

# Plasmodium Biology: Scientific Classification

Mohamed Moumaris\* 

Institute of Medical Sciences, Research and Development Company, Paris, France

## EDITORIAL

Morphological characterization and genetic techniques allow the description of the phylogenetic diversity of organisms. The *Plasmodium* genus belongs to the Plasmodiidae family, Haemospororida order, Aconoidasida class, Apicomplexa phylum, Alveolata superphylum, Halvaria infrakingdom, Harosa subkingdom, Chromista kingdom, and Eukaryote domain (Figure 1).

Five species that cause human Malaria are *Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium ovale*, *Plasmodium malariae*, and *Plasmodium knowlesi*. Artemisinin, mosquito nets, and vector control are antimalarial tools in endemic areas. It is crucial to have a good understanding of *Plasmodium* biology to implement effective control measures. Obtaining information about the structure and evolutionary processes of the *Plasmodium* can help achieve this understanding (Egwu et al., 2023).

Haemosporida are intracellular parasites that infect vertebrates and are transmitted by blood-sucking insects. Genetic analysis, particularly of the mitochondrial cytochrome b gene, is used to identify haemosporidian species (Bertotiené et al., 2019; Fecchio et al., 2020). Aconoidasida possesses an apical complex, which enables mobility and host cell invasion. This complex includes various organelles such as the polar ring, conoids, rhoptries, dense granules, microtubules, and micronemes (Figure 2). However, the *Plasmodium* species have a reduced or absent conoid. Recent proteomic and tomography studies have shown conoid structures across all *Plasmodium* life cycle forms (Koreny et al., 2021; Haase et al., 2022).

Apicomplexa are single-celled eukaryotes that parasitize metazoans. They possess apical complexes that secrete enzymes and are involved in host cell invasion. Apicomplexa is a taxonomic group that comprises entirely parasitic organisms (Swapna and Parkinson, 2017; Boisard and Florent, 2020). The Apicomplexa possess apicoplasts containing an additional circular DNA molecule that resembles the plastid DNA found in non-photosynthetic plants. This DNA molecule is approximately 35 kd and contains a palindromic sequence of genes responsible for subunit rRNAs, various tRNAs, proteins, and RNA polymerase subunits. The subunit rRNA genes are similar to those in mitochondrial

---

### Correspondence:

Mohamed Moumaris, Institute of Medical Sciences, Research and Development Company, 14 avenue René Boylesve 75016 Paris, France, ORCID: 0000-0002-6193-163X;  
Email mohamed.moumaris@sciencesettechnologies.com

Received Dates: November 25, 2025;

Accepted Date: February 27, 2026;

Published Date: March 05, 2026:

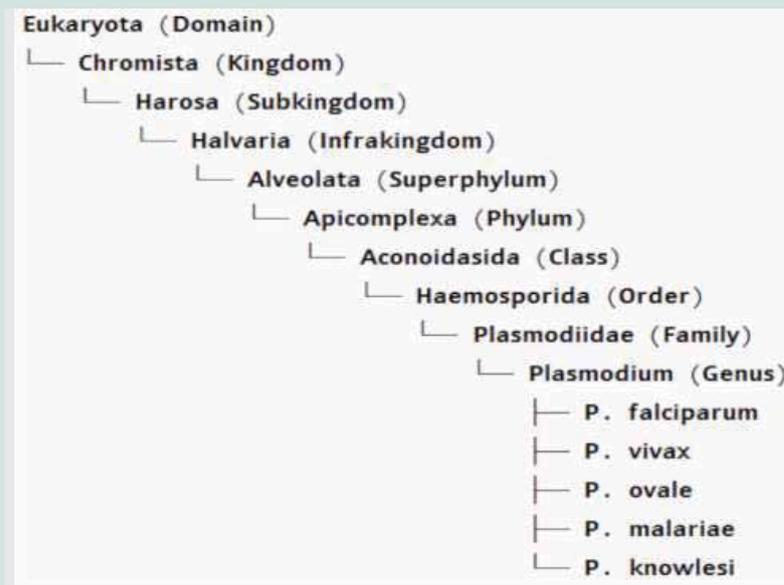


Figure 1: Taxonomic diagram of Plasmodium

or plastid sequences (Ng et al., 2018). This plastid-like DNA has been acquired through secondary endosymbiosis and conserved among organellar genomes. Apicomplexan parasites also have highly conserved organellar genomes with DNA similar to that found in mitochondria. This mitochondrial DNA consists of a 6 kb tandem repeat that codes for proteins, such as cytochrome b and cytochrome oxidase, as well as rRNAs (Verhoef et al., 2021).

Alveolata are single-celled organisms that have sub-membranous alveoli. The identification of Alveolata relies on the ultrastructure and molecular phylogenies of the 18S rRNA gene (Arzul and Carnegie, 2015; Gigeroff et al., 2023). Harosa is a monophyletic lineage with an RAB paralog (Rab1A), and it exhibits ciliary or pseudopodial locomotion with cortical alveoli. The Rab GTPase is a gene family with multiple paralogs that regulate the maintenance of the eukaryotic cell's compartmentalization system. Rab paralogs are regulators of membrane trafficking conserved in all eukaryotes (Cavalier-Smith, 2010; Cavalier-Smith et al., 2018; Morse et al., 2016).

The chromalveolates may have emerged from a process of chloroplast endosymbiosis between heterotrophic unicellular eukaryotes and unicellular red algae, based on molecular and morphological data of eukaryotic phylogeny. These organisms have evolved and specialized to thrive in specific environments, and establishing a new plastid organelle by secondary endosymbiosis is a highly complex process (Keeling, 2010; Walker et al., 2011; Sierra et al., 2013). Plasmodium, a

eukaryotic organism, undergoes schizogonies in recipient vertebrates and sporogonies in vector insects. It possesses specialized organelles, notably the nucleus, mitochondria, endoplasmic reticulum, Golgi apparatus, ribosomes, peroxisomes, and plastids (Cavalier-Smith, 1998; Simpson et al., 2004).

Understanding the taxonomical position, cellular architecture, and evolutionary history of Plasmodium is essential for advancing malaria research and improving control strategies. The integration of morphological, genetic, and molecular data allows researchers to decipher the complex biology of these parasites and their relationships within the phylogenetic tree of eukaryotes. Insights into organellar genomes, endosymbiotic origins, and technical invasion machinery deepen our knowledge of parasite evolution and provide serious targets for sanative intervention. Continued interdisciplinary research will be essential for developing modern tools to combat malaria and mitigate its orbicular impact (Moumaris et al., 1992 - 2025).

Keywords: Plasmodium, Malaria Parasites, Apicomplexa, Endosymbiosis, Phylogeny, Organellar genomes

Abbreviations

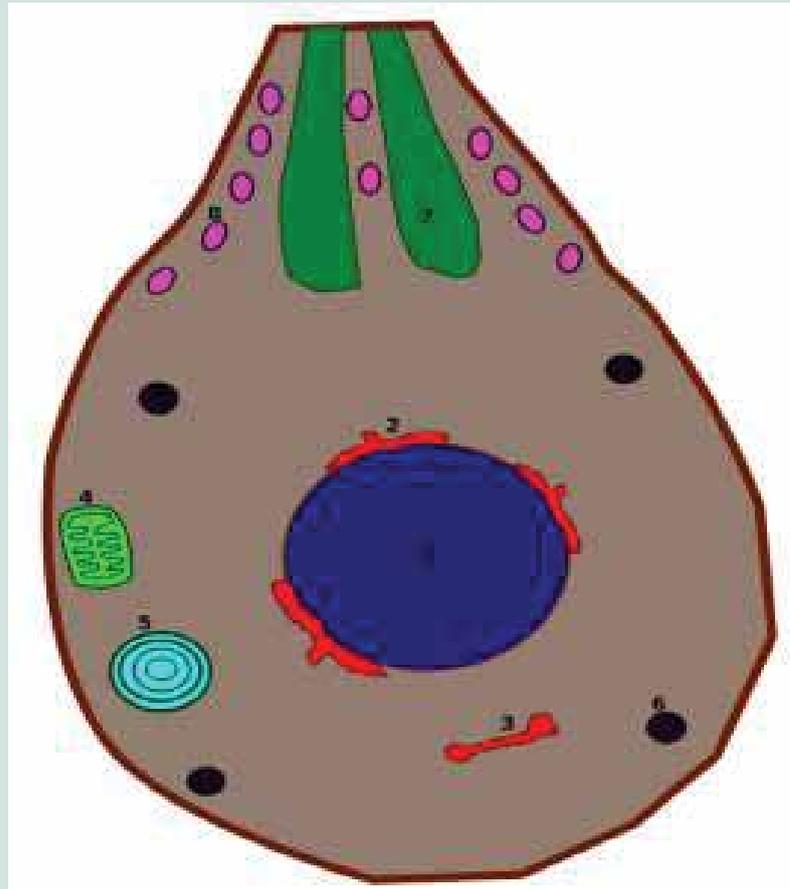
kb / kb: Kilobase (unit of DNA length)

kd / kDa: Kilodalton (unit of molecular mass)

Rab: Ras-related in brain (GTPase family)

CONFLICTS OF INTEREST

The author confirm that this article's content has no conflict of interest.



**Figure 2:** The Plasmodium merozoite (adapted from Moumaris M. Organelle Adaptations in Plasmodium: The Targets for Malaria Treatments. *Int J Zoo Animal Biol* 2025, 8(1): 000640). 1-Nucleus. 2- Endoplasmic reticulum. 3- Golgi apparatus. 4- Mitochondria. 5- Apicoplast. 6- Denses

**FUNDING:** No external funding received.

### ACKNOWLEDGMENTS

The author acknowledges Mrs. Norri Zahra and Mr. Re-gragui Moumaris. The author thanks Prof. Nisen Abuaf

(Sorbonne University and AP-HP) and Tech. Said Yousouf Chanfi (Sorbonne University). The author thanks Ing. Jean-Michel Bretagne (AP-HP). The author thanks Clr. Marie-Hélène Maës and SG. Monique Abuaf (Research and Development Company).

### REFERENCES

- Egwu, C. O., Alope, C., Chukwu, J., Nwankwo, J. C., Irem, C., Nwagu, K. E., Nwite, F., Agwu, A. O., Alum, E., Offor, C. E., & Obasi, N. A. (2023). Assessment of the antimalarial treatment failure in Ebonyi State, Southeast Nigeria. *J. Xenobiot.*, 13(1), 16–26. <https://doi.org/10.3390/jox13010003>
- Bernotienė, R., Žiegytė, R., Vaitkutė, G., & Valkiūnas, G. (2019). Identification of a new vector species of avian haemoproteids, with a description of methodology for the determination of natural vectors of haemosporidian parasites. *Parasit. Vectors*, 12(1), 307. <https://doi.org/10.1186/s13071-019-3559-8>
- Fecchio, A., Chagas, C. R. F., Bell, J. A., & Kirchgatter, K. (2020). Evolutionary ecology, taxonomy, and systematics of avian malaria and related parasites. *Acta Trop.*, 204, 105364. <https://doi.org/10.1016/j.actatropica.2020.105364>
- Koreny, L., Zeeshan, M., Barylyuk, K., Tromer, E. C., van Hooff, J. J. E., Brady, D., Ke, H., Chelaghma, S., Ferguson, D. J. P., Eme, L., Tewari, R., & Waller, R. F. (2021). Molecular characterization of the conoid complex in Toxoplasma reveals its conservation in all apicomplexans, including Plasmodium species. *PLoS Biol.*, 19(3), e3001081. <https://doi.org/10.1371/journal.pbio.3001081>
- Haase, R., Dos Santos Pacheco, N., & Soldati-Favre, D. (2022). Nanoscale imaging of the conoid and functional dissection of its dynamics in Apicomplexa. *Curr. Opin. Microbiol.*, 70, 102226. <https://doi.org/10.1016/j.mib.2022.102226>
- Swapna, L. S., & Parkinson, J. (2017). Genomics of apicomplexan parasites. *Crit. Rev. Biochem. Mol. Biol.*, 52(3),

254–273. <https://doi.org/10.1080/10409238.2017.1290043>

- Boisard, J., & Florent, I. (2020). Why the -omic future of Apicomplexa should include gregarines. *Biol. Cell*, 112(6), 173–185. <https://doi.org/10.1111/boc.202000006>
- Ng, C. S., Sinha, A., Aniweh, Y., Nah, Q., Babu, I. R., Gu, C., Chionh, Y. H., Dedon, P. C., & Preiser, P. R. (2018). tRNA epitranscriptomics and biased codon are linked to proteome expression in *Plasmodium falciparum*. *Mol. Syst. Biol.*, 14(10), e8009. <https://doi.org/10.15252/msb.20178009>
- Abstract
- Verhoef, J. M. J., Meissner, M., & Kooij, T. W. A. (2021). Organelle dynamics in apicomplexan parasites. *mBio*, 12(4), e0140921. <https://doi.org/10.1128/mBio.01409-21>
- Arzul, I., & Carnegie, R. B. (2015). New perspective on the haplosporidian parasites of molluscs. *J. Invertebr. Pathol.*, 131, 32–42. <https://doi.org/10.1016/j.jip.2015.07.014>
- Gigeroff, A. S., Eglit, Y., & Simpson, A. G. B. (2023). Characterisation and cultivation of new lineages of colpomeids, a critical assemblage for inferring alveolate evolution. *Protist*, 174(2), 125949. <https://doi.org/10.1016/j.protis.2023.125949>
- Cavalier-Smith, T. (2010). Kingdoms Protozoa and Chromista and the eozoan root of the eukaryotic tree. *Biol. Lett.*, 6(3), 342–345. <https://doi.org/10.1098/rsbl.2009.0948>
- Cavalier-Smith, T., Chao, E. E., & Lewis, R. (2018). Multigene phylogeny and cell evolution of chromist infrakingdom Rhizaria: Contrasting cell organisation of sister phyla Cercozoa and Retaria. *Protoplasma*, 255(5), 1517–1574. <https://doi.org/10.1007/s00709-018-1241-1>
- Morse, D., Webster, W., Kalanon, M., Langsley, G., & McFadden, G. I. (2016). *Plasmodium falciparum* Rab1A localizes to rhoptries in schizonts. *PLoS One*, 11(6), e0158174. <https://doi.org/10.1371/journal.pone.0158174>
- Keeling, P. J. (2010). The endosymbiotic origin, diversification and fate of plastids. *Philos. Trans. R. Soc. Lond. B Biol. Sci.*, 365(1541), 729–748. <https://doi.org/10.1098/rstb.2009.0103>
- Walker, G., Dorrell, R. G., Schlacht, A., & Dacks, J. B. (2011). Eukaryotic systematics: A user's guide for cell biologists and parasitologists. *Parasitology*, 138(13), 1638–1663. <https://doi.org/10.1017/S0031182010001708>
- Sierra, R., Matz, M. V., Aglyamova, G., Pillet, L., Decelle, J., Not, F., de Vargas, C., & Pawlowski, J. (2013). Deep relationships of Rhizaria revealed by phylogenomics: A farewell to Haeckel's Radiolaria. *Mol. Phylogenet. Evol.*, 67(1), 53–59. <https://doi.org/10.1016/j.ympev.2012.12.011>
- Cavalier-Smith, T. (1998). A revised six-kingdom system of life. *Biol. Rev. Camb. Philos. Soc.*, 73(3), 203–266. <https://doi.org/10.1017/s0006323198005167>
- Simpson, A. G., & Roger, A. J. (2004). The real “kingdoms” of eukaryotes. *Curr. Biol.*, 14(17), R693–R696. <https://doi.org/10.1016/j.cub.2004.08.038>

©2026 Moumaris M, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License 4.0 International License.

Cite this article as: Moumaris M, *Plasmodium Biology: Scientific Classification*, *Glob. Open Access J. Sci.*, 2026; 2(1):06-10.

