Colloquium

Molecular genetics and evolution of pheromone biosynthesis in Lepidoptera

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A great diversity of pheromone structures are used by moth species (Insecta: Lepidoptera) for long-distance mating signals. The signal/response channel seems to be narrow for each species, and a major conundrum is how signal divergence has occurred in the face of strong selection pressures against small changes in the signal. Observations of various closely related and morphologically similar species that use pheromone components biosynthesized by different enzymes and biosynthetic routes underscore the question as to how major jumps in the biosynthetic routes could have evolved with a mate recognition system that is based on responses to a specific blend of chemicals. Research on the desaturases used in the pheromone biosynthetic pathway for various moth species has revealed that one way to make a major shift in the pheromone blend is by activation of a different desaturase from mRNA that already exists in the pheromone gland. Data will be presented to support the hypothesis that this process was used in the evolution of the Asian corn borer, *Ostrinia furnacalis* species. In that context, moth sex-pheromone desaturase genes seem to be evolving under a birth-and-death process. According to this model of multigene family evolution, some genes are maintained in the genome for long periods of time, whereas others become deleted or lose their functionality, and new genes are created through gene duplication. This mode of evolution seems to play a role in moth speciation, as exemplified by the case of the Asian corn borer and European corn borer, *Ostrinia nubilalis* species.

For the full text of this article, see ref. 1.

1. Roelofs, W. L. & Rooney, A. P. (2003) *Proc. Natl. Acad. Sci. USA* **100,** 9179–9184.

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