Genomic B-cell immune profiles associated with clinical outcomes in Plasmodium vivax infection

Ada Vergara Olortegui

Universidad Peruana Cayetano Heredia (Peru)

It has been described that in the Peruvian Amazon Plasmodium vivax infected individuals can shift from an asymptomatic parasite carriage status to the development of symptomatic disease or viceversa. Although alterations in Bcell compartments have been described during malaria vivax, how peripheral blood B-cell responses differ between symptomatic (SY) and asymptomatic (ASY) P. vivax infection remains unclear.

Peripheral blood mononuclear cells from SY (n=17) and ASY (n=21) P. vivax–infected individuals and healthy controls (CTL, n=14) were analyzed using a 28-parameter flow cytometry panel (BD FACSymphony). Manual gating in FlowJo was performed to identify mature, memory and plasmablast subsets. Unsupervised FlowSOM clustering enabled multidimensional analysis and detection of subtle subpopulation changes among groups. SY showed increased naïve B cells with a compromised survival phenotype (BAFFR−). A mature CD40− naïve B-cell subset and CD1c+ marginal zone B cells were enriched in CTL and ASY but reduced in SY. SY also showed atypical proliferating IgM memory B cells (CD21−CD27−−CD71+Ki67+), reduced classical IgG memory B cells, and increased proliferating plasmablasts (CD71+Ki67+). In contrast, ASY displayed a profile closer to CTL, with only increased activated IgG memory B cells. These findings reveal distinct B-cell immune profiles associated with clinical status during P. vivax infection. SY was characterized by enhanced B-cell activation, proliferation, and altered memory B-cell composition, whereas ASY maintained a profile closer to CTL, suggesting more balanced humoral immune regulation. Overall, these results highlight the importance of studying ASY individuals to better understand immune mechanisms underlying divergent clinical outcomes in P. vivax infection.