julia Clarke**

2:00 DISCUSSION

3:30 COFFEE BREAK

4:00 DISCUSSION

### **EVENING EVENTS**

#### **PEABODY MUSEUM OF NATURAL HISTORY**

6:30 PEABODY COLLECTION TOUR

7:15 RECEPTION & BANQUET

## SUNDAY JULY 2, 2006

8:15 – 10:00 REGISTRATION

8:15 – 9:00 BREAKFAST

### **PHYLOINFORMATICS SYMPOSIUM**

**Conveners: Michael Donoghue & Nico Cellinese**

9:00 M. DONOGHUE: TBA

9:30 D. S. HIBBETT: Automated phylogenetic taxonomy and prospects for assembling the tree of life: A mycologist's perspective.

10:00 W. H. PIEL: Phylogenetic Databases and the PhyloCode

10:30 COFFEE BREAK

11:00 M. THOLLESSON: Regnum – Prospects and Pitfalls

11:30 M. THOLLESSON: Regnum - Demonstration

12:00 DISCUSSION

12:30 M. DONOGHUE: Closing Comments

## SUBMITTED ABSTRACTS

**D. A. BAUM**

NOMENCLATURAL IMPLICATIONS OF TREATING SPECIES AS RANKED CLADES.

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Within modern systematics, species are treated either as evolutionary entities, populations/lineages, or as taxonomic entities, units in the hierarchical system of named groups. These conceptions are at odds: if species are understood to be something other than clades, then they will not always show hierarchical nesting relations to clades, the entities that populate the rest of the taxonomic hierarchy. Thus, if species are viewed as taxonomic entities they should be equated with clades, but clades are not always evolutionary units. Given that both views of species are common among systematists, and that PN attempts to be as neutral as possible on taxonomic philosophy, we need to provide a nomenclatural system that can accommodate both views. As a proponent of the species-as-clades conception, I will focus on the question of how phylogenetic nomenclature can handle the application of species names to clades. Central to this is the recognition that ranks are compatible with PN provided that a change in rank does not change the correct name of any clade (though clades at particular ranks could be distinguished typographically). This reduces the nomenclatural significance of ranking decisions, which is desirable because ranking has a much less easily defined ontological basis than grouping. Suppose a scientist develops a systematization of a group of organisms in which all organisms are assigned to one and only one species clade, each denoted by the epithets of traditional species names. Even in the absence of changes in phylogenetic knowledge, a future researcher could modify the ranking decisions resulting in a new association between clades and species, but no change in the actual names of clades (some traditional epithets would now refer to clades that are not species). What is preventing such treatment of species as clades? Some have argued, rather myopically, that clades, by definition, cannot exist below the species level. This claim is unfounded and new analytical methods allow for the estimation of genealogical histories well within the confines of traditional species. Another common perspective is that species cannot be treated as clades until we agree upon an unambiguous species-ranking criterion. I do not believe this is a problem: species ranking guidelines are readily available within traditional taxonomic practice. Thus, we can simply allow individual specialists to make their best judgment on the assignment of clades to the species rank. No, the biggest problem in treating species as clades is a practical one: homonymy. To maintain continuity with current taxonomy, we would want to use species epithets for clade names, but species epithets are far from unique. I will propose, however, that provided that each traditional taxon name is only allowed to be converted once, relaxing the rules on homonymy is feasible and desirable given that it allows for the treatment of species-as-clades.

**P. E. BERRY**

**PHYLOGENETIC NOMENCLATURE THROUGH CONSENSUS RATHER THAN  
CODIFICATION: SETTING THE KEEL FOR STORMY SEAS AHEAD**

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The specter of a new code of phylogenetic nomenclature has stirred the muck from the bottom of the biological community pond. Both the complexity of issues and perceived inaccuracies on both sides have conjured conspiracy theories and personalized attacks or defenses. In part of this talk I will examine the psychological ramifications of shifting long-entrenched mindsets, as exemplified by the current biological nomenclature codes and the continual tinkering required (often contradictory to established rules) to make them functional. Generating a new code to replace the current codes raises both theoretical and practical issues, and most working taxonomists do not believe we are anywhere close to achieving that goal. Nonetheless, concepts of phylogenetic taxonomy and nomenclature are already working their way into traditional nomenclature systems. In plants, we are seeing hybrid systems appear as accepted norms in journal articles, textbooks, and web pages, in which Linnean binomials and ranks are used up to a certain (often ordinal) level, but after that, informal clade names are used for larger or more inclusive groups. This way, some of the vicissitudes of Linnean nomenclature can be avoided, such as excessive ranks and redundant names for monotypic groups. There are other issues that not even a good phylogenetic nomenclature code will resolve better than the traditional codes. These revolve mainly around diverging interpretation of similar data (i.e., differing species delimitations, or different phylogenetic interpretations based on different levels of sampling density or choice of analytical methods). As our understanding of phylogenetic relationships progresses in large groups such as plants, we need to acknowledge that it will be a long time before we attain a sufficient level of stability in our phylogenetic understanding of the organisms themselves for us to seriously consider a novel system that will accommodate their naming in a completely consistent manner. Taxonomic pluralism, as Paul Sereno asserts, may be inevitable, in fact, even desirable in our biopolitical society.

**Y. BERTRAND<sup>1,2</sup>**

**SPECIES NAMES: THE BEST OF ALL POSSIBLE WORDS?**

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The thesis I shall develop states that the so-called species problem in systematics derives not from our objective knowledge of organisms, but from the structure of our language framed by biological nomenclature. I define the species problem as our inability to agree on the meaning of species names. Two biologists may assume they are communicating about the same entity when uttering the same species name whereas their personal concepts of the same taxon name are, at best, slightly different but in some cases even incommensurable. I suggest that the roots of the species problem can be found in the first modern code of nomenclature: the Strickland Code. Among its writers, there was no common position on species definition. The authentic *tour de force*, which allows for overcoming the disagreement on a universal species definition in all subsequent codes of nomenclature, was the decision that species names are proper names. Proper names are associated with individuals. Individuals do not possess any necessary properties and, therefore, individuals do not need to be associated with a single definition. The focus of my study is the entity formed by a species name during time. Each utterance of a word is, according to the causal theory of reference, connected by a communication chain to the next utterance of that word. It implies that the different meanings of a word are also connected through time. Therefore, in the case of species, a linguistic individual is composed of all the meanings associated with the species name since its lexical introduction. In virtually all cases, according to the above account of a linguistic entity, the rigid connection between a name and a precise meaning is non-existent. As a consequence, meanings are withdrawn from conceptual selection inherent to normal scientific processes. No meaning can be refuted, or even challenged, since no clear meaning is explicitly associated with a species name. Thus, for each name, meanings cannot be expected to converge on a univocal sense. As the upshot, species names form imperfect memic entities, thus by escaping selection on their corresponding meanings, species names fail to form conceptual lineages. Therefore, I find it important to end the longstanding tradition of considering species names as proper names and instead make explicit what authors have in mind when coining a new name. This suggestion is in line with the PhyloCode for clades. Species names handled as common names must be associated with a definition.

**P. D. CANTINO<sup>1</sup> & K. DE QUEIROZ<sup>2</sup>**

PRECEDENCE, EMENDATIONS AND RECENT ADDITIONS TO THE PHYLOCODE

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Although phylogenetic nomenclature can be used without a code, the goal of clear communication about phylogeny will be best served if clade names are unique and stable. The PhyloCode achieves this goal by establishing precedence among competing names and definitions. Precedence is normally determined by priority of publication, but absolute adherence to publication priority can lead to instability in the context of a revised phylogeny if particular changes in the tree topology are not anticipated. In the current draft PhyloCode, only the Committee on Phylogenetic Nomenclature (CPN) can emend definitions; however, it may be desirable to allow emendation without CPN action under certain circumstances. We propose that such "unrestricted emendations" be permitted in order to preserve the original conceptualization of the clade and that they may involve changes in specifiers or qualifying clauses but must retain the original definition type, clade category (e.g., crown clade), and clade conceptualization (as interpreted from the protologue). In contrast, "restricted emendations", requiring CPN action, would change the original author's conceptualization of the clade through changes in definition type or specifiers. The purpose of a restricted emendation is to correct a definition that fails to associate a name with the clade to which it has traditionally referred.

Several changes and additions to the *PhyloCode* have been approved by the CPN since the last draft was posted on the Internet (June 2004). The most important additions are: 1) a recommendation that the most widely used name for a crown clade be adopted for the crown even if the name is also sometimes used for a larger clade that extends below the crown; 2) the recognition of a new class of names ("panclade names") that are to be applied to total clades (e.g., *Pan-Spermatophyta* would refer to the total clade of the crown clade *Spermatophyta*); 3) a recommendation that if the name of a crown clade refers etymologically to an apomorphy, the name of the clade stemming from the ancestor in which that apomorphy originated be formed by adding the prefix *Apo-* to the name of the crown clade (e.g., *Apo-Spermatophyta* for the clade stemming from the first species possessing seeds homologous with those in the crown clade *Spermatophyta*); 4) a mechanism to name a clade when the only preexisting name that has been widely applied to it has already been adopted for a different clade because it has a different meaning under two rank-based codes (e.g., *Prunella* applies to different organisms under the *ICZN* vs. the *ICBN*); and 5) a mechanism to give unique names to clades that correspond to subdivisions of genera under the rank-based codes.

**M. HABER**

THE VIRTUE OF DUAL AMBIGUITY IN SPECIES NAMES

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An advantage of the PhyloCode is the elimination of ambiguity of reference for proper names of higher taxa, where higher taxa are understood to be monophyletic groups. The referents of these names remain constant, though what our hypotheses tell us about these referents may change. In the PhyloCode, uncertainty of reference of higher taxa names reflects the uncertainty of phylogenetic hypotheses; in traditional codes, the ambiguity of reference of higher taxa names corresponds to genuine ambiguity, where no amount of empirical research will settle questions of reference. Uncertainty, in these kinds of cases, is preferable to ambiguity, as it maps onto and explicitly displays phylogenetic hypotheses. Hence the advantage of the PhyloCode. Traditional treatment of the definition of species names also involves ambiguities of reference, however these ambiguities are not as pernicious as those found in traditional treatment of higher taxon names. Species names include two categories of ambiguity – ontological and biological. The ontological ambiguity concerns what kind of thing a species is (*i.e.*, are species individuals, natural kinds, historical entities, etc.), whereas the biological ambiguity concerns what species concept is appropriate or correct. These ambiguities stem from scientific debates (both conceptual and empirical) about which the PhyloCode need not pronounce. Indeed, I will argue that for practical and theoretical reasons the PhyloCode should remain neutral with regard to both of these debates, and develop a species code that allows for taxonomic freedom with regard to decisions made about these debates. This will increase the compatibility between traditional codes and the PhyloCode, increase the utility of the code for practitioners, and produce definitions of species names that appropriately and stably pick out referents.

## **D. S. HIBBETT**

### **AUTOMATED PHYLOGENETIC TAXONOMY AND PROSPECTS FOR ASSEMBLING THE TREE OF LIFE: A MYCOLOGIST'S PERSPECTIVE**

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Fungi, which make up one of the major clades of life, pose difficult challenges for systematic mycologists. About 70,000 species of Fungi have been described, but this is thought to be a small fraction of extant species, and cryptic diversity within "well known" taxa seems to be the rule. Higher-level relationships are coming into focus through multi-locus analyses, but recent discoveries of major clades composed of obscure resupinate species suggest that there is still much to be learned about the higher-order structure of fungal phylogeny. Within major clades, it is common for there to be weakly supported resolution of early nodes, with strong support for more terminal groups.

Automated approaches to phylogenetic taxonomy have the potential to promote the discovery and communication of fungal diversity in the context of dynamic phylogenetic hypotheses and a rapidly growing sequence database. We have developed a prototype system for automated phylogenetic taxonomy, named *mor* (<http://mor.clarku.edu/>), which uses nuclear large-subunit rDNA sequences of mushroom-forming Fungi from GenBank. *Mor* performs a topologically constrained parsimony analysis and an unconstrained jackknife neighbor-joining analysis. The parsimony tree is then parsed using node-based taxon definitions in which the specifiers are individual sequence accessions. As of this writing, the trees produced by *mor* include over 2400 terminals, which have been parsed into seventeen clades. This system demonstrates that the core elements of taxonomy, namely tree-building and enumeration of the contents of clades, can be automated. However, the *mor* system is limited in that it only works with large subunit rDNA sequences from GenBank. To develop comprehensive trees and classifications, it will be necessary to integrate information from traditional taxonomies. This will be possible because taxonomic hierarchies have an inherent tree structure. It will also be necessary to incorporate sequences of the more variable internal transcribed spacer (ITS) region of nuclear rDNA, which will require automated approaches to supertree construction. ITS is widely used in molecular ecological studies, which frequently find sequences that have no close matches in GenBank. Automated integration of sequences based on specimens and those derived from environmental samples will promote sequence-based species discovery, but this also raises issues regarding typification of species names and the necessity of voucher specimens.

**T. M. KEESEY**

**A MATHEMATICAL APPROACH TO CLADE DEFINITIONS, USING ORDER RELATIONS ON SETS OF ORGANISMS**

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Clades, taxa consisting of an ancestor plus all descendants, are often defined based on conditions of ancestry and descent with objective rules for application. To date, such definitions have all taken the form of prose, but prose is an inherently ambiguous form. Furthermore, prose renders definitions difficult or impossible to interpret for computer applications and researchers not fluent in the definition's language. I propose a more rigorous and coherent form for taxon definition, based on preexisting forms of mathematical notation (logic, set, function, etc.), applicable to clades and, potentially, other types of taxa. This approach is granular to the level of the individual organism, not to the fuzzy, unstable levels of species or population. In order to accomplish this, the ancestor of a clade is defined as a "cladogenetic set," a set (or subset thereof) yielded by certain functions and consisting of one or more closely related organisms that are not ancestral to each other. The most basic phylogenetic statement, that one organism is ancestral to another, is codified as an order relation,  $<_h$ , on the universal set of all organisms,  $U$ , as is the opposite relation, descent ( $>_h$ ). From these I derive the following functions and operators:  $\min_h$  (initial members),  $\max_h$  (final members),  $\text{anc}$  (ancestors),  $\text{des}$  (descendants),  $\text{comanc}$  (common ancestors),  $\text{comdes}$  (common descendants),  $\text{homanc}$  (homologous ancestors),  $+_a$  (node-based ancestor),  $+_c$  (node-based clade),  $-_a$  (stem-based ancestor),  $-_c$  (stem-based clade),  $\text{apo}_a$  (apomorphy-based ancestor),  $\text{apo}_c$  (apomorphy-based clade),  $\text{crown}$  (crown clade),  $\text{pan}$  (total clade), and  $\text{NST}$  (node-stem triplet). I also provide means for referring to specific sets of individual organisms by pertinent specimens ( $\langle\langle\text{INSTITUTION ID}\rangle\rangle$ ), taxa with pertinent name-bearing type specimens ( $\langle\langle\text{Taxon}\rangle\rangle$ ), and character descriptions ( $\langle\langle\text{character description}\rangle\rangle$ ).

Example definitions:

Node-based.  $\text{Aves} := \langle\langle\text{Struthio}\rangle\rangle +_c \langle\langle\text{Tinamus}\rangle\rangle +_c \langle\langle\text{Vultur}\rangle\rangle$

Stem-based.  $\text{Panaves} := \langle\langle\text{Vultur}\rangle\rangle -_c \langle\langle\text{Crocodylus}\rangle\rangle$

Conditionally apomorphy- or stem-based.

$S := \text{apo}_c(\langle\langle\text{Vultur}\rangle\rangle, \langle\langle\text{feathers}\rangle\rangle)$

$\text{Avifilopluma} := \begin{cases} S, S \subseteq \text{Panaves}; \\ \text{Panaves}, S \not\subseteq \text{Panaves}. \end{cases}$

Node-stem triplet.

$(\text{Paleognathae}, \text{Pantinamidae}, \text{Panratitae}) := \text{NST}(\langle\langle\text{Tinamus}\rangle\rangle, \langle\langle\text{Vultur}\rangle\rangle)$

Example statements:

Heterodefinitional equivalence.

$\text{Panaves} = \text{pan Aves}$

$\text{Aves} = \text{crown Panaves}$

Composition.  $\text{Dinosauria} \supseteq \text{Megalosaurus} \cup \text{Hylaeosaurus} \cup \text{Iguanodon}$

Diagnosis.  $\text{Dinosauria} \supseteq \langle\langle\text{large sacrum composed of five ankylosed vertebræ} \dots\rangle\rangle \cap \langle\langle\text{broad} \dots$

$\text{coracoids}\rangle\rangle \cap \langle\langle\text{long and slender clavicles, whereby Crocodilian characters of the vertebral}$

$\text{column are combined with a Lacertian type of the pectoral arch}\rangle\rangle \cap \langle\langle\text{transitional or annectent}$

$\text{characters [of] the dental organs}\rangle\rangle \cap \langle\langle\text{bones of the extremities} \dots \text{ provided with large medullary}$

$\text{cavities and with well-developed} \dots \text{ processes, and terminated by metacarpal, metatarsal, and}$

$\text{phalangeal bones}\rangle\rangle$

(Clade definitions are from Gauthier and de Queiroz [2001]. "Dinosauria" refers to the original usage by Owen [1842]. Citations for specifier genera are omitted for brevity.)

**M. LAURIN**

## REPRESENTATION OF THE ISPN AND THE SUCCESS OF THE PHYLOCODE

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The development of the PhyloCode was initially (1998-2004) supervised by an advisory group composed of 26 people, in addition to the two authors (Cantino and de Queiroz). This committee included many of the initial proponents and early adepts of phylogenetic nomenclature. With the inauguration of the ISPN (International Society for Phylogenetic Nomenclature), the responsibility for amending the PhyloCode was transferred to the smaller CPN (Committee on Phylogenetic Nomenclature), composed of nine elected members, that currently represent four countries. Currently, the bylaws of the ISPN do not provide a mechanism to enable consultation of the membership to guide potentially important decisions made by the CPN. This is regrettable because the PhyloCode is a young code, that is still changing substantially, as shown by the recent incorporation of recommendations that deal with how to name clades, that could be argued to depart significantly from the spirit of earlier drafts of the code, that dealt almost exclusively with how to define clade names. This situation is arguably not ideal to promote the PhyloCode because the CPN is a very small committee (both in number of members and in geographical coverage), and because of this, for many scientists, the PhyloCode will not have the same legitimacy as rank-based codes. A simple comparison with the committees that amend the rank-based codes illustrates this point. The ICZN is amended by a commission currently composed of 21 members that represent 17 countries, whereas the ICBN is amended by the whole botanical congress (more than a thousand systematists from many countries).

The small size of the CPN and other committees of the ISPN reflects, to an extent, the relatively low proportion of systematists that currently use phylogenetic nomenclature. In this respect, we should not expect the ISPN to match the number of members and the diversity of geographic origin found in the societies that support the rank-based codes. Nevertheless, given the current growth of popularity of phylogenetic nomenclature among systematists, I suggest that we consider revising the bylaws of the ISPN in a near future to enable consultation of the membership of the society for the most important amendments of the PhyloCode, and that we try to broaden the geographical coverage of the membership and of the various committees of our society. This could only increase the legitimacy of the PhyloCode for many scientists and it may prevent incorporation into our code of articles that could prove unpopular in some countries or taxonomic fields. The PhyloCode is excellent, but getting it accepted by other systematists might be easier if the ISPN and its committees were more representative of the world-wide systematic community.

## D. MARJANOVIC

### THE IVORY TOWER: HOW CAN WE WIN THE NECESSARY ACCEPTANCE FOR PHYLOGENETIC NOMENCLATURE?

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The PhyloCode is not in a good starting position for taking off soon. Outside of a few universities and a few subdisciplines, few biologists have heard of, let alone understood, phylogenetic nomenclature. The handful of existing popular articles is uniformly abysmal; the PhyloCode critiques in scientific journals are without exception full of misunderstandings. Clearly we have been doing a very bad job explaining phylogenetic nomenclature.

However, many people dislike the PhyloCode because they dislike the proposed definitions of certain names. Often these are cases where PhyloCode advocates, too, use different definitions for the same name and vice versa. The purpose of the PhyloCode is to abolish these situations by introducing priority. The planned way to do this – the companion volume, edited by only three people who will likely be major contributors to the same volume – is already drawing criticism from self-designated PhyloCode skeptics.

I suggest registering name-definition combinations that the fewest people will dislike. These combinations can only be found in discussions that could need to take several years. Careful adherence to already existing Recommendations of the current draft of the PhyloCode will shorten this time. Following such discussions, different parts of the Tree of Life should have different starting dates for priority.

I will present examples of the care that should minimally be taken in defining converted clade names to maximize both stability of content and acceptance. Certain grade names should be given self-destructive definitions to remove them from circulation.

*Aves* L. 1758: branch; internal specifiers: *Passer domesticus*; external specifiers: *Velociraptor mongoliensis*, *Oviraptor philoceratops*, *Segnosaurus galbinensis*, *Troodon formosus*, *Sinornithoides youngi*, *Ornithomimus velox*, *Tyrannosaurus rex*, *Compsognathus longipes*, *Ornitholestes hermanni*, *Coelurus fragilis*, *Coelophysis bauri*, *Hypsilophodon foxii*, *Crocodylus niloticus*, *Sphenosuchus acutus*, *Euparkeria capensis*, *Megalancosaurus preonensis*, *Sorex araneus*

*Tetrapoda* unknown, before 1913: apomorphies: digits present and fin rays absent on all 4 limbs; int: *Salamandra salamandra*, *Sorex araneus*

*Theropsida* Goodrich 1916: branch; int: *Sorex araneus*; ext: *Passer domesticus*, *Lacerta agilis*

*Sauropsida* Huxley 1869: branch; int: *Passer domesticus*, *Lacerta agilis*; ext: *Sorex araneus*

*Diapsida* Osborn 1903: apo: upper temporal fenestra (with smooth, continuous edges, unlike fontanelle; larger than necessary to let nerves and/or blood vessels pass, unlike foramen; ventrally delimited by sutured/fused postorbital and squamosal bones); int: *Crocodylus niloticus*, *Sphenodon punctatus*

*Reptilia* ?Laurentius 1768: branch; int: *Lacerta agilis*, *Crocodylus niloticus*, *Testudo graeca*; ext: *Rana temporaria*, *Salamandra salamandra*, *Caecilia tentaculata*, *Passer domesticus*, *Sorex araneus*

*Sauria* MacCartney 1802: branch; int: *Lacerta agilis*, *Iguana iguana*, *Gekko gecko*, *Varanus niloticus*; ext: *Natrix natrix*

**J. REVEAL<sup>1,2</sup>**

**SUPRAGENERIC NAMES: DIFFICULT UNDER ANY CODE**

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Scientific names above the rank of genus (suprageneric names) as applied to groups of plants covered presently by the *International Code of Botanical Nomenclature* are variously created and recognized. Such names may or may not have priority, may or may not be based on an included generic name and thus may or may not have a type, are always ranked, and occasionally even validly published. Over the past half century the trends have been to recognize monophyletic suprageneric groups whose names are based on an included generic name, and to ascribe ranks in a more or less uniform manner. Over the last fifteen years efforts have been made to ascertain priority (at the ranks of family and below), determine validity, note current use, and more properly ascribe authorships and bibliographic references. With the creation of suprageneric names starting in the 1760s, promoted in the 1780s, and championed by numerous authors in the 1830s, there was a rather uniform set of names applied for all groups of plants. Names and ranks proliferated starting in the 1880s and continued well into the 1930s. Beginning anew, after the Second World War, authors took a “lumpers” or “splitters” view by recognizing few or many groups at basically a limited number of ranks. The problems for the proponents of the PhyloCode regarding suprageneric names are numerous. While rank is not an issue, it is clear that there are subclades within clades so that a hierarchical system of names would be useful. This can be accomplished by adopting a limited number of traditional terminations. Inasmuch as the PhyloCode is a new effort to bring nomenclatural stability to all organisms, both extant and fossil, this is a singular opportunity to adopt the best of the existing codes of nomenclature and establish a new system of nomenclature for suprageneric names. Accordingly, I urge adoption of a limited number of terminations and that all suprageneric names should be based on an included generic name. Even though clades, according to the PhyloCode, are defined by their circumscriptions, rather than types, use of a well-known included generic name, coupled with a limited set of terminations, would be a ready means of referring to any clade by non-taxonomists who, after all, are important clients for all of systematics.

## **S. L. RICHARDSON**

### **ASEXUAL SPECIES IN LIMBO: CAN THE PHYLOCODE ACCOMMODATE THE NAMING OF ASEXUAL ORGANISMS?**

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Clonal populations arising from the uniparental reproduction of a single organism constitute asexual “species” and have traditionally been assigned specific epithets under other nomenclatural codes (e.g. ICZN, ICBN, BC). According to the PhyloCode, asexual species could also be treated as clades, a clade being defined as “an ancestor (*an organism*, population, or species) and all of its descendants.” Conversion of specific epithets, however, is prohibited by the regulations stipulated in the current incarnation of the PhyloCode in that: (1) “a clade name may not be converted from a pre-existing specific or infraspecific epithet” (Article 10.1); and (2) “specimens that are not types may be used as specifiers only if the specimen does not belong to a named species under any code” (Article 11.5). These restrictions thus essentially prohibit the conversion of a large number of specific epithets that are currently valid under other nomenclatural codes. Difficulties may also arise when proposing phylogenetic definitions for the names of new asexual species, if the clades to be named are not based on published phylogenies (Rec. 9A), as is often the case in circumscribing species under the provisions of the ICZN/ICBN. Thus the potential exists for a large number of asexual taxa to remain in nomenclatural limbo until these issues are resolved. Examples of ways to apply the principles of phylogenetic nomenclature to definitions of asexual “species” or clades of *Foraminifera* (and their unicellular, photosynthetic eukaryotic endosymbionts) will be explored.

**I. N. SARKAR<sup>1</sup> AND D. P. REMSEN<sup>2</sup>**

**ENABLING BIOLOGICAL KNOWLEDGE INTEGRATION THROUGH SCIENTIFIC NOMENCLATURE**

1) Divisions of Invertebrate Zoology and Library Services, American Museum of Natural History, Central Park West at 79<sup>th</sup> Street, New York, NY 10044 USA

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Biological knowledge currently exists heterogeneously across many disparate knowledge bases. Towards the unification of pertinent biological knowledge, methods are required to reconcile differing representations for the same biological entity. In support of an infrastructure that would enable the use of uniform identifiers of life, such as “Life Science Identifiers” (LSIDs), all previously and currently used representations for the same entity need to be organized into federated, publicly accessible resources. To this end, we have been developing a set of automated techniques to extract string variants of scientific names from natural language text that can be reconciled into such a federated system. Here, we present the issues associated with how scientific names are currently represented in scientific literature (examining digitized volumes of heritage literature and contemporary biomedical resources) relative to a number of name catalogues (e.g., Species2000). By aggregating and reconciling the scientific names extracted from scientific literature and name catalogues, we have been developing a unified framework to navigate biological knowledge. We have developed a number of Web-based prototype applications (<http://portal.ubio.org>) that demonstrate the utility of organizing scientific names in a federated manner. This presentation aims to promote the integration of the PhyloCode nomenclature associated with organisms into the uBio system such that knowledge that may be referred to according to other formalisms (e.g., Linnaean nomenclature) can be readily identified. Such integration, we feel, will be essential for the ultimate success for PhyloCode names to be used as a primary reference for the Earth’s biota. As our heritage literature becomes available, largely due to the efforts of the Biodiversity Heritage Library consortium, the linking of legacy knowledge with contemporary knowledge can only benefit from having a stable nomenclature that can be mapped throughout taxonomy and time.

**C. P. SERENO**

**UNITARY TAXONOMY CONSIDERED**

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Given potential variation in structure and taxonomic content, phylogenetic definitions for a particular taxon are often theoretically limitless and therefore commonly unique in practice. Furthermore, a code that provides few limitations in definitional structure and little in the way of rationale for approaching high-level taxonomy ensures diverse and idiosyncratic application. Do these circumstances provide the foundation for a stable unitary taxonomy? Is a phylogenetically-based unitary taxonomy of supraspecific taxa functionally equivalent to typology in Linnean taxonomy? The pros and cons of established definitions, immutably enforced as unitary solutions by authority, are examined with an eye towards understanding their potential universal adoption, feasibility and necessity.

## **M. THOLLESON**

### **REGNUM – PROSPECTS AND PITFALLS**

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The PhyloCode requires that the names defined should also be registered in a public database. RegNum is a first shot at implementing this database, along with necessary interfaces, in accordance with requirements is outlined in Appendix A of the PhyloCode. Anyone can probably agree on the potential use for such a database when it comes to applying the names, avoiding or sorting out homonyms and synonyms, and so forth. There are also obstacles on the path, mainly relating to data integrity and the effort needed to keep and maintain such a database. I will here discuss some of these issues and how we have tried to solve them, as well as future potentially interesting applications and projects to harness the information in the database.

Furthermore, I will introduce a generalization to the kinds of definitions given by the PhyloCode (i.e., node-based, stem-based, ...), generalizations that are used in RegNum (this generalization also invites to its own flavor of shorthand notation). From these general definitions, the interface in RegNum can also provide the user with a phrasing of the definition that can be used in the protologue.

## USEFUL TELEPHONE NUMBERS

**Metro Taxi, 777-777**, Service from Tweed New Haven airport to hotels and campus (estimated \$10 to \$20 one way).

### HARTFORD: BRADLEY AIRPORT

Bradley Airport is located north of Hartford, about 1 hour from New Haven, 1 1/2 hours during rush hour; serviced by all major airline carriers.

From Bradley to New Haven:

- **CT Limo, (800) 472-5466, [www.ctlimo.com](http://www.ctlimo.com)** (\$90 round trip / \$47 one way, per passenger); drop off at New Haven's Long Wharf Terminal, a five-minute cab ride to hotels and campus. (Contact Metro Taxi 777-7777).
- Rental cars are also available from Bradley Airport.

### NEW YORK AREA AIRPORTS - KENNEDY, LaGUARDIA & NEWARK

Approximately 2 to 3 hours from campus.

- **CT Limo (800) 472-5466, [www.ctlimo.com](http://www.ctlimo.com)**, from Kennedy and LaGuardia Airports (\$126 round trip / \$65 one way, per passenger) and Newark (\$156 round trip / \$80 one way); drop off at New Haven's Long Wharf Terminal, a five-minute cab ride to hotels and campus. (Contact Metro Taxi 777-7777)
- **Prime Time Shuttle Service (800) 733-8267, [www.primetimeshuttle.com](http://www.primetimeshuttle.com)**, from Kennedy and LaGuardia Airports (\$94 round trip / \$49 one way, per passenger; 2 or more are \$32 per additional passenger); drop off at all New Haven hotels.
- **Red Dot Limousine Service (800) 673-3368, [www.18006reddot.com](http://www.18006reddot.com)**, from Kennedy and LaGuardia (\$106 round trip / \$53 one way, per passenger); drop off at the Omni, Courtyard by Marriott or Residence Inn, New Haven.

### TRAIN AND BUS

- **Amtrak (800) 872-7245, [www.amtrak.com](http://www.amtrak.com)**, The Acela Express offers expedient service between Boston and Washington DC. Amtrak services New Haven from Penn Station in New York. Average travel times by regular rail to New Haven are as follows: from Boston 3 hours, from New York 2 hours, from Philadelphia 4 hours. Taxis meet all trains and cost approximately \$12 to get to campus.
- **Metro North Commuter Railroad (800) 638-7646, [www.mta.nyc.ny.us](http://www.mta.nyc.ny.us)**, also offers frequent service to New Haven's Union Station from Grand Central Station in New York. Taxis meet all trains and cost approximately \$12 to get to campus.
- **Peter Pan (800) 343-9999, [www.peterpan-bus.com](http://www.peterpan-bus.com)**, and **Greyhound (800) 231-2222, [www.greyhound.com](http://www.greyhound.com)**, both serve New Haven.

## WHILE AT YALE...

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### **YALE UNIVERSITY ART GALLERY** <http://artgallery.yale.edu/>

The Yale University Art Gallery's permanent collection includes over 185,000 works, organized into ten curatorial areas: African Art, American Decorative Arts, American Paintings and Sculpture, Ancient Art, Art of the Ancient Americas, Asian Art, Coins and Medals, Early European Art, Modern and Contemporary Art and Prints, Drawings, and Photographs. The Gallery is located on Chapel at High Street. Opening hours: Tuesday-Saturday 10:00 am–5:00 pm; Thursday until 8:00 pm (Sept–June) Sunday 1:00–6:00 pm. Admission is free.



### **YALE CENTER FOR BRITISH ART** <http://ycba.yale.edu/index.asp>

Presented to the university by Paul Mellon (Class of 1929), the Yale Center for British Art houses the largest and most comprehensive collection of British art outside the United Kingdom. The Center is located at 1080 Chapel Street. Opening hours: Tuesday to Saturday 10 am to 5 pm; Sunday noon to 5 pm; Closed Mondays. Admission is free.

### **BEINECKE RARE BOOK AND MANUSCRIPTS LIBRARY** <http://www.library.yale.edu/beinecke/>



Directions From the New Haven Green: walk north on College Street to Wall Street. Take a left on Wall Street. Enter the plaza on the right in the middle of the first block. The Beinecke Library is the large white marble and gray granite building facing east. Visitors hours are Monday through Friday, 8:30 a.m. to 5 p.m.; Saturday, 10 a.m. to 5 p.m.



### **COLLECTIONS OF MUSICAL INSTRUMENTS**

<http://www.yale.edu/musicalinstruments/>

The Yale Collection of Musical Instruments is located in the heart of Yale's New Haven Campus on Hillhouse Avenue, once described by Charles Dickens as "the most beautiful street in America." Opening hours: Tuesday 1:00 to 4:00; Wednesday 1:00 to 4:00; Thursday 1:00 to 4:00. Closed in July and August. Admission is free.



### **PEABODY MUSEUM OF NATURAL HISTORY**

<http://www.peabody.yale.edu/>

The Yale Peabody Museum was founded in 1866 with a gift from philanthropist George Peabody, at the urging of his nephew, Yale's O.C. Marsh, the first professor of paleontology in North America and the Museum's first director. Marsh built many of the Peabody's great collections, and today you can see some of his most famous finds — the dinosaurs he named *Triceratops*, *Stegosaurus* and "Brontosaurus" — in the Museum's Great Hall. Along with more than 11 million specimens and objects in anthropology, botany, zoology, paleontology, entomology, ornithology, and historical scientific instruments in its collections, the Yale Peabody Museum is also home to Rudolph F. Zallinger's murals *The Age of Reptiles* and *The Age of Mammals*. The Museum is located at 170 Whitney Avenue. Opening hours: Monday through Saturday, 10 a.m. to 5 p.m.; Sunday, noon to 5 p.m. Admission is free for meeting participants.



### **STERLING MEMORIAL LIBRARY** <http://www.library.yale.edu/rsc/sml/>

Housing approximately 4 million volumes, Sterling Memorial Library is the largest library on the Yale campus and serves as the center of the library system. Over the course of three hundred years, Yale has developed special collections of exceptional depth and diversity. Researchers from Yale and beyond are encouraged to explore the unique primary resources that combine with extraordinary secondary resources at Yale to make its holdings world-renowned. The library is located on 120 High Street. Summer Hours: Monday through Wednesday: 8:30 a.m.-5:00 p.m.; Thursday: 8:30 a.m.-10:00 p.m.; Friday: 8:30 a.m.-5:00 p.m.; Saturday: 10:00 a.m.-5:00 p.m.; Sunday: closed