Foodborne Outbreaks Caused by Human Norovirus GII.P17-GII.17–Contaminated Nori, Japan, 2017

Technical Appendix

Technical Appendix Figure. Phylogenetic tree analysis of norovirus GII.P17-GII.17 strains associated with dried shredded nori–related and unrelated outbreaks during the 2016–17 endemic season, Japan, 2017. Analyses of viral genes encoding RdRp (A) and VP1 (B) are shown. Solid circles indicate strains from outbreaks with shredded nori. GII.P17 or GII.17_Wakayama/2017 is represented by LC318755, 1 of the 4 strains detected in outbreak 1 (LC318755–LC318758). GII.P17 or GII.17_Tokyo/2017 is represented by LC258403, 1 of the strains detected during outbreaks 2–5. GII.P17 or GII.17_Fukuoka/2017 is represented by LC311767, and GII.P17 or GII.17_Osaka/2017 is represented by LC318751 (Table). The evolutionary analysis was conducted by using MEGA7 software, with the maximum-likelihood method based on the Tamura-Nei model. The phylogenetic tree is drawn to scale, with branch lengths reflecting the number of substitutions per site.