

Selected by | Nico M. van Straalen

Evaluated 2 Oct 2006

[Relevant Sections](#)

Faculty Member

Comments

Nico M. van Straalen

Vrije Universiteit, Netherlands

ECOLOGY

New Finding

An expressed sequence tag (EST) project for the butterfly *Bicyclus anynana* (Satyridae) finds a number of genes expressed in the developing wing that have an ortholog in *Drosophila melanogaster* but are not involved in wing development in the latter species. The data suggest a mechanism of genetic co-option, the recruitment of existing pathways in a new setting to create evolutionary novelty. Like in many other EST projects, a great number of sequences turn out to be ribosomal proteins, and since these genes can be homologized across widely different taxonomic categories, the paper confirms the usefulness of EST sequencing for comparative purposes and reconstructing phylogenies. Also, the EST-project puts *B. anynana* on the map of lepidopteran genomic models, along with *Heliconius* and the silk moth. *Bicyclus* is a promising evo-devo model, since it combines genetic information with ecologically relevant wing pattern variation and seasonal polyphenism. So the paper illustrates that EST sequencing is a cost-effective and powerful strategy to start up studies into the ecological genomics of non-model species.

Evaluated 2 Oct 2006