29th ECCMID
Amsterdam, Netherlands
13 – 16 April 2019
The congress of ESCMID

O1201 Cross-sectional study reveals promising set of biomarkers to distinguish *Plasmodium falciparum* malaria from bacterial bloodstream infection

Marlow Zimmermann*[1], Nicole Gilberger[1], Daniel Eibach[1], Ralf Krumkamp[1], Eva Lorenz[1], Nimako Sarpong[2], Jürgen May[1]

[1] Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany, [2] Agogo Presby Hospital, Agogo, Ghana

Background: The differential diagnosis of malaria in Sub-Saharan Africa remains challenged by overlapping symptoms with viral, bacterial and other parasitic pathogens, as well as limited laboratory capacities. Our group set out to investigate whether cytokine expression profiles of febrile children could be used to correctly distinguish between malaria and bacterial induced sickness.

Materials/methods: We measured 55 cytokines in blood serum samples previously collected from children in rural Ghana. Of the samples available, 30 from confirmed bacteremia cases and 38 from malaria tropica cases were selected. Samples were measured with cytokine detection kits based on the XMAP® technology and were required to achieve a bead count of ≥ 30. We applied classification trees of single cytokines to preselect the most promising variables for the modeling process, i.e. predictive accuracy of ≥ 60%. To account for the high dimensionality of the data, we estimated predictive accuracy by constructing 100 random forest models with random test and training allocation of the samples, and reporting the range of accuracy among these models. To further test the loss of accuracy in smaller models, we used a backward elimination that would remove the least important variable of 100 random forest models and re-run the algorithm until the smallest model of one cytokine was obtained.

Results: 39 of the 55 cytokines measured, presented the required data quality in terms of bead counts. Fifteen further showed promising predictive strength in univariate classification trees and were included in the modeling process. Median predictive accuracy varied strongly between random forest models and ranged from 62% to 88% correctly classified children. The backward elimination further revealed, that a combination of nine cytokines achieved a median prediction accuracy of 88%.

Conclusions: Cytokine-based models show promising predictive power in distinguishing malaria from bacteremia in children. These findings however require further validation, as the selected sample was small and accuracy varied strongly between models with different random seeds.