Genomic surveillance suggested restricted largescale connectivity and contrasting resistance patterns in Plasmodium vivax across Latin America

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Genomic surveillance of Plasmodium vivax is essential for supporting malaria elimination in Latin America (LATAM) by improving our understanding of transmission dynamics and the emergence of drug resistance. Here, we used population genomic approaches to characterize parasite connectivity and investigate resistance associated variation across LATAM. Population genomic analyses suggested limited large-scale connectivity across the sampled regions of LATAM, supported by strong geographic structuring and high within-country relatedness. Distinct clustering in Amazonas (Peru), Acre (Brazil), Venezuela, and Tumbes (Peru) indicated genetically differentiated populations. In contrast, Ecuador clustered with Loreto (Peru), suggesting connectivity between western Amazonian regions. French Guiana, Colombia, and Honduras showed no clear clustering with neighboring countries. Relatedness networks and admixture analyses further supported these patterns, with minimal connectivity detected between Peru and other regions. Analysis of resistance-associated genes and the antigenic gene pvama1 revealed variable levels of genetic diversity across loci. High haplotypic diversity was observed in pvmrp2, pvmrp1, and pvama1, whereas pvcrt, pvabce1, and pvmdr1 showed limited variability. Antifolate resistance associated mutations were detected at moderate to high frequencies in pvdhps (A383G, 42.8%) and pvdhfr (S58R, 70.4%; S117N, 80.6%), while pvmdr1 variants linked to chloroquine resistance remained uncommon (F1076L, 5.4%; Y976F, 3.8%). Geographic structuring was further supported by location-specific variants in Amazonas, Tumbes, and Honduras. Together, these findings reveal a geographically structured P. vivax population landscape across sampled regions of LATAM and heterogeneous resistance-associated variation. Targeted genomic surveillance, particularly in neighboring cross-border regions, will be important for monitoring parasite movement, tracking resistance, and informing malaria elimination strategies.