Draft Genome Sequence of the Bactrocera oleae Symbiont “Candidatus Erwinia dacicola”

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“Candidatus Erwinia dacicola” is a Gammaproteobacterium that forms a symbiotic association with the agricultural pest Bactrocera oleae. Here, we present a 2.1-Mb draft hybrid genome assembly for “Ca. Erwinia dacicola” generated from single-cell and metagenomic data.

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REFERENCES

1. Petri L. 1909. Ricerche sopra i batteri intestinali della mosca olearia. Memorie della Regia Stazione di Patologia Vegetale di Roma, Rome, Italy.

2. Capuzzo C, Firrao G, Mazzon L, Squartini A, Girolami V. 2005. “Candidatus Erwinia dacicola,” a coevolved symbiotic bacterium of the olive fly Bactrocera oleae (Diptera: Tephritidae). Int J Trop Insect Sci 34:S123–S131. http://dx.doi.org/10.1017/S1742758414000174.

3. Estes AM, Hearn DJ, Bronstein JL, Pierson EA. 2009. The olive fly endosymbiont, “Candidatus Erwinia dacicola,” switches from an intracellular existence to an extracellular existence during host insect development. Appl Environ Microbiol 75:7097–7106. http://dx.doi.org/10.1128/AEM.00778-09.

4. Sacchetti P, Granchietti A, Landini S, Viti C, Giovannetti L, Belcari A. 2008. Relationships between the olive fly and bacteria. J Appl Entomol 132:682–689. http://dx.doi.org/10.1111/j.1439-0418.2008.01334.x.

5. Hagen KS. 1966. Dependence of the olive fly, Dacus oleae, larvae on symbiosis with Pseudomonas savastanoi for the utilization of olive. Nature 209:423–424. http://dx.doi.org/10.1038/209423a0.

6. Ben-Yosef M, Aharon Y, Jurkevitch E, Yuval B. 2010. Give us the tools and we will do the job: symbiotic bacteria affect olive fly fitness in a diet-dependent fashion. Proc Biol Sci 277:1545–1552. http://dx.doi.org/10.1098/rspb.2009.2102.

7. Ben-Yosef M, Pasternak Z, Jurkevitch E, Yuval B. 2014. Symbiotic bacteria enable olive flies (Bactrocera oleae) to exploit intractable sources of nitrogen. J Evol Biol 27:2695–2705. http://dx.doi.org/10.1111/jeb.12527.

8. Ben-Yosef M, Pasternak Z, Jurkevitch E, Yuval B. 2015. Symbiotic bacteria enable olive fly larvae to overcome host defences. R Soc Open Sci 2:150170. http://dx.doi.org/10.1098/rsos.150170.

9. Estes AM, Segura DF, Jessup A, Wornoayporn V, Pierson EA. 2014. Effect of the symbiont Candidatus Erwinia dacicola on mating success of the olive fly Bactrocera oleae (Diptera: Tephritidae). Int J Trop Insect Sci 34:S123–S131. http://dx.doi.org/10.1017/S1742758414000174.

10. Xin Z, Chen J. 2012. A high throughput DNA extraction method with high yield and quality. Plant Methods 8:26. http://dx.doi.org/10.1186/1746-4811-8-26.

11. Nurr S, Bankevich A, Antipov D, Gurevich A, Korobeynikov A, Lapidus A, Prijibelsky A, Pyshkin A, Sirotkin A, Sirotkin Y, Stepnaukhas R. 2013. Assembling genomes and mini-metagenomes from highly chimeric reads. Res Comput Mol Biol 7821:158–170.

12. Kumar S, Jones M, Koutsouvelos G, Clarke M, Blaxter M. 2013. Blobology: exploring raw genome data for contaminants, symbionts and parasites using taxon-annotated GC-coverage plots. Front Genet 4:237. http://dx.doi.org/10.3389/fgene.2013.00237.

13. Rinke C, Schwientek P, Sczyrba A, Ivanova NN, Anderson JJ, Cheng JF, Darling A, Malfatti S, Swan BK, Gies EA, Dodsworth JA, Hedlund BP, Tsimis G, Sievert SM, Liu WT, Eisen JA, Hallam SJ, Kyripides NC, Stepnaukhas R, Rubin EM. 2013. Insights into the phylogeny and coding potential of microbial dark matter. Nature 499:431–437. http://dx.doi.org/10.1038/nature12352.

14. Starr MP, Chatterjee AK. 1972. The genus Erwinia: enterobacteria pathogenic to plants and animals. Annu Rev Microbiol 26:389–426. http://dx.doi.org/10.1146/annurev.mi.26.100172.002133.

15. Moran NA. 1996. Accelerated evolution and Muller’s ratchet in endosymbiotic bacteria. Proc Natl Acad Sci U S A 93:2873–2878. http://dx.doi.org/10.1073/pnas.93.7.2873.

16. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. http://dx.doi.org/10.1093/bioinformatics/btu153.