

Wolbachia and mosquito genetics  
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The maternally inherited endosymbiont *Wolbachia* induces inter-population crossing sterilities known as cytoplasmic incompatibility (CI) in many mosquito species. We have observed complex patterns of CI between nine populations of *Culex quinquefasciatus* from diverse locations in the tropics, yet all are infected with a single strain of *Wolbachia* that shows no variation in the *Wolbachia* genes examined. Furthermore crossing type cannot be correlated with variation in *Wolbachia* density, estimated using quantitative PCR. However recent backcrossing data have shown that variation in maternally expressed host genes can have a major effect on CI rescue in embryos. Nuclear genes able to restore compatibility have clear adaptive value for the mosquito. The data help explain the complexity of crossing type observed in *Culex*, and also provide the basis for an alternative strategy for the utilization of *Wolbachia* as a gene drive system. Linkage of desirable transgenes to host nuclear genes able to restore complete CI rescue would provide a strong positive selection pressure, and this strategy will be explored using population modelling.

The *Aedes scutellaris* species complex of SE Asia and the South Pacific contains both important vectors of Bancroftian filariasis and some fully refractory species, with in some cases full fertility in interspecific crosses, providing excellent opportunities for exploring genetic replacement strategies. We are examining the mode of inheritance of susceptibility to *Brugia* and have isolated a number of polymorphic molecular markers for genetic mapping / population genetic studies. Finally we are also investigating the effects of chromosomal inversions on fertility in the *Anopheles gambiae* complex.