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## **Fate of *Culex pipiens*: Vector of Many Pathogenic Viruses**

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*Culex pipiens* mosquito has a large distribution that is affected by availability of water and temperature (Barker *et al.*, 2010; Azari-Hamidian *et al.*, 2011). The phytotelmata (water body with plants) having high water volumes with high solid contents and large canopy favors its growth (Adebote *et al.*, 2008; Jacob *et al.*, 2009). *C. pipiens* mosquito is a vector for many animals and human disease causing viruses e.g., Rift Valley Fever Virus (RVFV), West Nile Virus (WNV), Batai virus, Sindbis virus etc. (Reusken *et al.*, 2011). The distribution of these viruses is increasing day by day due the raise in temperature, rainfall and dispersal patterns (Gould and Higgs, 2009) and all these parameters favors' the growth of *C. pipiens*. Mandell and Flick (2011) while reviewing the occurrence and distribution of RVFV declared it an important potential threat to the human and livestock health. The food and temperature provided to insect poses a significant impact on virus infection and dissemination (Moutailler *et al.*, 2007; Anderson *et al.*, 2010). At temperature (30°C) the dissemination infection of WNV in *C. pipiens* was more than 90% (Dohm *et al.*, 2002a). WNV cause fever and neural epidemiology in birds, humans, horses and other mammals, its infection rate is high in already suffering organisms (Ulbert, 2011). It is also known that *C. pipiens* infected with virus in late summer, act as a carrier of virus in next spring (Dohm *et al.*, 2002b). Thus to stop the invasion of viruses the population of their vectors like *C. pipiens* should be diminish. Many studies have been conducted that were aiming to identify such pesticide which can effectively control *C. pipiens* adults and larvae (Hussein *et al.*, 2005; Khoobdel *et al.*, 2007; Reza and Abbas, 2007; Shonouda and Mehanney, 2000). But in some cases external application of pesticide is not so much effective due to the hard cuticle of insect (Ikbal *et al.*, 2007). Altalhi (2005) found the *Bacillus thuringiensis israelensis* (*Bti*, a bacterium) and duck weed (aquatic plant) as important biological controls of *C. pipiens*. According to him the presence of *Bti* in water cause toxic effect on the third and forth instars larvae in concentration dependant manner but *Bti* is expensive. Moreover he found that duck weed has cytochemical toxic effects on *C. pipiens* population, which lessened the need of high *Bti* concentrations. A more effective and economical biological control against *C. pipiens* is required.

*Wolbachia* are intercellular bacteria, infecting almost 66% of the pest (arthropods and nematodes), so it has great potential as biological control (Hilgenboecker *et al.*, 2008). *Wolbachia* inherit maternally; it shortens the life span of its host and can efficiently cause Cytoplasmic Incompatibility (CI) (McMeniman *et al.*, 2009). *Wolbachia* also cause infection in common house mosquito *C. pipiens* but rarely cause infertility, which is due to the presence of compatible *Wolbachia* strains (Duron *et al.*, 2011; Walker *et al.*, 2009). Atyame *et al.* (2011) conducted the PCR study of *Wolbachia* (*wPip*) strains in *Culex pipiens* mosquitoes, which sort out the reasons of compatibility and incompatibility caused by *Wolbachia*. The incompatible *Wolbachia* strains cause CI in mosquitoes and vice versa. According to them this CI property of *Wolbachia* depends upon *mod* and *resc* (lock and key) model and to evaluate its properties a total of 360 *C. pipiens* from

15 natural breeding sites of La Reunion Island were examined. From these mosquitoes 11 *wPip* strains were isolated; mobile genetic elements markers differentiate these strains on the basis of 1-4 genetic markers. These strains were genetically very similar as they contain the same sequence of different *ank2*, *pk1*, *pk2*, *GP12* and *GP15* alleles. Moreover these strains were mutually bidirectionally compatible. They also introduce the 4 new genetically distinct (*w5*, *w10*, *w1* and *w31*) *wPip* strains from 4 different *C. pipiens* of different geographical areas. The sequence analysis showed the La Reunion Island's *wPip* strains were extremely different from these 4 newly introduced strains. All the strains have different *mod/resc* functions having 11 compatible/incompatible crossing types out of which 5 compatible crossing types were identified in La Reunion Island. These different crossing types results due to the multiple *mod* and *resc* abilities i.e., one *resc* key would be compatible to more than one *mod* lock. These crossing types determine the viability and non-viability of *C. pipiens* eggs. The mating between *C. pipiens* with incompatible *wPip* strains would result in non-viable eggs with 0% egg Hatching Rate (HR). But the mosquitoes with compatible strains can produce viable eggs with HR more than 90%. Moreover, mating of infected males with uninfected females results in CI. These all *mod* and *resc* events occurring in host body are independent to the host genome. Thus this can be said that the mating compatibility of mosquitoes depends upon the *Wolbachia* strain present in them. If new genetically different *Wolbachia* strains are introduced in the La Reunion Island there will be more crossing types. Moreover the CI property of *Wolbachia* strains depends upon their crossing type and not on the host nuclear machinery.

*C. pipiens* is the potential vector of many viruses which infect both animals and humans. *Wolbachia* can be used as biological control of this insect as it causes the Cytoplasmic Incompatibility (CI) in *C. pipiens*. The *C. pipiens* of La Reunion Island has only genetically similar and compatible strains of *Wolbachia* therefore no CI was observed. But if the genetically different and incompatible strains of *Wolbachia* are introduced in this area then the CI can be increased in the mosquitoes. Thus the invasion of mosquitoes' population may be stopped by the intrusions of incompatible *Wolbachia* strains. This study conducted by Atyame *et al.* (2011) provides more detailed understanding of *Wolbachia* mode of action at molecular level, in future more research is required in order to use this bacteria more effectively against pathogens.

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