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Patrick Mavingui, Claire Valiente Moro, Van Tran-Van, Florence Wisniewski-Dyé, Vincent Raquin, et al.. Whole-Genome Sequence of Wolbachia Strain wAlbB, an Endosymbiont of Tiger Mosquito Vector *Aedes albopictus*. *Journal of Bacteriology*, 2012, 194 (7), pp.1840. 10.1128/JB.00036-12 . halsde-00723025

HAL Id: halsde-00723025

<https://hal.science/halsde-00723025>

Submitted on 17 May 2024

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Whole-Genome Sequence of *Wolbachia* Strain *wAlbB*, an Endosymbiont of Tiger Mosquito Vector *Aedes albopictus*

Patrick Mavingui,^a Claire Valiente Moro,^a Van Tran-Van,^a Florence Wisniewski-Dyé,^a Vincent Raquin,^a Guillaume Minard,^a Florence-Hélène Tran,^a Denis Voronin,^{a*} Zoé Rouy,^b Patricia Bustos,^c Luis Lozano,^c Valérie Barbe,^b and Víctor González^c

Université de Lyon, CNRS, UMR 5557, Ecologie Microbienne, Villeurbanne, France^a; CEA, DSV, IG, Genoscope, Evry, France^b; and Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, México^c

Although bacteria of the genus *Wolbachia* induced significant extended phenotypes to infected hosts, most molecular mechanisms involved are still unknown. To gain insight into the bacterial genetic determinants, we sequenced the whole genome of *Wolbachia wAlbB* strain, a commensal obligate intracellular of the tiger mosquito *Aedes albopictus*.

Mosquitoes are medically important vectors of pathogens. The tiger mosquito *Aedes albopictus* and its sister species *Aedes aegypti* transmitted a large number of arboviruses, notably dengue and chikungunya. In the absence of effective vaccines, transmission of pathogens can be reduced only by limiting mosquito densities by the mechanical eradication of breeding sites and by the application of insecticides that may affect nontarget organisms as well. There is an increasing interest in the use of microbes associated with arthropod vectors to interfere with the transmission of pathogens (1, 10). Indeed, bacteria of the genus *Wolbachia* have been shown to modulate the transmission of pathogens, like chikungunya (*Alphavirus* genus), dengue (*Flavivirus* genus), and parasites (*Brugia pahangi* and *Plasmodium galliceum*) by mosquito vectors through mostly unknown molecular mechanisms (3, 7, 8). To gain insight into the bacterial genetic determinants, we sequenced the whole genome of *Wolbachia wAlbB* strain of *A. albopictus*.

Genomic DNA was extracted from infected mosquito cell line Aa23 and subjected to multiple displacement amplification (6). A mate-paired library with 6-kb inserts was constructed and sequenced by 454 Titanium, generating 185,771 reads that corresponded to 56,058,332 bp and thus approximately 50× coverage. Assembly was performed using Newbler (version 2.3), and one run of Solexa sequencing (31,919,662 reads of 76 bp) allowed the correction of potential base errors. Coding sequence prediction and automatic functional annotation were performed using the MicroScope platform (9) (<http://www.genoscope.cns.fr/agc/microscope>). Manual validation of all the automatically annotated genes was carried out using the MaGe (Magnifying Genomes) interface.

The whole *Wolbachia wAlbB* genome consists of 165 contigs encompassing 49 scaffolds. It has 1,239,814 bp and an average GC content of 33.7%. The genome contains 1,209 predicted protein-coding sequences with an average length of 849 bp, 34 tRNA genes, and one rRNA copy split in 2 operons (16S and 5S-23S). Based on the phylogenetic analysis of 52 orthologous ribosomal proteins retrieved from the four complete *Wolbachia* genome sequences (2, 4, 5, 11), strain *wAlbB* appears to be most closely related to *Wolbachia wPip*, an endosymbiont of the mosquito *Culex pipiens* (4). Preliminary comparative analysis of those five whole-genome sequences of *Wolbachia* revealed 121 protein families present exclusively in strain *wAlbB*, which may suggest potential specific genomic bases for interaction with other coinfecting microorganisms and hosts.

Nucleotide sequence accession numbers. The genome sequence of *Wolbachia wAlbB* was deposited in EMBL under accession numbers [CAGB01000001](https://www.ebi.ac.uk/EMBL/nuclseq/CA/B01000001) to [CAGB01000165](https://www.ebi.ac.uk/EMBL/nuclseq/CA/B01000165). The sequence and annotations are also available from the MicroScope platform (<http://www.genoscope.cns.fr/agc/microscope>).

ACKNOWLEDGMENTS

This work was supported by grants ANR-06-SEST07 and FRB-CD-AOOI-07-012 and was carried out within the framework of GDRI “Biodiversité et Développement Durable à Madagascar.”

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Received 9 January 2012 Accepted 19 January 2012

Address correspondence to Patrick Mavingui, patrick.mavingui@univ-lyon1.fr.

* Present address: Molecular and Biochemical Parasitology, Liverpool School of Tropical Medicine, Liverpool, United Kingdom.

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doi:10.1128/JB.00036-12