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Review

Exploring functional genomics for drug target and therapeutics discovery in *Plasmodia*

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Abstract

Functional genomics approaches are indispensable tools in the drug discovery arena and have recently attained increased attention in antibacterial drug discovery research. However, the application of functional genomics to post-genomics research of *Plasmodia* is still in comparatively early stages. Nonetheless, with this genus having the most species sequenced of any eukaryotic organism so far, the *Plasmodia* could provide unique opportunities for the study of intracellular eukaryotic pathogens. This review presents the *status quo* of functional genomics of the malaria parasite including descriptions of the transcriptome, proteome and interactome. We provide examples for the *in silico* mining of the X-ome data sets and illustrate how X-omic data from drug challenged parasites might be used in elucidating amongst others, the mode-of-action of inhibitory compounds, validate potential targets and discover novel targets/therapeutics.

Keywords: Malaria; *Plasmodium*; Functional genomics; Transcriptome; Proteome; Interactome; Drug target; Therapeutics

Contents

Abbreviations: IDC, intraerythrocytic developmental cycle; MOA, mode-of-action; MudPIT, multidimensional protein identification technology; GO, gene ontology; SAGE, serial analysis of gene expression; ICAT, isotopically coded affinity tags; iTRAQ, isotope tags for relative and absolute quantification.

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