

# **The Current State of Insect Molecular Systematics: A Thriving Tower of Babel**

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Insect molecular systematics has undergone remarkable recent growth. Advances in methods of data generation and analysis have led to the accumulation of large amounts of DNA sequence data from most major insect groups. In addition to reviewing theoretical and methodological advances, we have compiled information on the taxa and regions sequenced from all available phylogenetic studies of insects. It is evident that investigators have not usually coordinated their efforts. The genes and regions that have been sequenced differ substantially among studies and the whole of our efforts is thus little greater than the sum of its parts. The cytochrome oxidase I, 16S, 18S, and elongation factor-1 $\alpha$  genes have been widely used and are informative across a broad range of divergences in insects. We advocate their use as standards for insect phylogenetics. Insect molecular systematics has complemented and enhanced the value of morphological and ecological data, making substantial contributions to evolutionary biology in the process. A more coordinated approach focused on gathering homologous sequence data will greatly facilitate such efforts.