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Daria Shipilina, PhD
Postdoctoral Fellow

Uppsala University,
Norbyvägen 18D,
Uppsala, Sweden
752 36

Dear Editors,

I am writing on behalf of coauthors to submit our manuscript entitled **“Gene expression responses to environmental cues shed light on components of the migratory syndrome in butterflies”** for consideration for publication in *Molecular Ecology*. This research represents a significant step forward in understanding the molecular mechanisms underlying a major ecological adaptation—migratory behavior. It contributes to the growing body of transcriptomic studies that align with the mission of *Molecular Ecology* to apply state-of-the-art molecular methods to fundamental ecological and evolutionary questions.

Migration is a complex behavior that involves synchronizing many physiological and behavioral processes. Therefore, environmental cues must be interpreted to decide how resources are allocated, such as choosing between migration and reproduction. Our study focuses on *Lepidoptera*, a clade not deeply covered before, and uses the long-distance migrant and charismatic emerging model species Painted Lady (*Vanessa cardui*). We investigate the transcriptomic response to two environmental cues associated with investment in reproduction or migration in butterflies: larval density and host plant availability for egg laying and as a food source. In an experiment designed to trigger the trade-off between migration and reproduction, we observed gene expression signatures consistent with the oogenesis-flight syndrome and highlighted the crucial role of hormonal regulation. By subjecting larvae to different environmental cues—food abundance and larval crowding—we examined the early predisposition for migratory plasticity. Our findings revealed that the peak response occurs during the last larval stage and emphasizes the role of genes involved in developmental regulation and metabolism.

Our findings provide novel insights into the molecular basis of migration and the ecological interactions between migratory insects and their environment and will be relevant to readers of *Molecular Ecology* interested in the genetic mechanisms underlying complex behavioral adaptations. Additionally, identification of candidate genes and pathways opens a broad field for future research on insect migration and comparative studies involving other groups exhibiting migratory behavior.

This manuscript has not been published elsewhere and is not under consideration by another journal. A preprint is available on bioRxiv (doi:10.1101/2024.07.17.602486). All authors have approved the manuscript and agree with its submission to *Molecular Ecology*.

Thank you for your consideration; we look forward to feedback from the editorial board and reviewers.

Sincerely,
Daria Shipilina
Postdoctorate Fellow
Uppsala University