

The Role of Olfaction in the Making of a Pest – A Genomic Analysis

Sukanya Ramasamy^{1,2}, Lino Ometto¹, Santosh Revadi^{1,3}, David Horner², Davide Pisani⁴,
Teun Dekker³, Gianfranco Anfora¹, Omar Rota Stabelli¹

¹Research and Innovation Centre, Fondazione Edmund Mach, Via E. Mach 1, 38010 San Michele all'Adige (TN), Italy;

² Università degli studi di Milano, via Celoria, Milano, Italy;

³ Chemical Ecology Unit, Swedish University of Agricultural Sciences, Alnarp, Sweden;

⁴ School of Biological Sciences and School of Earth Sciences, University of Bristol, UK

The emerging model pest *Drosophila suzukii* is characterized by the switch from a fermenting to a fresh fruit reproductive habit, but the genomic bases of this new trait are still widely unexplored. In this study, we have annotated the repertoire of olfactory genes in two populations of *D. suzukii* and in its closely related species, *D. biarmipes*, and performed thorough evolutionary studies on a 14 *Drosophila* phylogenetic framework. Compared to most other *Drosophila* species, the odorant receptors of *D. suzukii* are characterized by an increased turnover rate and a non-random distribution of evolutionary events (duplications, deletions, and positive selection), consistent with adaptation to a new ecological environment. In *D. suzukii*, odorant receptors that respond to some of the odours typical of ripening fruit have undergone duplication and show signs of positive selection; the most represented volatiles eliciting a response in these receptors include isoamyl acetate, for which we could confirm a functional role in *D. suzukii* using ad-hoc behavioural assays. Conversely, some of the key receptors used to detect volatiles produced during fermentation experienced loss of function and likely neo-functionalization in *D. suzukii*, a finding supported by physiological recordings; these genes are fairly divergent between European and American *D. suzukii* populations suggesting ancient multiple neo-functionalization events. Overall, our comparative analyses reveal unusual genomic evolutionary events in *D. suzukii* that can be associated with adaptations to new ecological behaviours, and unveil key genes and ligands that might become target of applied control strategies.