

# Where do the intermediates in fritillary butterflies come from: in the footsteps of genomic introgression

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Recent whole-genome and multilocus studies show that speciation via interspecific hybridization is widespread in nature. In the fritillary butterfly genus *Melitaea* (Lepidoptera, Nymphalidae) a high number of individuals and populations is known to have intermediate morphological characters between two distinct species. These intermediates were hypothesized to be a result of ancient or ongoing interspecific hybridization [3]. The recently described species *M. acentra* has male genitalia and wing color pattern that are intermediate between those found in the closely related allopatric species *M. persea* and distantly related sympatric species *M. didyma* [1]. Analysis of mitogenomes reveals two haplotypes within the *M. acentra* population. One of the haplotypes demonstrate slightly less sequence divergence (dxy) and fixation index (Fst) across the mitochondrial DNA with *M. persea* than with another haplotype of the same species.

Adaptive introgression between distantly related butterfly species was shown in genus *Heliconius* (Zhang et. al 2016), however, principles of formation of morphological features with intermediate structure are still unclear. We performed whole-genome resequencing of this three fritillary species to detect footprints of ancient or recent introgression, characterize patterns of genetics differentiation and propose possible model of speciation. Genome-wide admixture analysis has not revealed any evidences of interspecific hybridization between *M. didyma* and *M. persea*, but signs of sporadic hybridization between sympatric populations of *M. didyma* and *M. acentra* were found. More sensitive Pattersons D statistics (also known as ABBA-BABA test) was used in 25 kb sliding window to detect regions with the ancient introgression, and fd metrics was involved to calculate an admixture proportions (Martin et. al. 2014). Population genomics statistics (Fst, dxy and Tajimas D) were estimated across the genome to distinguish introgression from ancestral polymorphism and detect regions influenced

by directional selection. Obtained data allows us to propose a scenario of the *M. acentria* origin and evolution. According to this scenario, the combined effect of geographical isolation from the ancestral species (*M. persea*) and genomic introgression from *M. didyma* was the major driving force of the speciation.

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