CHRIS Covid-19 Study

Neutralizing Antibody

Version 1.0

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1. Introduction

This module stores information on SARS-COV-2 neutralizing antibody collected in the CHRIS COVID-19 study.

The CHRIS COVID-19 study was designed to estimate the distribution of SARS-CoV-2 infection cases in Val Venosta/Vinschgau since 1 February 2020, as well as the proportion of asymptomatic individuals among positive cases, to characterize transmission within households, to assess the relationship between antibody response and disease severity, to observe the evolution of antibody response over time, to identify environmental, molecular and genetic risk factors, to identify long-term sequelae.

The CHRIS COVID-19 study was organized in three stages:

Stage 1: A stratified random sample of 1812 CHRIS study participants was selected to represent the adult population of the Val Venosta/Vinschgau district. Out of this sample, 845 CHRIS participants replied to an online or paper questionnaire, underwent a molecular test based on a nasopharyngeal swab and a serum antibody test.

Stage 2: All 13,393 CHRIS study participants and their consenting cohabitants were invited to fill in an online questionnaire on their past and current health status, and on SARS-CoV-2 (potential) exposure and testing. Each CHRIS participant received ten access tokens to let them and their cohabitants register online. A shorter questionnaire was then sent repeatedly to all participants every 4 weeks for an update on their symptoms, COVID-19 exposure, and testing. All individuals at risk of positivity to SARS-CoV-2 infection and their cohabitants have been invited for a nasopharyngeal swab molecular test and a serum antibody test at the CHRIS study center.

Stage 3: To trace and monitor antibody response over time, all individuals testing positive to either the nasopharyngeal or the serum test in Stages 1 or 2 have been invited to repeat the serum antibody test every three months for a year, since their first measurement.

Biobanked serum of the participants to the random sample study (stage 1) was analyzed in the Laboratory of Virus-Cell Interaction, Centre for Integrative Biology, University of Trento, Italy. The ability of the serum to inhibit the transduction of a lentiviral vector pseudotyped with the SARS-CoV-2 spike protein was evaluated. As to the procedure workflow, pseudotyped vectors, transducing a gene encoding a fluorescent protein, were incubated along with scalar dilutions of serum that was then inoculated onto Huh-7 cells. Percentage of transduced fluorescent cells was next quantified using the High Content Molecular Device Image Xpress® Micro Confocal upon nuclei counterstaining with Hoechst 33,342. Finally, the serum dilution associated with 50% inhibition of transduction (ID50 value) was estimated from each derived sigmoidal curve.

2. History version changes

None

3. Data cleaning

1. The neutralizing antibody ID50 values were imported in Stata.

2. The information about batch and plate were added to the dataset.
3. Value “<75” of the neutralizing antibody ID50 variable ccna01 was transformed to -1024. missing values were set to “Unexpected missing” (-89).
4. The neutralizing antibody dataset was saved.

Stata v16.1 was used for the data cleaning process. The do file is available at the LINK-DO-cr_04_neutralAB.do.

4. Data structure

The variables listed in table 1 constitute all the variables associated with the neutralizing antibody measurement.

Table 1. Neutralizing antibody variables list

Variable	Description	Unit of reference	Coding	Filter	Notes	Version	Available	Derived
ccna01	Neutralizing antibody ID50 value	ID50	<float>				Yes	Yes
ccna02	Batch		1 First 2 Second 3 Third				Yes	No
ccna03	Plate		<integer>				Yes	No

5. Advices for the analysis

The analyst should account for possible batch effects.

The use of the sample weights (cc_esw, cc_rsw) should be considered to improve the generalizability of the results.

6. References

Pattaro C, Barbieri G, Foco L, Weichenberger CX, Biasiotto R, De Grandi A, Fuchsberger C, Egger C, Amon VSC, Hicks AA, Mian M, Mahlknecht A, Lombardo S, Meier H, Weiss H, Rainer R, Dejaco C, Weiss G, Lavezzo E, Crisanti A, Pizzato M, Domingues FS, Mascalzoni D, Gögele M, Melotti R, Pramstaller PP. Prospective epidemiological, molecular, and genetic characterization of a novel coronavirus disease in the Val Venosta/Vinschgau: the CHRIS COVID-19 study protocol. Pathog Glob Health. 2022 Mar;116(2):128-136. doi: 10.1080/20477724.2021.1978225. PubMed PMID: 34637685