Special Issue

Evolutionary Genetics and Phylogenetics of Mosquito Species

Message from the Guest Editors

Vector-borne diseases are responsible for approximately 17% of the global burden of communicable diseases and more than 700,000 deaths annually. As “the most dangerous animals in the world”, mosquitoes are fascinating, complex, and will likely always be with us. Across Culicidae, the diversity and heterogeneity of preferred ‘hosts’ range from the hemolymph of insect species through amphibians and reptiles to birds and mammals. What mechanisms are responsible for mosquito host choice? Spatiotemporal shifts in host-seeking, feeding, and resting behaviors have been documented and recent progress includes the detection of a single underlying ancestral component linked to human preference in *Aedes aegypti*. Current and predicted rapid urbanization and concurrent land use change worldwide may push mosquito evolution in the direction of increased human biting. In this Special Issue, original research articles and reviews are welcomed. Research areas may include (but not limited to) the following: the evolution of host preference, mechanisms underlying host-seeking, mosquito genome structure, and maintenance of mosquito diversity.

Guest Editors

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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