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Source: Journal of the North American Benthological Society, 29(1) : 147-169

Published By: Society for Freshwater Science

URL: <https://doi.org/10.1899/08-065.1>

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Taxonomy and systematics: contributions to benthology and *J-NABS*

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Abstract. Systematics, or taxonomy, is the study of the diversity of life on Earth. Its goals are to discover and describe new biological diversity and to understand its evolutionary and biogeographic origins and relationships. Here we review the contributions to the field of systematics and taxonomy published over the last 25 y in *J-NABS* and its predecessor *Freshwater Invertebrate Biology (FIB)*. We examined a total of 64 studies that we considered to be largely taxonomic in nature. We classified these studies into 2 major categories: morphological (e.g., descriptive taxonomy, taxonomic revisions) and molecular (e.g., deoxyribonucleic acid [DNA] barcoding, population genetics). We examined studies in 5-y increments for *J-NABS*. We also studied the period 1982 to 1985, during which *FIB* was published. On average, 12 taxonomic studies were published within each 5-y period. Molecular studies first appeared in 1986 and have slowly increased, reaching their greatest number within the last 5 y. Studies also were classified by their individual attributes. Morphological studies were, by far, the most common, but studies also included molecular data, biological information, distributional data, keys, and biogeographical analyses. Most studies included >1 of these attributes. Overall, the role of *J-NABS* in the development of benthic taxonomy has been minimal in terms of number of publications, but as part of the nexus of taxonomic literature, all contributions have been important to the discipline. We discuss these contributions and their impact on the following subject areas: taxonomy and revisionary systematics, phylogenetic and molecular systematics, taxonomic resources, taxonomic resolution, conservation and taxonomy, professional training, taxonomic certification, and graduate education. We also give an overview of new developments in the taxonomists' toolbox. These developments include DNA barcoding, online taxonomic resources, digital identification keys, cybertaxonomy, and modern museum collections and resources.

Key words: taxonomy, systematics, benthology, phylogenetics.

*Metals falling from industry like a nasty rain
but are they toxic or irrelevant
it's driving me insane*

*The answer is not easy
because I need to find
the names of each insect
from the hairs on its behind
(if only the taxonomists weren't dying off)⁶*

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⁶ Opening stanzas of a poem by Landis Hare, as reprinted in Mackay (2005)

Systematics, or taxonomy, is the study of the diversity of life on Earth. Its goals are to discover and describe new biological diversity, to understand its evolutionary and biogeographic origins and relationships, and to present this information in the form of biological classifications that serve as the general reference system for biology (Anonymous 1994). Systematics provides the historical perspective within which all biological inquiry ultimately becomes meaningful.

Systematists establish the nomenclatural and classificatory foundation upon which biological diversity is organized. Systematics has contributed to the broader development of biology in many ways, including our understanding of the nature of species, modes of speciation, the genetic structure of populations, and other fundamental evolutionary processes. Systematists traditionally have made the task of

identifying organisms easier for other scientists by constructing *keys* that use various features of organisms to distinguish them from one another. However, keys are produced as a service and by-product of what is the primary goal of systematics—to describe the diversity of organisms, to understand how organisms are related by evolutionary descent, and how they diverged into independent evolutionary entities. The phylogenetic trees inferred by taxonomists provide an objective basis on which to structure classifications and provide a framework on which to test hypotheses of coevolution, ecological associations, and behavior. Systematics also provides the necessary basis for the study of the distribution of organisms in space and time, i.e., historical biogeography and paleontology.

Overriding this discussion of taxonomy and its contributions to biology is the biodiversity crisis—the extinction of a considerable portion of the Earth's remaining species. Worldwide, loss of biological diversity has been accelerating at an alarming rate through habitat destruction, pollution, and global climate change (Wheeler 1990, Wilson 1992, Thomas et al. 2004a). The importance of assessing this ongoing loss is apparent, but biologists find it difficult to present even an approximate estimate of loss because relatively little is known about biodiversity in the first place (Wheeler 1990, 2007, Wilson 1992). Furthermore, insects and freshwater invertebrates might be experiencing extinction rates as great as, if not greater, than plants and vertebrates (Thomas et al. 2004b, Thomas 2005). This issue underscores the central role of taxonomy and systematics in addressing the biodiversity crisis (Mace 2004).

Recently, however, biology has recognized the “taxonomic impediment” (first coined by Taylor 1983, see also Giangrande 2003, Flowers 2007a, b): the acute shortage of taxonomic expertise, loss of positions at universities and museums, and limited resources (financial and technological) available to systematists to conduct fundamental taxonomic research. This taxonomic impediment, as the introductory poem describes, is a problem that clearly applies to benthic science, where species-level taxonomy is essential for documenting biodiversity. In addition, larval taxonomy is a requirement for biomonitoring (Bailey et al. 2001¹, Lenat and Resh 2001) and in studies of the life history of congeneric species (Rutherford and Mackay 1986, Beam and Wiggins 1987).

J-NABS has published systematic studies alongside both basic and applied studies throughout its lifetime.

¹ Boldface indicates paper was published in *J-NABS*

In a most basic sense, ecology and taxonomy are inherently intertwined, with taxonomy and systematics exploring and cataloging the diversity of organisms, and ecology using products, such as descriptions, distributions, keys, and phylogenies, as a foundation for studies of organisms or communities in their habitat, often returning products to taxonomy and systematics by providing clues to factors driving diversification and speciation. In our review, we summarize and examine taxonomic and systematic papers published in *J-NABS* while placing this literature within the broader contributions and development of systematics over the last 25 y. Major subject areas covered include taxonomic and revisionary systematics, phylogenetics and molecular systematics, and taxonomic resources, as well as the role of taxonomy in conservation and issues related to education and training in taxonomy. As we consider these subjects, we will discuss new developments in taxonomy and present our thoughts on current and future needs as the discipline applies to benthic organisms.

Historical Perspective

Taxonomy has an exceptionally long history dating back as early as Aristotle (Schuh 2000). The science became formalized when a standardized system for naming and classifying species was introduced by Linnaeus in his *Systema Naturae* (1758; Fig. 1), followed by the evolutionary framework of Darwin with the publication of his *Origin of Species* (1859; Fig. 1). The mid-20th century saw the advent of the new systematics (Huxley 1940) with its emphasis on intraspecific and population-level variation. In fact, one of the leaders in this development was Robert Usinger, an aquatic entomologist, best known among benthologists for his *Aquatic Insects of California* (Usinger 1956; Fig. 1), but who was also a coauthor of an influential textbook of the period (Mayr et al. 1953). Perhaps the single most important development in taxonomy in the latter half of the 20th century was the universal adoption of Hennig's principles of phylogenetic systematics or cladistics (Hennig 1950, 1966; Fig. 1). Cladistics uses an objective method, now strengthened by advanced analytical techniques (e.g., as implemented in the program PAUP by Swofford 2003), to reconstruct relationships among organisms based on shared common descent (Kitching et al. 1998). Cladistics has revolutionized the way taxa are classified, and it has great utility because of its inherent information content and predictive value (Farris 1979).

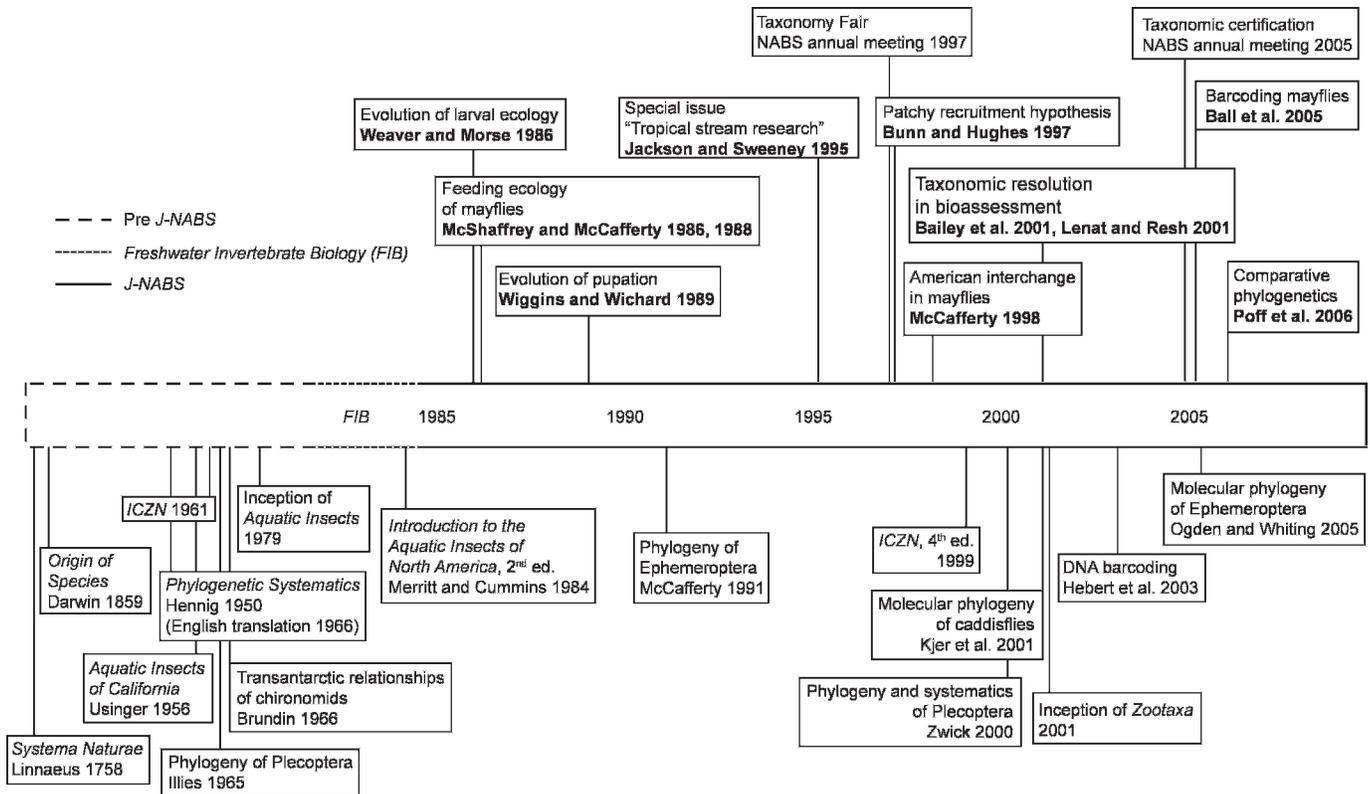


FIG. 1. Timeline of significant contributions to taxonomy and systematics of benthic macroinvertebrates from the early days (long dashes on left) to *Freshwater Invertebrate Biology (FIB)* (dashes) and *J-NABS* (solid line). Significant contributions in *J-NABS* are shown above the timeline in boldface, and other major contributions of relevance to taxonomy and systematics, especially of benthic organisms, are shown below the timeline. ICZN = International Code of Zoological Nomenclature. All studies are cited in the text except ICZN (1961, 1999), Illies (1965), Merritt and Cummins (1984), McCafferty (1991), Zwick (2000), and Ogden and Whiting (2005). NABS = North American Benthological Society, Ed. = edition.

Use of molecular data and new computer-based analytical methods also have revolutionized the field (Hillis et al. 1996, Felsenstein 2004). Molecular data, in the form of deoxyribonucleic acid (DNA) sequences, or their products, offer a vast suite of information for understanding evolutionary processes at the molecular level, including the evolution of genes and the evolution of how DNA is organized within the genome. In systematics, DNA sequences can serve as characters for inferring evolutionary relationships, can reveal cryptic species, and uncover evolutionary processes at the population level (Beaumont 1994).

Upon this solid historical foundation and these rigorous analytical techniques, systematics continues to advance through the development of new computational methods, such as Bayesian statistical inference in phylogeny reconstruction (Huelsenbeck and Ronquist 2001), and new syntheses with other disciplines, for example through community phylogenetics (Webb et al. 2002) and evolutionary developmental biology or “evo-devo” (Minelli 2007). The

presence of taxonomic information on the World Wide Web is ever-growing, and cybertaxonomy, the integration of taxonomic data with computers and the Internet across a network of taxonomists, will revolutionize the way taxonomy is practiced (Wheeler 2004, 2008a, b, Godfray et al. 2007). Even the staid subjects of nomenclature and formal classification have undergone recent suggestions for radical reform (Nixon et al. 2003, Cantino and de Queiroz 2007).

Methods and Summary of Literature Reviewed

We used JSTOR (<http://www.jstor.org/>) to inspect visually the tables of contents beginning with volume 1, issue 1 of *Freshwater Invertebrate Biology (FIB)* (1982–1985) through the latest issue of *J-NABS* at the time of this writing (1986–2009, volume 28, issue 3). We selected titles indicating content that was directly or indirectly related to taxonomy and systematics, including new taxonomic descriptions, larval descriptions, keys, taxonomic reviews and revisions, new

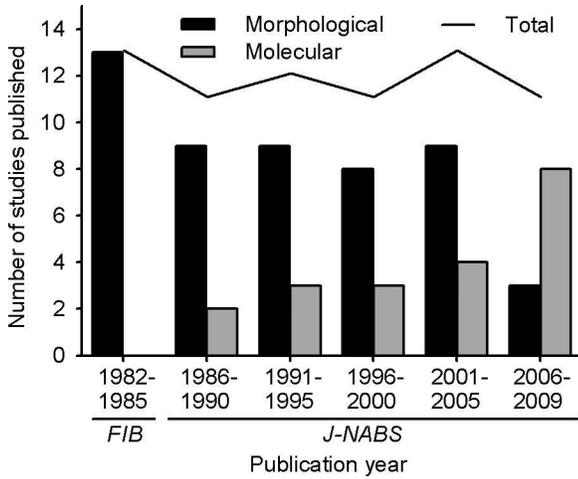


FIG. 2. Long-term publication trends of taxonomic studies in *J-NABS* and *Freshwater Invertebrate Biology (FIB)*. Studies were classified into morphological or molecular taxonomic studies and were grouped in 5-y increments. The total number of taxonomic studies published in *J-NABS* is indicated for each period.

distribution records, phylogenetic studies, classifications, nomenclature, morphology, molecular systematics, biogeography, population genetics, and book reviews of systematic or taxonomic works. Our review was not restricted by taxon, but for our more general discussions and examples from the literature, we mostly concentrated on insects and other aquatic macroinvertebrates, at the expense of aquatic plants and vertebrates; these groups are outside of our areas of expertise and represent taxa not included in *J-NABS* taxonomic contributions. We used the Web of Science (Institute for Scientific Information [ISI], Thompson Reuters, New York; http://thomsonreuters.com/products_services/scientific/Web_of_Science) available through the University of Minnesota Libraries and ran a cited reference search to compile data on subsequent citations of selected *J-NABS* papers or the advanced search feature for key word searches of certain subject areas. We conducted an additional search of the Web of Science for the keywords “taxonomic resolution” and “stream*” or “river*” to examine the role *J-NABS* has played in the discussion on taxonomic resolution in stream bioassessment. In the text, figures, and tables, we distinguish between papers published in *FIB* and *J-NABS*. Associate editors for *J-NABS* for taxonomy and systematics (we could not determine if *FIB* had an associate editor assigned to taxonomy) during the period covered included John C. Morse (1985–1989), W. Patrick McCafferty (1989–1992), Leonard C. Ferrington, Jr (1992–1995), Ralph W. Holzenthal

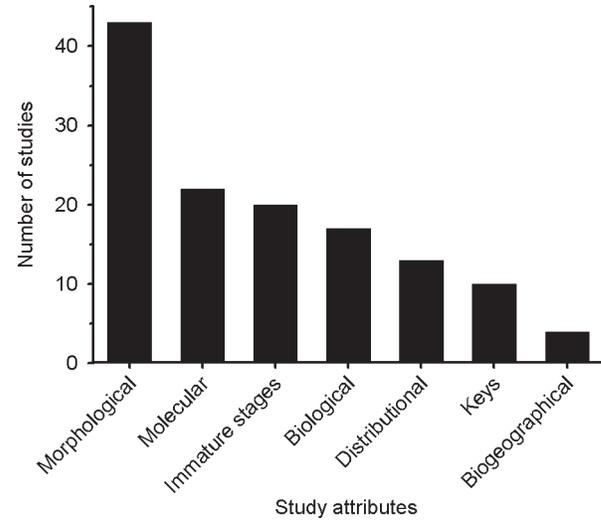


FIG. 3. Attributes of taxonomic studies in *J-NABS*. Studies were scored according to individual data sources or attributes. In some cases, a study was classified as having >1 type of attribute.

(1994–2006), and Atilano Contreras-Ramos (2006–present).

For the period reviewed (1982–2008), we examined a total of 71 studies that we considered to be largely taxonomic in nature. A summary of the number and type of contributions in morphological and molecular systematics and taxonomy over the life of the *J-NABS* is presented in Fig. 2. We classified these studies into 2 major categories: morphological (e.g., descriptive taxonomy, revisions) and molecular (e.g., population genetics, barcoding) for the purpose of examining long-term trends over the course of *J-NABS*’s history. We examined studies in 5-y increments for *J-NABS*. We also examined the period 1982 to 1985, which represents publications in *FIB*. On average, 12 taxonomic studies were published within each 5-y period (Fig. 2), and this average has been fairly consistent over the past 25 y. With the exception of the first 4 y of publication in *FIB*, which included a total of 13 morphological studies, on average, 9 morphological studies were published within each 5-y period. Molecular studies first appeared in the pages of *J-NABS* in 1986 (e.g., **Sweeney et al. 1986**) and have slowly increased, reaching their greatest number within the last 5 y. No taxonomic studies were published from 1990 to 1992.

These same studies also were classified by their individual attributes, and studies often contained attributes that fell into more than one category (Fig. 3). Morphological studies were, by far, the most common (43 studies; Fig. 3), but studies also included molecular data, biological information, immature

stages, distributional data, keys, and biogeographical analyses. Most studies included >1 of these attributes.

Taxonomy and Revisionary Systematics

Descriptive taxonomy, taxonomic revisions, and morphology

For the period reviewed, 39 taxa new to science were described in the pages of *J-NABS* and *FIB* (Table 1). These studies included the descriptions of 38 new species and 4 new genera (*Tempisquitoneura* Epler and de la Rosa, Chironomidae; *Prebaetodes* Lugo-Ortiz and McCafferty, Ephemeroptera; *Eocosmoecus* Wiggins and Richardson, Trichoptera; *Sineportella* Wood and Marsh, Ectoprocta). New taxa described included rotifers (1 species), copepods (1 species), pulmonate snails (1 species), ectoprocts (4 species), and aquatic insects (31 species). Among aquatic insects, Trichoptera accounted for 19 new species, Diptera 7, Megaloptera 2, Ephemeroptera 2, and Plecoptera 1. Almost ½ the taxa described in *J-NABS* (16 species, 1 genus) were published in a 1995 special issue on “Present Status and Future Directions of Tropical Stream Research” (Jackson and Sweeney 1995; volume 14, issue 1; Fig. 1) (Blahnik 1995, Contreras-Ramos 1995, Epler and de la Rosa 1995, Holzenthal 1995).

Taxonomic revisions and monographs accumulate all we know about the taxonomy and classification of a (preferably monophyletic) group of organisms. Except for the smallest clades, these publications are often several tens to hundreds of pages and are outside of the page limitations of *J-NABS* to publish. However, these large taxonomic monographs are of immediate benefit to benthology and will stand as definitive references for decades (e.g., Ruitter 1995). In general, new taxonomic descriptions published in *J-NABS* appeared within the context of comprehensive revisionary syntheses (e.g., Wiggins and Richardson 1989, Blahnik 1995, Moulton and Harris 1999, de Pinho et al. 2009), often including phylogenetic analyses (Whitlock and Morse 1994, Lugo-Ortiz and McCafferty 1996). Many of these papers included the descriptions of immature stages (e.g., Stark and Ray 1983, Wrubleski and Roback 1987, Ramirez and Novelo-Gutierrez 1999), observations of novel life stage information or habitat (Epler and de la Rosa 1995, Burian 2002, Paprocki et al. 2003, Morse and Lenat 2005), and keys to regional faunas (Glover and Floyd 2004).

Of particular interest and utility for *J-NABS* readers are studies dealing with the taxonomy of immature stages. Accordingly, new larval/pupal/nymphal associations, descriptions, and keys have appeared

relatively frequently in *J-NABS* (total of 20 contributions). Among the most noteworthy contributions are descriptions of new associations of genera (e.g., Monson et al. 1988, Huryn 1989, Contreras-Ramos and Harris 1998), and studies that included life-history data (e.g., Roback and Ferrington 1983) or novel techniques of life-history stage associations (Zloty et al. 1993, MacDonald and Harkrider 1999). Major contributions covering immature taxonomy and identification keys for the North American fauna during the period reviewed, but not published in *J-NABS*, include works of broad taxonomic coverage (e.g., Peckarsky et al. 1990, Smith 2001, Thorp and Covich 2001), the latest edition of *An Introduction to the Aquatic Insects of North America* (Merritt et al. 2008), and works focused on specific taxa (e.g., Floyd 1995, Glover 1996, Wiggins 1996, Stewart and Stark 2002). In spite of this advancement, most aquatic macroinvertebrate species (primarily the hemi- and holometabolous insects) are unknown in the immature stages. The importance of species-level identification of immature stages for bioassessment (Lenat and Resh 2001) and life-history studies cannot be overstated (see *Taxonomic resolution* below). Last, comprehensive identification guides are lacking for most of the tropical regions of the world, although recent works have improved our knowledge greatly for some taxa (e.g., Dominguez et al. 2006).

The study of aquatic insect morphology is not directly a taxonomic discipline, but it has contributed to advances to benthology and to science in general, for example, in the study of feeding behavior and mouthpart morphology (Cummins 1973, McShaffrey and McCafferty 1986 [Fig. 1], 1988 [Fig. 1]), functional morphology and hydrodynamics (Merritt et al. 1996), the origins of insect flight (Marden and Thomas 2003), and Hynes' (1970) classic coverage of the morphological adaptations of benthic organisms to the aquatic environment. Five papers published in *FIB* included purely morphological treatments: Sierszen et al. (1982) on the chaetotaxy of *Mysis*, Tozer (1982) on the antennal morphology of *Nectopsyche*, Smith (1983) on the sense organs of tubificid worms, Deutsch (1985) on female caddisfly leg morphology. Only a few *J-NABS* papers focused primarily on morphology. McShaffrey and McCafferty (1986, 1988) studied the functional morphology of mayfly feeding and Kennedy and Haag (2005) presented a morphometric analysis of glochidia (*Bivalvia*) shell size.

Nomenclature, checklists, and faunal surveys

Other important aspects of taxonomy are nomenclature, checklists, and faunal surveys and invento-

TABLE 1. New taxa described in *J-NABS* and *Freshwater Invertebrate Biology [FIB]* from 1983 to 2009.

Reference	Higher taxon	Status	Region	Taxa described (original combinations)
Stark and Ray (1983) ^a	Plecoptera:Perlodidae	New species	Nearctic	<i>Helopicus bogaloosa</i> Stark & Ray
Taylor and Jokinen (1984) ^a	Pulmonata:Physidae	New species	Nearctic	<i>Physa vernalis</i> Taylor & Jokinen
Vidrine et al. (1985) ^a	Rotifera:Conochilidae	New species	Nearctic	<i>Lacinularia causeyae</i> Vidrine, McLaughlin, & Willis ^b
Scheffer et al. (1986)	Trichoptera:Hydropsychidae	New species	Nearctic	<i>Hydropsyche aenigma</i> Scheffer, Wiggins, & Unzicker ^c
Wirth (1987)	Diptera:Ceratopogonidae	New species	Nearctic	<i>Dasyhelea sublettei</i> Wirth
Wrubleski and Roback (1987)	Diptera:Chironomidae	New species	Nearctic	<i>Procladius deltaensis</i> Roback
Wiggins and Richardson (1989)	Trichoptera:Limnephilidae	New genus	Nearctic	<i>Eocosmoecus</i> Wiggins & Richardson
Monson and Holzenthal (1993)	Trichoptera:Hydroptilidae	New species	Nearctic	<i>Oxyethira itasca</i> Monson & Holzenthal
Reid and Strayer (1994)	Copepoda:Cyclopidae	New species	Nearctic	<i>Diacyclops dimorphus</i> Reid & Strayer ^d
Whitlock and Morse (1994)	Trichoptera:Leptoceridae	New species	Nearctic	<i>Ceraclea enodis</i> Whitlock & Morse
Blahnik (1995)	Trichoptera:Hydropsychidae	New species	Neotropical	<i>Smicridea aries</i> Blahnik, <i>S. gomezi</i> Blahnik, <i>S. gomphotheria</i> Blahnik, <i>S. gemina</i> Blahnik, <i>S. catherinae</i> Blahnik, <i>S. hybrida</i> Blahnik
Contreras-Ramos (1995)	Megaloptera:Corydalidae	New species	Neotropical	<i>Chloronia convergens</i> Contreras-Ramos, <i>C. zacapa</i> Contreras-Ramos
Epler and de la Rosa (1995)	Diptera:Chironomidae	New genus, new species	Neotropical	<i>Tempisquitoneura merrillorum</i> Epler
Holzenthal (1995)	Trichoptera:Leptoceridae	New species	Neotropical	<i>Nectopsyche exophthalma</i> Holzenthal, <i>N. monticola</i> Holzenthal, <i>N. onyx</i> Holzenthal, <i>N. ortizi</i> Holzenthal, <i>N. tapanti</i> Holzenthal, <i>N. tuanis</i> Holzenthal, <i>N. utleyorum</i> Holzenthal
Lugo-Ortiz and McCafferty (1996)	Ephemeroptera:Baetidae	New genus, new species	Neotropical	<i>Prebaetodes sitesi</i> Lugo-Ortiz & McCafferty
Wood and Marsh (1996)	Ectoprocta:Victorellidae	New genus, new species	Nearctic	<i>Sineportella forbesi</i> Wood & Marsh
Wood (2001)	Ectoprocta:Plumatellidae	New species	Nearctic ^e	<i>Plumatella bushnelli</i> Wood, <i>P. nodulosa</i> Wood, <i>P. similirepens</i> Wood
Jacobsen and Perry (2002)	Diptera:Chironomidae	New species	Nearctic	<i>Manoa pahayokeensis</i> Jacobson
Paprocki et al. (2003)	Trichoptera:Hydropsychidae	New species	Neotropical	<i>Smicridea travertinera</i> Paprocki, Holzenthal, & Cressa
Glover and Floyd (2004)	Trichoptera:Leptoceridae	New species	Nearctic	<i>Nectopsyche waccamawensis</i> Glover & Floyd
Morse and Lenat (2005)	Trichoptera:Leptoceridae	New species	Nearctic	<i>Ceraclea joanna</i> Morse & Lenat
Funk et al. (2008a)	Ephemeroptera: Ephemereillidae	New species	Nearctic	<i>Eurylophella oviruptis</i> Funk
de Pinho et al. (2009)	Diptera:Chironomidae	New species	Nearctic, Oriental, Neotropical	<i>Skutzia epleri</i> de Pinho, Mendes, & Andersen, <i>S. inthanonensis</i> de Pinho, Mendes, & Andersen, <i>S. quetzali</i> de Pinho, Mendes, & Andersen

^a Published in *FIB*^b Transferred to the genus *Conochilopsis* Segers and Wallace (Rotifera:Conochilidae) (Segers and Wallace 2001)^c Included in the genus *Ceratopsyche* Ross & Unzicker by some authors (see Morse and Holzenthal 2008 for discussion)^d Transferred to the genus *Reidcyclops* Karanovic (Karanovic 2000)^e Also reported from New Zealand (Wood 2001)

ries, which have received little or no attention in *J-NABS*. Only one paper dealing with nomenclature was published in *FIB* (Loden and Harman 1982, designation of a *nomen novum*) and 4 *J-NABS* papers dealt with formal changes in taxonomic status: Smicrideinae new subfamily status (Trichoptera) (Scheffer 1996); *Ceratopsyche* new subgenus status (Trichoptera) (Scheffer et al. 1986); Melanemerellidae new family status (Ephemeroptera) (Molineri and Dominguez 2003); *Drunella cornuta* and *D. cornutella* (Ephemeroptera), revised species status (Funk et al. 2008b). Formal checklists are the primary source for maintaining up-to-date lists of taxonomic names, synonyms and associated taxonomic literature, for providing distributional information, and as starting points for taxonomic revisions and monographs (Morse 1997a). Checklists also are often the basis for any initial ecological or applied study that examines communities (e.g., Merritt et al. 2008). No formal checklists have been published in *J-NABS*.

Faunal surveys and inventories enable us to follow the expansion and contraction of species' ranges, to track the movement of invasive species, to monitor populations of threatened or endangered species, and to assess the recolonization of restored habitats or track a community's response to changes in water quality. These efforts often discover new species, new distribution records, or result in a better understanding of habitat requirements. The popularity of "BioBlitzes" (Lundmark 2003) often leads to new discoveries, as do more intensive, research-driven inventories, such as the National Park Service's Smoky Mountain "All Taxa Biodiversity Inventory," where >858 new species of organisms have been discovered (www.dlia.org)! The importance of survey and inventory efforts is also reflected in the National Science Foundation's investment in its "Biodiversity Surveys and Inventories" and "Planetary Biodiversity Inventories" programs. *J-NABS* is not seen as an outlet for survey data, but several significant new distribution records were published in *FIB*. These included Bingham and Hiltunen (1985) on a tubificid oligochaete, Smith (1985) on the range expansion of a freshwater mussel, Simpson and Abele (1984) on the range expansion of an exotic naidid oligochaete, and Seagle and Wetzel (1982) on an enchytraeid oligochaete. Distributional data have been published in *J-NABS* by Montz (1988), who added to Simpson and Abele's (1984) naidid records, and Smith (1988), whose new North American record of the freshwater ectoproct *Stephanella* included a review of its taxonomy and a detailed study of its morphology. Range discontinuities in some species or incidences of population declines, including Strayer et al. (1996) in

a population survey of an endangered mussel (*J-NABS*) and Smith (1982) on the contraction of a crayfish range (*FIB*), also have been reported.

Phylogenetics and Molecular Systematics

Cladistics and comparative phylogenetics

Coverage of phylogenetic studies in *J-NABS* has been limited. However, 2 key Trichoptera papers were published in *J-NABS*. Weaver and Morse (1986; Fig. 1) (32 citations) and Wiggins and Wichard (1989; Fig. 1) (28 citations) examined the phylogenetic importance of larval feeding ecology and case-making behavior, and pupation, respectively. Both papers have been cited frequently since their appearance, primarily in entomological literature, but also in studies of phylogeny reconstruction using ecological (Miller and Wenzel 1995) and behavioral traits (Wenzel 1992). Specifically, Weaver and Morse (1986) was the first study in *J-NABS* to use a comparative phylogenetic approach to infer an hypothesis of the ecology of the trichopteran ancestor. Together with Ross (1967), these papers contributed to the debate on the basic phylogenetic hypotheses of major lineage evolution in Trichoptera (for a review see Morse 1997b), and thereby, serve as the basis for recent and ongoing studies to resolve these basal relationships (Frانيا and Wiggins 1997, Kjer et al. 2001 [Fig. 1], 2002, Holzenthal et al. 2007). Other cladistic studies published in *J-NABS* include McCafferty and Wang (1994) on the *Timpanoga* complex (Ephemeroptera:Ephemerillidae), Scheffer's (1996) work on the subfamilies of Hydropsychidae (Trichoptera), Stuart and Currie's (2002) phylogeny of lepto-cerid caddisflies using behavioral characters of case construction, Molineri and Dominguez' (2003) study on the placement of *Melanemerella* (Ephemeroptera), and Lugo-Ortiz and McCafferty's (1996) study on the *Baetodes* group (Ephemeroptera).

Comparative phylogenetic approaches, the use of independently derived phylogenetic trees to compare traits among species (Harvey and Pagel 1991), also have been used in applied benthic ecology as a response to the recent inclusion of ecological and behavioral characters (species traits) in community analysis. For example, Poff et al. (2006; Fig. 1) used a comparative approach to identify species traits that were not strongly influenced by phylogeny for application in multivariate community ecology studies. Historically, species-traits approaches in benthic ecology are based on the riverine habitat templet of Townsend and Hildrew (1994), an adaptation of Southwood's (1977) habitat templet concept, and describe the influence of the physical habitat as the

primary factor influencing autecology. The use of traits in benthic ecology was developed further by a number of authors (e.g., Resh et al. 1994, Statzner et al. 1997), but also by a contribution in *J-NABS* by Poff (1997) with the introduction of the concept of the habitat as a filter for biological traits. Additional studies published in *J-NABS* have used species traits of benthic macroinvertebrates (Townsend et al. 1997, Lamouroux et al. 2004, Resh et al. 2005, Dolédec et al. 2006, Paillex et al. 2007) as an alternative to taxonomic approaches. Although it is too soon to measure how the comparative phylogeny approach will stand the test of time, we think it likely that the approach of Poff et al. (2006) will be influential in species-traits studies.

Historical biogeography

Aquatic insects studies, most notably the work of Brundin (1966; Fig. 1) on trans-Antarctic midges and Andersen (1982) on water striders, have contributed greatly to the development of the discipline of historical biogeography. The often-narrow habitat requirements and limited dispersal abilities of aquatic macroinvertebrates make them ideal organisms with which to study global patterns of biogeography in space and time (e.g., Dillon and Robinson 2009). Four papers dealing with historical biogeography have appeared in *J-NABS*. In their paper describing a new species of *Manoa* (Chironomidae) from the Everglades, Jacobsen and Perry (2002) discussed the possible Gondwanan origin of the genus. McCafferty (1998; Fig. 1) presented a comprehensive review of various dispersal and vicariance hypotheses of the interchange of generic lineages and species of mayflies between North and South America. Based on phylogenetic analysis of DNA sequence data, Page et al. (2008) inferred that the origin of Caribbean atyid shrimp genera was an ancient evolutionary radiation via vicariance or dispersal. An analysis of cytochrome c oxidase I (COI) DNA sequence data concluded that high levels of generic diversity in pleurocerid snails in the Appalachian highlands of eastern North America suggest an ancient, Paleozoic origin of the populations (Dillon and Robinson 2009). These papers are excellent examples of the application of modern analytic tools in systematics to test hypotheses of regional patterns of distribution.

Biochemical and molecular systematics

The use of molecular sequence data to infer phylogenetic relationships among taxa has revolutionized the field of systematics. However, *J-NABS*

coverage of molecular and biochemical systematic work is very limited. Several studies published in *J-NABS* address DNA barcoding issues (see below), but only a few studies examine between-species relationships with biochemical methods or sequence data. Busack (1989) examined the evolutionary relationships within a recently diverged clade of *Procambarus* crayfish. Funk et al. (2006, 2008b) examined the species boundary between the obligately parthenogenetic mayfly *Centroptilum triangulifer* and its sexually reproducing sister species *C. alamanca*, and among 3 species of *Drunella* in eastern North America. Page et al. (2008) used mitochondrial DNA sequences as a tool to examine the evolutionary history of a radiation of Caribbean atyid shrimps (see above).

Other molecular and biochemical studies published in *J-NABS* have focused on intraspecific variation, in particular population structure (Sweeney et al. 1986, Hughes et al. 1995, Gibbs et al. 1998, Geenen et al. 2000, Elderkin and Klerks 2001, Monaghan et al. 2002, Yam and Dudgeon 2005, Pauls et al. 2009), phylogeography (Kauwe et al. 2004), speciation (Thomas et al. 1994), cryptic species (Duan et al. 2000), genetic differentiation and its implication in conservation (Geenen et al. 2000), and larval differentiation (MacDonald and Harkrider 1999). A few population genetic studies have formulated hypotheses that have been acknowledged and tested widely in the literature. The most prominent example is the patchy recruitment hypothesis, which explains local isolation of populations within streams by a combination of limited larval dispersal within streams and adult dispersal between streams, but with only a few adult females founding and maintaining each population (Schmidt et al. 1995, Bunn and Hughes 1997 [Fig. 1], Schultheis and Hughes 2005). Robinson et al. (1992) linked genetic diversity and life-history traits to show that genetic diversity is lower in populations living where environmental conditions are more stable.

DNA barcoding

DNA barcoding entails the use of one universally suitable gene region to differentiate among species (Hebert et al. 2003; Fig. 1). Its pros and cons have been actively debated. DNA barcoding (Miller 2007) or DNA taxonomy (sensu Vogler and Monaghan 2006) can help circumscribe biodiversity but cannot stand on its own or, by any means replace, morphology-based taxonomy (e.g., Ebach and Holdrege 2005, Will et al. 2005, Hickerson et al. 2006, Meier et al. 2006, Wheeler 2008b). For aquatic insects in particular, DNA barcoding has the appeal of facilitating and

quicken the process of associating different life stages of species (eggs, larvae, pupae, and adults) without time-consuming and often difficult rearing (Graf et al. 2005, Miller et al. 2005, Waringer et al. 2007, 2008; but see also Cameron et al. 2006 for a discussion on the cost of barcoding in other applications). Knowing and describing the immature stages is a vital prerequisite for applied (see *Taxonomic resolution* below), ecological, and evolutionary studies of aquatic insects (Weaver and Morse 1986, Wiggins and Wichard 1989, Pauls et al. 2008). The first application of DNA barcodes to associate life stages published in *J-NABS* was Zhou et al. (2007; Fig. 1) who used the method to associate larvae and females of Chinese Hydropsychidae (Fig. 3). DNA barcoding also carries great potential in associating sexes in adults (Willassen 2005, Johanson 2007).

DNA barcoding also has been used for species identification (e.g., Hebert et al. 2003, 2004, Monaghan et al. 2005). One of the first studies to test DNA barcodes for species identification was published in *J-NABS* (Ball et al. 2005; Fig. 1). This work on mayflies was the first of its kind and addressed a taxon relevant to all readers, taxonomic and applied, of *J-NABS*. The paper was recognized well beyond hydrobiologists (a total of 15 citations) and has been cited mostly in evolutionary biology journals. Although the general literature on barcoding has grown dramatically, only a few *J-NABS* papers have addressed its utility for identifying taxa from macroinvertebrate studies. Alexander et al. (2009) showed that in North American *Ephemera* our taxonomic knowledge is still insufficient to successfully use DNA barcodes for species identification. Carew et al. (2007) examined the utility of COI restriction-fragment length polymorphism (RFLP) and barcoding sequence data for determining the Tanytarsini (Chironomidae) from an environmental monitoring sample.

It will be interesting to see how DNA barcoding develops as a means for species identifications because enormous efforts are being made to catalog the barcodes of all described species (www.barcodinglife.org). Only when these large and taxonomically extensive data sets are analyzed in the future, will we actually be able to assess the limitations of barcoding as a means for species identification in ecological data sets. Also, as more studies investigate the utility of a single gene region, reassessment of the validity of using a single marker for DNA-based identifications, life stage associations, and other taxonomic studies (Roe and Sperling 2007) will become important. However, DNA barcoding is only one of many tools in the taxonomist's toolbox and a DNA barcode is basically useless unless it can

be linked to a formally established species name and compared with the morphology and DNA of type specimens (Miller 2007).

Taxonomic Resources

Book reviews and NABS bibliographies

J-NABS also has published reviews of books and other works published elsewhere. These reviews are not primary taxonomic resources per se, but *J-NABS* book reviews often have been of taxonomic revisions (e.g., Smith 1987), monographs (e.g., Wallace 1991), atlases (e.g., Kalff 1986), identification guides (e.g., Wood 1992), catalogs (e.g., Moulton 2001), or other works of importance to systematists and the *J-NABS* readership in general. These reviews (45 in total) have covered works treating taxa as diverse as fish (e.g., Angermeier 1998), annelids (e.g., Pennak 1986), mussels (e.g., Gordon 1994), general insects (e.g., Oswood 1998), diatoms (e.g., Parker 1997), and with either regional (e.g., Molloy 1987) or world-wide focus (e.g., Hynes 1987). Such reviews are an important contribution by *J-NABS* to the community. Of similar importance to taxonomy are the North American Benthological Society's (NABS) "Current and Selected Bibliographies on Benthic Biology." This publication is separate from *J-NABS*, but it has been an invaluable resource for accessing and keeping abreast of taxonomic literature, especially before the advent of CD-ROM or online searchable literature databases.

Online resources

Checklists, bibliographies, and distribution maps traditionally have been published in print format. However, once printed, they can quickly become out of date (Godfray et al. 2007). Online digital resources have the potential to reflect up-to-date taxonomy, classification, and phylogenetic placement (e.g., Tree of Life Web Project; Maddison et al. 2007). Thus, they have become increasingly more important to taxonomy than traditional print publication methods for both aggregation and dissemination of taxonomic and other information. In addition to *Zoological Record*, which has persisted for over 100 y as the primary resource for searching taxonomic literature, digital resources, such as taxonomic databases, faunal checklists, and online keys, have emerged to reduce barriers to access to information (Godfray et al. 2007) and to present this information in a searchable format. These contributions fall primarily into 3 categories: 1) large-scale database initiatives, 2) checklists, bibliographies, and distribution maps, and 3) interactive digital identification keys (Table 2).

TABLE 2. Some examples of digital and online taxonomic resources. Digital resources available online include taxonomic databases, large database cataloging initiatives, checklists, bibliographies, distribution data, and digital keys. In this table, checklists, bibliographies and distribution information are limited to those that address aquatic insect taxa.

Online resource	URL
Databases	
Animal Diversity Web	animaldiversity.ummz.umich.edu/site/index.html
Catalogue of Life	www.catalogueoflife.org
Encyclopedia of Life	www.eol.org
Global Biodiversity Information Facility (GBIF)	www.gbif.org
Integrated Taxonomic Information System (ITIS)	www.itis.gov
iSpecies	www.ispecies.org
Species2000	www.sp2000.org
Tree of Life	www.tolweb.org
ZooBank	www.zoobank.org
Zoological Record	www.scientific.thomson.com/products/zr (access by subscription only)
Checklists, bibliographies, and distribution information	
Ephemeroptera Galactica	www.famu.org/mayfly
Mayfly Central	www.entm.purdue.edu/Entomology/research/mayfly/mayfly.html
Plecoptera Society of North America Valid Stonefly Names	plsa.inhs.uiuc.edu/plecoptera/validnames.aspx
Plecoptera Species File Online	plecoptera.speciesfile.org/HomePage.aspx
Odonata Central	www.odonatacentral.org
Trichoptera World Checklist	entweb.clemson.edu/database/trichopt/index.htm
Trichoptera Literature Database	www.trichopteralit.umn.edu
Trichoptera Africana	www.senckenberg.de/trichoptera
Zobodat	www.zobodat.at
The Taxa and Autecology Database for Freshwater Organisms	www.freshwaterecology.info
Fauna Europaea	www.faunaeur.org
Nomina Insecta Nearctica	www.nearctica.com/nomina/main.htm
Interactive digital identification keys	
Interactive Key to the Aquatic Insect Orders of North America	www.entomology.umn.edu/museum/projects/keys
Eutaxa	www.eutaxa.com
Interactive Key to the Benthic Macroinvertebrate Orders and Families of North America	www.unb.ca/cri/bmi
Digital Key to the Aquatic Insects of North Dakota	www.waterbugkey.vcsu.edu
Aquatic Insects of Michigan	insects.ummz.lsa.umich.edu/~ethanbr/aim
Identification Key to the Orders (and Families) of Saskatchewan Aquatic Insect Larvae and Adults	www.aquatax.ca/TaxaKey.html
European Limnofauna	nlbif.eti.uva.nl/bis/limno.php

Large database initiatives to catalog species-level biodiversity online have emerged within the last 10 y, and have built largely on checklists and other online database resources (Table 2). The Global Biodiversity Information Facility (GBIF) is an international consortium whose mission is to facilitate digitization and global dissemination of primary biodiversity data. The Integrated Taxonomic Information System (ITIS) is a US federal government program, in partnership with Canada and Mexico, to create an easily accessible database with reliable information on species names and their hierarchical classification. Of particular importance to taxonomy and nomenclature is ZooBank, the official online registry of zoological nomenclature and its proposed mandatory registration of

names and nomenclatural acts (Polaszek et al. 2005). Most recently, the Encyclopedia of Life (EOL) has emerged as the main venue to pool taxonomic information at the species level. However, 2 issues are apparent in most of these large-scale database resources: 1) data on arthropods are probably the least complete, with species-level pages listing little other than taxonomic information if any is listed at all (e.g., photographs, distribution, biology, conservation status), and 2) these initiatives depend on the voluntary efforts of taxonomists to contribute to the completeness and quality of information and its maintenance (Armitage 2007, Flowers 2007b).

Interactive online digital identification keys have the potential to be used by a larger community of

benthologists than many of the other freely accessible and available taxonomic resources. Digital keys can link images (both illustrations and photographs) with morphological descriptions and provide multiple pathways for identification, a feature perhaps most useful to a novice user (Walter and Winterton 2007). Volunteer macroinvertebrate monitors require additional morphological figures for successful identification (Nerbonne and Vondracek 2003). These resources are increasingly available online (Table 2), but are also available in CD-ROM formats (e.g., Holzenthal et al. 2008, Lechtaler 2008). With the appropriate software, researchers can contribute keys that are adjustable to the level of the user. Given the growth of community and volunteer biomonitoring (Firehock and West 1995), online keys might provide inexpensive and accessible identification tools to a range of potential users. To date, however, online keys to benthic organisms that identify below the family level are still highly geographically regionalized in North America and are limited mainly to the mid-western region of the US (Table 2).

Museums and voucher collections

The 2.5 billion specimens estimated to be housed in the world's museums and natural history collections are far more than curios for the acquisitive. They represent the comparative material on which the science of systematics functions, and they serve to track the historical spread of human diseases, monitor changes to the environment, study species and genetic diversity, act as reference specimens for identification, and educate the next generation of systematists (Winston 2007). Despite their value, the decline in taxonomic expertise has come hand in hand with a decline in support for natural history collections (Winston 2007). A vast array of data on taxonomy, historical and contemporary distributions, seasonal occurrence, habitat type, host plant-parasite records, and ecological associations are associated with specimens. Polymerase chain reaction (PCR) technology and modern extraction protocols can be used to obtain DNA from museum specimens collected decades ago. The value of these data for tracking the imperilment status of aquatic insects and other species is especially enhanced when museum specimen data are georeferenced, databased, and publicly accessible (Shaffer et al. 1998, Graham et al. 2004, Winker 2004, DeWalt et al. 2005, Gaubert et al. 2006). In some instances, especially because of the biodiversity crisis, the only information we might ever have about some species will be from museum material.

Voucher collections, especially of material associated with ecological and bioassessment studies, are of

particular importance to benthology. Voucher collections, a subset of specimens for each taxonomic unit identified in the study, should be set aside and deposited in museums or other permanent repositories accessible to the scientific community to serve as a physical record of the application of the scientific name. Without vouchers, identifications, no matter how good the taxonomic literature or skill of the identifier, are always open to question. It is notable that *J-NABS*, unlike other journals (for example those published by the Entomological Society of America), does not have an explicit recommendation regarding voucher specimens. Often, material collected in basic or applied ecological studies might be more abundant than that collected by taxonomists or might have been collected over a longer period of time than that afforded to taxonomists during their often limited field work. As such, the probability that this material might yield new distribution records, new species, new ecological associations, or new life-history associations is high. Ecologists, applied benthologists, and taxonomists should work hand-in-hand to ensure that this material is deposited in museums and is recorded in the published scientific literature.

Taxonomic Resolution

J-NABS has actively led the discussion regarding the level of taxonomic resolution that is best suited to assess streams and rivers for different purposes. Our Web of Science search for "taxonomic resolution" and "stream*" or "river*" revealed 161 papers (search done 21 September 2009). Twenty-three of these (14.2%) were published in *J-NABS*, 11.2% were published in *Hydrobiologia*, and 9.3% were published in *Freshwater Biology*. Each journal seems to have maintained a regional focus with respect to the issue of taxonomic resolution. *J-NABS* focuses primarily on North America (76.2%); *Hydrobiologia* and *Freshwater Biology* are primary outlets for European (72.2% and 80%, respectively) and Australasian studies (44% and 40%, respectively). Our survey also showed that the topic is controversial. Since 1990, the number of studies has increased steadily, and from 2000 to 2008, an average of 14.55 papers were published every year (20 in 2008). Many of the *J-NABS* papers, in particular the discourse between Bailey et al. (2001; Fig. 1) and Lenat and Resh (2001; Fig. 1) on whether species-level or higher-level resolution is best, have been key to the discussion in North America and elsewhere. Both 2001 papers argue their points of view, which often differ dramatically, but both conclude that neither extreme position (all family vs all species-level identification) is sufficient or feasible. Like many of the authors who cite these 2

landmark papers (e.g., **Chessman et al. 2007**), they argue for a scaled approach, adapted to the area being surveyed. Diverse taxonomic groups with various ecologies should be determined to lowest possible level, and other taxa that only have few representatives with similar ecologies and tolerances should be determined to a higher level, e.g., family level as applied in North America (**Carter and Resh 2001**).

This scaled philosophy leads to application of differing levels of taxonomic resolution in different regions of world. The trend is toward higher resolution in regions where the fauna is well known and of moderate to high diversity. In central Europe, authors of many studies argue that species-level identifications are more discriminating, and thus, result in better assessment (Haase et al. 2004, Schmidt-Kloiber and Nijboer 2004, Gabriels et al. 2005, Verdonschot 2006). In northern Europe, the fauna is less diverse, and only a few species occur per genus and family. Thus, higher-level determination is sometimes sufficient (Heino and Soininen 2007, Raunio et al. 2007). In southern Europe or South America, the fauna is very diverse, but the species-level taxonomy is only poorly known (Feio et al. 2006, Verdonschot 2006). Based on the current state of knowledge, little additional resolution is obtained with genus/species-level identifications over family-level identifications (Dolédéc et al. 2000, Melo 2005, Feio et al. 2006). In North America and Australasia, most studies show that higher-level taxonomic resolution is sufficient for broad-scale and general bioassessment. However, the fauna in these regions is only moderately well known at the species level for many taxonomic groups. When considering diverse families or genera, where species-level identification is possible, species-level identifications do provide more resolution in bioassessment (**Waite et al. 2000, Lenat and Resh 2001, King and Richardson 2002, Arscott et al. 2006**). In North America, most taxa, even many Ephemeroptera, Plecoptera, and Trichoptera (EPT) genera, cannot be identified to species or their identification is problematic, even among experts (e.g., **Stribling et al. 2008**). For example, only 30% of the North American Trichoptera species are known as larvae (Wiggins 1996) or can be identified only by a depleted number of taxonomic experts (DeWalt et al. 2005). If the species-level taxonomy and ecology of these diverse and sensitive groups were better known and understood, assessments using species-level information probably would be more informative, more accurate, and more sensitive at identifying ecosystem integrity and changes.

Another problem with use of identifications above the species level is that most trait or tolerance-value

assignments are based on genus- or, sometimes, family-level identification and often bear little or no relationship to the actual traits, ecology, or tolerance of species (**Lenat and Resh 2001, Bried and Ervin 2007**). Species-level information could help dramatically in refining our assessment tools. Creators of new Internet databases (Vieira et al. 2006, ELC 2007) are attempting to compile all known data for species-level trait assignments where possible. Knowledge of where individual species occur and their ecological and morphological traits has the potential to improve greatly the resolution and accuracy of assessment schemes. New taxonomic tools, such as DNA taxonomy or DNA barcoding, can facilitate and quicken the process of identifying and differentiating benthic invertebrates. Clearly, our best chance of understanding diversity, species traits, and ecosystem function comes with species-level identifications for species-diverse taxa.

Conservation and Taxonomy

Freshwater habitats and the species they harbor are perhaps the most endangered in the world (Abell 2002, Saunders et al. 2002). The leading threats to freshwater biodiversity include agricultural nonpoint-source pollution, altered hydrological regimes, alien invasive species, changes in land use, and global climate change (**Richter 1993, Sala et al. 2000, Dextrase and Mandrak 2006, Brown et al. 2007**). In North America, freshwater ecosystems are particularly imperiled and might be experiencing species depletion rates as great, if not greater, than those of tropical forests (Ricciardi and Rasmussen 1999). Huge declines in stonefly, mollusk, crayfish, crustacean, and fish species have been reported (Master et al. 2000, **Strayer and Malcom 2007, Lysne et al. 2008**), and the International Union for Conservation of Nature and Natural Resource (IUCN) Red List of Threatened Species (IUCN 2008) includes hundreds of North American aquatic species listed at some level of concern (extinct, endangered, threatened, or vulnerable). However, only 48 aquatic insects appear on the Red List, and these insects are mostly odonates (IUCN 2008). Furthermore, only 4 aquatic insect species are currently protected by the US Endangered Species Act (an elmid beetle, a dryopid beetle, a dragonfly, and a naucorid bug) and a single EPT species, the limnephilid caddisfly, *Glyphopsyche sequatchi* Etnier and Hix (1999), from Tennessee, is a candidate for protection by the US Fish and Wildlife Service (USFWS 2007). Undoubtedly, these numbers do not adequately reflect the actual imperilment status of aquatic insects (DeWalt et al. 2005). Although less documented, EPT

taxa (especially stoneflies), which are particularly sensitive to human disturbances, have experienced a great decline in numbers (DeWalt et al. 2005).

J-NABS has published numerous articles related to conservation (Benke 1990, Brouha 1993, Careless and Barnese 1993, Coyle 1993, Mackay 1993, Pringle and Aumen 1993, Richter 1993, Dewberry and Pringle 1994, Strayer 2006, Strayer and Dudgeon 2010), yet only one of the reviewed works has discussed the importance of taxonomy and systematics in aquatic species conservation (Perez and Minton 2008). Indeed, systematists have the opportunity to play a critical role in conserving aquatic species by discovering new biodiversity, documenting species distributions, clarifying taxonomy, and resolving phylogenies.

The importance of continual documentation of biodiversity, both temporally and spatially, cannot be overstated. Morse et al. (1993) evaluated 74 EPT taxa from Appalachia (USA) to determine their imperilment status, but noted that a lack of historical baseline data prevented a more precise determination of their true status. By conducting taxonomic surveys, describing new species, and documenting their habitat, systematists make available this vital historical baseline data. Retroactive capture of specimen records in natural history collections could provide at least some historical data. Taxonomic revisions might provide an opportunity to contribute additional information about species distributions and abundances. Polhemus (1993) conducted an intensive survey to collect additional specimens to include in his taxonomic revision of the Hawaiian damselfly genus *Megalagrion*, and found that several species were no longer present in areas where they had been collected historically. The survey of *Megalagrion* and resulting information on its possible imperilment certainly contributed to the placement of several *Megalagrion* species as candidates for protection under the Endangered Species Act. Systematists can further assist policy makers by providing species data to the Fish and Wildlife Service about taxa that should be considered as candidates for future listings (Opler 1993).

Taxonomic revisions also provide comprehensive information on the identity of species and a stable nomenclature and classification “so that scientists and resource managers know exactly what it is they are trying to save” (Polhemus 1993). For example, a phylogenetic analysis of the pleurocerid snail genus *Lithasia* revealed 2 new imperiled cryptic species that had previously been included inappropriately in a widely distributed species (Minton and Lydeard 2003). Systematic studies can help guide conservation

priorities by determining areas of high phylogenetic diversity in the form of evolutionary significant units (Moritz 1994, Faith and Baker 2006, Perez and Minton 2008).

Professional Training, Taxonomic Certification, and Graduate Education

As an organization, NABS has recognized the value and importance of taxonomy in benthic science. The society has initiated the very popular annual Taxonomy Fairs (in 1997; Fig. 1) and technical workshops held at its annual meetings as responses to the limited taxonomic training most biology majors receive. An increasing number of members also list taxonomy as their primary interest area (Johnson 2007). NABS also has recognized that academic support for faculty positions and student training related to nonmolecular, organismal taxonomy is declining. Concerns have been expressed to the NABS leadership by a number of state and federal agencies (NABS 2008). In addition, DeWalt et al. (2005) suggested that the trend toward the use of lower taxonomic resolution (family- and genus-level) in bioassessment is a result of the lack of well-trained taxonomists able to identify or circumscribe taxa at the species-level. To counteract this trend, NABS has been a leader among its peer organizations in initiating a Taxonomic Certification Program (in 2005; Fig. 1) that specifically recognizes that “high quality taxonomy is crucial to credible ecological studies and reliable bioassessment programs.” A stated goal of the program, in addition to providing professional taxonomic certification, is to promote graduate training of new taxonomic experts (NABS 2008). To support this latter goal, NABS has initiated a campaign to establish an endowment to support graduate student travel and research in taxonomy and systematics.

Traditionally, a formal education in biology involved gaining a broad knowledge of organismal diversity and related aspects, such as functional morphology, embryology, and physiology, as well as scientific reasoning, history, and philosophy (Ball 1988). Students of biology were expected to devote a great deal of their time to learning the basic skills needed to observe, collect, identify, and describe the natural world (Ball 1988, Godfray and Knapp 2004). In other words, they learned taxonomy. However, during the last few decades, the discipline of taxonomy has taken a back seat in the biological curriculum. This decline in teaching and funding for taxonomy has been attributed to the growth of the field of molecular biology (Godfray and Knapp 2004). Studying taxonomy came to be viewed as passé as

new biology students flocked to what was perceived as the “sexier” end of the field, molecular biology (Godfray and Knapp 2004, Raven 2004). The result has been a long-term decline in both professional and amateur taxonomists (Gaston and May 1992, Hopkins and Freckleton 2002, Godfray and Knapp 2004). Today, <6000 professional taxonomists exist worldwide (Wilson 2004). Furthermore, a large mismatch exists between the number of taxonomists studying a particular taxon and that taxon’s species diversity (Gaston and May 1992).

In light of the biodiversity crisis, this lack of investment in taxonomic training is perhaps the greatest obstacle to conservation research (Gotelli 2004). Recognition of the urgent need to train new taxonomists led to the creation of the US National Science Foundation Partnership for Enhancing Expertise in Taxonomy (PEET) program (Rodman and Cody 2003, Rodman 2007). The PEET program provides training of students in basic descriptive, revisionary, and monographic taxonomy, with an emphasis on lesser known, yet extremely species diverse organisms (DRR was a PEET-funded graduate student). The PEET program has been touted as a successful model for tackling the taxonomic impediment and attracting young workers to the field (Boero 2001, Rodman and Cody 2003, Rodman 2007). In addition, new molecular techniques applied to taxonomy and the introduction of cybertaxonomy have made the field “fashionable” again (Gewin 2002, Mallet and Willmott 2003, Pyle et al. 2008, Wheeler 2008a). The core of taxonomy is the discovery of biodiversity, an exciting prospect that has lured many young workers into the field. Still, convincing students to enter a particular field is difficult if they perceive that they will not be hired once they are trained. Surveys have shown that most PEET-trained taxonomists are indeed gaining employment; however, they are likely to be hired in positions where they cannot fully practice taxonomy (Agnarsson and Kuntner 2007, Rodman 2007) or in positions that do not afford an opportunity to train graduate students (e.g., undergraduate teaching institutions). Therefore, to confront the impediment fully and to attract new workers in taxonomy, newly trained professionals must be employed to practice the taxonomy they have been taught.

Conclusions

Systematics has contributed fundamentally to our understanding of the natural world. Systematic contributions in *J-NABS* have been few compared to contributions in other areas of benthology, but as part

of the nexus of taxonomic literature, all contributions have been important to the discipline. Contributions also have traced the overall development of systematics in general; for example, all recent systematics contributions to *J-NABS* (2006–2008) have included biochemical or molecular data (e.g., allozymes or DNA sequences). As systematics continues to develop new approaches to studying biological diversity and confronts emerging challenges, these topics are sure to be reflected in the pages of *J-NABS*.

J-NABS can be viewed as a truly collaborative venue for benthic science. The disciplines of its contributors range in specialization but are united by their study organisms and the habitat features of those organisms. In consequence, we see many avenues where taxonomy can continue to contribute to *J-NABS* as stand-alone descriptive and phylogenetic studies and in a collaborative framework within which life-history and ecological studies can include insights from taxonomy to produce what can be viewed as “complete packages” of information for species. In addition, phylogenetic studies that synthesize ecological or behavioral information already have illustrated how important it is to understand the interactions of biological attributes in an evolutionary context. However, we stress the primacy of descriptive taxonomy and comparative morphology in benthic science for providing the foundation for phylogenetic analysis and its subsequent application to studies of functional morphology, community ecology, life-history investigations, trophic interactions, or behavior (Wheeler 2004, 2008b).

In spite of their great importance, the impact factor of descriptive taxonomic papers is low (Agnarsson and Kuntner 2007). Of the papers listed in Table 1 (excluding the first 3, published in *FIB*), only 1 (**Lugo-Ortiz and McCafferty 1996**) received significant subsequent citations in the literature (17), but of these, 14 citations were in other works published by the authors. The remaining works listed in Table 1 have received 6 (1 paper), 5 (1 paper), 3 (3 papers), 2 (3 papers), 1 (5 papers), or no (6 papers) subsequent citations (search done 18 September 2009). Evaluating the significance of taxonomic contributions by simple tallies of numbers of subsequent citations, or by more formal impact factor measures of journals themselves, misses the enduring importance of taxonomic contributions (Minelli 2003, Agnarsson and Kuntner 2007, Padial and de la Riva 2007, Rosser et al. 2007). In the future, examinations of the user interactions from scholarly literature portals (e.g., Web of Science, J-STOR, etc.) by the academic community might be more indicative of real usage than counts of citations (Bollen et al. 2009). These assessments of citations

could become less applicable to taxonomy and systematics in general. Underlying the initiatives to make taxonomic resources available online is a larger conversation within the taxonomic community suggesting that taxonomy should be approached and communicated more as an “e-science” where alpha taxonomy is conducted primarily online (Godfray et al. 2007, Mayo et al. 2008, Clark et al. 2009). University assessment metrics for “scholarly activity” will have to be adjusted to assess contributions of the taxonomic community in this nonjournal venue.

Certainly the descriptive taxonomic contributions in *J-NABS* on benthic organisms are far fewer than those occurring in other journals, especially *Aquatic Insects* (began in 1979; Fig. 1) and, more recently, *Zootaxa* (began in 2001; Fig. 1). New species are being discovered continuously, even within the well-known North American fauna, and new species descriptions have appeared in *J-NABS* (e.g., **Wood 2001, Jacobsen and Perry 2002, Glover and Floyd 2004, Funk et al. 2008a**) (Table 1). Although it is often considered the most traditional branch of systematics, descriptive and revisionary taxonomy is still of fundamental importance (Wheeler 2004, 2007) and the “Age of Discovery” is far from over (Donoghue and Alverson 2000, May 2004). The original description (and the act of typification) serves to anchor all subsequent published information of a species in the literature (Minelli 2003). This historical nexus of literature is an enduring legacy of taxonomy.

Cybertaxonomy holds great promise to democratize taxonomy by providing to a community of integrated users the technological tools necessary to collect, describe, and catalog the world’s biodiversity and to use this information in concert with conservation efforts to address the biodiversity crisis (Page et al. 2005, Godfray et al. 2007). PEET and other funding programs designed to train a new generation of taxonomists have the potential to stem the tide of declining taxonomic expertise; funding for this program should be increased and similar programs at other agencies should be established. NABS’s support for taxonomy is evidenced by its recently established endowment to support graduate student research in taxonomy and systematics and its long-standing taxonomy fairs and workshops. The Society for Systematic Biology’s Mini-PEET grants program (<http://systbiol.org/>) is also an excellent investment in the future of the discipline. Perhaps NABS should follow suit.

Museums and natural history collections harbor an invaluable treasure trove of specimens and associated records. These specimens are the sine qua non of taxonomic research. Museum curators are engaged in

exciting new initiatives to capture digital images of holotypes (E-Type Initiative: <http://insects.oeb.harvard.edu/etypes/index.htm>) and morphological characters (Morphbank: <http://www.morphbank.net/>; MorphoBank: <http://morphobank.geongrid.org/>), to georeference locality records and other specimen-level data, and to upload this information into searchable, online databases. Interactive identification keys and other online identification resources offer new ways of identifying taxa, with the added benefit of almost limitless links to illustrations, photographs, and online sources of additional information. Rather than suffer through more years of insufficient support, the world’s natural history collections should be infused with new funding to support their critical service to society. Administrators, granting agencies, and tenure committees should recognize the value of taxonomic contributions, even if these contributions and the journals in which they are published have little “impact.” DNA-barcoding offers an exciting new technology to aid species identification, but only taxonomy can provide the scientific paradigm within which these identifications will be meaningful.

Taxonomy is a multidimensional discipline spanning all levels of biological organization and incorporating the latest technological advances. It is a discipline rich in opportunities for students and researchers with varied talents, interests, and expertise, all united by a passion to study the diversity of life on Earth. It is now poised, largely through the creative skills and perseverance of its own practitioners, to meet the challenges of collecting, describing, and cataloging the rich biological diversity of the planet and to confront the biodiversity crisis.

Acknowledgements

This paper is dedicated to the taxonomists who have and will continue to contribute so importantly to the success of *J-NABS* and to the science of benthology in general. We are grateful to Pamela Silver for inviting us to participate in this anniversary issue. Alan Steinman was of great help in steering us through the process and offered many useful suggestions. The review benefited greatly from the many suggestions, ideas, and insights of our colleagues: Brian Armitage, Roger Blahnik, David Bowles, Atilano Contreras-Ramos, Wills Flowers, Jolanda Huisman, Karl Kjer, Manny Pescador, Andy Rasmussen, Dave Ruitter, and Johann Waringer. Our sincere appreciation is extended to the following sources of support: University of Minnesota Graduate School Doctoral Dissertation Fellowship (DDR), University of

Minnesota Graduate School Post-Doctoral Fellowship (PKM), and the German Academy of Sciences Leopoldina Fellowship (BMBF-LPD 9901/8-169) (SUP). This material is based upon work supported by the National Science Foundation under Grant No. 0117772. Additional support came from the University of Minnesota Experiment Station under project numbers 34-15 and 34-17. This support is gratefully acknowledged.

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Received: 10 April 2008
Accepted: 6 October 2009