

RESEARCH

Open Access



Establishment of *Wolbachia* infection in *Aedes aegypti* from Pakistan via embryonic microinjection and semi-field evaluation of general fitness of resultant mosquito population

Muhammad Sajjad Sarwar^{1,2*} , Nusrat Jahan², Azeem Ali³, Hafiz Kamran Yousaf¹ and Iqra Munzoor¹

Abstract

Background: Dengue is a mosquito-borne viral disease that is mainly spread by *Aedes aegypti*. It is prevalent on five continents, predominantly in tropical and sub-tropical zones across the world. *Wolbachia* bacteria have been extensively used in vector control strategies worldwide. The focus of the current study was to obtain a natural population of *Ae. aegypti* harbouring *Wolbachia* and to determine the impact of this bacteria on the new host in a semi-field environment.

Methods: *Wolbachia*-infected *Aedes albopictus* was collected from the city of Lahore, Punjab, Pakistan, and *Wolbachia* were successfully introduced into laboratory-reared *Ae. aegypti* via embryonic microinjection. The stable vertical transmission of *wAlbB* in the host population was observed for eight generations, and the impact of *Wolbachia* on the general fitness of the host was evaluated in semi-field conditions.

Results: In the laboratory and semi-field experiments, *wAlbB* *Wolbachia* presented a strong cytoplasmic incompatibility (CI) effect, evidenced as zero egg hatching, in crosses between *Wolbachia*-infected males and wild (uninfected) females of *Ae. aegypti*. *Wolbachia* infection had no noticeable impact on the general fitness ($P > 0.05$), fecundity, body size (females and males) and mating competitiveness of the new host, *Ae. aegypti*. However, there was a significant decrease in female fertility (egg hatch) ($P < 0.001$). In addition, under starvation conditions, there was a remarkable decrease ($P < 0.0001$) in the life span of *Wolbachia*-infected females compared to uninfected females (4 vs. > 5 days, respectively).

Conclusions: *Wolbachia* strain *wAlbB* has a great potential to control the dengue vector in *Ae. aegypti* populations by producing 100% CI with a limited burden on its host in natural field conditions. This strain can be used as a biological tool against vector-borne diseases.

Keywords: *Wolbachia*, *Aedes aegypti*, *Aedes albopictus*, Embryonic microinjection, Cytoplasmic incompatibility

Background

Aedes aegypti is a mosquito of medical importance as it spreads dengue virus (4 serotypes) to millions of people worldwide annually. Pakistan has experienced the reoccurrence of dengue outbreaks during the last two

*Correspondence: mssravian@gmail.com; sarwarms@uo.edu.pk

¹ Department of Zoology, University of Okara, Okara 56300, Pakistan
Full list of author information is available at the end of the article



© The Author(s) 2022. **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

decades. According to the WHO, 102,404 dengue cases and 278 deaths were reported in Pakistan within a 3-year period (2019–2021) [1]. To control dengue vectors, mainly *Aedes aegypti* mosquitoes but to a lesser extent *Aedes albopictus* mosquitoes, insecticides are imported into the country as a cost of billions of rupees annually. In addition to the high cost, the use of traditional insecticides is associated with many negative effects on the environment and communities. In the absence of a vaccine or antiviral drug against dengue virus, suppressing or replacing the vector population through novel methods are important approaches for disease control. One such approach is the use of the *Wolbachia*, a Gram-negative alpha-proteobacteria, which is now being used in various countries as a biological agent to control the progression of various vector-borne diseases, including dengue [2–6].

Wolbachia is a bacterium that is naturally present in many invertebrate species, particularly in nematodes and various arthropods, including insects, such as termites and springtails [7–11]. *Wolbachia* causes several reproductive modifications, such as cytoplasmic incompatibility (CI) [12], parthenogenesis, male-killing [13] and feminization, in their hosts [14]. Of these modifications, CI is the most common phenomenon, present in a wide range of insects that fail to complete karyogamy, conceivably by delaying nuclear envelope breakdown and mitosis. This mechanism may promote *Wolbachia* invasion of uninfected populations because infected females can mate and produce offspring successfully with both infected and uninfected males, whereas uninfected females are unable to produce offspring when they mate with *Wolbachia*-infected males [15].

Aedes aegypti lacks natural *Wolbachia* infection and, consequently, it may be artificially infected with *Wolbachia* naturally occurring in insects to utilize the unique features of this bacterium [16]. Different strains of *Wolbachia* can be used to control a particular disease through manipulation of the biology of the insect host in various ways, such as vector population suppression, direct interference with the transmission of pathogens to humans and negative effects on the fitness of different hosts (e.g. fecundity, fertility, larval development and longevity of mosquito vectors) [17–23]. In the last two decades, various laboratory and field experiments had been conducted with the aim to evaluate numerous strains of *Wolbachia* within mosquito vectors.

Aedes albopictus is naturally infected with two strains of *Wolbachia*: *wAlbA* and *wAlbB* [24]. The application of the proposed strategy requires transfection of a suitable *Wolbachia* strain through microinjection. The transfer can be carried out embryonically, by microinjection the cytoplasm of the *Wolbachia*-infected embryo of the donor insect (mosquitoes and fruit flies, etc.)

to the recipient [25]. Artificial transinfection of *Wolbachia* strain from the native host (*Culex* or *Drosophila*) to another distantly related new host can be challenging [25–29]. Since the effect of different strains is highly variable on the hosts, however, the best strain for vector control has complete maternal transmission, maximum CI induction, low fitness cost, strong virus blocking ability and high occurrence under field conditions [30–33]. *wAlbB* was first introduced into *Ae. aegypti* in 2005, and was found to induce CI [29]. This strain inhibits dengue and other viruses from being transmitted by *Ae. aegypti* [34]. Moreover, *wAlbB* is more heat resistant than other *Wolbachia* strains [35], and *wAlbB* has been released in field trials, successfully reducing dengue transmission [36].

Given this background, we selected wild *Ae. albopictus* as a donor of *Wolbachia wAlbA* and *wAlbB* strains for transinfection to local *Ae. aegypti* mosquitoes collected from Lahore, Pakistan. It was expected that these *Wolbachia wAlbA* and *wAlbB* strains would be better adapted to the local warm environment and would have a better chance of inducing CI, spreading in the wild mosquito population and blocking the transmission of viruses. The fitness of the transinfected mosquito population was also evaluated in the semi-field conditions to obtain data allowing a better prediction in field conditions. This study provides baseline data for the experimental release of *Wolbachia*-infected dengue-resistant mosquitoes in the specific study area of population suppression and replacement.

The present study is designed to transfect the local strain of *Wolbachia* and investigate its effects on the local population of the host *Ae. Aegypti*. The objectives involve the transfection of *Wolbachia* from *Ae. albopictus* collected in Pakistan into the local *Ae. aegypti* population via embryonic microinjection and semi-field evaluation of the impact of *wAlbB* on the general fitness of the host population through the assessment of fecundity, fertility, larval to pupal development, CI induction potential, male competitiveness and life span.

Methods

Field collection and rearing of mosquito strains

A donor of *Wolbachia*, *Ae. albopictus*, and recipient, *Ae. aegypti* (hereafter referred to as “RAG”), adult mosquito populations were locally collected from Lawrence Garden, Lahore Pakistan (31°33′17.9″ N, 74°19′44.4″ E) in 2015 using a CDC backpack mosquito aspirator (model 1412; John W. Hock Co., Gainesville, FL, USA). Geographical coordinates were collected as DMS (degrees, minutes, seconds) using a GPS apparatus (model 76CSx; Garmin GPSMAP® USA, Olathe, KS, USA). Both populations were reared separately in an insectary at Govt.

College University, Lahore, Pakistan, at 27 ± 0.5 °C ambient temperature and $80 \pm 5\%$ relative humidity, under a photoperiod of 12/12-h light/dark with 30 min of gradual transition of light as per standard rearing procedures [37]. Females aged about 5–6 days were blood-fed on defibrinated sheep blood through a membrane feeder for 20 min. Eggs were incubated for a minimum of 1 week.

Detection of *Wolbachia* in *Ae. albopictus*

The presence of *Wolbachia* in *Ae. albopictus* was confirmed by PCR and then the transfection experiments were performed. Dissection of the reproductive organs of the field-collected *Ae. albopictus* and genomic DNA extraction and quantification were done as described by Sarwar et al. [38]. The extracted DNA (template) was exponentially amplified in a Techne Progene PCR thermal cycler (Marshall Scientific, Hampton, NH, USA) in a total reaction volume of 50 μ l containing $1 \times$ Taq buffer, 1.5 mM MgCl₂, 0.2 mM dNTPs, 0.4 μ M each primer, 1 U Taq DNA polymerase and approximately 50 ng of DNA. Genomic DNA of RAG and *Culex quinquefasciatus* were used as the negative and positive control, respectively. Details on the general primer of *Wolbachia* (*Wolbachia* surface protein [*wsp*]) along with PCR conditions are given in Additional file 1: Figure S1a. The amplified products were then analysed by gel electrophoresis as reported by Sarwar et al. [39]. The presence of double infection of *Wolbachia* strains was also tested using *wAlbA* and *wAlbB* strain-specific *wsp* gene primers [40]. Details on these procedures are given in Additional file 1: Figure S1b, c.

Embryonic microinjection for *Wolbachia* transfection

The microinjection protocol was adapted from Xi et al. [29]. Micropipettes (length: 10 cm) were prepared from Quartz tubing filaments (outside and inside diameters: 1.0 and 0.70 mm, respectively) using a laser-based micropipette puller (model PMP-102Q; MicroData Instrument, South Plainfield, NJ, USA). The sharp tip was then mechanically ground using MicroData Instrument's Microelectrode Beveler (model MFG-5AP) to create the bevelled surface of the tip. For the microinjection, 10 blood-fed donor and recipient females were allowed to oviposit separately for about 60–90 min. The grey-coloured eggs were selected and aligned on a slide. The eggs of RAG mosquitoes were desiccated for a short period and then protected by a drop of halocarbon 700 oil (Sigma-Aldrich Co., St. Louis, MO, USA) to avoid further desiccation. Similarly, the *Ae. albopictus* eggs were aligned on the slide but without desiccation. In total, 376 RAG eggs were microinjected in four experimental groups. The injected embryos were considered to be filial

generation zero (F_0) and incubated in the insectary for 1 week, ultimately developing into adults.

The establishment of and screening for *Wolbachia* infection were carried out as described by Xi et al. [29]. Briefly, the first filial generation (F_1) eggs of *Wolbachia*-positive F_0 females of *Ae. aegypti* were reared (the trans-fected mosquito line is hereafter referred to as “WAG”), and all remaining (*Wolbachia*-uninfected) F_1 eggs were discarded. The F_1 females were separated at the pupal stage to keep them virgin and allowed to mate with RAG (uninfected) males in a 1:1 ratio. After mating, 5- to 6-day-old F_1 females were blood fed, and F_1 individual females were isolated and allowed to oviposit. Following oviposition, F_1 females were also tested for *Wolbachia* infection using the PCR assay. Those F_1 females of WAG that tested negative for the presence of *Wolbachia* were discarded along with their progeny. The F_1 females carrying a double infection of *Wolbachia* strains (*wAlbA* + *wAlbB*) were selected to establish a *Wolbachia*-infected *Ae. aegypti* line. A maximum of 30 virgin WAG females were outcrossed with 30 RAG (uninfected) males (at a 1:1 ratio) for up to four generations to decrease genetic bottleneck effects in the WAG line [41]. The egg hatching rate of WAG was compared with that of RAG and the graph was plotted.

Confirmation of *Wolbachia* infection in WAG at F_5

A total of 15 virgin females and males were randomly selected from the WAG F_5 stock line. Whole genomic DNA was extracted from the dissected ovaries of WAG. Double infection of *Wolbachia* strains was screened for by PCR, using the same procedure as mentioned above (for details, see Additional file 1: Figure S1b, c).

Generation of aposymbiotic line

The aposymbiotic line was generated by removing *Wolbachia* infection from about 50 WAG mosquitoes at the F_5 generation. The adults were fed a 10% sugar solution containing tetracycline solution at 1 mg/ml, pH 7 (Sigma-Aldrich; catalogue #T7660-5G) for 5 days per week for two consecutive generations to observe the impact of *Wolbachia* on the *Ae. aegypti* host. The mosquitoes were transferred from the stock cage to new cages using a handheld mechanical aspirator (model 2809 A; BioQuip Products Inc. Compton, CA, USA). The removal of *Wolbachia* was confirmed by the PCR, as mentioned above, in subsequent generations. This aposymbiotic line is referred to hereafter as “TWAG”.

General fitness of WAG in the semi-field conditions

Semi-field evaluation was carried out from August to October 2016 in the GCUL Botanic Garden, Lahore (31°33'24.9" N, 74°19'38.4" E) to determine the effect

of *wAlbB Wolbachia* at the F_8 - F_9 generations on reproductive fitness (female fecundity and fertility), the time required for larval development, mosquito body size, mating competitiveness of WAG males to wild males, life span and degree of CI induction. All the semi-field experiments were done in triplicate independently.

The field cage was made up of a rounded rectangular shaped mosquito net ($2.25 \times 1.25 \times 1.00$ m). A two-cage design was employed to reduce the potential for accidental escape of laboratory-reared mosquitoes or the accidental introduction of wild mosquitoes (Additional file 1: Figure S2). Thus, the field cage itself was covered with a larger mosquito bed net on all sides and over the top. The field cage unit was kept on a wooden platform with the legs of the platform in water-filled bowls, and placed under a tree canopy *Alstonia scholaris* with climbing shrub *Vallaris solanacea*. However, as an additional protection from extensive sunlight and rainfall, a canvas tarpaulin (3×5 m) was suspended over each cage at a height of 2 m. The cage was provided with a flowerpot as a resting area and containers of a 10% sugar solution. Four semi-field cages were installed in the same environment. Environmental parameters, including temperature, relative humidity, light intensity and rainfall were recorded using a data logger at set intervals of 1 h, and mean values of each day were plotted.

Female fecundity and fertility

The average number of eggs laid per female (fecundity) was estimated in the RAG, WAG (at F_8) and TWAG groups of mosquitoes. In the semi-field cages, one hundred 5- to 6-day-old gravid females of each group were transferred to twenty 50- μ l Falcon tubes, five females per tube, and allowed to lay eggs. The egg hatching rate (fertility) of the three groups was also evaluated. After day 7 of incubation, the egg strips of each group were immersed in deoxygenated water, and the hatching rate was scored at 48-h post immersion. To see the effect of *Wolbachia* on oviposition, we used analysis of variance (ANOVA) to compare the difference in the means of all pairs. The proportion of egg hatching was tested using a Chi-square test of association. We proposed three hypotheses regarding the equality of: (i) RAG and WAG; (ii) WAG and TWAG; and (iii) TWAG and RAG; these were tested against the alternative hypotheses of no equality.

Larval development and wing length measurement

Post egg hatching, 100 larvae of each group were transferred to rearing pans. An equal amount of larval food (6% liver powder) was given to all groups daily. Pupae formation was recorded at 12-h intervals. A test of

association was applied to days and pupae formation. The test hypothesis states that the number of days required for pupae formation and the number of pupae are independent. The alternative hypothesis states that these are not independent and that the number of days required for pupae formation and the number of pupae are associated. Wing length/area was considered to be an estimate of body size [42]; the latter has a strong impact on the fecundity of female and male mosquitoes. Wing length was measured as previously described by Joshi et al. [41]. The results of wing length measurement were analysed using the Wilcoxon–Mann–Whitney test.

Cytoplasmic incompatibility

To determine the ability of WAG to induce CI, four types of crosses in three biological replicates were designed between RAG and WAG F_9 mosquito strains (RAG $\text{♀} \times$ RAG ♂ , RAG $\text{♀} \times$ WAG ♂ , WAG $\text{♀} \times$ RAG ♂ and WAG $\text{♀} \times$ WAG ♂). In each cross-group, 20 newly emerged females and 20 newly emerged males were transferred to each cage and reared as mentioned above. Briefly, 5-day-old females were offered a blood meal and the eggs subsequently harvested. Post hatching, the number of viable larvae from each cross was used to determine the level of *wAlbB*-induced CI. The number of hatched eggs was counted under the dissecting microscope and recorded. CI was statistically analysed under the following hypothesis: at least one pair of all groups is insignificant as compared to the average percentage egg hatch against the alternative that there is at least one difference.

Mating competitiveness

The male competitiveness index (C) calculation was adopted from Zhang et al. [43]. Briefly, the mating competitiveness trial of WAG involved four WAG:RAG male ratios (0:40, 20:20, 30:10, 40:0). The 40 virgin (WAG/RAG) males (72–96 h post emergence) followed by 30 virgin RAG females (48–72 h post emergence) were released into field cages. ANOVA was used to compare the groups under the following hypotheses. (i) H_{11} , at least in one group the number of laid eggs is different; (ii) in H_{12} , at least in one group the hatch proportion is different.

Life span (with and without food)

The longevity of 25 virgin WAG F_8 (*Wolbachia*-infected) adults (females and males) was estimated while maintained on 10% glucose only or without any food. Triplicates of RAG adults were used as control. Larvae could pupate as described above, and all the male and female pupae were manually separated based

on body size. To ensure virginity, the pupae were then transferred to an individual test tube (13 × 100 mm; Fisher Scientific Company LLC, Pittsburgh, PA, USA) containing 40 ml of distilled deionized water. Pupae remained in test tubes until adult emergence. Twenty-five mosquitoes, either males or females, were transferred to round paper cups (volume: 946.4 ml; model H4325-J8000, Symphony®; Dart Container, Mason, MI, USA) having a white fine fabric net on the top. Dead mosquitoes were recorded and removed from the opening at the bottom of the container every day until no viable mosquitoes were left.

Overview of data analysis

The data of all the experiments were analysed using the appropriate parametric and non-parametric statistical tests, such as the Chi-square test of association and ANOVA test for parametric data, and the Wilcoxon–Mann–Whitney test and Mantel–Cox test for non-parametric data. Data on fecundity, mating competitiveness and CI assays were tested using ANOVA at a 95% CI, using the SPSS software package (SPSS IBM Corp., Armonk, NY, USA). The details of each test have been mentioned above with the corresponding experimental design.

Results

Wolbachia transinfection via microinjection

Four experimental groups of RAG eggs (total $n = 376$) received cytoplasm via microinjection from the donor *Ae. albopictus* carrying *wAlbA* and *wAlbB* *Wolbachia* strains. Only 44 of the inoculated WAG eggs hatched, with 25 neonate larvae surviving up to the second instar. From these 25 larvae, 20 adults ultimately emerged, nine of which were morphologically identified as female and the remaining 11 as male (Additional file 1: Table S1); these adults were denoted the F_0 generation. None of the eggs hatched in the second experiment and, therefore, this group was discarded. All nine WAG virgin females were outcrossed with RAG males (uninfected *Ae. aegypti*); thus, F_1 WAG eggs were obtained from each F_0 female separately for 2 days. All F_0 adults were then screened by PCR targeting the *wsp* gene using *wAlbA* and *wAlbB* primers separately, as described in the [Methods](#) section.

In total, 13 F_0 WAG (7 females, 6 males) mosquitoes were found to be positive for *Wolbachia* infection (Additional file 1: Table S2). A gel image of the PCR products using strain-specific *wsp* gene primers is shown in Additional file 1: Figure S3. The remaining uninfected F_0 7

adults were discarded along with their eggs. In addition, the males were not used in subsequent steps to establish the *Wolbachia* infected line and, therefore, a gel image of infection status in males is not shown.

Double infection in WAG in the F_0 and F_1 generations

The WAG F_0 females were found to be infected with *wAlbA* and/or *wAlbB* *Wolbachia* in all three possible combinations. One, four and two females were harboured a single *wAlbA*, double *wAlbA* + *wAlbB* and single *wAlbB* infection, respectively. Screening showed that four and two F_0 males were double infected (*wAlbA* + *wAlbB*) and *wAlbB* single infected, respectively (Additional file 1: Table S3).

A total of 334 F_1 WAG eggs were harvested from the five F_0 females. Of these, 132 eggs hatched, with 115 larvae surviving to become F_1 adults (Additional file 1: Table S4). In total, 17 F_1 females were *Wolbachia*-infected (Additional file 1: Table S5), of which five, two and 10 females were infected with *wAlbA*, *wAlbA* + *wAlbB* and *wAlbB*, respectively (Additional file 1: Table S6). Two females carrying double *Wolbachia* strains were selected to establish the WAG line.

Wolbachia infection in WAG at the F_5 generation

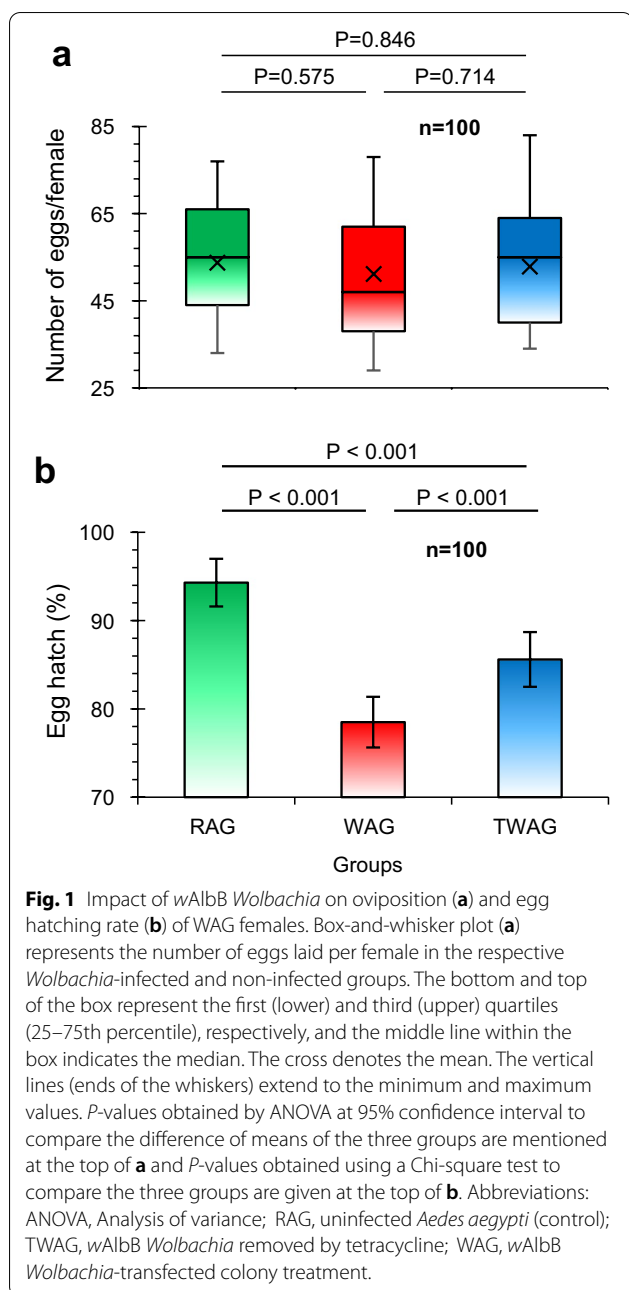
Randomly selected 12 virgin females and 12 males from the WAG F_5 stock line were screened for double infection of *Wolbachia* strains using the PCR assay. All individuals were found infected by *wAlbB* only. Not a single female (Additional file 1: Figure S4) or male was infected with *Wolbachia* *wAlbA* single infection or with *wAlbA* + *wAlbB* double infection, possibly due to the low infection rate of the *wAlbA* strain. Subsequently, randomly selected individuals from stock cages were screened at various generations, and *Wolbachia* infection was consistently confirmed up to the F_{85} generation.

Egg hatching rate in WAG up to the F_8 generation

An overview of the egg hatching rate of WAG mosquitoes over eight generations after *Wolbachia* transfection is shown in Additional file 1: Figure S5. In the first three generations, the fertility of WAG was low, ranging from 45 to 29%. However, a 70% egg hatch was achieved in the F_5 generation, and after the F_6 generation the fertility of WAG was observed to be stable at $80 \pm 5\%$.

Weather conditions during the semi-field experiments

Average daily temperatures and relative humidity during the 3 months of the semi-field trials ranged from 18 °C to 31 °C, and from 54% to 92%, respectively. Total rainfall

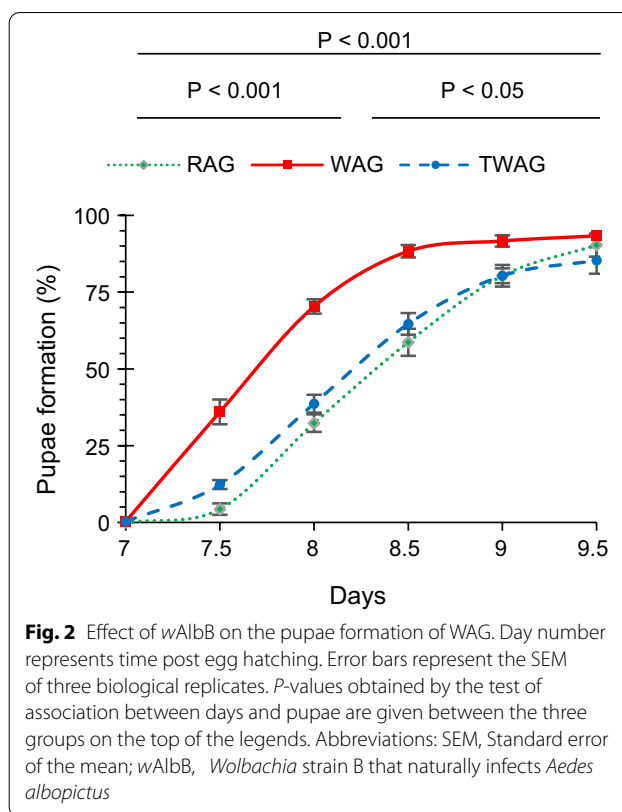


was noted as 442.2 mm in > 15 episodes, resulting in suitable weather conditions for the mosquito population (Additional file 1: Figure S6).

General fitness of WAG in the semi-field experiments

Female fecundity and fertility

Fecundity is a measure of the reproductive potential of female mosquitoes. There was no significant difference ($P > 0.05$) in egg-laying capacity (mean: 52.6 per female) between the three groups (Fig. 1a). Egg hatching rates

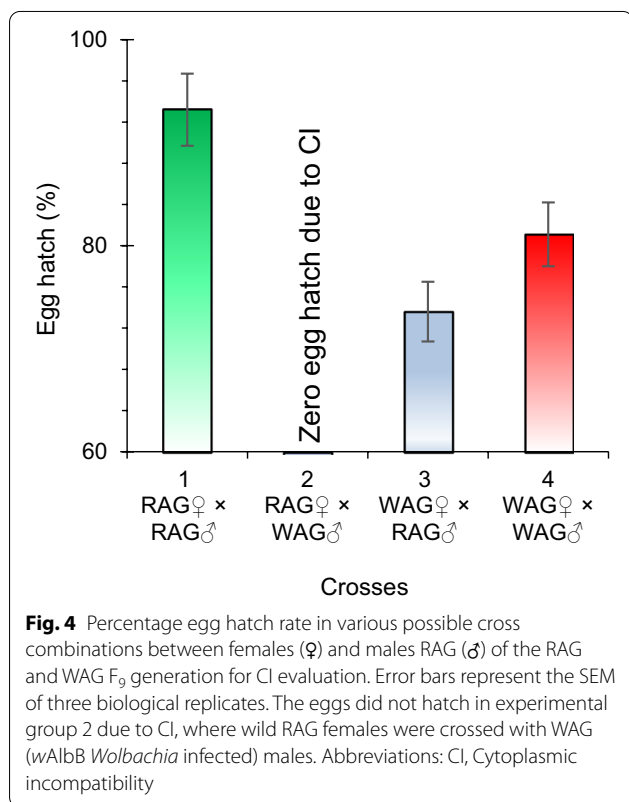
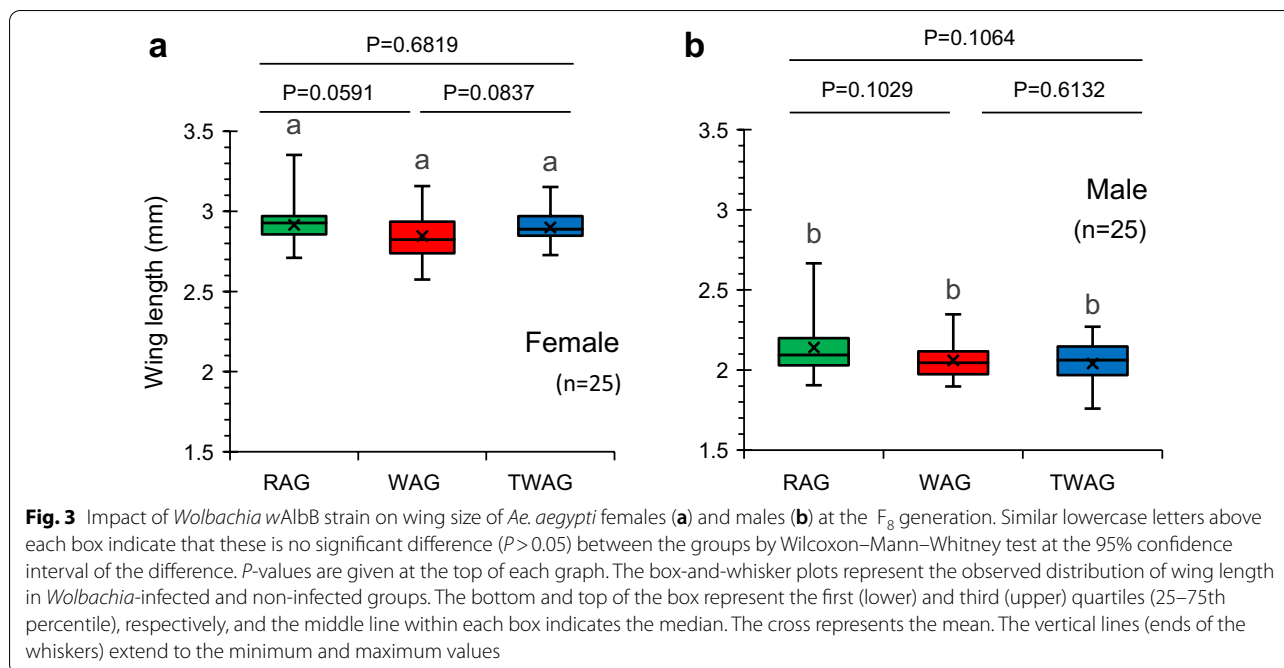


of the RAG, WAG and TWAG groups were 94.3, 78.5 and 85.6%, respectively. The Chi-square test of association indicated that egg hatching rates among all the three groups were significantly different ($P < 0.001$) (Fig. 1b). This result demonstrated that there was no considerable effect of *wAlbB* on fecundity whereas a remarkable decrease in fertility was noted with *Wolbachia* infection.

Larval development and wing-length measurement

Figure 2 shows that pupal emergence was significantly higher ($P < 0.001$) at day 7.5 in the WAG group than in the RAG group (36% vs. 4%, respectively). In addition, at day 8.5, pupal emergence was 88% in WAG and 59% RAG. However, a 93% pupal emergence was recorded in WAG as compared to 90% in RAG at day 9.5. Based on these observations, it could be inferred that *wAlbB* induced the earlier development of larvae to pupal formation in *Ae. aegypti*.

Analysis of the data sets on wing lengths of RAG, WAG and TAG females (range: 2.57–3.16 mm) and males (range: 1.57–2.92 mm) indicated no significant between-group difference ($P > 0.05$) using the Mann–Whitney U-test (Fig. 3). Therefore, we concluded that infection with *wAlbB* did not affect the body size of the host, based on wing length in either sex.



Cytoplasmic incompatibility

The potential of *wAlbB* to induce CI was determined by allowing WAG mosquitoes to cross with RAG mosquitoes. A maximum egg hatch of 93.2% was noted in a cross between RAG female mosquitoes (RAG♀) × RAG male mosquitoes (RAG♂), while 0% egg hatch was observed in the cross between RAG♀ × WAG♂. Therefore, complete (100%) CI was induced. An average of 73.6% egg hatch was observed in the WAG♀ × RAG♂ group. In addition, the egg hatch was 81.1% in a group involving WAG♀ × WAG♂ (Fig. 4).

These results indicated that the *wAlbB* *Wolbachia* strain induced complete CI in *Ae. aegypti* when *Wolbachia*-infected males were crossed with uninfected females ($P > 0.001$). The least significant difference test (LSD) was applied, and results indicated that one pair was not significant among the six pairs tested.

Mating competitiveness assays

Thirty female and 40 male mosquitoes were placed together in the same cage for 2 days. A maximum of 1684 eggs was collected from the control group (RAG♂ × RAG♀). No remarkable difference in egg-laying capacity was noted in all four groups. However, the number of eggs that eventually hatched was significantly different ($P < 0.001$), indicating that the number

Table 1 Competitiveness index of different ratios of F₈ WAG males measured at different ratios of RAG males in semi-field conditions

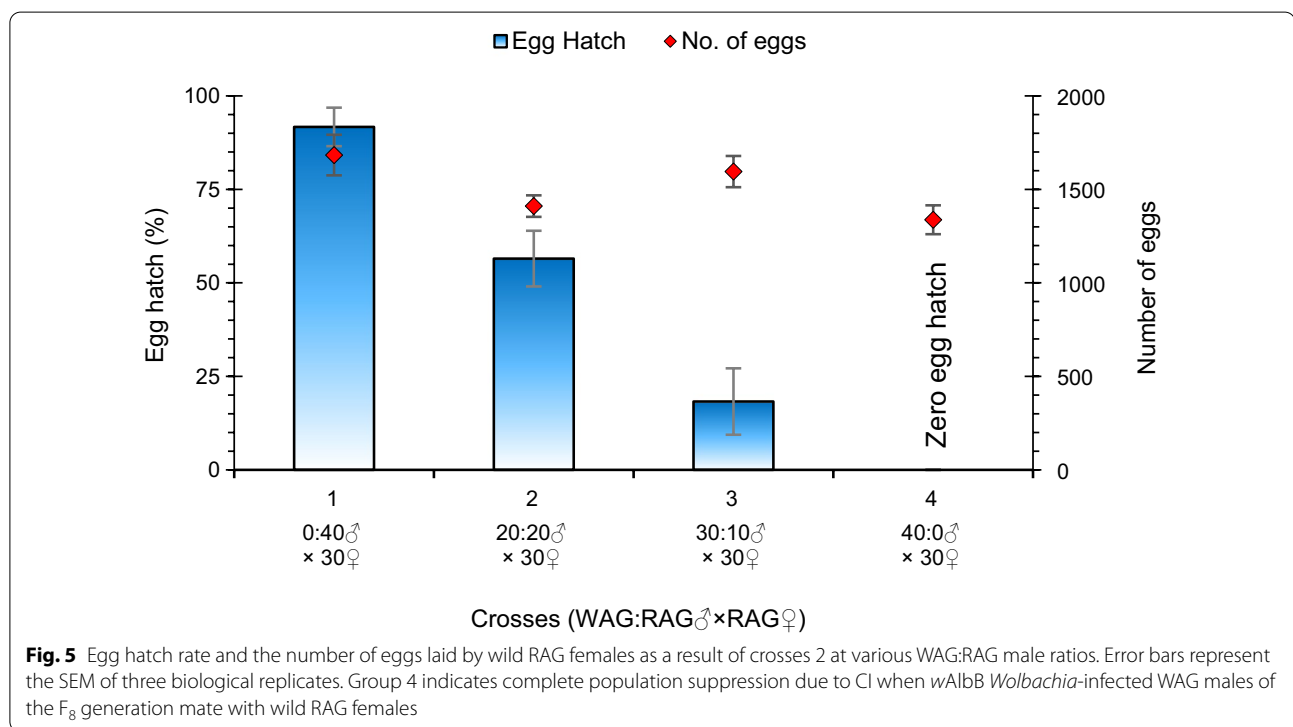
Male ratio WAG:RAG	♂ × ♀ WAG:RAG × RAG	Egg hatch ^a (n eggs)	Hc-Hr	Hr-Hi	Cm/In	Competitiveness index ^b
0:1	0:40 × 30 Hc	91.7% ± 5.1 ^a (1684)	Negative control group			
1:1	20:20 × 30 Hr	56.5% ± 8.1 ^b (1411)	35.2 ± 11.8	56.5 ± 8.1	1	0.63 ± 0.3
3:1	30:10 × 30 Hr	18.3% ± 5.9 ^c (1595)	73.4 ± 11.0	18.3 ± 5.9	0.33	1.38 ± 0.6
1:0	40:0 × 30 Hi	0.0% ± 0.0 ^d (1338)	Positive control group			

All values are given as ± standard error of the mean of triplicate measures

RAG Uninfected *Aedes aegypti* (control), TWAG wAlbB *Wolbachia* removed by tetracycline, WAG wAlbB *Wolbachia*-transfected colony treatment

^a Different lowercase letters indicate that the values are statistically different ($P < 0.05$) in all crosses using Tukey mean procedure test

^b Competitiveness index = $\frac{Hc-Hr}{Hr-Hi} \times \frac{Cm}{In}$, where Hc = hatch rate of eggs harvested from the cross RAG♂ × RAG♀ (compatible); Hr = hatch rate of eggs harvested from the cross WAG:RAG♂ × RAG♀; Hi = hatch rate of eggs harvested from the cross WAG♂ × RAG♀ (incompatible); Cm = number of compatible males (RAG); In = number of incompatible males (WAG)

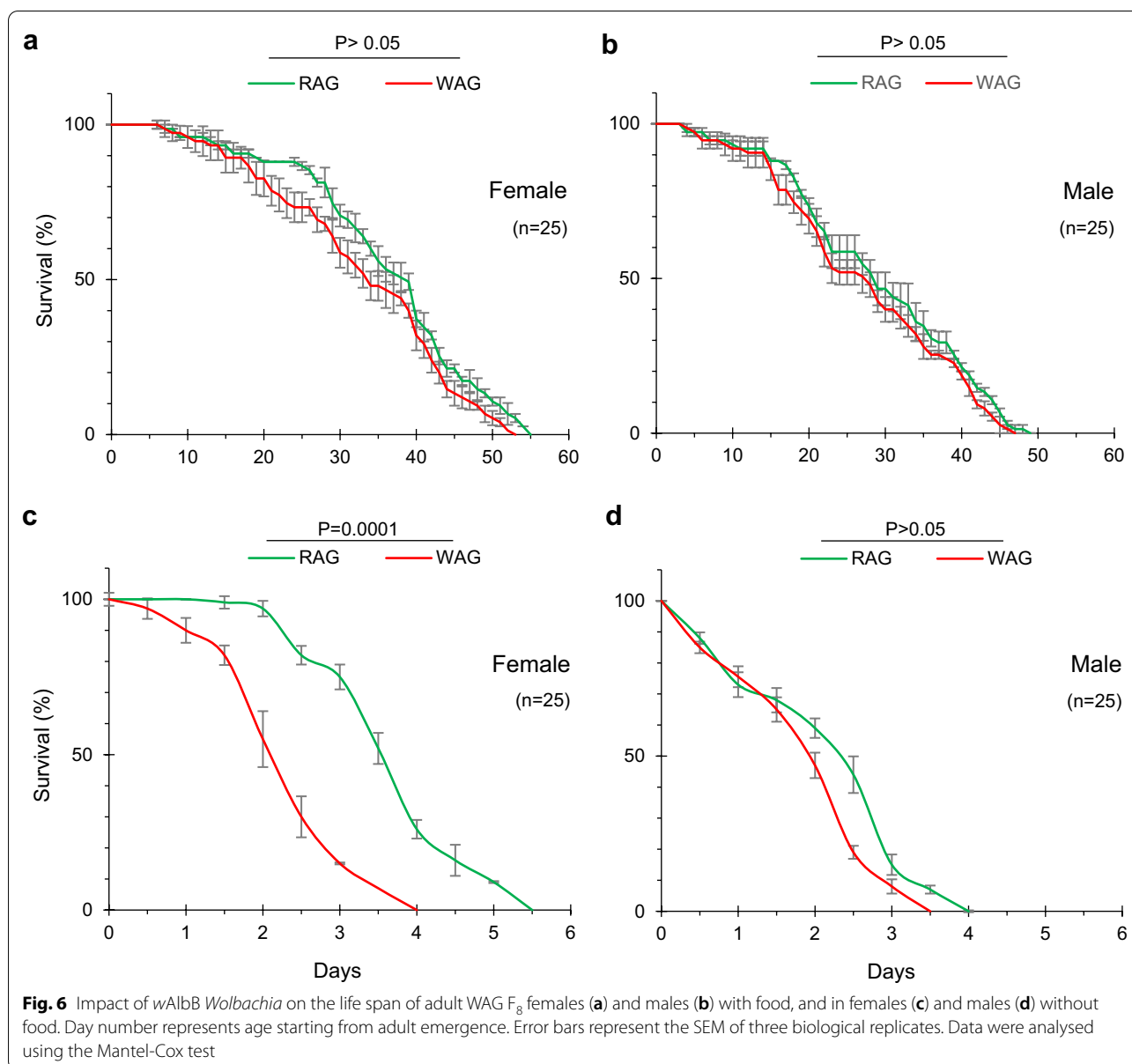


of compatible matings was different in each group. The egg hatch in the compatible cross (RAG♂ × RAG♀) was 91.7%. At a ratio of 20:20 WAG:RAG males, egg hatching was 56.5%, giving a competitiveness index of 0.63. This means that compatible (RAG) males were slightly more competitive than incompatible (WAG) males (Table 1). A 35.2% reduction in egg hatch was noted when WAG males mated with RAG females when in competition with RAG males. At a 3:1 WAG:RAG release ratio, egg hatching was reduced to 18.3% due to maximum matings

of incompatible males (WAG♂) (Fig. 5). Thus, egg hatch was significantly influenced by the ratio of WAG males.

Life span (with and without food)

Longevity was not significantly different in RAG and WAG females (Mantel–Cox test, $P > 0.05$). Maximum survival of RAG and WAG females was 54 and 52 days, respectively. The survival curve was almost similar between the two groups up to 14 days (at 93% survival). However, a noticeable decrease in survival in WAG



females was observed from 15 days (89% survival) up to 26 days (73% survival). After 40 days, the death rate was similar in both groups (Fig. 6a). Similarly, RAG and WAG males showed similar survival patterns (Mantel-Cox test, $P > 0.05$), with an initial survival stability of 2 weeks. The survival curve was notably similar, with $> 90\%$ of male mosquitoes alive up to 15 days. At 28 days, 51–55% of males were still alive in both groups. A maximum survival of 49 and 47 days was observed in the male RAG and WAG groups, respectively (Fig. 6b).

Under conditions of complete starvation, WAG females had a significantly shorter life span, with a

maximum survival of 4 days, than RAG females, with a maximum survival of > 5 days (Mantel-Cox test, $P < 0.0001$). After 1.5 days, the number of WAG females began to gradually decrease (Fig. 6c). Life span assays indicated no significant difference in the survival curve of RAG and WAG males under conditions of complete starvation ($P > 0.05$) (Fig. 6d). Males of both groups had a maximum life span of 4 days. *wAlbB* remarkably reduced the survival of WAG *Ae. aegypti* females compared with RAG females under starvation conditions, while *wAlbB* did not affect the survival rate of male *Ae. aegypti* under the same conditions.

Discussion

The results of the current study suggest that embryonic microinjection is a suitable strategy for the interspecific transfer of *Wolbachia*. *Wolbachia* affects various phenotypes of the mosquitoes in which it is present, such as reductions in life span and fecundity, respectively [44–48]. In our study, the *Wolbachia* donor (*Ae. albopictus*) and recipient (*Ae. aegypti*) mosquitoes were locally collected from Lahore, Pakistan. It was expected that these indigenous mosquito species that have a local mitochondrial haplotype would be better adapted to the warm climate of the country than nonlocal species and that these *Wolbachia*-infected mosquitoes would have high chances of survival and progression in the natural weather conditions following field releases. These mosquitoes would thus have a high chance of mating with the females of the wild population. Similarly, the local *Wolbachia* strain would show good CI induction, virus inhibition and fitness cost on the host, among other effects.

In the present study, *wAlbB Wolbachia* was successfully established in naturally uninfected *Ae. aegypti* from wild-collected *wAlbA + wAlbB* double-infected *Ae. albopictus*. The recipient *Ae. aegypti* colony was initially double infected at the F_0 generation and then later the double infection was replaced by a single infection of *wAlbB Wolbachia* within five generations post microinjection. The exact number of filial (F_1 – F_5) generations needed for the loss of *wAlbA* infection to occur or the reason behind this removal was not assessed. However, it is important to mention here that to eliminate genetic bottlenecks, we performed outcrosses of double-infected (*wAlbA + wAlbB*) F_0 females with uninfected males. One of the possible reasons for the loss of *Wolbachia* is the low titre of the *wAlbA Wolbachia* in the F_0 females. The *wAlbA* might be removed simultaneously or gradually during these outcrosses. Afterwards, the *wAlbB* infection is currently stable in successive generations (up to F_{85} and thereafter). Xi et al. [29] reported the transfer of embryonic cytoplasm from double-infected *Ae. albopictus* to *Ae. aegypti*. The *wAlbA* infection was unstable, and only the *wAlbB* strain of *Wolbachia* was established successfully in *Ae. aegypti* (WB1). Similarly, the cytoplasm of double-infected *Ae. albopictus* was microinjected separately into the aposymbiotic *Wolbachia*-removed *Ae. albopictus* (Houston) as well as the *Ae. aegypti* (WB2). A single stable *wAlbB* infection was established in the host [29, 49]. In contrast, the *wAlbA* strain was not always lost after transinfection [50, 51].

Many studies have reported that the *wAlbB* strain of *Wolbachia* has the potential to be used as a biocontrol

agent for the control of different diseased vectors [29, 30, 36, 41, 47, 52–54]. The current study was also focused on evaluation of the effect of *wAlbB* on the general fitness of the host, such as fecundity, wing length, life span assays and, most importantly, the CI of *Ae. aegypti* under semi-field conditions. The field conditions are highly variable in any part of the world as compared to standard laboratory conditions. Factors such as temperature, humidity, wind, rainfall and the day/night cycle greatly affect the efficiency or even survival of laboratory-reared mosquitoes. Experiments under semi-field conditions therefore provide more reliable data for predicting the results of field trials.

To assess the changes in the physiology of the host, natural or artificial *Wolbachia* infection can be removed from insects by treatment with various antibiotics, including tetracycline [55, 56] and rifampicin [57]. The results of the present study suggest that *Wolbachia* did not affect the physiology of *Ae. aegypti*, as indicated by the fecundity and wing length measurements. Similarly, Calviti et al. [58] reported that the removal of *Wolbachia* infection had no observable effect on the fitness of the natural host *Ae. albopictus* under either laboratory conditions or in greenhouses.

In the current study, *Wolbachia* strain *wAlbB* had no impact on the fecundity of *Wolbachia*-infected females in the semi-field experiments, which is consistent with the results from previous laboratory studies [59, 60]. However, a significant decrease in the egg hatching rate was noted, which is also consistent with results of previous studies [25, 29, 61]. On the other hand, different authors [41, 62] have suggested that *wMel*-infected *Ae. aegypti* and *wAlbB*-infected *Anopheles stephensi* females showed reduced fecundity compared to uninfected mosquitoes at high temperature.

Wing-length measurements have been used in mosquito studies to infer the overall body size, which in turn is a measure of general fitness, including the mating potential of the mosquitoes [42, 63, 64]. In the current study, *wAlbB Wolbachia* did not have any negative impact on the wing size of the host. These results are consistent with the findings of Axford et al. [65]. No significant impact of *wAlbB Wolbachia* was reported on the body size of *Ae. aegypti*. Furthermore, current results are also consistent with previous reports of *wAlbB* and *wMel* not having any significant impact on the wing length/body size of *Ae. aegypti* [62] and *An. stephensi* [41], respectively.

By releasing different ratios of RAG and WAG males to RAG females, we found that *Wolbachia*-infected males were competitive with wild males. These findings

are consistent with those of a previous study [66]. Conversely, Xi et al. [67] reported that *Wolbachia* reduced the mating competitiveness of transfected male mosquitoes.

It is well documented that the same strain of *Wolbachia* not only imparts a different impact on the host of another species but also on the host of the same species. In search of the *Wolbachia* strain for better features, different insects have been screened. It is also evident from the results that the selected *wAlbB* strain affected the host differently. The current results are broadly consistent with previously published data, with minor differences regarding egg hatching, larval development and life span that could be due to genetic differences in background or density of the *wAlbB* strain. It is important to mention that *Wolbachia*-infected mosquitoes have been released in the field in Australia [2] and China [68]. Moreover, *Wolbachia* strain *wAlbB* has been documented to reduce dengue transmission in Malaysian populations of *Ae. aegypti* in field trials [36].

Conclusions

In the present study, *Wolbachia* strain *wAlbB* produced complete CI by affecting fertility in the new host *Ae. aegypti* and reduced the life span of only females under starvation conditions in the semi-field experiments. *Wolbachia* strain *wAlbB* did not affect the fecundity of female mosquitoes but significantly decreased the rate of egg hatching. This *wAlbB* strain has a great potential to control the dengue vector *Ae. aegypti* population by producing 100% CI without affecting the general fitness of the host under natural conditions. As such, this strain could be used as biocontrol for vector-borne diseases.

Abbreviations

♀: Female(s); ♂: Male(s); ANOVA: Analysis of variance; CI: Cytoplasmic incompatibility; F: Filial; RAG: *Aedes aegypti* lacking *Wolbachia* naturally; SEM: Standard error of the mean; TWAG: *wAlbB* infection removed in WAG by antibiotic treatment; WAG: *wAlbB*-infected *Ae. aegypti*; *Wsp*: *Wolbachia* outer surface protein.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s13071-022-05317-4>.

Additional file 1: Fig. S1. General (a) and strain-specific primer sequences (b, c) showing estimated product size along with thermal cycler conditions for the detection of *Wolbachia* by targeting the *wsp* gene. **Fig. S2.** A semi-field cage was used for the evaluation of the fitness of WAG. **Fig. S3.** Gel electrophoresis analysis of PCR products using *wsp* gene-based strain-specific *wAlbA* (a) and *wAlbB* (b) primers targeting gDNA of WAG F_0 females. **Fig. S4.** Gel electrophoresis analysis of PCR products using *Wolbachia* *wAlbA*-specific (a, c) and *wAlbB*-specific (b, d) primers targeting the *wsp* gene from WAG F_2 females (a, b) and males (c, d). **Fig. S5.** Egg hatching rate of WAG females from F_1 to F_8 generation. **Fig. S6.** Weather conditions from August to October 2016 during

semi-field experiments: mean daily temperature (a), relative humidity (b) and rainfall (c). **Table S1.** Survival details of *Ae. aegypti* embryos (F_0) post microinjection of cytoplasm from *Ae. albopictus* embryos. **Table S2.** *Wolbachia* infection along with gender distribution in WAG F_0 adults post microinjection. **Table S3.** Distribution of double infection of *Wolbachia* strains in parental (F_0) WAG adults post microinjection. **Table S4.** Egg hatching rate of WAG F_1 eggs. **Table S5.** Survival and *Wolbachia* infection details of WAG F_1 . **Table S6.** Details of *Wolbachia* positive WAG F_1 females post microinjection.

Acknowledgements

We are grateful to the management of GCUL Botanic Garden for granting permission to set the semi-field experiments on their premises. We also wish to thank Mr Adnan Saleem, Lab Attendants, for providing support in the field.

Author contributions

MSS and NJ contributed to the conception and design of the study, conducting the experiments and collecting data. NJ supervised the whole work. AA and IM contributed to data analysis and processing. HKY wrote the first draft of the manuscript. All authors read and approved the final manuscript.

Availability of data and materials

Further details of the current study are available from the corresponding author on reasonable request.

Declarations

Ethics approval and consent to participate

This study was carried out in strict accordance with the recommendations in the Animal Ethics Procedures, and the protocol was reviewed and approved by the Approval Committee, GCUL (Ref. No. 1027/ORIC/14).

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

¹Department of Zoology, University of Okara, Okara 56300, Pakistan. ²Department of Zoology, Government College University, Katchery Road, Lahore, Pakistan. ³Department of Statistics and Computer Science, University of Veterinary and Animal Sciences, Lahore, Pakistan.

Received: 4 November 2021 Accepted: 9 May 2022

Published online: 06 June 2022

References

- WHO. Dengue fever—Pakistan. World Health Organization. 2021. <https://www.who.int/emergencies/disease-outbreak-news/item/dengue-fever-pakistan>. Accessed 15 Dec 2021.
- Beebe NW, Pagendam D, Trewin BJ, Boomer A, Bradford M, Ford A, et al. Releasing incompatible males drives strong suppression across populations of wild and *Wolbachia*-carrying *Aedes aegypti* in Australia. *Proc Natl Acad Sci USA*. 2021;118:e2106828118.
- Pinto SB, Riback TIS, Sylvestre G, Costa G, Peixoto J, Dias FBS, et al. Effectiveness of *Wolbachia*-infected mosquito deployments in reducing the incidence of dengue and other *Aedes*-borne diseases in Niteroi, Brazil: a quasi-experimental study. *PLoS Negl Trop Dis*. 2021;15:e0009556.
- Indriani C, Tantowijoyo W, Rances E, Andari B, Prabowo E, Yusdi D, et al. Reduced dengue incidence following deployments of *Wolbachia*-infected *Aedes aegypti* in Yogyakarta, Indonesia: a quasi-experimental trial using controlled interrupted time series analysis. *Gates Open Res*. 2020;4:50.
- Ahmad NA, Mancini MV, Ant TH, Martinez J, Kamarul GMR, Nazni WA, et al. *Wolbachia* strain *wAlbB* maintains high density and dengue inhibition

- following introduction into a field population of *Aedes aegypti*. *Philos Trans R Soc Lond B Biol Sci.* 2018;376:20190809.
6. Ahmad NA, Endersby-Harshman NM, Mohd Mazni NR, Mohd Zabari NZA, Amran SNS, Ridhuan Ghazali MK, et al. Characterization of sodium channel mutations in the dengue vector mosquitoes *Aedes aegypti* and *Aedes albopictus* within the context of ongoing *Wolbachia* releases in Kuala Lumpur, Malaysia. *Insects.* 2020;11:529. <https://doi.org/10.3390/insects11080529>.
 7. Wasala SK, Brown AMV, Kang J, Howe DK, Peetz AB, Zasada IA, et al. Variable abundance and distribution of *Wolbachia* and *Cardinium* endosymbionts in plant-parasitic nematode field populations. *Front Microbiol.* 2019;10:964.
 8. Czarnetzki AB, Tebbe CC. Detection and phylogenetic analysis of *Wolbachia* in *Collembola*. *Environ Microbiol.* 2004;6:35–44.
 9. Diouf M, Miambi E, Mora P, Frechault S, Robert A, Rouland-Lefevre C, et al. Variations in the relative abundance of *Wolbachia* in the gut of *Nasutitermes arborum* across life stages and castes. *FEMS Microbiol Lett.* 2018;365:fny046. <https://doi.org/10.1093/femsle/fny046>.
 10. de Oliveira CD, Goncalves DS, Baton LA, Shimabukuro PH, Carvalho FD, Moreira LA. Broader prevalence of *Wolbachia* in insects including potential human disease vectors. *Bull Entomol Res.* 2015;105:305–15.
 11. Lopez-Madrigal S, Duarte EH. Titer regulation in arthropod-*Wolbachia* symbioses. *FEMS Microbiol Lett.* 2019;366(23):fnz232. <https://doi.org/10.1093/femsle/fnz232>.
 12. Beckmann JF, Ronau JA, Hochstrasser M. A *Wolbachia* deubiquitylating enzyme induces cytoplasmic incompatibility. *Nat Microbiol.* 2017;2:17007.
 13. Perlmutter JJ, Meyers JE, Bordenstein SR. Transgenic testing does not support a role for additional candidate genes in *Wolbachia* male killing or cytoplasmic incompatibility. *mSystems.* 2020;5:e00658-19. <https://doi.org/10.1128/mSystems.00658-19>.
 14. Herran B, Geniez S, Delaunay C, Raimond M, Lesobre J, Bertaux J, et al. The shutting down of the insulin pathway: a developmental window for *Wolbachia* load and feminization. *Sci Rep.* 2020;10:10551.
 15. Chen H, Zhang M, Hochstrasser M. The biochemistry of cytoplasmic incompatibility caused by endosymbiotic bacteria. *Genes.* 2020;11:852.
 16. Ross PA, Callahan AG, Yang Q, Jasper M, Arif MAK, Afizah AN, et al. An elusive endosymbiont: does *Wolbachia* occur naturally in *Aedes aegypti*? *Ecol Evol.* 2020;10:1581–91.
 17. Hussain M, Lu G, Torres S, Edmonds JH, Kay BH, Khromykh AA, et al. Effect of *Wolbachia* on replication of West Nile virus in a mosquito cell line and adult mosquitoes. *J Virol.* 2013;87:851–8.
 18. Lu P, Bian G, Pan X, Xi Z. *Wolbachia* induces density-dependent inhibition to dengue virus in mosquito cells. *PLoS Negl Trop Dis.* 2012;6:e1754.
 19. Moreira LA, Iturbe-Ormaetxe I, Jeffery JA, Lu G, Pyke AT, Hedges LM, et al. A *Wolbachia* symbiont in *Aedes aegypti* limits infection with dengue, Chikungunya, and *Plasmodium*. *Cell.* 2009;139:1268–78.
 20. Magori K, Legros M, Puente ME, Focks DA, Scott TW, Lloyd AL, et al. Skeeeter Buster: a stochastic, spatially explicit modeling tool for studying *Aedes aegypti* population replacement and population suppression strategies. *PLoS Negl Trop Dis.* 2009;3:e508.
 21. Nguyen TH, Nguyen HL, Nguyen TY, Vu SN, Tran ND, Le TN, et al. Field evaluation of the establishment potential of *wMelPop Wolbachia* in Australia and Vietnam for dengue control. *Parasit Vectors.* 2015;8:563.
 22. Ross PA, Axford JK, Callahan AG, Richardson KM, Hoffmann AA. Persistent deleterious effects of a deleterious *Wolbachia* infection. *PLoS Negl Trop Dis.* 2020;14:e0008204.
 23. Ross PA, Turelli M, Hoffmann AA. Evolutionary ecology of *Wolbachia* releases for disease control. *Annu Rev Genet.* 2019;53:93–116.
 24. Hu Y, Xi Z, Liu X, Wang J, Guo Y, Ren D, et al. Identification and molecular characterization of *Wolbachia* strains in natural populations of *Aedes albopictus* in China. *Parasit Vectors.* 2020;13:28.
 25. Ant TH, Herd CS, Geoghegan V, Hoffmann AA, Sinkins SP. The *Wolbachia* strain *wAu* provides highly efficient virus transmission blocking in *Aedes aegypti*. *PLoS Pathog.* 2018;14:e1006815.
 26. Zabalou S, Riegler M, Theodorakopoulou M, Stauffer C, Savakis C, Bourtzis K. *Wolbachia*-induced cytoplasmic incompatibility as a means for insect pest population control. *Proc Natl Acad Sci USA.* 2004;101:15042–5.
 27. Zabalou S, Apostolaki A, Livadaras I, Franz G, Robinson A, Savakis C, et al. Incompatible insect technique: incompatible males from a *Ceratitis capitata* genetic sexing strain. *Entomol Exp Appl.* 2009;132:232–40.
 28. Blagrove MS, Arias-Goeta C, Failloux AB, Sinkins SP. *Wolbachia* strain *wMel* induces cytoplasmic incompatibility and blocks dengue transmission in *Aedes albopictus*. *Proc Natl Acad Sci USA.* 2012;109:255–60.
 29. Xi Z, Khoo CC, Dobson SL. *Wolbachia* establishment and invasion in an *Aedes aegypti* laboratory population. *Science.* 2005;310:326–8.
 30. Joshi D, Pan X, McFadden MJ, Bevins D, Liang X, Lu P, et al. The maternally inheritable *Wolbachia* *wAlbB* induces refractoriness to *Plasmodium berghei* in *Anopheles stephensi*. *Front Microbiol.* 2017;8:366.
 31. Fraser JE, O'Donnell TB, Duyvestyn JM, O'Neill SL, Simmons CP, Flores HA. Novel phenotype of *Wolbachia* strain *wPip* in *Aedes aegypti* challenges assumptions on mechanisms of *Wolbachia*-mediated dengue virus inhibition. *PLoS Pathog.* 2020;16:e1008410.
 32. Puggioli A, Calvitti M, Moretti R, Bellini R. *wPip Wolbachia* contribution to *Aedes albopictus* SIT performance: advantages under intensive rearing. *Acta Trop.* 2016;164:473–81.
 33. Hoffmann AA, Ross PA, Rašić G. *Wolbachia* strains for disease control: ecological and evolutionary considerations. *Evol Appl.* 2015;8:751–68.
 34. Bian G, Xu Y, Lu P, Xie Y, Xi Z. The endosymbiotic bacterium *Wolbachia* induces resistance to dengue virus in *Aedes aegypti*. *PLoS Pathog.* 2010;6:e1000833.
 35. Ross PA, Wiwatanaratanaabutr I, Axford JK, White VL, Endersby-Harshman NM, Hoffmann AA. *Wolbachia* infections in *Aedes aegypti* differ markedly in their response to cyclical heat stress. *PLoS Pathog.* 2017;13:e1006006.
 36. Nazni WA, Hoffmann AA, NoorAfizah A, Cheong YL, Mancini MV, Golding N, et al. Establishment of *Wolbachia* strain *wAlbB* in Malaysian populations of *Aedes aegypti* for dengue control. *Curr Biol.* 2019;29:4241-8 e5.
 37. Zheng ML, Zhang DJ, Damiens DD, Lees RS, Gilles JR. Standard operating procedures for standardized mass rearing of the dengue and chikungunya vectors *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae)-II-egg storage and hatching. *Parasit Vectors.* 2015;8:348.
 38. Sarwar MS, Jahan N, Shahbaz F. Molecular detection and characterization of *Wolbachia pipientis* from *Culex quinquefasciatus* collected from Lahore, Pakistan. *Am J Trop Med Hyg.* 2018;98:154–61.
 39. Sarwar MS, Jahan N, Batool F, Kalim B. *Wsp* gene based detection and characterization of *Wolbachia* in indigenous *Drosophila*. *J Bio & Env Sci.* 2017;10:1–8.
 40. Yang C, Xi Z, Zhu J, Luo Y. Detection primer, detection method and detection kit of *Aedes B* type *Wolbachia*. China: Patent CN 104878111 A. 2015.
 41. Joshi D, McFadden MJ, Bevins D, Zhang F, Xi Z. *Wolbachia* strain *wAlbB* confers both fitness costs and benefit on *Anopheles stephensi*. *Parasit Vectors.* 2014;7:1–9.
 42. Armbruster P, Hutchinson RA. Pupal mass and wing length as indicators of fecundity in *Aedes albopictus* and *Aedes geniculatus* (Diptera: Culicidae). *J Med Entomol.* 2002;39:699–704.
 43. Zhang D, Lees RS, Xi Z, Bourtzis K, Gilles JR. Combining the sterile insect technique with the incompatible insect technique: Ill-robust mating competitiveness of irradiated triple *Wolbachia*-infected *Aedes albopictus* males under semi-field conditions. *PLoS ONE.* 2016;11:e0151864.
 44. Hoffmann AA, Montgomery BL, Popovici J, Iturbe-Ormaetxe I, Johnson PH, Muzzi F, et al. Successful establishment of *Wolbachia* in *Aedes* populations to suppress dengue transmission. *Nature.* 2011;476:454–7.
 45. Lau MJ, Ross PA, Hoffmann AA. Infertility and fecundity loss of *Wolbachia*-infected *Aedes aegypti* hatched from quiescent eggs is expected to alter invasion dynamics. *PLoS Negl Trop Dis.* 2021;15:e0009179.
 46. Shaw WR, Marcenac P, Childs LM, Buckee CO, Baldini F, Sawadogo SP, et al. *Wolbachia* infections in natural *Anopheles* populations affect egg laying and negatively correlate with *Plasmodium* development. *Nat Commun.* 2016;7:11772.
 47. McMeniman CJ, Lane RV, Cass BN, Fong AW, Sidhu M, Wang YF, et al. Stable introduction of a life-shortening *Wolbachia* infection into the mosquito *Aedes aegypti*. *Science.* 2009;323:141–4.
 48. Schraiber JG, Kaczmarczyk AN, Kwok R, Park M, Silverstein R, Rutaganira FU, et al. Constraints on the use of lifespan-shortening *Wolbachia* to control dengue fever. *J Theor Biol.* 2012;297:26–32.
 49. Xi Z, Dean JL, Khoo C, Dobson SL. Generation of a novel *Wolbachia* infection in *Aedes albopictus* (Asian tiger mosquito) via embryonic microinjection. *Insect Biochem Mol Biol.* 2005;35:903–10.
 50. Ruang-Areerate T, Kittayapong P. *Wolbachia* transinfection in *Aedes aegypti*: a potential gene driver of dengue vectors. *Proc Natl Acad Sci USA.* 2006;103:12534–9.

51. Ant TH, Sinkins SP. A *Wolbachia* triple-strain infection generates self-incompatibility in *Aedes albopictus* and transmission instability in *Aedes aegypti*. *Parasit Vectors*. 2018;11:295.
52. Flores HA, de Bruyne JT, O'Donnell TB, Tuyet Nhu V, Giang NT, Trang HTX, et al. Multiple *Wolbachia* strains provide comparative levels of protection against dengue virus infection in *Aedes aegypti*. *PLoS Pathog*. 2020;16:e1008433.
53. Bian G, Zhou G, Lu P, Xi Z. Replacing a native *Wolbachia* with a novel strain results in an increase in endosymbiont load and resistance to dengue virus in a mosquito vector. *PLoS Negl Trop Dis*. 2013;7:e2250.
54. Rasgon JL, Gamston CE, Ren X. Survival of *Wolbachia pipiensis* in cell-free medium. *Appl Environ Microbiol*. 2006;72:6934–7.
55. Bishop C, Parry R, Asgari S. Effect of *Wolbachia* wAlbB on a positive-sense RNA negev-like virus: a novel virus persistently infecting *Aedes albopictus* mosquitoes and cells. *J Gen Virol*. 2020;101:216–25.
56. Hoerauf A, Volkmann L, Nissen-Paehle K, Schmetz C, Autenrieth I, Büttner DW, et al. Targeting of *Wolbachia* endobacteria in *Litomosoides sigmodontis*: comparison of tetracyclines with chloramphenicol, macrolides and ciprofloxacin. *Trop Med Int Health*. 2000;5:275–9.
57. Aljanyoussi G, Tyrer HE, Ford L, Sjöberg H, Pionnier N, Waterhouse D, et al. Short-course, high-dose rifampicin achieves *Wolbachia* depletion predictive of curative outcomes in preclinical models of lymphatic filariasis and onchocerciasis. *Sci Rep*. 2017;7:210.
58. Calvitti M, Moretti R, Porretta D, Bellini R, Urbanelli S. Effects on male fitness of removing *Wolbachia* infections from the mosquito *Aedes albopictus*. *Med Vet Entomol*. 2009;23:132–40.
59. Joubert DA, Walker T, Carrington LB, De Bruyne JT, Kien DHT, Hoang NLT, et al. Establishment of a *Wolbachia* superinfection in *Aedes aegypti* mosquitoes as a potential approach for future resistance management. *PLoS Pathog*. 2016;12:e1005434.
60. Dobson SL, Rattanadechakul W, Marsland EJ. Fitness advantage and cytoplasmic incompatibility in *Wolbachia* single- and superinfected *Aedes albopictus*. *Heredity*. 2004;93:135–42.
61. Ross PA, Gu X, Robinson KL, Yang Q, Cottingham E, Zhang Y, et al. A wAlbB *Wolbachia* transinfection displays stable phenotypic effects across divergent *Aedes aegypti* mosquito backgrounds. *Appl Environ Microbiol*. 2021;87:e0126421.
62. Turley AP, Zalucki MP, O'Neill SL, McGraw EA. Transinfected *Wolbachia* have minimal effects on male reproductive success in *Aedes aegypti*. *Parasit Vectors*. 2013;6:1–10.
63. Foo IJ, Hoffmann AA, Ross PA. Cross-generational effects of heat stress on fitness and *Wolbachia* density in *Aedes aegypti* mosquitoes. *Trop Med Infect Dis*. 2019;4:13.
64. Honěk A. Intraspecific variation in body size and fecundity in insects: a general relationship. *Oikos*. 1993;66:483–92. <https://doi.org/10.2307/3544943>.
65. Axford JK, Ross PA, Yeap HL, Callahan AG, Hoffmann AA. Fitness of wAlbB *Wolbachia* infection in *Aedes aegypti*: parameter estimates in an outcrossed background and potential for population invasion. *Am J Trop Med Hyg*. 2016;94:507–16.
66. Axford JK, Ross PA, Yeap HL, Callahan AG, Hoffmann AA. Fitness of wAlbB *Wolbachia* infection in *Aedes aegypti*: parameter estimates in an outcrossed background and potential for population invasion. *Am J Trop Med Hyg*. 2016;94:507–16.
67. Xi Z, Khoo CC, Dobson SL. Interspecific transfer of *Wolbachia* into the mosquito disease vector *Aedes albopictus*. *Proc Biol Sci B*. 2006;273:1317–22.
68. Zheng X, Zhang D, Li Y, Yang C, Wu Y, Liang X, et al. Incompatible and sterile insect techniques combined eliminate mosquitoes. *Nature*. 2019;572:56–61.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Ready to submit your research? Choose BMC and benefit from:

- fast, convenient online submission
- thorough peer review by experienced researchers in your field
- rapid publication on acceptance
- support for research data, including large and complex data types
- gold Open Access which fosters wider collaboration and increased citations
- maximum visibility for your research: over 100M website views per year

At BMC, research is always in progress.

Learn more biomedcentral.com/submissions

