

## Why *Drosophila* is not *Drosophila* any more, why it will be worse and what can be done about it?

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Formally, *Drosophila melanogaster* Meigen, 1830 is still *Drosophila*; however, it just waits for the first formal revision of the genus. On the basis of a 23 : 4 vote, the International Commission on Zoological Nomenclature rejected the proposal (Kim van der Linde et al., 2007) to make an exception to the rules and to switch the type of the genus *Drosophila* from *D. funebris* to *D. melanogaster* in order to retain for ever the name *Drosophila melanogaster* for the species that represents probably the most important model organism in many branches of biological research. The results of molecular taxonomic studies have shown that the correct name of this species should be *Sophophora melanogaster* rather than *Drosophila melanogaster* (O'Grady, 2010; van der Linde et al., 2010). Taxonomists and phylogeneticists are not concerned too much with this as *Drosophila/Sophophora melanogaster* represents for them just one of many millions of species. The nontaxonomists, i.e., the remaining approximately seven billion inhabitants of our planet, are in a worse situation. When they want to communicate precisely about the fly that eats their fruit, that is a vector of bacterial pathogens in food processing or healthcare facilities, that is a carrier of an interesting gene, or that is considered as the subject of a regulation or a rule to be formulated, they have a problem.

The genera like *Drosophila* are just a tip of the iceberg. In the past decade, i.e. after the advent of multigene or even whole-genome studies, molecular phylogenetics evolved from an amusing toy for molecular biologists searching for a “cheap publication” or for a simple project for a pregraduate or postgraduate student to a potent tool that can provide a reliable picture of the phylogeny of particular groups of organisms. With this advance, more and more biologists have been forced to admit that many traditional taxa, including the genera, were wrongly constructed and needed to be redefined or even abandoned. Molecular analyses often show that a particular clade *B* of a phylogenetic tree comprising species with a typical and distinct morphology is, in fact, an internal sub-clade of another clade, *A*, of the phylogenetic tree consisting of clades comprising, again, species with a typical and distinct morphology, but different from that of the species on clade *B*. Usually, this surprising result of the molecular analysis is sooner or later confirmed by a focused analysis of classical, e.g., morphological, traits. When the species of clade *A* were originally assembled into taxon *A* and species of clade *B* were originally assembled into taxon *B* of the same or higher taxonomic rank as taxon *A* then new results change the status of taxon *A* from monophyletic (holophyletic in Ashlock's (1971) terminology) to paraphyletic (polyphyletic in Hennig's (1966) terminology). Paraphyletic taxa violate the fundamental principle of the current, cladistic, taxonomy—any two species of a particular taxon should be more related to one another (should have a more recent common ancestor) than to any other species from a different taxon of the same or higher taxonomic level (Hennig, 1966).

This issue can be correctly resolved in two different ways. One possibility is to cancel the inserted taxon *B* while redirecting all its species to taxon *A*, despite the fact that they may differ from the remaining species more than other representatives of *A* do from members of a sister taxon of taxon *A*. When this solution is chosen and when clades *A* and *B* have the taxonomic rank of genus, the scientific name of the species of genus *B* should be changed. And if genus *B* was described and properly named earlier than the genus *A*, all genus *A* species rather than genus *B* species should be renamed. In speciose genera like *Drosophila*, such change of the generic name could bring about various taxonomic problems. For example, lumping all drosophilas into one genus to allow *Drosophila melanogaster* to keep its name would result in four species ending up with the name *Drosophila serrata* and another four with the name *Drosophila carinata* (van der Linde & Yassin, 2010).

The other option is to keep both genera. In such a case, however, only a part of the original genus *A* would be retained and all groups of species of genus *A* that branched earlier than genus *B* would be classified into their own (new) genera and would be given new scientific names, despite the fact that the representatives of most new genera would look

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