Hindawi Publishing Corporation
Journal of Biomedicine and Biotechnology
Volume 2012, Article ID 754054, 2 pages
doi:10.1155/2012/754054

Letter to the Editor

Comment on "Emerging Functions of Transcription Factors in Malaria Parasite"

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Received 19 January 2012; Accepted 18 March 2012

In a recent Journal of Biomedicine and Biotechnology special issue on Immunology and Cell Biology of Parasitic Disease (2011), Tuteja et al. [1] authored a review summarizing transcription factors in the malaria parasite, *Plasmodium*. It is well known that there are very few characterized transcriptional regulators in the malaria parasite [2–4]. To date, the sole family of transcriptional regulators in *Plasmodium* consists of a conserved group of proteins containing a DNA-interaction domain with high homology to the *Arabidopsis* APETELA2 (AP2) DNA-binding domain [5]. Related AP2-integrase DNA-binding domains are also present in various *Tetrahymena* species, a few viruses, and cyanobacteria (reviewed in [6]). However, there have been no reports of an AP2 expansion in any other eukaryote other than the Apicomplexans. This lineage-specific expansion is now known as the Apicomplexan AP2 (ApiAP2) protein family [5], and since these proteins represent the first family of putative specific transcriptional regulators in the malaria parasite, their characterization has generated a flurry of recent reports [7–10]. The authors of this review, unfortunately, report an incorrect association between the ApiAP2 proteins (pfam PF00847) and the Activator Protein-2 (AP-2) (pfam PF03299) found in higher eukaryotes (reviewed in [11]). Despite the similarity in nomenclature, there is absolutely no evolutionary conservation (homology) or functional relationship between the mammalian AP-2 and the malarial ApiAP2 proteins as the authors suggest. The authors also incorrectly cite a recent in-depth review of the ApiAP2 protein family as a source for this information [12]. As an international journal with a diverse readership, it is pertinent that this misleading information is corrected so as to prevent further confusion.

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