**SUPPLEMENTAL MATERIAL**

***Laboratory methods***

**Diagnosis of SARS-CoV-2 was made by an in-house one-step real-time PCR (Forward Primer: RdRP\_Fi 5´-GTCATGTGTGGCGGTTCACT-3´, Reverse primer: RdRP\_Ri 5´-CAACACTATTAGCATAAGCAGTTGT-3´, Probe: RdRP\_P 5´- CAGGTGGAACCTCATCAGGAGATGC-3´ (FAM-BHQ1). Running conditions: 46°C for 30 min; 95°C for 1 min; and 45 repeat cycles with 95°C for 15 sec and 56°C for 1 min) or the Roche Cobas 6800 assay (Roche Diagnostics, Rotkreutz, Switzerland). Samples with a cycle threshold (Ct) value below 33 were selected for WGS and phylogenetic analysis.**

**RNA was extracted from NPS using a MagNA Pure Total Nucleic Acid Isolation kit (Roche Diagnostics, Basel, Switzerland) on the MagNA Pure LC automated extractor. Quantification of RNA was performed using TaqMan 1-Step RT-qPCR Master Mix and TaqMan 2019-nCoV Assay kit v1 (Thermo Fisher, Waltham, MA, USA). RNA libraries were prepared in accordance with the protocol for Ion AmpliSeq SARS-CoV-2 Research Panel (Thermo Fisher). Briefly, RNA was reverse transcribed with the SuperScript VILO cDNA synthesis kit on an IonCode 96-well PCR Plate (Thermo Fisher). Subsequently, library preparation was performed on the Ion Chef platform using the Ion AmpliSeq Kit for Chef DL8. Final libraries were quantified using the Ion Library TaqMan Quantification kit (Thermo Fisher) and the sequence size estimated using High Sensitivity D1000 DNA Kit on Agilent 4200 TapeStation system (Agilent Technologies). For template preparation, libraries were pooled to a final concentration of 30 pM. Thereafter, the Ion Chef Platform was used to ligate the libraries onto spheres using the Ion 510, 520, 530 Kit-Chef (Thermo Fisher). Following clonal amplification, libraries were loaded onto Ion 530 Chip and sequencing was performed on the S5 System (XL, Prime; Thermo Fisher) according to the manufacturer’s protocol for 200 bp read length.**

***Bioinformatics and phylogenetic analysis***

**Reads were quality trimmed and mapped to a SARS-CoV-2 reference sequence (GenBank acquisition number NC.045512) and a consensus sequence was independently determined using the Torrent Suite plugin IRMAreport (Thermo Fisher) and CLC Genomics Workbench version 12.0.3 (Qiagen, Aarhus, Denmark). Consensus sequences used in phylogenetic analyses were collected from the IRMAreport pipeline. Low coverage samples resulting in non-complete genomes (less than 95% of the reference genome) were excluded. Alignments were made in CLC using the Alignment tool and trimmed at ends to create equally long consensus sequences. Apart from the samples included in this study, alignment was made with community samples sequenced by the Public Health Agency of Sweden by the method described in this article 1. All reported SARS-CoV-2 sequences circulating in Western Sweden during the outbreak period available for download, were included in the phylogenetic analysis. Clades were determined using the NeXT clade web-based method with associated nomenclature 2**

***Statistical analysis***

**Variables were compared using Mann-Whitney U-test (SPSS Software package version 25 IBM Armonk New York US).**

**Supplemental Table 1.** Clinical characteristic of patients including median and range for age, Charlson co-morbidity index 3, cycle threshold value, length of hospital stay, cause of admission and health-care association are listed below. Variables were compared using Mann-Whitney U-test.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Patient characteristics | All cases(n=32) | Survivors (n=18) | Deceased (n=14) | *P* |
| Female sex n (%) | 15 (47%) | 10 (56%) | 5 (36%) | 0.357 |
| Age (years)  | 84 (67-96) | 80 (67-96) | 86 (67-96) | 0.235 |
| CCI score | 6 (2-10) | 6 (2-10) | 6 (3-10) | 0.694 |
| Ct value | 20 (15-39) | 22 (17-39) | 19 (15-28) | ***0.018*** |
| Total LOS (days) | 18 (6-85) | 17 (6-85) | 20 (8-28) | 0.398 |
| LOS until NPS (days) | 9 (4-21) | 7 (4-21) | 10 (6-21) | 0.168 |
| LOS from NPS until death (days) | - | - | 8 (2-30) | - |
|  |  |  |  |  |
| *Cause of admission* |  |  |  |  |
| Hip fracture | 12 (38%) | 8 (44 %) | 4 (29%) | 0,464 |
| Femur fracture | 8 (25%) | 4 (22%) | 4 (29%) | 0.779 |
| Other  | 12 (38%) | 6 (33%) | 6 (43%) | 0.667 |
|  |  |  |  |  |
| *HCAI* |  |  |  |  |
| Indeterminate  | 10 (31%) | 8 (44%) | 2 (14%) | 0.156 |
| Suspected | 18 (56%) | 8 (44%) | 10 (71%) | 0.071 |
| True | 4 (13%) | 2 (11%) | 2 (14%) | 0.722 |
|  |  |  |  |  |

***CCI= Charlson Comorbidity index, Ct= Cycle threshold, LOS= Length-of-stay, NPS= nasopharyngeal sample, HCAI=Healthcare-associated infection***

**REFERENCES**

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**3.** Charlson ME, Pompei P, Ales KL, MacKenzie CR. A new method of classifying prognostic comorbidity in longitudinal studies: development and validation. *J Chronic Dis* 1987;40:373-383.