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Infecciones por Wolbachia pipientis en poblaciones de Aedes albopictus en la ciudad de València (España): implicaciones para el control de mosquitos

Authors declare that there is no conflict of interests.

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Pilot survey of *Wolbachia pipientis* infections in populations of *Aedes albopictus* in the city of València (Spain): implications for mosquito control

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ABSTRACT

BACKGROUND // The presence of *Aedes albopictus*, of high sanitary and social impact, was first reported in València (eastern Spain) in 2015. Innovative tools for its control include the use of the endosymbiotic bacterium *Wolbachia pipientis*. The release of male mosquitoes infected with the wPip strain, has proven very promising for large-scale Incompatible Insect Technique (IIT) applications. Before this strategy can be implemented in València, it is important to know whether the natural local mosquito populations are *Wolbachia*-infected and, if so, identifying the infecting strains/supergroups.

METHODS // Eggs were collected from the 19 districts of the València city between May and October 2019. A total of 50 lab-reared adult *Ae. albopictus* individuals were processed and analyzed for *Wolbachia* detection and molecular characterization. These actions took place within the framework of a collaboration established with the Department of Health and Consumers of the city council of València.

RESULTS // Our study revealed that 94% of the analyzed samples were naturally infected with *Wolbachia*. Both wAlbA and wAlbB supergroups were identified, with most samples (72% of the infected ones) carrying co-infections.

CONCLUSIONS // These data provide the first characterization of the *Wolbachia* presence in natural populations of *Ae. albopictus* in the Mediterranean area of Spain. This information is relevant to evaluate the potential use of *Wolbachia* strains in order to achieve the suppression of the Asian tiger mosquito populations through massive release of artificially infected males.

KEYWORDS // *Aedes albopictus*; *Wolbachia*; València; Insect Incompatible Technique (IIT); Biological control; Mosquito control; 16S rRNA gene; *wsp*.

RESUMEN

FUNDAMENTOS // La presencia de *Aedes albopictus*, de alto impacto sanitario y social, se informó por primera vez en Valencia en 2015. Las herramientas innovadoras para su control incluyen el uso de la bacteria endosimbótica *Wolbachia pipientis*. La liberación de mosquitos machos infectados con la cepa wPip ha demostrado ser muy prometedora para aplicar la Técnica de Insectos Incompatibles (IIT) a gran escala. Antes de que esta estrategia pueda implementarse, es importante saber si las poblaciones locales de mosquitos silvestres están infectadas por *Wolbachia* y, de ser así, identificar las cepas/supergrupos infectantes, siendo estos los objetivos del presente trabajo.

MÉTODOS // Se recolectaron huevos de los diecinueve distritos de València entre mayo y octubre de 2019, y se mantuvieron en el laboratorio hasta llegar a adultos. Un total de cincuenta individuos adultos de *Ae. albopictus* fueron procesados y analizados para detectar la presencia de *Wolbachia* y su caracterización molecular. Estas acciones se enmarcaron en la colaboración establecida con la Concejalía de Salud y Consumo del Ayuntamiento de València. La prueba exacta de Fisher fue utilizada para detectar la significación estadística de las diferencias entre grupos.

RESULTADOS // El 94% de las muestras analizadas estaban infectadas de forma natural con *Wolbachia*. Se identificaron los supergrupos wAlbA y wAlbB, y la mayoría de las muestras (72% de las infectadas) presentaban coinfecciones.

CONCLUSIONES // Los datos proporcionan la primera caracterización de la presencia de *Wolbachia* en poblaciones naturales de *Ae. albopictus* en el área mediterránea de España. Esta información es relevante para evaluar el potencial uso de cepas de *Wolbachia* de cara a la supresión de poblaciones de mosquito tigre asiático mediante la liberación masiva de machos infectados artificialmente.

PALABRAS CLAVE // *Aedes albopictus*; *Wolbachia*; València; Técnica de Insectos Incompatibles (IIT); Control biológico; Control de mosquitos; Gen de rRNA 16S; *wsp*.

THE INVASION OF *Aedes albopictus* (Skuse, 1894), known as Asian tiger mosquito, has been reported worldwide (1). Its recognized clinical importance lies in its potential to transmit several pathogens causing diseases like *dirofilariasis* and different exotic anthroponotic arboviruses including dengue (DENV), *chikungunya* (CHIKV), or Zika fever (ZIKV) (2-5). The increased risk of transmission is due to several concomitant reasons, including climatic and socio-economic factors, international travel and trade, and public health systems (6). In this context, Mediterranean countries such as Italy, France, Croatia and Spain have declared cases of autochthonous DENV, CHIKV and ZIKV transmission in recent years (5,7-10). Among them, the situation of DENV is particularly worrying since dengue has emerged as the most important viral mosquito-borne disease globally in recent years (11). In Southern Europe autochthonous dengue transmission episodes have occurred on several occasions (12), with a first European detection of *Ae. albopictus* mosquitoes infected with DENV in Spain in 2015 (13). Traditional control measures to reduce mosquito populations include source reduction, public education, and insecticide application, routinely implemented by hundreds of municipalities across Europe (14). However, in some cases, success may be limited due to low levels of community participation, lack of coordination between different administrations and poor practices in the application of insecticides. Moreover, insecticide resistance cannot be discarded as an additional problem to achieve optimal results on *Ae. albopictus* control in Europe (15). Therefore, there is a great consensus among the scientific community about the need to search for innovative and complementary *Ae. albopictus* control methods in urban environments.

nia to the rest of the Mediterranean area including the Balearic Islands (17), as well as other inland and northern regions in Spain such as Madrid, Extremadura and Basque Country (18-20). In 2015 it was reported for the first time in the city of Valencia (21). Thenceforth, its control has become a major goal for municipal public health services (22). Major control measures include treatment with insecticides of breeding places, community participation, as well as biological strategies. The latter overcome some of the drawbacks of insecticide use, namely lack of specificity against certain insects, toxicity to humans and the environment, as well as the possibility of developing resistance (6,23).

Different biological strategies have been used worldwide (24), such as the application of biolarvicides mostly based on *Bacillus thuringiensis* formulates, the release of radiated males (Sterile Insect Technique, SIT), insect transgenesis techniques, or the use of endosymbionts like *Wolbachia* to cause the death of the embryos due to cytoplasmic incompatibility (CI) between the parental gametes (Incompatible Insect Technique, IIT) (25,26). IIT has the advantage that it does not involve the release of mutant or genetically manipulated organisms. Population suppression of *Aedes* mosquitoes through the implementation of a *Wolbachia* strategy is considered a high impact method for insecticide resistance management (27).

Wolbachia pipiensis (Alphaproteobacteria: Rickettsiales) is a maternally transmitted endosymbiont that is estimated to be able to infect up to 66% of known insect species (28). This single species of the genus *Wolbachia* is classified into supergroups A to U (29). Supergroups A and B infect only arthropods, where they act mostly as reproductive parasites. In these cases, distinct *Wolbachia* strains cause different alterations in their hosts to increase their transmission to the next generation, with CI as the most frequent manipulation (30). *Wolbachia* has been used for pest

Ae. albopictus was first reported in Spain in 2004 (16). Since then, it has spread from Catalo-

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and disease vector control because it not only alters host reproduction, but also blocks virus replication and transmission (31). For this reason, endosymbiont-infected populations are being released into the field for two main purposes: population re-placement and population suppression (32). The success of both approaches relies on the ability of the new infecting *Wolbachia* strain to induce CI in the native mosquito population. Thus, the presence of some *Wolbachia* infections in wild mosquito populations might interfere with disease control programs, making population replacement or suppression challenging or even impossible.

The presence of *Wolbachia* strains wAlbA and wAlbB, belonging to the A and B supergroups respectively (33,34), has been widely described in natural populations of *Ae. albopictus*, where infected individuals usually carry one or both strains (35). No other strains have been found naturally in this mosquito species, although it cannot be discarded, since *Wolbachia* is known to undergo horizontal transmission between phylogenetically distant insect species (36). Pioneering studies performed in Italy, described the generation in the laboratory of a new *Ae. albopictus* ARwP line in which the natural *Wolbachia* strains have been replaced by the wPip strain obtained from *Culex pipiens* (Linnaeus, 1758) (37); very recently, the same group reported the first field experiment in Europe to assess the incapacity of the male mosquitoes of the ARwP line to produce viable offspring after mating with wild *Ae. albopictus* females (38). These studies provide further support to the IIT as a suitable approach to reduce and/or suppress *Ae. albopictus* populations in the Mediterranean area.

In the present study, as a first step towards the implementation of an IIT strategy similar to the successful one mentioned above, we have investigated the presence of *Wolbachia* in natural populations of *Ae. albopictus* in the city of València (Spain).

MATERIALS AND METHODS

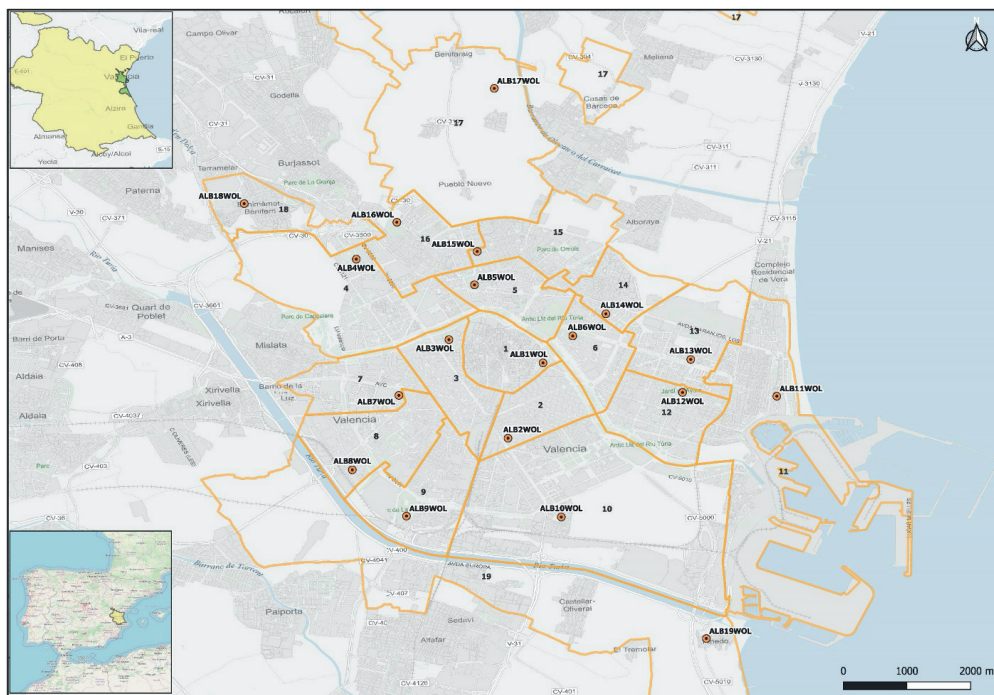


Mosquito sampling. Eggs were collected using standard ovitraps (9). Black plastic bowls (0.4 L volume) filled with water (2/3 of capacity) and supplemented with a wooden stick as oviposition support were used. Sampling was carried out in 2019, between May and October, coinciding with most relevant activity period of the species, in the 19 districts of the city of València, Spain [Figure 1; ANNEX I]. Sampling was spatiotemporally done as follows: May, urban center districts 1, 2 and 3; June, bordering urban districts 4, 5 and 6; July, bordering urban districts 7, 8 and 9; August, bordering urban districts 10, 11 and 12; September, bordering urban districts 13, 14, 15 and 16; October, peripheral rural districts 17, 18 and 19. Number of eggs collected by ovitraps per district ranges from 9 to 112. Specific microhabitats where ovitraps were installed are characterized by shady places well covered by vegetation. Field-collected eggs were reared under laboratory conditions until adult emergence, as previously described (39). Seven to ten days' adult insects, both male and female, were frozen at -20°C to kill them and were maintained in the freezer until total DNA extraction. Species identification and sex separation was confirmed under binocular microscope according to Schaffnet *et al.* criteria (40). The selection of individuals for *Wolbachia* analyses was done randomly by choosing at least 1 male and 1 female per district.

***Wolbachia* genotyping: DNA extraction, amplification, sequencing and phylogenetic analysis.** Individual adult mosquitoes were lysed and homogenized in 200 µL of phosphate buffered saline (PBS) with the aid of sterile toothpicks. After centrifugation at low speed (800xg) for 20 min, total genomic DNA was extracted using DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany) following the manufacturer's protocol, and using a final elution volume of 100 µL. The quality and quantity of DNA was determined with a NanoDrop ND-1000 spectrophotometer.



Figure 1
Spatial distribution of the sampling sites for collecting *Ae. albopictus* eggs in the 19 districts of the city of Valencia, Spain (in numbers).



Dots indicate sampling points.

All tDNA samples were screened for the presence of *Wolbachia* based on polymerase chain reaction (PCR) amplification of the molecular markers *wsp* (primers: 81F, 5'-TGGTCCAATAAGTGATGAAGAAAC-3'; 691R, 5'-AAAAATTAAACGCACTCCA-3'), and 16S rRNA gene (primers: WolbF, 5'-GAAGATAATGACGGTACTCAC-3'; WspecR, 5'-AGCTTCGAGTGAAACCAATTG-3') (41). Negative samples were tested with primers to amplify host ribosomal S7 gene to test DNA quality (5'ATGGT-TTTCGGATCAAAGGT-3' and 5'-CGACCTGTG-TTCAATGGTG-3') (42). Positive samples were then analyzed with forward *wsp*-primers specific for strains wAlbA (328F, 5'-CCAGCAGATACTATTGCG-3') and wAlbB (183F, 5'-AAGGAACCGAAGTTCATG-3'), together with the above mentioned reverse primer 691R (35).

Briefly, PCR amplifications were performed on 2-5 µL of insect's total DNA in 50 µL of reaction with 0.2 µM of each appropriate primer 1X Key Buffer, 2.5 mM MgCl₂, 0.2 mM of each dNTP, 1 unit of Taq DNA Polymerase (VWR) and PCR-grade water up to final volume. 4% DMSO was added to the mix when the first PCR reaction failed. The thermal cycling profile was as follows: initial denaturation at 95 °C for 4 min, followed by 40 cycles of denaturation at 95 °C for 1 min, annealing at 55 °C for 1 min, and extension at 72 °C for 1 min, plus a final extension step of 10 min at 72 °C. The PCR amplification process was performed on two replicates for each sample, and all PCR experiments included positive and negative controls. As a positive control, we used tDNA of an *Ae. albopictus* line coinfecting with *Wol-*

bachia wAlbA and wAlbB, kindly provided by Drs. Nuria Busquets and Sandra Talavera (Universitat Autònoma de Barcelona, Spain). In the negative control, water was added to the PCR reaction instead of tDNA. The amplicons size was checked by 2% agarose gel electrophoresis, stained with SafeView™ Classic stain (NBS Biologicals, Huntingdon, Cambridgeshire, UK), and visualized with UV light.

ABI sequencing was performed on selected amplified products at the sequencing facility of the Universitat de València (Servicio Central de Soporte a la Investigación Experimental, SCSIE) to confirm their identity. Sequencing reads were quality surveyed and assembled using the Staden Package (<http://staden.sourceforge.net>) (43). The obtained sequences were compared with *Wolbachia* sequences already available in GenBank through BLAST searches (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) (44). The DNA sequences determined in this study have been deposited in GenBank (see Accession numbers in **TABLE 1**). Selected *Wolbachia* sequences available in GenBank [**TABLE 1**] were used to perform a sequence alignment with MEGA (45). Phylogenetic analysis was performed by maximum likelihood with GTR+G+I Model. Bootstrap analysis was performed with 1,000 replications. The FigTree v1.4.0 software (<http://tree.bio.ed.ac.uk/software/figtree/>) was used to visualize and edit the phylogenetic tree.

RESULTS AND DISCUSSION

OUR DATA REVEALED THAT 94% OF THE analyzed samples were naturally infected with *Wolbachia*, 72.3% of which were superinfected with strains wAlbA and wAlbB [**TABLE 2, ANNEX I**]. We searched for the presence of *Wolbachia* in 50 adult insects (25 females and 25 males) by PCR, using generic *wsp* primers. Of these, 47 samples (24 females and 23 males) tested positive, revealing a very high infection rate. The possibility of negative results due to an amplification problem caused by a low quality of purified tDNA was ruled out,

as all three negative samples were positive for the host ribosomal S7 gene. Since co-infection with wAlbA and wAlbB strains has been frequently described worldwide (33), the positive samples were subsequently tested with strain-specific primers in separate reactions (35). All amplified and sequenced samples were identical to the *wsp* sequences of wAlbA and wAlbB found in GenBank, and grouped with the corresponding sequences in a phylogenetic analysis [**FIGURE 2**].

The results obtained in our study confirm the possibility of implementing the IIT based on the release of *Ae. albopictus* males infected with wPip in the city of Valencia in a near future, since the wild populations of Asian tiger mosquito are not naturally infected by this endosymbiont strain. Our next steps will focus on the selection of appropriate substrains of wPip naturally infecting the autochthonous *Cx. pipiens* populations, and transfer them by egg microinjection to *Ae. albopictus*, to obtain and maintain in captivity an artificial colony whose males could be released into the field and cause CI after mating with wild females.

Recent research in Italy supports the release of males of a *Wolbachia* wPip-infected *Ae. albopictus* line (ARwP) for autocidal suppression strategies against the Asian tiger mosquito (51,52). Before a similar initiative could be implemented in a new territory, the detection and identification of the *Wolbachia* strains present in local wild *Ae. albopictus* populations is convenient to prevent unexpected effects such as inefficient loss of compatibility (53).

This high rate of *Wolbachia* infection in a wild population of *Ae. albopictus* (94.0%) is similar to the prevalence found in Asian countries like China (93.3 and 95.52%) (54,55), Thailand (100%) (56), or Korea (99%) (57), as well as in the US (95%) (58), and Brazil (99.3%) (59), and far from the low prevalence found in Mexico (a median of 38%) (60).

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Table 1
Wolbachia partial *wsp* sequences included in the phylogenetic analysis.

Accession number	Insect host	Reference
AF020058	<i>Aedes albopictus</i>	33
AF020059	<i>Aedes albopictus</i>	33
AY462863	<i>Aedes albopictus</i>	44
HM007832	<i>Aedes albopictus</i>	45
JX129187	<i>Aedes albopictus</i>	45
OP066400	<i>Aedes albopictus</i>	This study
OP066401	<i>Aedes albopictus</i>	This study
AF020061	<i>Culex pipiens</i>	33
AY462861	<i>Culex quinquefasciatus</i>	44
AF020072	<i>Drosophila melanogaster</i>	33
AF020068	<i>Drosophila simulans</i>	46
AF020070	<i>Drosophila simulans</i>	46
AB039284	<i>Dryinid</i> wasp	47
AF020076	<i>Ephestia cautella</i>	33
AF020077	<i>Glossina austeni</i>	33
AF020079	<i>Glossina morsitans</i>	33
AF020080	<i>Laodelphax striatellus</i>	33
AF020071	<i>Muscidifurax uniraptor</i>	33
AF481181	<i>Nilaparvata lugens</i>	48
AF020082	<i>Phlebotomus papatasi</i>	33
AF020083	<i>Tribolium confusum</i>	33
AF020084	<i>Trichogramma deion</i>	33

Table 2
Infection status of the individual adult *Aedes albopictus* mosquitoes analyzed in this study.

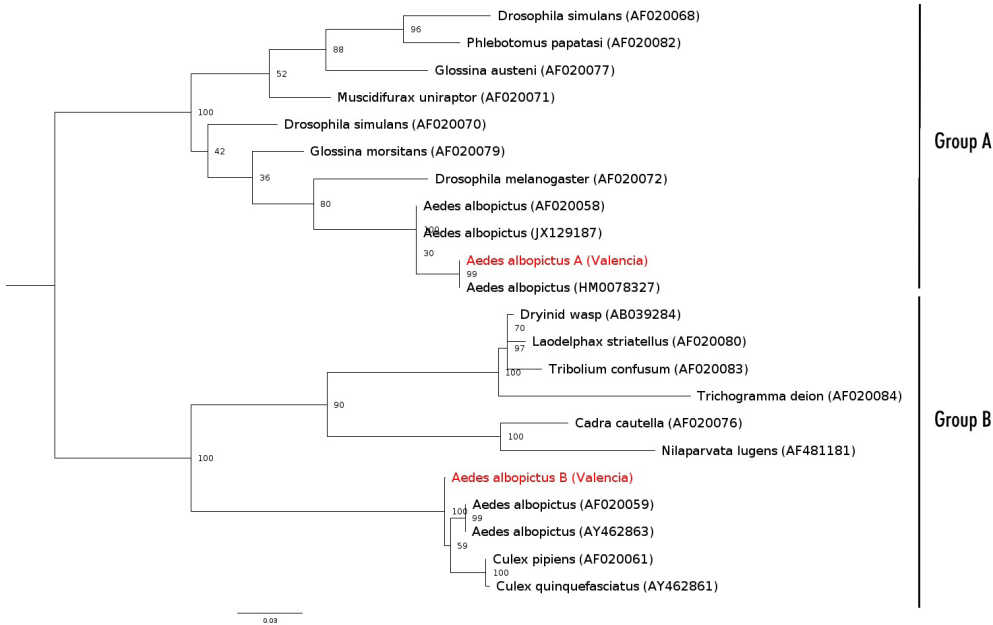
Sex	A+B+	A+B-	A-B+	A-B-
Females	21	3	0	1
Males	13	1	9	2

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Figure 2

Phylogenetic analysis of the *wsp* partial nucleotide sequences of *Wolbachia* obtained from *Ae. albopictus* collected in València, Spain (in red).



Scale bar represents substitutions per site.

Very few reports have been published in the Mediterranean countries, with large differences found in different locations in France (metropolitan and Corsica) (53,61), and Greece (53).

In our survey, the infectious status of males and females differed significantly (p-value 0.0067 using Fisher's exact test). Most infected mosquito females carried superinfections (84%); in the case of males, 54% of them carry also both *Wolbachia* strains, but 36% of them present single infection with wAlbB. These results are in accordance with what had been found previously, with superinfections virtually fixed among females (33,35,56), and loss of wAlbA with age in males (53).

A recent study using ARwP infected males and released in urban areas of Rome (Italy) have confirmed the feasibility of IIT as a way of controlling *Ae. albopictus* populations (38). The authors presented promising results, as 30% of females collected in the release spots were sterile, and 20% had strongly reduced fertility compared with controls. Furthermore, male longevity is not affected by wPip infection in the ARwP line, as they survived up to 2 weeks after release, which is considered adequate for the preservation of reproductive fitness in males, and very similar to wild Asian tiger mosquito males in the field under normal conditions (62). These results are in the same line that those found in a previous laboratory study by the same group (63),

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where no differences were found between uninfected and ARwP *Ae. albopictus* males regarding longevity, mating rate, sperm capacity and mating competitiveness in laboratory condition and greenhouses.

Finally, it is important to address the status of the regulatory aspects of using *Wolbachia*-based control approaches in Europe. Any product to be used to control unwanted organisms (including mosquitoes) that are harmful to human or animal health, or to the environment, or simply can cause damage to human activities, should be registered in Europe as a biocide according to the *EU Biocidal Products Regulation 528/2012* (66). After collecting information about the use of *Wolbachia* as a potential biocide in Europe, the European Commission has recently approved its use stating as follows: “*The bacteria of the genus Wolbachia, or any preparation containing those bacteria, used for the purpose of inoculating those bacteria into mosquitoes, with the objective of creating non-naturally infected mosquitoes for vector control purposes, shall be considered a biocidal product; while non-naturally infected mosquitoes,*

regardless of the infection technique used, shall be considered neither a biocidal product nor a treated article” (65). Considering these regulations, there is a clear route now for the introduction process of *Wolbachia* into the vector control programs of Europe according to European laws. In this context, the València City Council is supporting an initiative regarding the implementation of *Wolbachia* strains for the control of *Ae. albopictus* populations which will be pioneering in Spain.

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Annex I

Demographic profile (sex, site code, location), *Wolbachia* detection status and of supergroup classification for all individual adult *Aedes albopictus* mosquitoes used in this study.

Sample	Sex	Site	Coordinates		wAlbA	wAlbB	Infection
			Latitude	Longitude			
ALB1WOL1F	F	D1	39,4727	-0.3695	+	+	AB
ALB1WOL1M	M	D1	39,4727	-0.3695	+	+	AB
ALB2WOL1F	F	D2	39,4589	-0.3759	+	+	AB
ALB2WOL1M	M	D2	39,4589	-0.3759	+	-	A
ALB3WOL1F	F	D3	39,4769	-0.3867	+	+	AB
ALB3WOL1M	M	D3	39,4769	-0.3867	-	+	B
ALB3WOL2M	M	D3	39,4769	-0.3867	-	+	B
ALB4WOL1F	F	D4	39,4916	-0.4036	+	+	AB
ALB4WOL1M	M	D4	39,4916	-0.4036	+	+	AB
ALB5WOL1F	F	D5	39,4869	-0.382	+	-	A
ALB5WOL1M	M	D5	39,4869	-0.382	+	+	AB
ALB5WOL2M	M	D5	39,4869	-0.382	-	+	B
ALB6WOL1F	F	D6	39,4776	-0.3641	+	-	A
ALB6WOL1M	M	D6	39,4776	-0.3641	-	+	B
ALB7WOL1F	F	D7	39,4667	-0.3958	+	+	AB
ALB7WOL2F	F	D7	39,4667	-0.3958	-	-	0
ALB7WOL1M	M	D7	39,4667	-0.3958	+	+	AB
ALB8WOL1F	F	D8	39,4531	-0.4043	+	-	A
ALB8WOL2F	F	D8	39,4531	-0.4043	+	+	AB
ALB8WOL1M	M	D8	39,4531	-0.4043	-	-	0
ALB9WOL1F	F	D9	39,4446	-0.3944	+	+	AB
ALB9WOL1M	M	D9	39,4446	-0.3944	+	+	AB
ALB9WOL2M	M	D9	39,4446	-0.3944	+	+	AB
ALB10WOL1F	F	D10	39,4444	-0.3661	+	+	AB
ALB10WOL2F	F	D10	39,4444	-0.3661	+	+	AB

Pilot survey of *Wolbachia pipiensis* infections in populations of *Aedes albopictus* in the city of Valencia (Spain): implications for mosquito control.

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Annex I (continues)
Demographic profile (sex, site code, location), *Wolbachia* detection status and of supergroup classification for all individual adult *Aedes albopictus* mosquitoes used in this study.

Sample	Sex	Site	Coordinates		wAlbA	wAlbB	Infection
			Latitude	Longitude			
ALB10WOL1M	M	D10	39,4444	-0.3661	-	+	B
ALB11WOL1F	F	D11	39,4666	-0.3267	+	+	AB
ALB11WOL1M	M	D11	39,4666	-0.3267	-	+	B
ALB12WOL1F	F	D12	39,4673	-0.34	+	+	AB
ALB12WOL1M	M	D12	39,4673	-0.34	-	+	B
ALB13WOL1F	F	D13	39,4733	-0.3425	+	+	AB
ALB13WOL1M	M	D13	39,4733	-0.3425	+	+	AB
ALB14WOL1F	F	D14	39,4816	-0.358	+	+	AB
ALB14WOL1M	M	D14	39,4816	-0.358	+	+	AB
ALB15WOL1F	F	D15	39,493	-0.3815	+	+	AB
ALB15WOL1M	M	D15	39,493	-0.3815	+	+	AB
ALB16WOL1F	F	D16	39,4984	-0.3962	+	+	AB
ALB16WOL2F	F	D16	39,4984	-0.3962	+	+	AB
ALB16WOL3F	F	D16	39,4984	-0.3962	+	+	AB
ALB16WOL4F	F	D16	39,4984	-0.3962	+	+	AB
ALB16WOL1M	M	D16	39,4984	-0.3962	+	+	AB
ALB16WOL2M	M	D16	39,4984	-0.3962	+	+	AB
ALB16WOL3M	M	D16	39,4984	-0.3962	-	-	0
ALB16WOL4M	M	D16	39,4984	-0.3962	+	+	AB
ALB17WOL1F	F	D17	39,5229	-0.3784	+	+	AB
ALB17WOL1M	M	D17	39,5229	-0.3784	+	+	AB
ALB18WOL1F	F	D18	39,5018	-0.4241	+	+	AB
ALB18WOL1M	M	D18	39,5018	-0.4241	-	+	B
ALB19WOL1F	F	D19	39,4222	-0.3396	+	+	AB
ALB19WOL1M	M	D19	39,4222	-0.3396	-	+	B

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