Genetic Diversity of *Plasmodium vivax* in a Border Region of the Guiana Shield: Epidemiological and Antimalarial Resistance Implications

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The Guiana Shield represents a major challenge for malaria control and elimination in the Americas, as it includes high-transmission settings associated with mining activities and intense cross-border human mobility among malaria-endemic countries. In this context, Roraima stands out as an area of high epidemiological relevance, accounting for the largest number of imported malaria cases in Brazil and showing an increase in coinfections by *Plasmodium vivax* and *P. falciparum*. This study aimed to characterize the genetic diversity and population structure of *P. vivax* in a border region of the Guiana Shield, focusing on genes associated with antimalarial resistance. We analyzed 449 *P. vivax* isolates, including samples collected for this study in Roraima (n = 116) and publicly available data from other Brazilian states and neighboring countries. Parasite DNA was subjected to selective whole-genome amplification (sWGA) followed by targeted next-generation sequencing of 11 candidate resistance genes, yielding high-quality data with a mean coverage of 96%. The results revealed high genetic diversity in Roraima compared with other Amazonian states, consistent with high-transmission scenarios driven by population mobility and frequent coinfections. Genetic proximity was observed among isolates from Roraima, French Guiana, and Guyana (Fst < 0.05), indicating regional gene flow. High frequencies of mutations in *pvmdr1* and *pvmrp1* were detected in Roraima, including the F1240I variant, rare or absent elsewhere, suggesting local selective pressure associated with antimalarial use. High sequencing depth (median of ≈ 1563x) also enabled detection of low-frequency variants, consistent with polyclonal infections. Overall, these findings indicate that Roraima acts as an epidemiological and genetic hotspot for *P. vivax* within the Guiana Shield, highlighting the need for continuous

genomic surveillance and coordinated cross-border control strategies in the Amazon region.