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| Abstract title | The genome of <i>Drosophila subpulchrella</i> and the importance of sister-species comparison in agricultural pest science |
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Genomics is often used to clarify the biology of agricultural pests and to define management strategies against them. There is however one crucial aspect often neglected: the comparison between a pest and its closest non-pest sister species. In the absence of a sister species, genome comparisons cannot discriminate characters that are unique to the pest, from those shared with other members of its clade. To highlight the benefit of a sister species comparison, we sequenced a draft genome of *D. subpulchrella*, the closest known non-pest sister species of model fruit pest *D. suzukii*. First, our evolutionary analyses could set the age of speciation of *D. suzukii*, clarified its paleo-ecological context, and revealed genetic admixtures that should be taken into account when modeling pest population in the field. Second, and probably more importantly, we could polarize various genomic event on the phylogenetic tree, revealing a set of key chemosensory genes that will ease the development of trapping strategies based on lures. Finally, we could disentangle the evolutionary significance of *Wolbachia* symbionts which may serve as bio-control agents. Our results show that applying a sister species concept to applied research agenda can enhance and speed up the definition of new management strategies.

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