

Letter to the Editor

Comment on “Emerging Functions of Transcription Factors in Malaria Parasite”

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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.

References

- [1] R. Tuteja, A. Ansari, and V. S. Chauhan, “Emerging functions of transcription factors in malaria parasite,” *Journal of Biomedicine and Biotechnology*, vol. 2011, Article ID 461979, 6 pages, 2011.
- [2] L. Aravind, L. M. Iyer, T. E. Wellems, and L. H. Miller, “Plasmodium biology: genomic gleanings,” *Cell*, vol. 115, no. 7, pp. 771–785, 2003.
- [3] T. J. Templeton, L. M. Iyer, V. Anantharaman et al., “Comparative analysis of apicomplexa and genomic diversity in eukaryotes,” *Genome Research*, vol. 14, no. 9, pp. 1686–1695, 2004.
- [4] R. M. R. Coulson, N. Hall, and C. A. Ouzounis, “Comparative genomics of transcriptional control in the human malaria parasite *Plasmodium falciparum*,” *Genome Research*, vol. 14, no. 8, pp. 1548–1554, 2004.
- [5] S. Balaji, M. Madan Babu, L. M. Iyer, and L. Aravind, “Discovery of the principal specific transcription factors of Apicomplexa and their implication for the evolution of the AP2-integrase DNA binding domains,” *Nucleic Acids Research*, vol. 33, no. 13, pp. 3994–4006, 2005.
- [6] S. R. Wessler, “Homing into the origin of the AP2 DNA binding domain,” *Trends in Plant Science*, vol. 10, no. 2, pp. 54–56, 2005.
- [7] M. Yuda, S. Iwanaga, S. Shigenobu, T. Kato, and I. Kaneko, “Transcription factor AP2-Sp and its target genes in malarial sporozoites,” *Molecular Microbiology*, vol. 75, no. 4, pp. 854–863, 2010.

- [8] M. Yuda, S. Iwanaga, S. Shigenobu et al., "Identification of a transcription factor in the mosquito-invasive stage of malaria parasites," *Molecular Microbiology*, vol. 71, no. 6, pp. 1402–1414, 2009.
- [9] C. Flueck, R. Bartfai, I. Niederwieser et al., "A major role for the Plasmodium falciparum ApiAP2 protein PfSIP2 in chromosome end biology," *PLoS Pathogens*, vol. 6, no. 2, Article ID e1000784, 2010.
- [10] T. L. Campbell, E. K. de Silva, K. L. Olszewski, O. Elemento, and M. Llinás, "Identification and Genome-Wide Prediction of DNA Binding Specificities for the ApiAP2 family of regulators from the malaria parasite," *PLoS Pathogens*, vol. 6, no. 10, Article ID e1001165, 2010.
- [11] D. Eckert, S. Buhl, S. Weber, R. Jäger, and H. Schorle, "The AP-2 family of transcription factors," *Genome Biology*, vol. 6, no. 13, article no. 246, 2005.
- [12] H. J. Painter, T. L. Campbell, and M. Llinás, "The Apicomplexan AP2 family: integral factors regulating Plasmodium development," *Molecular and Biochemical Parasitology*, vol. 176, no. 1, pp. 1–7, 2011.