Molecular and Biochemical Parasitology

Volume 134, Issue 1, March 2004, Pages 75-88

Identification of regulatory elements in the *Plasmodium falciparum* genome â˜†

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https://doi.org/10.1016/j.molbiopara.2003.11.004

Abstract

There is little information regarding regulatory sequences in the newly sequenced genome of the malaria parasite, *Plasmodium falciparum*. Thus, for the first time, a bioinformatic strategy was utilized to identify regulatory elements in this genome using the *P. falciparum heat shock protein* (*hsp*) gene family as a model system. Our analysis indicates that the *P. falciparum hsp* genes do not contain standard eukaryotic regulatory elements. However, a novel G-rich regulatory element named the G-box was identified upstream of several *P. falciparum hsp* genes and the *P. yoelii yoelii*, *P. berghei*, and *P. vivax hsp*86 genes. Remarkably, the *Plasmodium* sp. G-boxes were required for maximal reporter gene expression in transient transfection assays. The G-box is not homologous to known eukaryotic elements, and is the best-defined functional element elucidated from *Plasmodium* sp. Our analysis also revealed several other elements necessary for reporter gene expression including an upstream sequence

element, the region surrounding the transcription start site, and the 5â€² and 3â€² untranslated regions. These data demonstrate that unique regulatory elements are conserved in the genomes of *Plasmodium* sp., and demonstrate the feasibility of bioinformatic approaches for their identification.

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Abbreviations

hsp, heat shock protein

Keywords

Plasmodium; Malaria; Promoter; Transcription; Transfection; Luciferase

â˜† Supplementary data associated with this article can be found, in the online version, at doi: 10.1016/j.molbiopara.2003.11.004.

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