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## Guest Editorial

### ***Wolbachia*: Why These Bacteria are Important to Genome Research**

Intracellular bacteria of the genus *Wolbachia* were first discovered in mosquitoes in the 1920s. Their superficial similarity to pathogenic rickettsia initially raised interest in them as potential human pathogens. However, injection experiments with mice showed that they were non-pathogenic, and they were subsequently classified as symbionts of insects. Despite their early discovery, relatively little work was done with *Wolbachia* until recently.

In the last decade there has been an exponential increase in *Wolbachia*-related reports appearing in the scientific literature. This upsurge in interest can be attributed to a number of factors. Until the 1970s, *Wolbachia* was considered to infect a limited number of species of mosquitoes. It is now clear that *Wolbachia* is an extremely common intracellular agent of invertebrates, infecting nearly all the major groups of arthropods and other terrestrial invertebrates. Its wide host range and abundance can be attributed partly to the unusual phenotypes it exerts on the host it infects. These include the induction of parthenogenesis (the production of female offspring from unmated mothers) in certain insects, the feminization of genetic male crustaceans to functional phenotypic females, and the failure of fertilization in hosts when males and females have a different infection status (cytoplasmic incompatibility). All of these phenotypes favor maternal transmission of the intracellular *Wolbachia*. In the last year, *Wolbachia* has also been shown to be a widespread symbiont of filarial nematodes. It appears that *Wolbachia* is needed by the adult worm for normal fertility, indicating that *Wolbachia* is behaving like a classic mutualist in this case. This discovery exemplifies that the extent of the host range of *Wolbachia* and its associated phenotypes is still far from fully understood.

The reductionist paradigm of molecular and cell biology this century has made huge strides in understanding the biology of individual organisms and life processes. The obvious frontier for the next century will be to apply this reductionist approach to understanding the molecular basis for organismal interactions. Organisms that show intimate and prolonged interactions will be well suited for this approach. In this context, *Wolbachia* with its diversity of hosts (including model organisms, such as *Drosophila*) together with the diversity of phenotypic outcomes of association will be an ideal model system for understanding the molecular basis of organismal interactions.

The possibility of generating complete genomic sequence data from a number of *Wolbachia* strains, as outlined in the Meeting Summary of the *Wolbachia* Genome Consortium by Slatko et al. in this issue, will open the door to making the *Wolbachia* system tractable to such studies. In addition, the biology of *Wolbachia* suggests that this information might also be useful for the possible application of *Wolbachia* to reduce disease transmission from insects to humans, plants, and livestock as well as the possible development of new therapies for the control of filarial infections and the direct reduction of pest abundance.

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