



JIP06-COVID19-COVRIN-D.2.1.1

Workpackage 2

Responsible Partners:
INSA (36), ANSES (01)

Contributing partners:
All partners



GENERAL INFORMATION

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Other contributors	All partners		
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Dissemination <i>Author's suggestion to inform the following possible interested parties.</i>	<div> OHEJP WP 1 <input type="checkbox"/> OHEJP WP 2 <input type="checkbox"/> OHEJP WP 3 <input type="checkbox"/> OHEJP WP 4 <input type="checkbox"/> OHEJP WP 5 <input type="checkbox"/> OHEJP WP 6 <input type="checkbox"/> OHEJP WP 7 <input type="checkbox"/> Project Management Team <input checked="" type="checkbox"/> Communication Team <input checked="" type="checkbox"/> Scientific Steering Board <input type="checkbox"/> National Stakeholders/Program Owners Committee <input type="checkbox"/> EFSA <input type="checkbox"/> ECDC <input type="checkbox"/> EEA <input type="checkbox"/> EMA <input type="checkbox"/> FAO <input type="checkbox"/> WHO <input type="checkbox"/> OIE <input type="checkbox"/> Other international stakeholder(s): Social Media: Other recipient(s): </div>		



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JIP06-WP2-T2.1 Genome analyses

D.2.1.1 Report on the established website protocol repository

Description of the task

The two main overall operational objectives of COVRIN WP2 are: i) to identify drivers for the emergence and spread of SARS-CoV-2; ii) to generate data and build models for risk assessment of SARS-CoV-2.

Within WP2, **Task 2.1 is focused on the analyses of whole genome sequences of SARS-CoV-2 strains circulating in humans and animals**. In particular, Task 2.1. involves **methodologies exchange** among partners [from wet-lab Next-generation sequencing (NGS)-related procedures to Bioinformatics pipelines], as well as **phylogenetic analysis and investigation for potential virulence traits** (e.g., mutations known to play a direct role in receptor binding or antibody recognition). This approach aims not only at promoting protocol sharing/harmonization, but also at **mapping evolutionary changes of SARS-CoV-2 viruses isolated within and across human and different animal species**, as a means to identify mutations and recombination events driving adaptation to alternative hosts. In parallel, this task also supports the selection of strains that may be used for downstream biological characterization *in vivo* and *in vitro*.

In this context, the first **T2.1 sub-task (ST2.1.1 - Protocol repository)** focused on building a **NGS-related protocol repository** to be kept “alive” as the project develops. This allows partners to **carry out methodology comparison/harmonization and to enhance their capacity to generate, analyse and interpret viral genomic data**. The protocol repository also provides guidance on the procedures to be applied in subsequent T2.1 subtasks (ST2.1.2 – harmonization sampling and methods NGS; ST2.1.3 – phylogenetic analyses).

This deliverable describes the activities and first outcomes of the ST2.1.1.

Description of the deliverable

In order to lay the foundation for the compilation of a comprehensive NGS-related protocol repository for SARS-CoV-2 (and other coronaviruses), two Excel surveys were circulated among COVRIN partners to collect the following information:

- 1) A **summary description of the methodologies used for sample preparation for NGS and subsequent data analysis**, named “Protocol Repository NGS procedures”.

*In particular, partners were asked to list the main techniques used for **RNA extraction, cDNA generation, PCR, PCR product purification, Library preparation, Sequencing and Bioinformatics pipeline** (until the consensus genome sequence). A general protocol description and related publications were also detailed.*

- 2) An overview of the **key steps of the bioinformatics pipeline(s) used for the analysis of SARS-CoV-2 NGS data**, named Survey Bioinformatics pipeline.



*In particular, partners were asked to indicate which **bioinformatics platform(s)/pipeline(s)** they are using **for routine SARS-CoV-2 genomic surveillance and/or research**. The survey followed a Yes/No format, and aimed at gathering/comparing the **flexibility, diversity, completeness (start-to-end) and integrative mode** of the currently applied pipelines. It covers the following computations/bioinformatics features: **Installation/code/interface, Software parameters; NGS input data; Reads Quality control (QC); Consensus generation; Mutation detection and annotation; Nucleotide and amino acid alignment; Phylogenetics and metadata visualization; Classification (Clade/Lineage)**.*

Responses were obtained from eleven partners: **ANSES (01), APHA (21), FLI (10), INSA (36), IZSLER (29), IZSAM (28), PIWET (34), Sciensano (04), SVA (41), UoS (P23) and WVBR (31)**.

A 'live' version will be made available in the COVRIN group on the EJP website, being accessible for continuous consultation and edition by all COVRIN participants. A final and more comprehensive version of the protocol repository will be publicly released at the end of the project.