

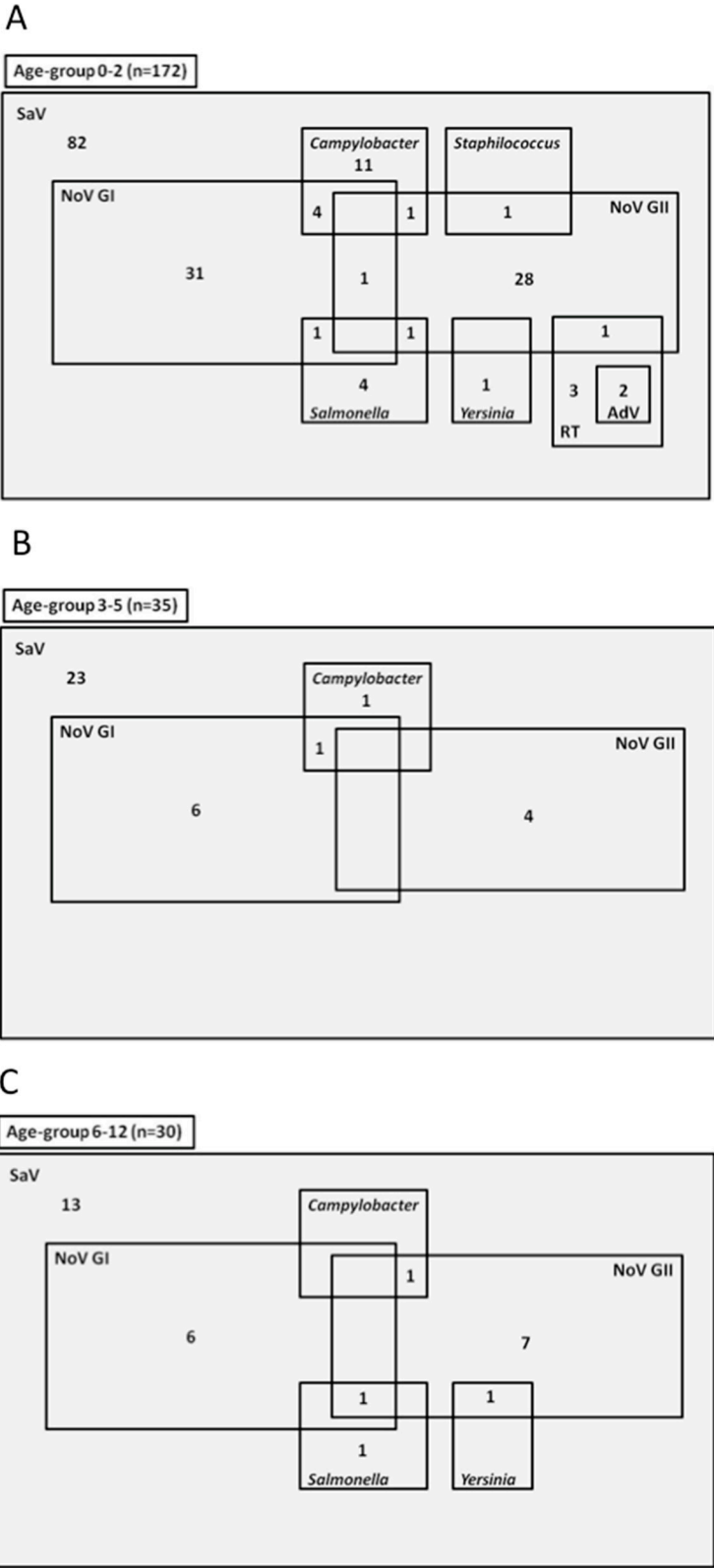
**Human sapovirus among outpatients with acute gastroenteritis in Spain: a one year
study**

Miguel F Varela, Enrique Rivadulla, Alberto Lema, Jesús L Romalde

Department of Microbiology and Parasitology, CIBUS-Faculty of Biology, Universidade de Santiago de Compostela. 15782, Santiago de Compostela, Spain

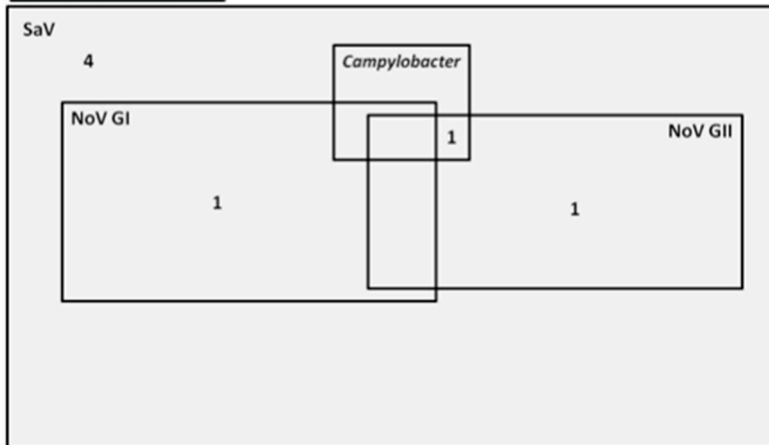
Supplementary Material

Supplementary Figure S1. Each of the 6 images (A-F) shows the number of coinfections cases of SaV with other viral and bacteriological agents for the different age-group analysed. Data for other pathogens obtained from previous study [16].



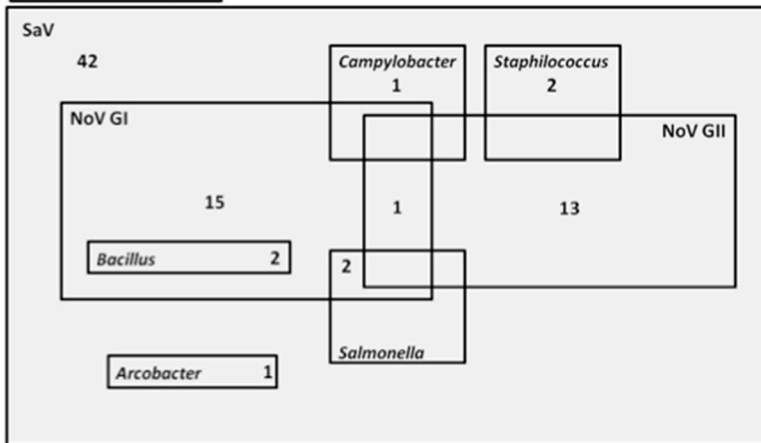
D

Age-group 13-18 (n= 7)



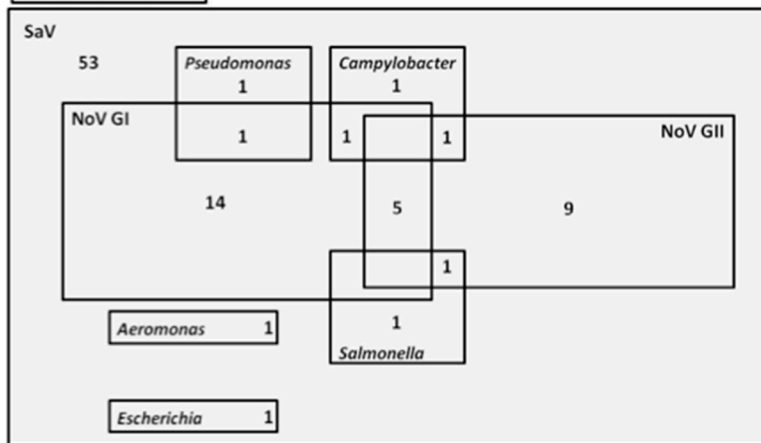
E

Age-group 19-59 (n=79)



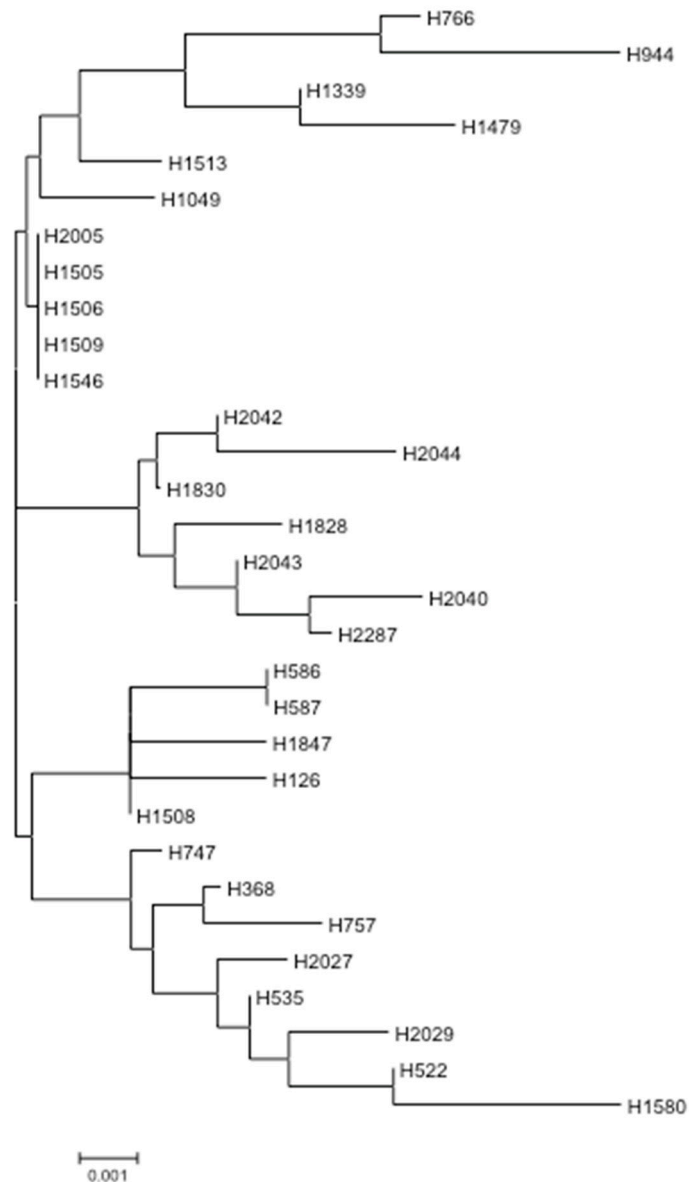
F

Age-group >60 (n=90)

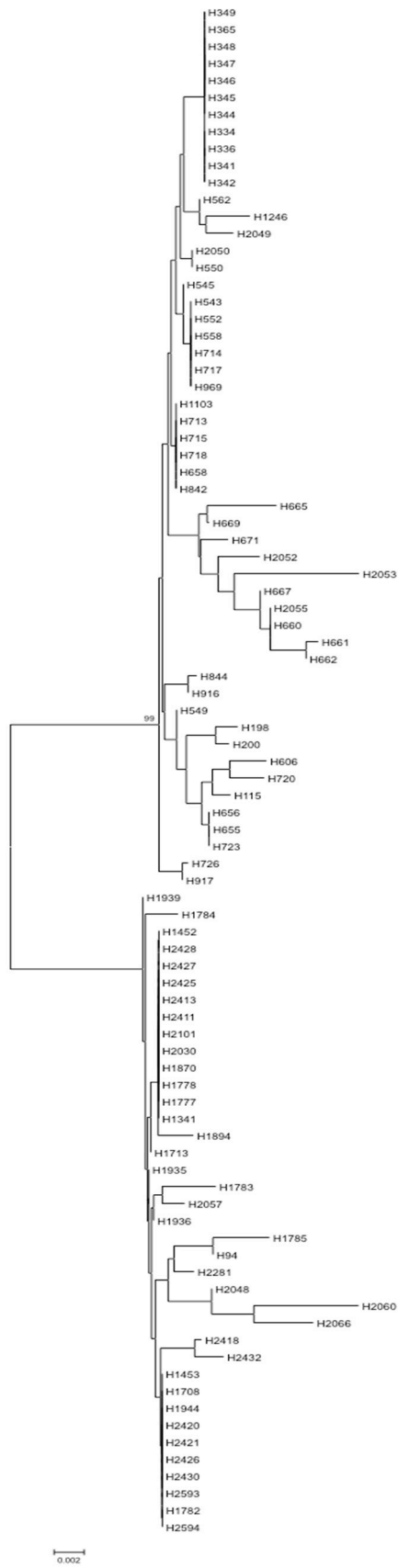


Supplementary Figure S3. Phylogenetic trees based on the partial capsid gene sequences of SaV using the Neighbor-Joining algorithm for the sequences obtained in the present study belonging to genotype GI.2 (A), GI.1 (B), GII.1 (C) and GII.4 (D). Bootstrap values (greater than 70 %) are shown at each node as percentages of 1,000 replicates. Bar, nucleotide substitutions per site.

A



B



C



D

