

## Complete Genome Sequence of "Candidatus Portiera aleyrodidarum" BT-QVLC, an Obligate Symbiont That Supplies Amino Acids and Carotenoids to *Bemisia tabaci*

Diego Santos-Garcia, Pierre-Antoine Farnier, Francisco Beitia, Einat Zchori-Fein, Fabrice Vavre, Laurence Mouton, Andrés Moya, Amparo Latorre and Francisco J. Silva  
*J. Bacteriol.* 2012, 194(23):6654. DOI: 10.1128/JB.01793-12.

---

Updated information and services can be found at:  
<http://jb.asm.org/content/194/23/6654>

---

### REFERENCES

*These include:*

This article cites 19 articles, 7 of which can be accessed free at:  
<http://jb.asm.org/content/194/23/6654#ref-list-1>

### CONTENT ALERTS

Receive: RSS Feeds, eTOCs, free email alerts (when new articles cite this article), [more»](#)

---

Information about commercial reprint orders: <http://journals.asm.org/site/misc/reprints.xhtml>  
To subscribe to to another ASM Journal go to: <http://journals.asm.org/site/subscriptions/>

# Complete Genome Sequence of “*Candidatus Portiera aleyrodidarum*” BT-QVLC, an Obligate Symbiont That Supplies Amino Acids and Carotenoids to *Bemisia tabaci*

Diego Santos-Garcia,<sup>a</sup> Pierre-Antoine Farnier,<sup>b</sup> Francisco Beitia,<sup>c</sup> Einat Zchori-Fein,<sup>d</sup> Fabrice Vavre,<sup>b</sup> Laurence Mouton,<sup>b</sup> Andrés Moya,<sup>a,e</sup> Amparo Latorre,<sup>a,e</sup> and Francisco J. Silva<sup>a,e</sup>

Institut Cavanilles de Biodiversitat i Biologia Evolutiva, Universitat de València, Valencia, Spain<sup>a</sup>; Université Claude Bernard Lyon 1, Laboratoire de Biométrie et Biologie Evolutive, UMR CNRS 5558, Villeurbanne, France<sup>b</sup>; Instituto Valenciano de Investigaciones Agrarias, Unidad Asociada de Entomología IMA/CIB-CSIC, Valencia, Spain<sup>c</sup>; Agricultural Research Organization, Department of Entomology, Newe Ya'ar Research Center, Ramat Yishay, Israel<sup>d</sup>; and Unidad Mixta de Investigación en Genómica y Salud (Centro Superior de Investigación en Salud Pública [CSISP]), Valencia, Spain<sup>e</sup>

**The genome of “*Candidatus Portiera aleyrodidarum*,” the primary endosymbiont of the whitefly *Bemisia tabaci* (Mediterranean species), is reported. It presents a reduced genome (357 kb) encoding the capability to synthesize, or participate in the synthesis of, several amino acids and carotenoids, being the first insect endosymbiont capable of supplying carotenoids.**

Whiteflies are small sap-sucking insects belonging to the family Aleyrodidae (2). *Bemisia tabaci*, which is able to feed on many plant species, being one of the worst agricultural pests, has been described as a species complex composed of 24 indistinguishable species (formerly called biotypes) (3). The most important biotypes (based on economic losses) are B (or Middle East-Asia Minor 1 species), which is the most widespread, and Q (or Mediterranean species), which shows more resistance to insecticides (9).

*B. tabaci* harbors a primary (obligate) endosymbiont, “*Candidatus Portiera aleyrodidarum*,” which is located in specialized cells called bacteriocytes (1), and also may contain different secondary (facultative) symbionts (7).

We report here the complete genome of the primary symbiont “*Ca. Portiera aleyrodidarum*” BT-QVLC from *B. tabaci* (Mediterranean species) strain QHC-VLC, which also harbors “*Candidatus Hamiltonella defensa*” (13) and “*Candidatus Cardinium hertigii*” (20).

Enriched bacterial samples were obtained by following a modified Harrison protocol (8) and used for sequencing single-end and 3-kb pair-end libraries using 454 GS-FLX Titanium and a 5-kb mate-pair using HiSeq2000. Filtered reads were used for MIRA *de novo* hybrid assembly, and the software program Gap4 was used for editing and closing the genome (41× combined coverage). The software program Prodigal and the BASYS and RAST servers were used for the initial gene calling, followed by hand curation.

“*Ca. Portiera aleyrodidarum*” has a small chromosome (357,472 bp) with 26.1% G+C content and 68% coding density, values derived from a strong genome reduction process (5, 12, 14), being in the frontier between reduced and extremely reduced symbiotic genomes (10, 11, 16). The genome contains 246 coding genes, 8 pseudogenes, and 38 noncoding RNA genes (33 tRNAs, 3 rRNAs, *rnpB*, and *tmRNA*). It includes an almost complete information transfer gene repertoire (4) but lacks the genes encoding the aminoacyl-tRNA synthetases for arginine, methionine, threonine, and tryptophan. “*Ca. Portiera aleyrodidarum*” is able to synthesize the essential amino acids threonine and tryptophan and the nonessential serine and lacks the last gene of the phenylalanine, valine, leucine, and isoleucine pathways. The lysine pathway

is also incomplete, lacking the *dapF* and *lysA* genes, with *dapB* pseudogenized. Moreover, the histidine pathway is disrupted, lacking the two last enzymes of the pathway. In addition, for the methionine pathways, it encodes only the last enzyme. These results suggest potential complementations with the insect, or the secondary endosymbionts, to complete the missing steps (6, 18, 19). Interestingly, “*Ca. Portiera aleyrodidarum*” has the ability to produce carotenoids, compounds that insects usually obtain from the diet. They are a source for insect pigments and have a canonical antioxidant action. Recently, carotenoids have been proposed, using light as a source to generate electrons, to reduce NAD<sup>+</sup> in the pea aphid (17).

The genome of this species from the B biotype has been recently described (15). Gene content in the two genomes is the same, although there are some discrepancies due to differences in annotation (pseudogenes, hypothetical proteins, and noncoding RNA genes). The average nucleotide identity between genes of the two strains is 99.3%.

In summary, we propose “*Ca. Portiera aleyrodidarum*” as a symbiont able not only to supplement the diet of its host but to use carotenoids as a way of protecting against oxidative stresses by supplying it with reducing power.

**Nucleotide sequence accession number.** The genome was deposited in GenBank under accession number CP003835.

## ACKNOWLEDGMENTS

This work was supported by grants BFU2009-12895-CO2-01 from the Spanish Ministry of Science and Innovation and Prometeo 92/2009 from Generalitat Valenciana (Spain) and by EU COST Action FA0701. These results have been achieved within the framework of the 1st call on Mediterranean agriculture carried out by ARIMNet, with funding from MOARD (IL), ANR (FR), INIA (ES), NAGREF-DEMETER (GR), and GDAR (TR). D.S.-G. is a recipient of a contract from Prometeo 92/2009.

Received 20 September 2012 Accepted 25 September 2012

Address correspondence to Francisco J. Silva, francisco.silva@uv.es.

Copyright © 2012, American Society for Microbiology. All Rights Reserved.

doi:10.1128/JB.01793-12

## REFERENCES

1. Baumann L, et al. 2004. Sequence analysis of DNA fragments from the genome of the primary endosymbiont of the whitefly *Bemisia tabaci*. *Curr. Microbiol.* 48:77–81.
2. Byrne DN, Bellows TS. 1991. Whitefly biology. *Annu. Rev. Entomol.* 36:431–457.
3. De Barro PJ, Liu SS, Boykin LM, Dinsdale AB. 2011. *Bemisia tabaci*: a statement of species status. *Annu. Rev. Entomol.* 56:1–19.
4. Gil R, Silva FJ, Pereto J, Moya A. 2004. Determination of the core of a minimal bacterial gene set. *Microbiol. Mol. Biol. Rev.* 68:518–537.
5. Gomez-Valero L, Latorre A, Silva FJ. 2004. The evolutionary fate of nonfunctional DNA in the bacterial endosymbiont *Buchnera aphidicola*. *Mol. Biol. Evol.* 21:2172–2181.
6. Gosalbes MJ, Lamelas A, Moya A, Latorre A. 2008. The striking case of tryptophan provision in the cedar aphid *Cinara cedri*. *J. Bacteriol.* 190: 6026–6029.
7. Gottlieb Y, et al. 2008. Inherited intracellular ecosystem: symbiotic bacteria share bacteriocytes in whiteflies. *FASEB J.* 22:2591–2599.
8. Harrison CP, Douglas AE, Dixon AFG. 1989. A rapid method to isolate symbiotic bacteria from aphids. *J. Invertebr. Pathol.* 53:427–428.
9. Khasdan V, et al. 2005. DNA markers for identifying biotypes B and Q of *Bemisia tabaci* (Hemiptera: Aleyrodidae) and studying population dynamics. *Bull. Entomol. Res.* 95:605–613.
10. McCutcheon JP, Moran NA. 2012. Extreme genome reduction in symbiotic bacteria. *Nat. Rev. Microbiol.* 10:13–26.
11. Moya A, Pereto J, Gil R, Latorre A. 2008. Learning how to live together: genomic insights into prokaryote-animal symbioses. *Nat. Rev. Genet.* 9:218–229.
12. Perez-Brocal V, et al. 2006. A small microbial genome: the end of a long symbiotic relationship? *Science* 314:312–313.
13. Rao Q, et al. 2012. Draft genome sequence of “*Candidatus Hamiltonella defensa*,” an endosymbiont of the whitefly *Bemisia tabaci*. *J. Bacteriol.* 194:3558.
14. Silva FJ, Latorre A, Moya A. 2001. Genome size reduction through multiple events of gene disintegration in *Buchnera* APS. *Trends Genet.* 17:615–618.
15. Sloan DB, Moran NA. Endosymbiotic bacteria as a source of carotenoids in whiteflies. *Biol. Lett.*, in press.
16. Tamames J, et al. 2007. The frontier between cell and organelle: genome analysis of *Candidatus Carsonella ruddii*. *BMC Evol. Biol.* 7:181. doi: 10.1186/1471-2148-7-181.
17. Valmalette JC, et al. 2012. Light-induced electron transfer and ATP synthesis in a carotene synthesizing insect. *Sci. Rep.* 2:579. doi:10.1038/srep00579.
18. Wilson AC, et al. 2010. Genomic insight into the amino acid relations of the pea aphid, *Acyrtosiphon pisum*, with its symbiotic bacterium *Buchnera aphidicola*. *Insect Mol. Biol.* 19(Suppl. 2):249–258.
19. Wu D, et al. 2006. Metabolic complementarity and genomics of the dual bacterial symbiosis of sharpshooters. *PLoS Biol.* 4:1079–1092.
20. Zchori-Fein E, Perlman SJ, Kelly SE, Katzir N, Hunter MS. 2004. Characterization of a ‘*Bacteroidetes*’ symbiont in *Encarsia* wasps (Hymenoptera: Aphelinidae): proposal of ‘*Candidatus Cardinium hertigii*’. *Int. J. Syst. Evol. Microbiol.* 54:961–968.