Fulgoroid Phylogeny: Using Combined Molecular Datasets to Unravel Planthopper Evolution (Insecta, Hemiptera, Fulgoroidea)

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The planthopper superfamily Fulgoroidea comprises more than 12,000 described species in 20 families. While Fulgoroidea is monophyletic (Asche, 1987; Bourgoin et al., 1997), the relationships among the fulgoroid families remain largely contentious. A number of hypotheses of planthopper phylogeny have been proposed based on morphological evidence (Muir, 1923, 1930; Asche, 1987; Emeljanov, 1990; Bourgoin, 1993). Although there is congruence concerning relationships among some planthopper families (e.g., the monophyly of Delphacidae + Cixiidae, and of Kinnaridae + Meenoplidae), the results of these studies are otherwise incongruous with respect to relationships among all 20 families.

More recently, DNA nucleotide sequence data have been employed to attempt to elucidate planthopper phylogeny (Bourgoin et al., 1997; Yeh et al., 1998; Yeh & Yang, 2001). These studies concluded with several points of concordance, suggesting the overall utility of molecular data for resolving fulgoroid phylogeny. However, many of their conclusions were discordant, both with each other and with the previous morphological studies, leaving many questions regarding the phylogeny of Fulgoroidea unanswered.

In an attempt to better reconstruct fulgoroid phylogeny, I will discuss results of analyses including approximately 60 taxa in 17 planthopper families based on DNA nucleotide sequence data from three genetic loci. These results will be interpreted in light of the phylogenetic trends in ovipositor structure proposed by Asche (1987) and Bourgoin (1993), as well as what is known concerning host plant associations (based on Wilson et al., 1994).

Additionally, I will present results of an ongoing phylogenetic investigation of the planthopper family Fulgoridae. Although fulgorid planthoppers have received attention based on their often bizarre morphology and wax production (O'Brien, 2002), no phylogenetic hypothesis has yet been proposed for this group. My analyses, to date, include approximately 50 taxa in 35 genera based on DNA nucleotide sequence data from three genetic loci.

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