Members of the genus *Stenotrophomonas* reside in a broad range of environments and are commonly identified as multidrug-resistant opportunistic pathogens of humans (1). However, they are most frequently found in soils or in association with plants (2), where they are able to form symbiotic interactions (3). *Stenotrophomonas* spp. are also associated with multiple insect species (4–8), including three members of the *Bactrocera*, *Cucurbita*, *B. tau*, and *B. zonata* (9, 10). Due to a lack of phenotypic data, the nature of these interactions is not understood. However, the draft genome sequence of *Stenotrophomonas maltophilia* SBo1 presented here will aid future investigations into the mechanisms that underlie insect-microbe interactions and will contribute to a community-level examination of the *B. oleae* microbiota (11).

*S. maltophilia* SBo1 was cultured from the gut of the fruit fly *Bactrocera oleae*. The draft genome sequence presented here will inform future investigations into the nature of the interaction between insects and their microbiota.

Bacteria of the genus *Stenotrophomonas* are ubiquitous in the environment and are increasingly associated with insects. *Stenotrophomonas maltophilia* SBo1 was cultured from the gut of *Bactrocera oleae*. The draft genome sequence presented here will inform future investigations into the nature of the interaction between insects and their microbiota.
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