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Scientists Find Multiple *Wolbachia* Genomes Integrated in a *Drosophila* Chromosome

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Investigators demonstrated multiple complete bacterial genomes integrated into an animal genome in a study led by a team at the Institute for Genome Sciences (IGS) at the University of Maryland School of Medicine.

The international team's work involves lateral gene transfer (LGT), the transmission of genetic material between organisms in the absence of sexual reproduction. This team re-sequenced and analyzed three *Drosophila ananassae* genomes and found multiple complete bacterial genomes integrated into an animal genome. Their findings appear in the December 12th issue of *BMC Genomics*.

Lateral gene transfer (LGT) can allow organisms to acquire novel traits that are unique from those that are vertically inherited and occasionally results in higher fitness. Although LGT has been described in many organisms over the last decades, fewer cases have been found in animals than in bacteria or plants. When identified in animals, the donors are often cytoplasmic inhabitants, like mitochondria and endosymbionts, like *Wolbachia*. Previously, the leader of this team detected LGT from bacterial *Wolbachia* endosymbionts – or organisms living within another organism – in almost 20% of arthropod and nematode genome sequencing projects.

The international team of investigators found that multiple copies of the *Wolbachia* genome are transferred to the *Drosophila* nuclear genome in all three lines. With only low levels of expression from genes in the lateral gene transfers, it seems unlikely that the genes transferred are functional. Yet 20% of one chromosome in the insect is made up of bacterial DNA.

“Our results demonstrate a massive transfer of bacterial DNA to an animal chromosome,” says Julie Dunning Hotopp, Associate Professor, Department of Microbiology and Immunology at the Institute for Genome Sciences at the University of Maryland School of Medicine and lead author of the study. “It is clear from all the recent findings on LGT over the past decade that large amounts of bacterial DNA continue to frequently integrate into invertebrate genomes, sometimes yielding functional and adaptive mutations.”

The multi-institutional team of investigators included scientists from Uppsala University, Sweden and the University of Maryland School of Medicine. The project was supported by grants to JCDH from the NSF Microbial Sequencing Program (EF-0826732) and NIH New Innovator Award Program (1-DP2-OD007372) and grants to SGEA from the Swedish Research Council, the European Union, and the Knut and Alice Wallenberg Foundation.

About the Institute for Genome Sciences

The Institute for Genome Sciences (IGS) is an international research center within the University of Maryland School of Medicine. Comprised of an interdisciplinary, multidepartment team of investigators, the Institute uses the powerful tools of genomics and bioinformatics to understand genome function in health and disease, to study molecular and cellular networks in a variety of model systems, and to generate data and bioinformatics resources of value to the international scientific community. www.igs.umaryland.edu

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