

Appendix

S1 Details regarding the sample collection for each dataset

Samples were taken from three separate LC-MS studies into different infections with pathogens associated with febrile disease. For D_{VL}, plasma was taken from 20 adult patients from Fuenlabrada (Madrid, Spain) diagnosed with visceral leishmaniasis at the Hospital Universitario de Fuenlabrada between January 2013 and June 2015. Blood samples were collected during the period of active disease and infection by *Leishmania infantum* was confirmed by *Leishmania* specific nested PCR; the presence of *Leishmania*-specific plasma antibodies were determined by rK39 immunochromatographic test (Inbios, USA) and indirect immunofluorescence test. Data obtained were compared with those of 20 matched healthy controls obtained from volunteers at the Blood Bank of the Hospital Universitario de Fuenlabrada [1]. For D_Z, patients included in the Zika virus group had presented to hospital seeking assistance for febrile symptoms confirmed as Zika virus infection by PCR (n=10). The healthy control group was composed of women attending their routine prenatal care (n=10). Samples from all participants were collected by using a red cap vacuum blood tube of 4 mL, without clot activator. After blood collection, the tubes were maintained in the rack, at room temperature for 30 minutes. After this time, samples were maintained at 4°C until centrifugation (which was performed in less than 5 hours). Centrifugation was carried out at 2000 x g for 10 minutes. Serum samples were then placed in 1.5 microtubes and stored at -80°C until metabolites extraction [2]. Regarding D_M, the malaria patients are described in detail in [3].

References

- [1] Jarrin EP, Cordeiro FB, Medranda WC, Barrett M, Zambrano M, Regato M. A Machine Learning-Based Algorithm for the Assessment of Clinical Metabolomic Fingerprints in Zika Virus Disease. In: 2019 IEEE Latin American Conference on Computational Intelligence (LA-CCI); 2019. p. 1–6.14.
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- [3] Milne K, Ivens A, Reid AJ, Lotkowska ME, O'Toole A, Sankaranarayanan G, et al. Mapping Immune Variation and Var Gene Switching in Naive Hosts Infected with *Plasmodium falciparum*. *eLife*. 2021;10:e62800.doi:10.7554/eLife.62800