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Dear Editors,

Please find attached a research article with the title Linkage mapping and genome annotation give novel insights into gene family expansions and regional recombination rate variation in the painted lady (*Vanessa cardui*) butterfly", for consideration for publication in Genomics.

Gene family expansions and crossing over are two main mechanisms for generating novel genetic variants that can be picked up by natural selection. Therefore, characterization of these processes is crucial for understanding how organisms adapt to the environment. Here, we develop a high-density linkage map and detailed genome annotation based on information from a high-contiguity genome assembly to investigate lineage specific gene family expansions and characterize the recombination landscape in the painted lady butterfly (*Vanessa cardui*) - a non-diapausing, highly polyphagous species famous for its long-distance migratory behavior and almost cosmopolitan distribution range.

Our results reveal a complex interplay between regional recombination rate variation, gene duplications and transposable element activity shaping the genome structure of the painted lady. A key result is that we identify several lineage specific gene family expansions which consist of regional clusters of gene copies in tandem. The functions of these gene families are mainly associated with protein and fat metabolism, detoxification, and defense against infection - critical functions for the painted lady's unique life-history characteristics. We discuss the relevance of these specific gene family expansions for the evolution of long-distance migration in insects in detail. Furthermore, the detailed recombination maps allow us to characterize the regional recombination landscape, data that reveal a strong effect of chromosome size on the recombination rate, a limited impact of GC-biased gene conversion and a positive association between recombination and short interspersed elements.

Given the combination of traditional linkage mapping, detailed genome annotation and comparative genomics approaches, where we both characterize the genome structure and recombination landscape of a model species for migratory research and identify candidate genes for adaptations to a migratory life-style, we believe that the study fits very well within the scope of Genomics. We foresee that the results will attract interest from a broad audience of readers interested in recombination rate and genome evolution in general, and the genetic underpinnings of complex phenotypes in particular.

The study contains no statements of personal communication or other issues related to permissions. All raw data generated in the study will be available via the European Nucleotide Archive (ENA) under accession number PRJEB52289, pending publication. All gene names used in the paper adhere to approved nomenclature guidelines.

Thank you for considering this manuscript, and we look forward to hearing from you.

Authors