SUPPLEMENTARY MATERIAL

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The present file contains supplementary information about the vibriosis surveillance system in the study countries, as well additional information of the vibriosis cases and related isolates of the project. Phylogenetic trees of *V. alginolyticus* and *V. parahaemolyticus* supporting our findings are also included.

**Table S1. Characteristics of national surveillance systems of vibriosis in study countries, 2018**

| Country | Surveillance introduced | Data source | Reporting | Comprehensiveness | Design | Data reported by | Data collection on all types of samples, regardless of infection severity |
|---------|------------------------|-------------|-----------|--------------------|--------|-----------------|---------------------------------------------------------------------|
| Norway  | No¹                    | Laboratory database | Compulsory | Other²,³       | Passive | L               | Yes                                                                  |
| Sweden  | Yes                    | National surveillance | Compulsory | Comprehensive | Passive | L, Ph, H        | Yes                                                                  |
| Denmark | No⁵                    | Laboratory database | Compulsory | Other⁴       | Passive | L               | Yes                                                                  |
| Finland | Yes                    | National surveillance | Compulsory | Comprehensive | Passive | L               | Yes                                                                  |
| Poland  | Yes                    | National surveillance | Compulsory | Other⁵       | Passive | L, Ph           | Yes                                                                  |
| Estonia | Yes                    | Laboratory database | Compulsory | Comprehensive | Passive | L               | Yes                                                                  |

¹ Data reported by: L – laboratories, Ph – physicians, H – hospitals.
² Severe infections (e.g. septicemia, wound infections and necrotizing fasciitis) and non-severe infections (e.g. otitis, skin infections, gastroenteritis).
³ Vibrio cholerae cases are routinely notified and isolates sent to the national reference laboratory at the national institute for the detection of cholera markers, whereas for non-cholerae Vibrio spp. this was the case for *V. parahaemolyticus* isolated from patients with gastrointestinal infections, only. Until 2019, other vibriosis were reported and isolates forwarded to the national institute in case of suspected outbreaks. Since 2019, vibriosis (irrespective of detected species) is a mandatory notifiable disease in Norway.
⁴ Data collected through nationwide laboratories survey for the year 2018.
⁵ Laboratory findings are automatically logged into the Danish Microbiology Database (MiBA), including infections caused by all Vibrio spp.
⁶ Vibriosis cases were reported in the group “other bacterial foodborne infections” with only *V. parahaemolyticus* (ICD10 A05.3) specified as a separate vibriosis pathogen.
| Isolate name | Sequence type | Accession no. | Assembly statistics | FASTQ Statistics |
|--------------|--------------|--------------|--------------------|-----------------|
| **NO VA 18** |            |              |                    |                 |
| NO VA 18_16  | 96h          | ERS5890681   | 5421232            | 176             |
| NO VA 18_06  | 138          | ERS5890687   | 5417902            | 190             |
| NO VA 18_01  | 180          | ERS5890743   | 5040727            | 145             |
| SE VA 18_07  | 181          | ERS5890679   | 5595925            | 107             |
| NO VA 18_13  | 182          | ERS5890690   | 5329433            | 158             |
| NO VA 18_22  | 183          | ERS5890693   | 3743229            | 125             |
| NO VA 18_02  | 184          | ERS5890742   | 5262397            | 164             |
| SE VA 18_05  | 185          | ERS5890741   | 5294713            | 232             |
| NO VA 18_18  |              | ERS5890739   | 5161131            | 106             |
| NO VA 14_12  |              | ERS5890686   | 4074567            | 164             |
| NO VA 18_24  |              | ERS5890695   | 5156195            | 205             |
| NO VA 17_03  |              | ERS5890688   | 5123679            | 145             |
| SE VA 18_01  |              | ERS5890699   | 5209691            | 206             |
| SE VA 18_03  |              | ERS5890683   | 5245702            | 178             |
| NO VA 14_08  |              | ERS5890644   | 5344746            | 125             |
| NO VA 18_21  |              | ERS5890698   | 5248046            | 113             |
| NO VA 14_09  |              | ERS5890697   | 5126912            | 195             |
| NO VA 14_10  |              | ERS5890689   | 4856867            | 687             |
| NO VA 16_14  |              | ERS5890741   | 5275994            | 185             |
| SE VA 18_02  |              | ERS5890678   | 5105536            | 150             |
| NO VA 18_16  |              | ERS5890685   | 5175692            | 190             |
| NO VA 18_17  |              | ERS5890691   | 5199821            | 124             |
| NO VA 15_19  |              | ERS5890737   | 5221100            | 112             |
| NO VA 18_11  |              | ERS5890677   | 5371247            | 247              |
| NO VA 06_07  |              | ERS5890740   | 5092698            | 148             |
| NO VA 18_15  |              | ERS5890682   | 5276788            | 213             |
| NO VA 08_05  |              | ERS5890694   | 5342958            | 191             |
| NO VA 08_07  |              | ERS5890800   | 5268605            | 123             |
| NO VA 23_20  |              | ERS5890692   | 5204394            | 124             |
| SE VA 18_04  |              | ERS5890738   | 5075931            | 187             |
| NO VA 14_04  |              | ERS5890676   | 5179496            | 165             |
| SE VA 18_18  |              | ERS5890762   | 3850592            | 165             |
| NO VA 17_02  |              | ERS5890648   | 3994385            | 228             |
| FI VA 18_04  |              | ERS5890649   | 4123998            | 410             |
| PL VA 18_02  |              | ERS5890660   | 3992736            | 139             |
| PL VA 18_05  |              | ERS5890663   | 3966014            | 103             |
| FI VA 18_25  |              | ERS5890668   | 4060283            | 228             |
| FI VA 18_10  |              | ERS5890645   | 4014291            | 281             |
| FI VA 18_13  |              | ERS5890744   | 3952491            | 144             |
| SE VA 18_24  |              | ERS5890703   | 3964416            | 199             |
| SE VA 18_27  |              | ERS5890734   | 3969652            | 204             |
| DK VA 18_02  |              | ERS5890673   | 4065772            | 132             |
| SE VA 18_22  |              | ERS5890707   | 3948328            | 93              |
| SE VA 18_43  |              | ERS5890630   | 3948644            | 71              |
| SE VA 18_43  |              | ERS5890735   | 4032206            | 120             |
| FI VA 18_34  |              | ERS5890652   | 4460675            | 660             |
| FI VA 18_33  |              | ERS5890653   | 4102663            | 466             |
| FI VA 18_42  |              | ERS5890709   | 4044664            | 220             |
| FI VA 18_29  |              | ERS5890643   | 4040074            | 317             |
| NO VA 15_06  |              | ERS5890755   | 4093649            | 191             |
| DK VA 18_03  |              | ERS5890672   | 3988972            | 234             |
| DK VA 18_04  |              | ERS5890670   | 3884611            | 346             |

**Table S2. Summary table of assembly and FASTQ statistics for Vibrio spp. isolates from study countries, 2014-2018 (Isolates are sorted by species).**

- **Genome size**: Size of the genome in base pairs.
- **No. Contigs**: Number of contigs in the assembly.
- **Average size**: Average size of contigs in base pairs.
- **N50**: Size of the largest contig such that 50% of the genome size is contained in contigs of at least this size.
- **No Reads**: Number of reads for the isolate.
- **Coverage**: Mean coverage of reads for the isolate.
- **Mean size read**: Average read length.
- **SD Read length**: Standard deviation of the read lengths.

**Statistics**

- **Size**: Size of the isolate in base pairs.
- **Statistics**: Various statistical metrics for the isolates.

- **Mean**: Mean value of a specific metric for the isolate.
- **10.7875**: Value for a specific metric.

**2014-2018** (Isolates are sorted by species).
## Table S3. Summary of key characteristics of non-travel related vibriosis cases in the study countries, 2018.

| Characteristic                      | Countries | Total |
|-------------------------------------|-----------|-------|
|                                     | Denmark   | Sweden | Norway | Finland | Poland and Estonia |
| Reported cases, n                  | 170       | 147    | 92     | 30      | 605               |
| Male-to-female ratio (cases)       | 1.5 (101/69) | 2.2 (101/46) | 1.0 (47/45) | 4.0 (24/6) | 2.0 (42/21) |
| Notification rate per 100,000       | 2.9       | 1.4    | 1.7    | 0.5     | ND                |
|                                     |           |        |        |         | ND                |
| Age, years                         | median    | 53     | 58     | 42      | 39                |
|                                     | range     | 2-93   | 1-101  | 3-91    | 3-87              |
|                                     |           |        |        |         | ND                |
|                                     | Age group, n (%) |       |        |         | ND                |
| 0-4                                 | 2 (1.2%)  | 3 (2%) | 2 (2.2%) | 2 (6.7%) | 0 (0%)           | 9 (2%) |
| 5-14                                | 34 (20%)  | 24 (16.3%) | 24 (26.1%) | 7 (23.3%) | 2 (33.3%) | 91 (20.4%) |
| 15-24                               | 20 (11.8%) | 14 (9.4%) | 10 (10.8%) | 2 (6.7%) | 1 (16.7%) | 47 (10.6%) |
| 25-44                               | 20 (11.8%) | 16 (10.9%) | 13 (14.1%) | 5 (16.7%) | 0 (0%) | 54 (12.1%) |
| 45-64                               | 28 (16.4%) | 31 (21.1%) | 18 (19.6%) | 4 (13.3%) | 2 (33.3%) | 83 (18.7%) |
| 65-79                               | 49 (28.8%) | 35 (23.8%) | 18 (19.6%) | 6 (20%) | 1 (16.7%) | 109 (24.5%) |
| 80+                                 | 17 (10%)  | 24 (16.3%) | 7 (7.6%) | 4 (13.3%) | 0 (0%) | 52 (11.7%) |
|                                     |           |        |        |         | ND                |
|                                     | Season, n (%) |       |        |         | ND                |
| Summer                              | 134 (78.8%) | 109 (74.2%) | 57 (61.9%) | 22 (73.4%) | 4 (66.7%) | 326 (73.3%) |
| Autumn                              | 29 (17.1%) | 29 (19.7%) | 31 (33.7%) | 6 (20%) | 1 (16.7%) | 96 (21.6%) |
| Winter                              | 4 (2.3%)  | 5 (3.4%) | 2 (2.2%) | 1 (3.3%) | 1 (16.6%) | 13 (2.9%) |
| Spring                              | 3 (1.8%)  | 4 (2.7%) | 2 (2.2%) | 1 (3.3%) | 0 (0%) | 10 (2.2%) |
|                                     |           |        |        |         | ND                |
| Vibrio species, n (%)               |           |        |        |         | ND                |
| V. alginolyticus                    | 70 (41.2%) | 19 (12.9%) | 63 (68.5%) | 0 (0%) | 0 (0%) | 152 (34.2%) |
| Non-toxigenic V. cholerae           | 3 (1.8%)  | 64 (43.5%) | 2 (2.2%) | 26 (86.7%) | 5 (83.3%) | 100 (22.5%) |
| V. parahaemolyticus                 | 55 (32.4%) | 19 (12.9%) | 12 (13.0%) | 3 (10.0%) | 0 (0%) | 89 (20.0%) |
| V. vulnificus                       | 16 (9.4%) | 19 (12.9%) | 9 (9.8%) | 1 (3.3%) | 0 (0%) | 45 (10.1%) |
| Vibrio spp.                         | 26 (15.3%) | 26 (17.7%) | 6 (6.5%) | 0 (0%) | 1 (16.7%) | 59 (13.3%) |

* Data source: mandatory surveillance system (Sweden); nationwide surveying of public health microbiology laboratories (Norway); reporting of clinical sample analyses (Denmark, Finland, Poland, and Estonia). See material and methods for details on data acquisition.

Note: ND – not determined.

## Table S4. Whole genome sequenced Vibrio isolates in the study countries, 2014-2018.

| Characteristic                      | Grand total | Total vibriosis | Vibrio alginolyticus | Non-toxigenic Vibrio cholerae | Vibrio parahaemolyticus | Vibrio vulnificus |
|-------------------------------------|-------------|-----------------|----------------------|-------------------------------|-------------------------|------------------|
|                                     |             | nT T            | nT T                 | nT T                          | nT T                    | nT T             |
| Country                             |             |                 |                      |                               |                         |                  |
| Norway                              | 58          | 35 (12) 3 (8)   | 16 (7) 0 (1)         | 2 (2) 1 (6)                   | 6 (3) 2 (1)             | 11 0             |
| Denmark                             | 8           | 6 2             | 0 0                  | 2 2                           | 0 0                     | 4 0              |
| Sweden                              | 68          | 66 2            | 6 1                  | 41 1                          | 8 0                     | 11 0             |
| Finland                             | 28          | 27 0 (1)        | 0 0                  | 26 0 (1)                      | 0 0                     | 1 0              |
| Poland                              | 3           | 1 (2) 0         | 0 0                  | 1 (2) 0                       | 0 0                     | 0 0              |
|                                     |             |                 |                      |                               |                         |                  |
| Clinical                            |             |                 |                      |                               |                         |                  |
| Blood                               | 46          | 43 (3) 0        | 1 (1) 0              | 18 (1) 0                      | 4 (1) 0                 | 20 0             |
| Faeces                              | 20          | 7 (2) 4 (7)     | 0 (1) 0              | 6 3 (7)                       | 1 (1) 1                 | 0 0              |
| Ear-related                         | 47          | 37 (6) 3 (1)    | 14 (3) 1 (1)         | 23 (2) 1                      | 0 (1) 1                 | 0 0              |
| Wound-related                       | 34          | 32 (1) 0 (1)    | 5 (1) 0              | 14 0                          | 8 0 (1)                 | 5 0              |
| Other                               | 18          | 16 (2) 0        | 2 (1) 0              | 11 (1) 0                      | 1 0                     | 2 0              |
| Environmental                       | 13          | 13 0            | 0 13                 |                               |                         |                  |
| Year                                | 2018        | 142             | 135 7                | 22 1                          | 72 4                    | 14 2             |
|                                     | 2014-2017   | 23 14 9         | 7 1                  | 4 7                           | 3 1                     | 0 0              |

nT – non-travel related clinical isolates or travel status unknown; T – travel related clinical isolates; All environmental were seawater isolates. Numbers indicate isolates of 2018 and in parenthesis isolates collected during 2014-2017.
Figure S1. SNP based phylogeny of 31 V. alginolyticus genomes from study countries. The V. alginolyticus ASM35417v2 sequence was used as reference. The scale bar indicates the number of substitutions per site.

Note: VA, V. alginolyticus, NO – Norway, SE – Sweden, MLST – multilocus sequence typing, ST – sequence type. The first number represents the isolation year and the second number denotes the isolate number.
Figure S2. SNP based phylogeny of 20 V. parahaemolyticus genomes from study countries. The V. parahaemolyticus ASM19609v1 sequence was used as reference. The scale bar indicates the number of substitutions per site.

Note: VP – V. parahaemolyticus, NO – Norway, SE – Sweden, MLST – multilocus sequence typing, ST – sequence type. The first number represents the isolation year and the second number denotes the isolate number. Pandemic strain ST3 is bolded.