

Appendix Table. Amino acid identity rates of all genomic RNA segments between rotavirus reference strains and GER126-08*

| Strain | Genogroup† | Genotype | VP1 | VP2 | VP3 | VP4 | VP6 | VP7 | NSP1 | NSP2 | NSP3 | NSP4 | NSP5 | NSP6 |
|-------------|------------|----------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|-------------|
| Wa | Wa-like | G1P[8] | 99.1 | 96.8 | 96.0 | 94.4 | 98.2 | 77.6 | 82.7 | 95.8 | 98.0 | 96.5 | 94.4 | 89.1 |
| DS-1 | DS-1-like | G2P[4] | 90.1 | 89.3 | 80.8 | 91.3 | 92.6 | 75.4 | 69.3 | 88.0 | 82.2 | 84.0 | 81.8 | 80.4 |
| AU-1 | AU-1-like | G3P[9] | 91.5 | 91.3 | 83.2 | 65.1 | 92.4 | 79.1 | 58.0 | 88.0 | 84.1 | 85.1 | 87.8 | NC‡ |
| P | Wa-like | G3P[8] | 98.6 | 98.4 | 97.7 | 97.5 | 99.4 | 79.4 | 83.3 | 96.2 | 99.3 | 97.1 | 98.9 | NC‡ |
| ST3 | Wa-like | G4P[6] | 98.0 | 97.9 | 96.5 | 76.9 | 99.7 | 73.3 | 92.5 | 94.6 | 99.0 | 93.1 | 97.9 | 94.5 |
| B3458 | Wa-like | G9P[8] | 98.6 | 97.9 | 98.4 | 98.1 | 99.2 | 80.9 | 94.8 | 94.9 | 98.3 | 95.4 | 100 | 93.4 |
| 14B2 | | G12 | NA§ | NA§ | NA§ | NA§ | NA§ | 97.8 | NA§ | NA§ | NA§ | NA§ | NA§ | NA§ |
| B4633-03 | Wa-like | G12P[8] | 98.5 | 97.2 | 99.1 | 98.0 | 99.7 | 96.9 | 94.7 | 99.3 | 99.0 | 94.2 | 100 | 94.5 |
| Dhaka25-02 | Wa-like | G12P[8] | 98.4 | 97.2 | 99.2 | 98.5 | 99.4 | 96.9 | 96.3 | 99.6 | 97.4 | 94.8 | 100 | 96.7 |
| GER172-08 | Wa-like | G12P[6] | 98.4 | 98.5 | 99.0 | 78.3 | 99.2 | 96.9 | 95.5 | 98.4 | 98.7 | 94.8 | 100 | 93.4 |
| L26 | DS-1-like | G12P[4] | 90.0 | 89.2 | 95.3 | 91.0 | 92.1 | 92.6 | 68.7 | 95.2 | 82.9 | 84.5 | 97.9 | 95.6 |
| Matlab13-03 | Wa-like | G12P[6] | 98.4 | 97.1 | 96.6 | 78.1 | 99.4 | 95.3 | 96.3 | 99.0 | 83.2 | 94.2 | 100 | 94.5 |
| RU172 | | G12P[7] | NA§ | NA§ | NA§ | NA§ | 94.4 | 92.3 | NA§ | NA§ | NA§ | 94.8 | 97.9 | 96.7 |
| RV161-00 | DS-1-like | G12P[6] | 90.3 | 89.0 | 81.0 | 78.4 | 92.6 | 96.6 | 69.3 | 89.2 | 83.5 | 94.2 | 82.0 | 78.2 |
| T152 | AU-1-like | G12P[9] | 91.3 | 91.6 | 84.1 | 63.8 | 99.4 | 95.7 | 51.9 | 89.2 | 83.8 | 85.7 | 88.3 | 78.2 |

*VP, viral protein; NSP, nonstructural protein; NA, not available. All values given in percentages.

†According to Matthijnssens et al. (11), the genogroup was assigned if at least 7 gene segments belonged to the respective Wa-, DS-1-, or AU-1-like genotype. Results of the second G12 strain detected in this study (GER172-08) are highlighted in gray. **Boldface** indicates highest percentages per column. GenBank accession numbers of these highly homologous genomic RNA segments used in comparison: 14B2 VP7 AAZ79294; B3458 NSP5 ABV57763; B4633-03 VP6 ABA34210, NSP5 ABA34247; Dhaka 25-02 VP3 ABA34200, VP4 ABA34206, NSP1 ABA34223, NSP2 ABA34228, NSP6 DQ146659; Matlab13-03 NSP1 ABA34225, NSP5 ABA34250; P NSP3 ABV53278, NSP4 ABV53281; RU172 NSP6 DQ204739 ST3 VP6 ABU87857; Wa VP1 ABF67546.

‡Amino acid identities were not calculated because different open reading frames result in longer and shorter NSP6 proteins, respectively.

§Full-length sequence information was not available.