

Role and Perspective of Molecular Approaches in Insect Systematics: A case study for higher classification of the family Tephritidae.

Ho-Yeon Han

Department of Life Science, Yonsei University

Phylogeny underlies our efforts to examine, explain, and manage the natural world. At the lower level, clear demarcation of species boundaries is essential if we are to develop any sorts of workable management plan for pest species. We must know what constitutes a species and have some basis for recognizing whether a population in a novel place or with a novel ecology belongs in a previously identified species concept or merits separate designation. Further, the relationships among species provide a basis for higher classification, but of greater importance are the evolutionary implications of these relationships. A well-defined phylogeny permits us to evaluate any number of ecological, behavioral, and physiological traits, many of which are very important in dealing with pest taxa. A phylogenetic framework provides the baseline for understanding the evolution of host choice and breadth, population biologies that might be associated with propensity for pest status, and natural variation or evolved changes in efficacy of control tactics. Without phylogenetic knowledge, we have limited abilities to predict biological features of an unstudied species. With such knowledge, we at least have a starting point for inferring the biological attributes of the species.

The fly family Tephritidae (Diptera) contains some of the most significant agricultural pests in the world and has some importance as a source taxon for the biological control of weeds. Species such as the Mediterranean fruit fly and Oriental fruit fly cause unquantified damage worldwide and create further difficulties in agricultural trade, since they are pests of quarantine significance. With increasing world trade in agricultural commodities a certainty, it is also a certainty that new tephritid pests will appear; species not previously described

or whose biologies have never been studied. A well-defined phylogeny of the major lineages within this family is presently lacking and is essential for further research on these flies. Furthermore, a solid phylogenetic framework permits accurate predictions of life-history characteristics for species of unknown biology and an educated assessment of the evolution of traits of agricultural interest.

Morphology has resolved little in tephritid classification and phylogeny. At present, three subfamilies are recognized, each containing a number of different tribes. However, characters defining these taxa are often weak, the relationships among the taxa are undefined, and classification schemes do not serve as a predictor of evolutionary relationships. Recent molecular studies indicate that variable regions of the mitochondrial genes have the potential to help resolve these relationships. My molecular data already have significantly contributed toward the sound classification of the family Tephritidae. Some of the examples of such contributions are the confirmations of the following systematic hypothesis based on the 16S rDNA data: (1) monophyly of the tribe Trypetini ; (2) monophyly of the *Chetostoma* group; (3) monophyly of the *Trypeta* group; and (4) non-monophyletic nature of the previous concept of *Hemilea*. More rigorous phylogenetic tests can be achieved if we improve the dataset by better taxon sampling and more sequence data across the mitochondrial genome.