FUNCTIONAL TRAIT NICHES OF NORTH AMERICAN LOTIC INSECTS: EVOLUTIONARY CONSTRAINTS ON TRAIT-BASED ECOLOGICAL APPLICATIONS

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SUPPLEMENTAL METHODOLOGY

Resolution of the Phylogenetic Tree

Phylogenetic relationships of the North American lotic insects were resolved based on a compilation of morphology- and molecular-based phylogenetic analyses, and classifications. The tree was constructed using MacClade (Maddison and Maddison, 2001). A group-membership character (Farris, 1973) was constructed for each resolved clade. Each group-membership character was named for the reference upon which it was coded.

The tree was resolved as follows. Relationships among the orders followed Wheeler et al. (2001) as the most comprehensive phylogenetic analysis available at this level. When multiple phylogenetic analyses were performed in a study on different data partitions (as in Wheeler et al., 2001), the simultaneous analysis of all characters (A. G. Kluge, 1989; Nixon and Carpenter, 1996) was used to resolve the relationships. All orders, families, subfamilies, and tribes were resolved as clades unless there was contrary evidence available. Contrary evidence was found for two cases: Kathroperla was removed from the Chloroperlidae following Terry and Whiting (submitted), and Apatania was moved from the Lomnephilidae to the Apataniidae following Morse (2004).

The following eight guidelines were followed in cases of conflicting relationships inferred among studies. First, molecular analyses with greater bootstrap (Felsenstein, 1985) / jackknife (Farris et al., 1996) support and character sampling were used instead of molecular analyses with lower bootstrap / jackknife support and character sampling. As a result, Hovmöller et al. (2002) was used instead of Saux et al. (2004) for the resolution of the Lestidae within the Odonata. Also, Terry and Whiting (submitted), rather than Thomas et al. (2000) was used for resolution of the interfamilial relationships within the Plecoptera. Second, molecular phylogenetic analyses with clades supported by $\geq$ 63% bootstrap or jackknife support were used instead of morphology-based phylogenetic analyses in which no branch support was reported. Clades with $\geq$ 63% bootstrap or jackknife support are supported by the equivalent of at least one uncontradicted synapomorphy (Farris et al., 1996). Following this guideline, Osborne et al. (2004) was followed instead of McCafferty and Wang (1994) where they conflicted for resolution within the Ephemerellidae. Terry and Whiting (submitted) was used in place several earlier studies where they conflicted in the Plecoptera: Zwick (2000) for resolution of the Capniidae, Leuctridae, and Nemouridae; Surdick (1985) for resolution within the Chloroperlidae; Shepard and Baumann (1995) for resolution within the Leuctridae; Baumann (1975) for
resolution within the Nemouridae; Nelson (1979) within the Perlidae; and Stark and Szczytko (1988) within the Perlodidae.

Third, morphology-based analyses were followed over molecular-based analyses in which the clades were supported by < 63% bootstrap or jackknife support. As such, Scheffer (1996) was followed instead of Kjer et al. (2002) for resolution of Simicridea and Diplectrona (Hydropsychidae). Fourth, recent phylogenetic analyses with clades supported by ≥ 63% bootstrap or jackknife support were preferred over resolution in The Tree of Life Web Project (http://tolweb.org/tree/phylogeny.html) that was not entirely based on a single phylogenetic analysis. Therefore, when they conflicted, Terry and Whiting (submitted) was followed instead of resolution in The Tree of Life Web Project for the Capniidae, Chloroperlidae, Perlidae, and the Taeniopterygidae.

Fifth, classifications were used instead of molecular-based phylogenetic analyses for which the clades had < 63% bootstrap or jackknife support. Following this guideline, resolution of the Aeshnidae, Corduliidae, and the Gomphidae followed Trueman and Rowe (2001) instead of Misof et al. (2001). Also, Carle (1986) was used instead of Misof et al. (2001) for resolution within the Gomphidae, and Bechly (2004) was used in place of Saux et al. (2003) for resolution of the Cordulegastridae. Finally, Wiggins (1996) was used instead of Kjer et al. (2002) for resolution of Diplectrona and Homoplectra. Sixth, classifications were used when explicit phylogenetic analyses were not available. Therefore, Morse (2004) was used for resolution within the Hydroptilidae). Seventh, more recent and comprehensive classifications were used over earlier and less comprehensive classifications. As such, N. J. Kluge (1998, 2004) was used instead of Peters and Campbell (1991) for the Ephemeroptera. Eighth, phenetic analyses were used when neither cladistic analyses nor classifications were available. As a result, Nelson (1979) was used for determining the resolution of Attaneuria within the Perlidae.

Three genera from the Plecoptera were excluded from our tree: Alaskaperla, Bisancora, and Diploperla. We were unable to find a phylogenetic analysis or classification that allowed us to resolve Alaskaperla within the Chloroperlidae or Diploperla within the Perlodidae. Although Bisancora was sampled by Surdick (1985), due to conflict and differential sampling relative to Terry and Whiting (submitted), we were unable to resolve it within the Chloroperlidae.

Mapping Ecological Characters onto the Tree

The consistency and retention indices (A. G. Kluge and Farris, 1969; Farris, 1989) were calculated for each of the 20 ecological characters using MacClade. All characters were treated as unordered (i.e., one step between every character state). All character states were included in these calculations – parsimony-uninformative character states were not excluded (see Davis et al., 1998). The consistency index measures homoplasy (convergence and/or reversal events) by comparing the observed number of steps for each character relative to the minimum possible number of steps (e.g., a two-state character would have a minimum of one step; a four-state character would have a minimum of three steps). In contrast, the retention index measures homoplasy relative to the maximum possible number of steps (e.g., an analysis of 250 taxa, in which 230 taxa have state 1 and 20 taxa have state 2, would have a maximum of 20 steps). Both indices range from zero (maximum homoplasy) to one (no homoplasy). The retention index can equal zero, whereas the consistency index can asymptotically approach, but never equal, zero. For ease of interpretation, we have limited our analyses to the consistency index (the more intuitive of the two indices), but report both indices for completeness.
Unfortunately, our phylogenetic tree of the North American allotic insects was not fully resolved (i.e., dichotomous), and included some large polytomies (e.g., the 13 genera within the Baetidae were unresolved relative to one another). MacClade was set to treat polytomies as uncertainty in resolution and therefore calculated the minimum possible number of steps when optimizing the characters onto the tree. Therefore, the actual number of steps, and consequently the number of inferred convergences and/or reversals, may be underestimated due to lack of resolution. Other potentially confounding factors that were not taken into account in our analyses include the exclusion of extinct fossil taxa, terrestrial taxa, and allotic-insect taxa that are native to North America. We anticipate that the rigor of this study will be improved upon by increasing taxonomic sampling and as more insect taxa are included in well supported phylogenetic analyses, which may be used to update our inferred tree.

Each of the ecological characters was mapped onto the entire tree, the Ephemeroptera-Plecoptera-Trichoptera tree, as well as each of the seven orders that included at least four terminals (Coleoptera: 9; Diptera: 18; Ephemeroptera: 62; Hemiptera: 12; Odonata: 36; Plecoptera: 79; Trichoptera: 87) independently of one another. Note that due to the differences in number of taxa and degree of resolution within each of these nine analyses, the consistency and retention indices are not directly comparable among them. For example, the fewer taxa and the less resolution within an order, the higher the consistency index is expected to be given that there are fewer opportunities to infer character-state changes, and hence homoplasy (Sanderson and Donoghue, 1989). However, the relative degree of homoplasy among ecological characters will be directly comparable across orders. For example, character X may be more homoplasious than character Y within the Coleoptera, but character Y may be more homoplasious than character X within the Trichoptera.

Some characters are constant within orders. For these constant characters, both the consistency and retention indices are undefined (indicated by “N/A” in the Table). For characters that are variable, but the minimum number of steps is identical to the maximum number of steps (i.e., characters for which only one state is present in two or more taxa), the consistency index is 1.0 and the retention index is undefined.

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REFERENCES


