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## The molecular evolutions of amylase duplicate genes in *D. melanogaster* group

**Sammer Marzouk**

University of Chicago, USA

Within *D. melanogaster*, the amylase gene designation is made up of duplicate genes that can be designated as proximal or distal genes. Studies have divided up *Drosophila* coding regions by these classifications. And within these subgroups, there are significant evolutionary similarities and differences. These overlaps have caused for there to be an ambiguity when it comes to the relationship between these two subgroups. Do proximal and distal genes evolve independently (if distal genes cluster with their orthologs) or not (if the paralogs cluster)? By looking at the DNA material of nine species from the *D. melanogaster* group, this paper conducts advanced genetic and statistical analyses using specialized software. By creating dependent and independent phylogenies for the nine species and conducting advanced bootstrap parameters on them, the paper demonstrates that it is more likely that the relationship between the proximal and distal genes is one of dependent evolution. This supports the notion that there exists a form of positive selection acting upon a coding region. For future research, the same analysis could be done using amylase regulatory region. This analysis could provide insight into the relationship of upstream sequences of proximal and distal genes, multiple alignments and putative regulatory elements. And in future follow-ups, it could focus on the nucleotide divergence that appears to be taking place.

marzouk.sammer@gmail.com