

Shared signature of recent positive selection on the TSBP1-BTNL2-HLA-DRA genes in five native populations from North Borneo

ABSTRACT

North Borneo (NB) is home to more than 40 native populations. These natives are believed to have undergone local adaptation in response to environmental challenges such as the mosquito-abundant tropical rainforest. We attempted to trace the footprints of natural selection from the genomic data of NB native populations using a panel of 2.2 million genome-wide single nucleotide polymorphisms. As a result, an 13-kb haplotype in the Major Histocompatibility Complex Class II region encompassing candidate genes TSBP1–BTNL2–HLA-DRA was identified to be undergoing natural selection. This putative signature of positive selection is shared among the five NB population sandis estimated to have arisen5.5thousand years(220generations) ago, which coincides with the period of Austronesian expansion. Owing to the long history of endemic malaria in NB, the putative signature of positive selection is postulated to be driven by Plasmodium parasite infection. The findings of this study imply that despite high levels of genetic differentiation, the NB populations might have experienced similar local genetic adaptation resulting from stresses of the shared environment.