**Supplementary Material**

**Supplementary Figure 1.** Flowchart of study selection for review Symbiotic *Wolbachia* in mosquitoes and its role in reducing the transmission of mosquito-borne diseases:updates and prospects



**Supplementary Table 1.** Field infected and trans-infection of mosquito by Wolbachia and its prevention effect of vector-borne diseases.

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| Topic | *Wolbachia* strain | Vector/s species | Research strategy & methodology  | Main findings |
| *Aedes* spp. |
| Epidemiology | wAlb and Pip | *Ae. albopictus* | PCR based approach | Maternal transmission is nearly 100% [1] |
| *Wolbachia* | *Ae. aegypti* | Trans-infection technique | Inherited microorganisms [2] |
| Wsp | *Ae. albopictus* | On field-collected PCR-based approach | Infections prevalence 86.7% [3] |
| Infection | Wsp | *Aedes* and *Culex* | PCR-based approach | Predominately found in the reproductive tissues but infection rates varied according to host species [4] |
| wAlbA+wAlbB | *Ae. albopictus* | PCR-based and antibody-based approaches | Distributed in host somatic and germ-line tissues [5] |
| Wsp | *Ae. albopictus* | On-field infection and PCR-based approach | Modify vector populations and deliver pathogen-blocking genes [6] |
| Wsp | *Ae. albopictus* | PCR-based approach | No differences in oviposition responses and strain-specific differences in mating, and host-seeking behavior [7] |
| wAlbA &wAlbB | *Ae. albopictus* | PCR-based approach | Effect on immature survivorship, developmental rate, adult size, larval nutrition, and CI level causing reduced larval survival and food computation [8] |
| wPip  | *Ae. albopictus* | Genes-editing approach | Bidirectional reproductive barriers between infected and uninfected mosquitoes [9] |
| wPip , wMel, wAlbA &wAlbB | *Ae. albopictus* | Induced sterility and virus protection  | Reducing transmission of CHIKV and DENV [10] |
| Mel, AlbA and Pip | *Ae. albopictus,**Cx.quinquefasciatus* | Field data screened by PCR-based approach s | Reduce viral and other bacterial replication [11] |
| wMelPop | *Ae. aegypti* | PCR-based and antibody-based approaches | Predominately found in the fat body, Malphgian tubules, ovaries, and Salivary glands, inducing phenotype change and adult lifespan reduction [12] |
| wMelPop | *Ae. aegypti* | PCR-based approaches | Anatomical changes, unable to successfully insert stylet into human skin, reducing feeding success, Infection and lifespan [13] |
| wMelPop | *Ae. aegypti* | Blood-feeding trials in response to humans | Anatomical changes, "bendy" proboscis, reducing feeding success, Infection and lifespan [14] |
| wMel | *Ae. aegypti* | In field challenge and PCR-based approach | Infected and uninfected distributed in the same body tissues, wMel reduce viral infection [15] |
| *wMelPop-CLA* | *Ae. aegypti* | Morphometric assessments | Infected mosquitoes have low infection fitness in the field [16] |
| wMelPop | *Ae. aegypti* | Microarray and PCR-based approach | Vector was less susceptible to filariasis infection by immune responses up regulation and sorter lifespan [17]  |
| wMel | *Ae. aegypti* | Laboratory larval competition  | Density and sex dependent effect, males development inhibition [18]  |
| wMel | *Ae. aegypti* | Effects of infected larval nutrition  | Both nutrition level and infection showed interference in larval development and diet one also showed Larval development is impaired in infected mosquitoes but not strain [19] |
| wMel | *Ae. aegypti* | Odor cues response in the field  | Reduction of adult lifespan and blood feeding success not alteration of odor attraction [20] |
| wMel | *Ae. aegypti* | *Wolbachia*-infected mosquitoes release into the field | Reduction of mosquito populations and virus-amplification in the female mosquito [21] |
| wAlbB-wsp | *Ae. aegypt* | PCR-based approaches | Density-dependent increased CI basal immunity and longevity, reduced lifespan [22] |
| wMelBr | *Ae. albopictus**Ae. aegypti* | Wild and trans-infected mosquitoes interspecific competition | *Larvae* had superior survivorship, faster development rate and a higher performance index in *Ae albupictus* than *Ae. aegypti* both infected and uninfected groups [23] |
| wMel | *Ae. aegypti* | PCR-based approach | Resources competition induced gene expression, metabolic homeostasis, and physiological processes causing ROS and NOs expression [24] |
| wMelPop | *Ae. aegypti* | PCR-based approach | Infection alters lipid/cholesterol metabolism including differential cholesterol and lipid profiles [25] |
| wMelPop-CLA | *Ae. aegypti* | PCR-based approach | Strain-dependent GATA4 expression inhibiting virus assembly [26] |
| Different strain | *Ae. aegypti* | *Wolbachia* usage and surveillance  | High support from the community [27] |
| *wMel* | *Ae. aegypti* | PCR-based approach | Reduced vector competence for ZIKV [28] |
| wMelPop | *Ae. aegypti* | PCR-based approach | Long period infection reduces adult life span and DENV transmission [29] |
| wMelPop | *Ae. aegypti* | On-Field blood meal, PCR based and antibody-based approaches | Innate immune system priming and limited cellular resources are required for pathogen replication [30] |
| *wMel* | *Ae. aegypti* | Released *Wolbachia*-infected mosquito  | Reduced vector competence for CHIKV, extremely high viral titers detected in the blood meal but no infectious virus in saliva [31] |
| wBm | *Ae. aegypti.* | PCR-based and antibody-based approaches  | *Wolbachia* depletion blocks transmission of lymphatic filariasis preventing chitinase-dependent parasite escheatment, causes depletion of *Wolbachia* , leads to a block of MF development to stage 3 [32] |
| *Anopheles* spp. |
| Epidemiology | coxA haplotypes | *An. stephensi* | PCR-based approaches  | 10.9% of *An. stephensi* screened positive from *An. stephensi* with multiple haplotypes and supergroups A and B [33] |
| Wsp | *An. gambiae* | PCR-based approaches | High *Wolbachia* 16S rRNA sequence diversity, low abundance, and no congruence between host and symbiont phylogenies *Wolbachia* sequences were detected [34] |
| wAnfu-A and wAnfu-B | *An. fenstusts* | PCR-based approaches | New strains were isolated, the discovery of natural infection [35] |
| Wanga | *An. gambiae* | PCR-based approaches | Naturally harbor these bacteria and Novel *Wolbachia* strain, isolated [36] |
| Infection | *wAlbB* | *An. stephensi* | PCR-based approaches | Reduced female fecundity and caused a minor decrease in male mating competitiveness [37] |
| *wAlbB* | *An. stephensi* | PCR-based approaches | Reduction in parasite numbers of up to 92% at the sporozoite stage and more than half at the oocyst stage [38] |
| *Wsp* | *An. gambiae* | PCR-based approaches | natural infection, reducing the life span of vectors and providing resistance to pathogen infection [39] |
| wAlbB,wMelPop | *An. gambiae* | PCR-based approaches | Differences in interference of pathogen development in mosquitoes. The wAlbB strain significantly increases *P. berghei* oocyst levels in the mosquito midgut while wMelPop modestly suppresses oocyst levels [40] |
| *wMelPop and wAlbB* | *An.**gambiae* | PCR-based and antibody-based approaches  | wMelPop disseminates widely in the fat body, head, sensory organs and other tissues but is absent from the midgut and ovaries, significantly inhibiting *P.falciparum* oocyst levels in the mosquito midgut [41] |
| Wanga | *An. gambiae , An. coluzzii* | PCR-based approaches | Relatively higher prevalence and intensity of infection-detected significantly reduced the prevalence and intensity of sporozoite infection [42] |
| WAnga-M | *An.gambiae* and *An. coluzzii* | PCR-based approaches | wAnga influenced mosquito egg-laying behaviour ,phenotypic change of the vector, inhibition to *P. falciparum* development [43] |
| WAnga | *An. coluzzii,* | PCR based and antibody-based approaches | negative correlation between the presence of *Plasmodium* parasites and *Wolbachia* infection, wAnga does not induce CI but affects oviposition to reduce malaria prevalence [44] |
| Wanga | *An. arabiensis & An. funestus,* | PCR-based approaches  | confirmation of natural *Wolbachia* in malaria vectors but low prevalence and density within species, limits the malaria parasite *P. falciparum* infections [45] |
| *Culex* spp. |
| Epidemiology | Wsp | *Cx pipiens* | PCR-based approaches  | Prevalence 87.3% wild-caught mosquitoes, rate of infection females 61.5% to 100% while males 80% to 100%. horizontal transfer between unrelated host organisms, results in a high proportion of infection prevalence and rate [46] |
| Wsp | *Culex pipiens and Culex torrentium* | PCR-based approaches  | The prevalence of *Wolbachia* in *Cx. pipiens* was 97% (95% CI 94.8–97.6%), while only 0.7% (95% CI 0.19–2.45%) in *Cx. torrentium* [47] |
| Infection | Group A and B | *Different strains* | PCR-based approaches | Wolbachia supergroup A prefer cooler temperatures than uninfected ones, On the other hand, supergroup B infected-hosts prefer warmer temperatures [48] |
| Wolbachia spp. | *Cx. quinquefasciatus* | PCR-based approaches | *Wolbachia* reduces vector competence in *Cx. quinquefasciatus*, and potentially in other Wolbachia-infected mosquito vectors [49] |
| Different strains | *Cx. pipiens* | PCR-based approaches | A new host-*Wolbachia* symbioses had a higher survival rate than in old host-*Wolbachia* symbioses. Induction of host innate immune responses [50] |
| Wpip | *Cx. pipiens* | PCR-based approaches  | A considerable amount of *Wolbachia* diversity can be generated within a single host species in a short time, and playing a key role in their evolution [51] |
| *Different strain* | *Cx pipiens* | Insecticide resistance stages | High infection densities do not increase CI or maternal transmission efficiency relative to low infection densities and increase insecticide resistance. Increased density could contribute to the fitness cost of resistance [52] |
| Different strain | *Cx. pipiens* | PCR-based approaches | Insecticide-resistant strains, sharing the same cytoplasmic and nuclear background has an insecticide-susceptible strain, the higher *Wolbachia* density, correlated to insecticide resistance, and increase the physiological costs of insecticide resistance [53] |
|  | Different strain | *Cx pipiens.* | PCR-based approaches  | Strains harboring the resistance gene had more density than a susceptible strain with the same genetic background, the resistant mosquitoes had significantly higher infection rates than the susceptible ones [54] |
| Different strain | *Cx quinquefasciatus* | PCR-based approaches  | No correlation between susceptibility of two lines in response to DDT while they represented a significant correlation for deltamethrin, infection increased the susceptibility to deltamethrin but had a neutral effect on DDT susceptibility [55] |
|  | WpipSJ | *Cx. Quinquefasciatus* | PCR-based approaches  | Native wPipSJ infection is more resistant to the pathogenic action of the three mosquitocidal bacterial strains, naturally infected with wPipSJ is less susceptible, while susceptible to *B. thuringiensis* subsp. israelensis than to the other [56] |

coxA: cytochrome c oxidase subunit, CI: cytoplasmic incompatibility; CHIKV: Chikungunya virus; DENV: dengue virus, Wsp: *Wolbachia* surface antigen, MF: Microfilaria.

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