

Mechanisms and evolution of female-limited Batesian mimicry in *Papilio* butterflies

Haruhiko FUJIWARA

University of Tokyo (Emeritus Professor)

haruh@edu.k.u-tokyo.ac.jp

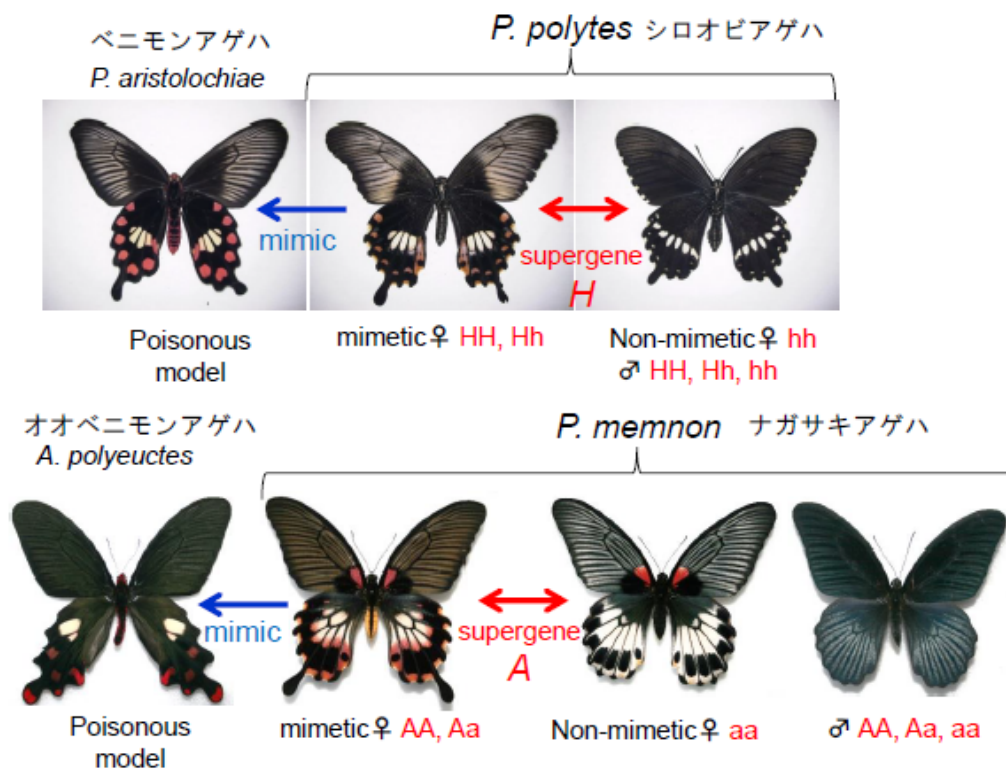


To deceive predators, palatable species often resemble color patterns and morphology of unpalatable species, which is called Batesian mimicry. Many animals employ the Batesian mimicry, which mechanisms and evolution remain largely unknown. In two closely related swallowtail butterflies, *Papilio polytes* and *P. memnon*, there are two types (mimetic and non-mimetic coloration) females, while males show non-mimetic pattern. The female-limited Batesian mimicry of these butterflies attract public interest from Darwin and Wallace's era. In both species, mimetic phenotype is superior to non-mimetic and known to be controlled by a single autosomal locus (*H* in *polytes* and *A* in *memnon*). Thus, the mimetic female genotype is HH or Hh (AA or Aa) and non-mimetic is hh (aa), while all males with any genotype are non-mimetic. Fisher RA (1930) suggested that this polymorphic female-limited mimicry is regulated by "supergene", which is a cluster of multiple genes tightly linked together.

Recent genome projects revealed many supergenes involved in various complex adaptive phenomena, but the functional unit of supergene has not been clarified in any cases. We have identified the mimicry supergene locus (*H* for *P. polytes* and *A* for *P. memnon*) in a region around *doublesex* (*dsx*) of chromosome 25 (1): The region includes several genes, *dsx*, *UXT*, *U3X* (only for *polytes*) and *Nach-like*, which sequences are highly diversified between *H* and *h* (*A* and *a*) due to recombination suppression, caused by chromosomal inversion in *P. polytes* but probably by repetitive sequences without inversion in *P. memnon* (2, 3). To identify the functional unit of mimicry supergene, we performed knock-down of candidate gene function by electroporation mediated RNAi in mimetic female wings of *P. polytes*. We found that *dsx-H* was responsible for switching from the non-mimetic to mimetic traits, and that not only *UXT* within highly diversified region (HDR) but also *sir2* adjacent to HDR affected the wing pattern (4). Furthermore, it was suggested that *U3X* regulates both *dsx-H* and *UXT* expression. These results indicate that *dsx-H* works as a mimicry gene and other flanking genes as modifier and that functional unit of mimicry supergene is expanded to a wider region than we thought before. In the symposium, I also discuss how two mimicry supergenes in *Papilio* species have evolved.

References

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- (3) Komata, S. et al. (2022) Genomic architecture and functional unit of mimicry supergene in female limited Batesian mimic *Papilio* butterflies. *Philos Trans R Soc Lond B Biol Sci.* B 377 (1856), 20210198.
- (4) Komata, S. et al. (2023) Functional unit of supergene in female-limited Batesian mimicry of *Papilio polytes*. *Genetics* 223, iyac177.



Female limited Batesian mimicry in *P. polytes* and *memnon*