Mail corresp. 8-6-2020

Dear 5.1.2e) and 5.1.2e),

Attached you will find the RIVM serological data for the COVID-19 eligibility panel (n=12) and the harmonization panel (n=38).

In brief, the data refer to quantitative arbitrary units (AU/ml) of IgG antibodies reacting to either S1 spike or nucleoprotein (N) in a multiplex reaction (Luminex platform). An arbitrary antibody concentration-unit of '100' was assigned on the basis of the mean fluorescence intensity (MFI) signal in the upper limit of linearity of a 3-fold serial dilution of a reference, which is pooled Cov-19 convalescent serum.
The respective cut-off values for S1 (2.37 AU/ml) and N (19.7 AU/ml) have been determined on basis of extensive non-COV-19 ILI and hCov serum panels, using a specificity optimized cut-off by ROC analysis (> 99%) at a sensitivity ranging from 84-96%, depending on COVID19 cohort selection (manuscript submitted). Using the NIBSC temporary standard we will be able to convert to International units in the near future.

In the table, positive quantitative IgG values are indicated in red, and also indicated qualitatively as a pos or neg test result. The results are expressed as GMC, from 3 independent experiments. We have also added an illustration of the GMC (Y-axis) against 'day post hospitalization' (X-axis).

Notable outcomes for the longitudinal sera:
118 (3 sera) remains seronegative for both S1 and N
058 (3 sera) shows values around the cutoff for S1 (2x pos, 1x neg) for S1, but does not show any change in concentration, nor did we detect any antibodies against nucleoprotein. We have doubts whether this is COV-19 specific seroconversion.

We are very much interested in how our MIA test results relates to your serological data. We encountered a few sera with extreme high antibody concentrations and those sera were difficult in the measurements resulting in high CV%.
It would be good to disscuss this (TC?) and see how we pursue with the other samples.

Regards,

5.1.2e

on behalf of 5.1.2e , 5.1.2e and 5.1.2e

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