

Special Issue

Pathogenesis of *Plasmodium falciparum* Malaria

Message from the Guest Editor

Malaria is one of the most important vector-borne diseases. Out of the various species causing malaria infection, *Plasmodium falciparum* is the most prevalent and causes severe infections. Resistance to antimalarial drugs, lack of a potent antimalarial vaccine, and genetic diversity among the circulating *P. falciparum* species pose challenges in the eradication of malaria from endemic areas. In *P. falciparum*, an indirect correlation of the clinical manifestation has been reported with the biological characteristic of the parasites which determines the virulence to some extent. Studying genetic diversity enables the prediction of patterns of emergence and spread of phenotype of the novel antigenic variants leading to diverse clinical complication, drug resistance, or escape of vaccine-induced immunity. In this Special Issue, we invite authors to share their latest research on *P. falciparum* genetic diversity and drug resistance. This issue also welcomes authors to publish their studies establishing a relationship between genetic diversity and clinical manifestations and ultimately pathogenesis of the disease.

Guest Editor

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