

# WORLDWIDE CIRCUMSPOROZOITE PROTEIN VARIANTS (VK210, VK247 AND *P. VIVAX*-LIKE) DISTRIBUTION IN *ANOPHELES* SPP MOSQUITOES

Marrara P. Sampaio<sup>a,b</sup>, Marcelo Cerilo-Filho<sup>a,b</sup>, Yasmin de A. G. do Amaral<sup>a</sup>, Maria Naely G. Almeida<sup>a</sup>, Rayanne I. Correa<sup>a</sup>, Dulce J.V. Fernando<sup>ab</sup>, Raísa P. Braz<sup>ab</sup>, Andréa R. S. Baptista<sup>a,b</sup>, Ricardo L. D. Machado<sup>a,b</sup>

Corresponding author: marrarapereira@id.uff.br

<sup>a</sup>Centro de Investigação de Microrganismos. Instituto Biomédico. Departamento de Microbiologia e Parasitologia. Universidade Federal Fluminense. Niterói – RJ, Brasil.

<sup>b</sup>Programa de Pós-Graduação em Microbiologia e Parasitologia Aplicadas. Instituto Biomédico. Departamento de Microbiologia e Parasitologia. Universidade Federal Fluminense. Niterói – RJ, Brasil.

**Introduction:** Circumsporozoite Protein of *Plasmodium vivax* (PvCSP) is a leading candidate for a malaria vaccine. Since *Anopheles* mosquitoes are the primary vectors responsible for *Plasmodium* sp transmission, understanding how different *Anopheles* species influence the global distribution of PvCSP variants (VK210, VK247 and *P.vivax*-like) could ultimately lead to more targeted strategies for controlling malaria transmission and improving vaccine efficacy. **Objective:** This study aims to evaluate global distribution of PvCSP variants in *Anopheles* mosquitoes through a systematic review following the PRISMA statement. **Methods:** Articles were searched in Pubmed, Science direct, Scopus and Google scholar databases using the PICO format to structure the research question. Selection criteria included duplicate removal, title and abstract screening, eligibility assessment, and risk of bias analysis using the Joanna Briggs Institute. **Results:** Twenty-nine articles, published between 1993 and 2023, were analyzed and a total of 188,786 mosquitoes were compiled, with 85 species observed: 74.76% were from South America, 23.93% from Asia, 0.66% from Africa, and 0.65% from North America, according to the articles found. In Africa, 12 species were analyzed, with only *A. gambiae* and *A. stephensi* testing positive for VK210 monoinfection. In Asia, more than 36 species were analyzed, with 24 testing positive for VK210 (n=19) and VK247 (n=16) monoinfections, with mixed infections (n=6), where *A. karwari*, *A. minimus* and *A. maculatus* showed susceptibility to all three conditions. In North America, *A. albimanus* and *A. pseudopunctipennis* were positive for VK210, VK247, and mixed infections, with *A. pseudopunctipennis* showing greater susceptibility to the VK247 variant in Mexico. In South America, 12 out of 24 species showed VK210 monoinfection, and 10 species were positive for VK247, with *A. darlingi* as the primary vector for VK210 and VK247 monoinfections on the continent. *Anopheles oswaldoi* and *A. daeneorum* were positive for the *P. vivax*-like variant, found only in Brazil, additionally, *A. triannulatus* and *A. aquasalis* were found exclusively with VK210+VK247 mixed infections. **Conclusion:** This data underscores the heterogeneity in the distribution of PvCSP variants across different *Anopheles* spp and regions. This diversity can affect the parasite's distribution in human hosts, posing a significant challenge to developing an effective universal vaccine.

**Key-words:** Vector Competence; Genetic Diversity; Malaria; Molecular epidemiology

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