

Supplementary Table S1. National Center for Biotechnology Information (NCBI) accession numbers for Hawaiian Drosophilidae gene sequences selected for phylogenetic reconstruction of individual species having a verified *Wolbachia* infection, and genome accessions for outgroup taxa (also infected). Gene names and abbreviations are elongation factor 1-gamma (*EF1g*), glycerol-3-phosphate dehydrogenase (*Gpdh*), phosphoglucose isomerase (*Pgi*), and yolk protein 2 (*Yp2*).

Sample ID	Species Name	Accession Number (NCBI)					Reference
		<i>EF1g</i>	<i>Fz4</i>	<i>Gpdh</i>	<i>Pgi</i>	<i>Yp2</i>	
M09120	<i>Scaptomyza cyrtandrae</i>	JN815467.1	JN815636.1	JN815794.1	JN815958.1	JN816160.1	[1]
M09124	<i>Scaptomyza crassifemur</i>	JN815471.1	----	JN815798.1	JN815962.1	JN816164.1	[1]
M09127	<i>Scaptomyza reducta</i>	JN815474.1	----	JN815801.1	JN815965.1	JN816167.1	[1]
M09245	<i>Scaptomyza caliginosa</i>	JN815560.1	JN815714.1	JN815878.1	JN816041.1	JN816245.1	[1]
M09011	<i>Scaptomyza nasalis</i>	JN815359.1	JN815639.1	JN815722.1	JN815886.1	JN816052.1	[1]
M09015	<i>Scaptomyza undulata</i>	JN815363.1	JN815568.1	JN815724.1	JN815888.1	JN816056.1	[1]
M09066	<i>Drosophila perissopoda</i>	JN815413.1	JN815594.1	JN815751.1	JN815915.1	JN816106.1	[1]
M09028	<i>Drosophila quasiexpansa</i>	JN815376.1	JN815632.1	JN815790.1	JN815954.1	JN816153.1	[1]
M09075	<i>Drosophila atroscutellata</i>	JN815422.1	JN815603.1	JN815760.1	JN815924.1	JN816115.1	[1]
M09073	<i>Drosophila ancyla</i>	JN815420.1	JN815601.1	JN815758.1	JN815922.1	JN816113.1	[1]
M09228	<i>Drosophila nigrocirrus</i>	----	JN815701.1	JN815864.1	----	JN816230.1	[1]
M09230	<i>Drosophila</i> "large spots"	JN815548.1	JN815703.1	JN815866.1	JN816029.1	JN816232.1	[1]
M09095	<i>Drosophila kikiko</i>	JN815442.1	JN815621.1	JN815779.1	JN815943.1	JN816135.1	[1]
M09037	<i>Drosophila hawaiiensis</i>	JN815385.1	JN815573.1	JN815730.1	JN815894.1	JN816077.1	[1]
M09043	<i>Drosophila micromyia</i>	JN815390.1	JN815577.1	JN815734.1	JN815898.1	JN816083.1	[1]
M09096	<i>Drosophila engyochracea</i>	JN815443.1	JN815622.1	JN815780.1	JN815944.1	JN816136.1	[1]

Sample ID	Species Name	Accession Number (NCBI)					Citation
		<i>EF1g</i>	<i>Fz4</i>	<i>Gpdh</i>	<i>Pgi</i>	<i>Yp2</i>	
M09059	<i>Drosophila murphyi</i>	JN815406.1	JN815588.1	JN815745.1	JN815909.1	JN816080.1	[1]
M09061	<i>Drosophila ochracea</i>	JN815408.1	JN815590.1	JN815783.1	JN815911.1	JN816101.1	[1]
M09091	<i>Drosophila prolaticilia</i>	JN815438.1	JN815565.1	JN815719.1	JN815939.1	JN816131.1	[1]
M09063	<i>Drosophila prostopalpis</i>	JN815410.1	JN815592.1	JN815749.1	JN815913.1	JN816103.1	[1]
M09189	<i>Drosophila heteroneura</i>	JN815516.1	JN815675.1	JN815838.1	JN816002.1	JN816205.1	[1]
M09018	<i>Drosophila basimacula</i>	JN815366.1	----	----	----	JN816059.1	[1]
M09030	<i>Drosophila seclusa</i>	JN815378.1	----	----	----	JN816071.1	[1]
M09025	<i>Drosophila redunca</i>	JN815373.1	----	----	----	JN816066.1	[1]
N/A	<i>Drosophila suzukii</i>	CAKG01035181.1	CAKG01024421.1	CAKG01004152.1	CAKG01035649.1	CAKG01056334.1	[2]
N/A	<i>Drosophila melanogaster</i>	NT_033777.3	NC_004354.4	NT_033779.5	NT_033778.4	NC_004354.4	[3]
N/A	<i>Drosophila simulans</i>	NT_479536.1	NC_029795.1	NT_479533.1	NT_479534.1	NC_029795.1	[4]
N/A	<i>Culex quinquefasciatus</i>	NW_001887359.1	----	NW_001886703.1	NW_001886829.1	----	[5]
N/A	<i>Aedes albopictus</i>	NW_017857380.1	----	NW_017856043.1	NW_017857316.1	----	[6]

References

- Magnacca, K.N.; Price, D.K. Rapid adaptive radiation and host plant conservation in the Hawaiian picture wing *Drosophila* (Diptera: Drosophilidae). *Mol. Phylogenetics Evol.* **2015**, *92*, 226–242.
- Ometto, L.; Cestaro, A.; Ramasamy, S.; Grassi, A.; Revadi, S.; Siozios, S.; Moretto, M.; Fontana, P.; Varotto, C.; Pisani, D.; et al. Linking genomics and ecology to investigate the complex evolution of an invasive *Drosophila* pest. *Genome Biol. Evol.* **2013**, *5*, 745–757.
- dos Santos, G.; Schroeder, A.J.; Goodman, J.L.; Strelets, V.B.; Crosby, M.A.; Thurmond, J.; Emmeret, D.B.; Gelbart, W.M.; FlyBase Consortium. FlyBase: Introduction of the *Drosophila melanogaster* Release 6 reference genome assembly and large-scale migration of genome annotations. *Nucleic Acids Res.* **2015**, *43*, D690–D697.
- Hu, T.T.; Eisen, M.B.; Thornton, K.R.; Andolfatto, P. A second-generation assembly of the *Drosophila simulans* genome provides new insights into patterns of lineage-specific divergence. *Genome Res.* **2013**, *23*, 89–98.
- Arensburger, P.; Megy, K.; Waterhouse, R.M.; Abrudan, J.; Amedeo, P.; Antelo, B.; Bartholomay, L.; Bidwell, S.; Caler, E.; et al. Sequencing of *Culex quinquefasciatus* establishes a platform for mosquito comparative genomics. *Science* **2010**, 86–88.
- Miller, J.R.; Koren, S.; Dilley, K.A.; Puri, V.; Brown, D.M.; Harkins, D.M.; Thibaud-Nissen, F.; Rosen, B.; Chen, X.G.; et al. Analysis of the *Aedes albopictus* C6/36 genome provides insight into cell line utility for viral propagation. *Gigascience* **2018**, *7*, 1–13.