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Core genome and lineage specific expansion in malaria parasites

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Abstract

Malaria is an important global infectious disease, responsible for over 1 million deaths yearly. Genome sequencing of the causative agents *Plasmodium* predicted novel therapeutic targets. Here we present a comprehensive analysis of the genomes of six malaria parasite species. The core genome is composed of 3,351 genes. These genes play important roles in fundamental functions as well as in parasite-specific activities. They represent the minimum requirement to maintain a successful life cycle that spans hosts and mosquito vectors. We further investigated the distribution and features of genes that have been expanded in specific parasite lineage(s). Although the functions of most families remain unknown, these Lineage-Specific Expansions could reveal components in parasite networks that, by their enhanced genetic variability, can contribute to pathogenesis, virulence, stress responses, or interesting phenotypes.

Biography

Yufeng Wang received her Ph.D. degree in Bioinformatics and Computational Biology from Iowa State University, USA. She is an Associate Professor at the University of Texas at San Antonio. She has expertise is in the area of bioinformatics, computational biology, systems biology and molecular evolution. Her current research interests include comparative genomics, molecular evolution, and population genetics, with a special emphasis on the evolutionary mechanisms and systems biology of infectious diseases.

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