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Analysis of recent gene duplication and conversion in the *Drosophilamelanogaster* genome

Using the genomic sequences of *D. melanogaster* subgroup, we investigate the pattern of gene duplication and interlocus gene conversion. Our analysis with careful visual inspections enabled accurate identification of a number of duplicated blocks. The orthologous parts of those duplicated blocks were also identified in the *D. simulans* and *sechellia* genome, by which we were able to clearly classify most blocks into *pre-* and *post*-speciation duplicated blocks. We found 28 *post*-speciation duplicated genes, from which the rate of gene duplication (from one copy to two copies) is estimated to be 1.0×10^{-9} per single-copy gene per year. Our analysis demonstrate that gene conversion between duplicated regions is a common and genome-wide phenomenon in the *D. melanogaster* genome, and its role should be especially significant in the early stages of duplicated genes. Based on a population genetic prediction, we applied a new genome-scan method to test for signatures of selection for neofunctionalization, and found a strong signature in a pair of transporter genes.

Short CV

Experience

2009–Present:	Adjunct Associate Professor, National Cheng-Kung University, Tainan, Taiwan.
2005–Present:	Scientific researcher, National Institute of Biomedical innovation, Osaka, Japan.
2004-2005:	Scientific researcher, National Institute of Infectious Diseases, Tokyo, Japan.
2003- 2004:	Research Associate, University of Chicago, IL, US.
2002:	Research Associate, University of Tokyo, Tokyo, Japan.
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