ORT_09 - Laboratory diagnosis of human parvovirus B19 infection in acute febrile illnesses in a malaria- endemic area on the border of Brazil and French Guiana

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Introduction: Human parvovirus B19 (B19V) infection can cause a block in erythropoiesis, resulting in severe anemia in patients with inherited hemolytic diseases. There are reports showing that B19V infection may worsen anemia in children living in areas endemic for *Plasmodium falciparum* infection. However, the effect of B19V coinfection on malaria caused by P. vivax in Brazil has not been determined. Accurate diagnosis is therefore essential.

Objectives: The aim of this study was to perform serological and molecular diagnosis of B19V infection in individuals living in the municipality of Oiapoque, Amapá State.

Methodology: A total of 300 sera collected in 2014-2015 were tested for B19V IgM and IgG using a commercial enzyme immunoassay (EIA) (Serion, Brazil). B19V-DNA detection was performed by both conventional PCR (cPCR) and quantitative PCR (qPCR) targeting the non-structural region. Of these 300 individuals, 148 tested positive (malaria+) and 152 tested negative (malária-) for *P. vivax*. Statistical differences between different categorical groups were determined using Fisher's exact test, available in GraphPad Prism® v.9.0.0. and $p<0.05$ was considered significant.

Results: By EIA, 132 sera (79 malaria+ and 53 malaria-) tested B19V IgM positive and 156 IgM negative. By cPCR and/or qPCR, 26 IgM negative sera tested B19V DNA positive. The viral load ranged from $6.5x10^3$ to $5.5x10^6$ IU/mL (mean: $2.8x10^5$IU/mL). Using both EIA and PCR, recent B19V infection was diagnosed in 63.4% (92/145) of malaria+ and 45% of malaria- (68/151) individuals, and this difference was statistically significant (p=0.0017). The B19V infection status could not be determined in about 1% (4/300) of the individuals. Only 9% (27/300) were negative for both EIA and PCR. Overall, B19V IgG antibodies were detected in 78% of the serum samples from malaria+ (115/148) and malaria- (119/152) individuals and this difference was not statistically significant (p=1.000).

Conclusion: Similar to what has been reported by others, these results support the need for multiple tests to accurately differentiate recent from past B19V infection. Our results confirm the findings that 2014 to 2015 was an epidemic year for B19V infection in this country.

Keywords: Parvovirus B19; Laboratory Diagnosis; *P. vivax*