

Supplementary material;

Recombinant strains of human parechovirus in rural areas in the North of Brazil

Élcio Leal^{1,*}, Adriana Luchs², Flávio Augusto de Pádua Milagres^{3,4,5,6}, Shirley Vasconcelos Komninakis^{7,8}, Danielle Elise Gill¹², Márcia Cristina Alves Brito Sayão Lobato^{4,6}, Rafael Brustulin^{4,5,6}, Rogério Togisaki das Chagas^{4,6}, Maria de Fátima Neves dos Santos Abrão^{4,6}, Cássia Vitória de Deus Alves Soares^{4,6}, Fabiola Villanova¹, Steven S. Witkin⁹, Xutao Deng^{10,11}, Ester Cerdeira Sabino^{3,12}, Eric Delwart^{10,11} and Antônio Charlys da Costa¹²

- 1 Institute of Biological Sciences, Federal University of Pará, Pará 66075-000, Brazil
- 2 Enteric Disease Laboratory, Virology Center, Adolfo Lutz Institute, São Paulo 01246-000, Brazil
- 3 LIM/46, Faculty of Medicine, University of São Paulo, São Paulo 01246-903, Brazil
- 4 Secretary of Health of Tocantins, Tocantins 77453-000, Brazil
- 5 Institute of Biological Sciences, Federal University of Tocantins, Tocantins 77001-090, Brazil.
- 6 Public Health Laboratory of Tocantins State (LACEN/TO), Tocantins 77016-330, Brazil
- 7 Postgraduate Program in Health Science, Faculty of Medicine of ABC, Santo André 09060-870, Brazil
- 8 Retrovirology Laboratory, Federal University of São Paulo, São Paulo 04023-062, Brazil
- 9 Department of Obstetrics and Gynecology, Weill Cornell Medicine, 1300 York Avenue New York, NY 10065 USA
- 10 Blood Systems Research Institute, San Francisco, 94143 CA, USA
- 11 Department Laboratory Medicine, University of California San Francisco, San Francisco, 94143 CA, USA
- 12 Institute of Tropical Medicine, University of São Paulo, São Paulo 05403-000, Brazil

* Correspondence:

Élcio Leal; elcioleal@gmail.com

Vp1 gene tree

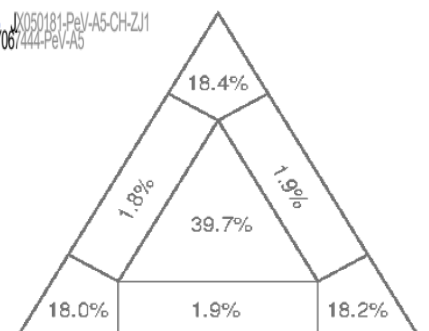
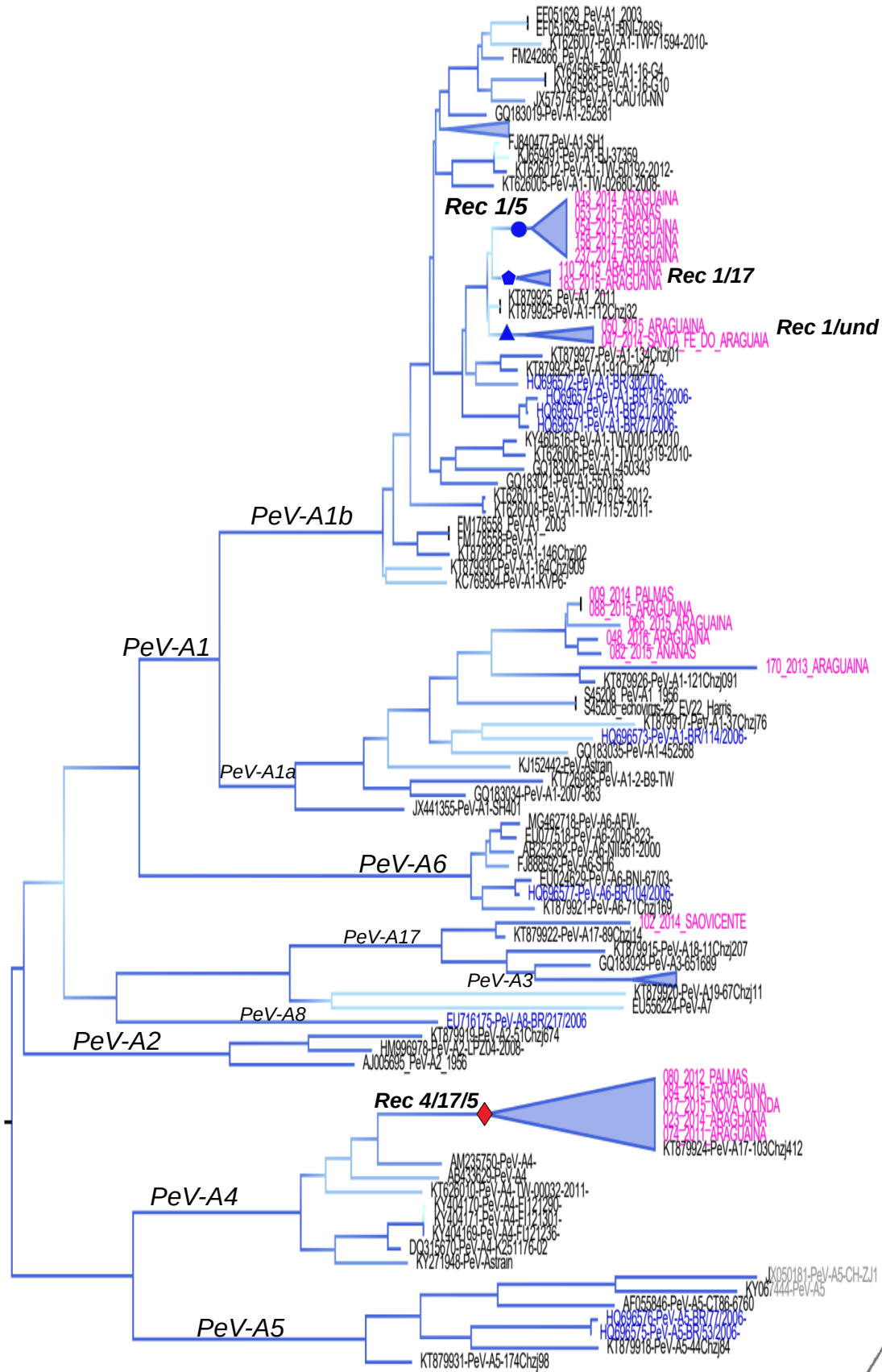


Figure S1. VP1 tree of PeV

Maximum likelihood tree constructed using VP1 gene region of PeVs.

Branch colors indicate the statistical support of each node that were calculated using aLRT. A colored scale indicating the aLRT values is also shown in the trees. Phylogenetic groups corresponding to the main genotypes are indicated by names above branches. Brazilian isolates were colored: blue indicate strains from Bahia and magenta indicate strains from Tocantins. Recombinant strains identified in this study are indicated by gray areas. The triangle in the base of tree is the likelihood map and it shows 39.7% of unresolved trees in the PeV genome alignment. Tree was constructed using maximum likelihood criteria implemented in the FastTree software ¹, assuming GTR model plus gamma correction distributions and the proportions of variable sites in the alignment. Likelihood mapping was obtained using the software Tree-puzzle (version 5.3)².

3D gene tree

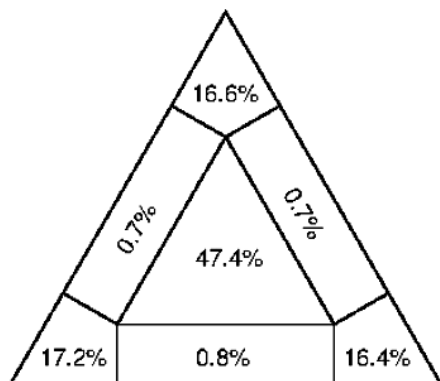
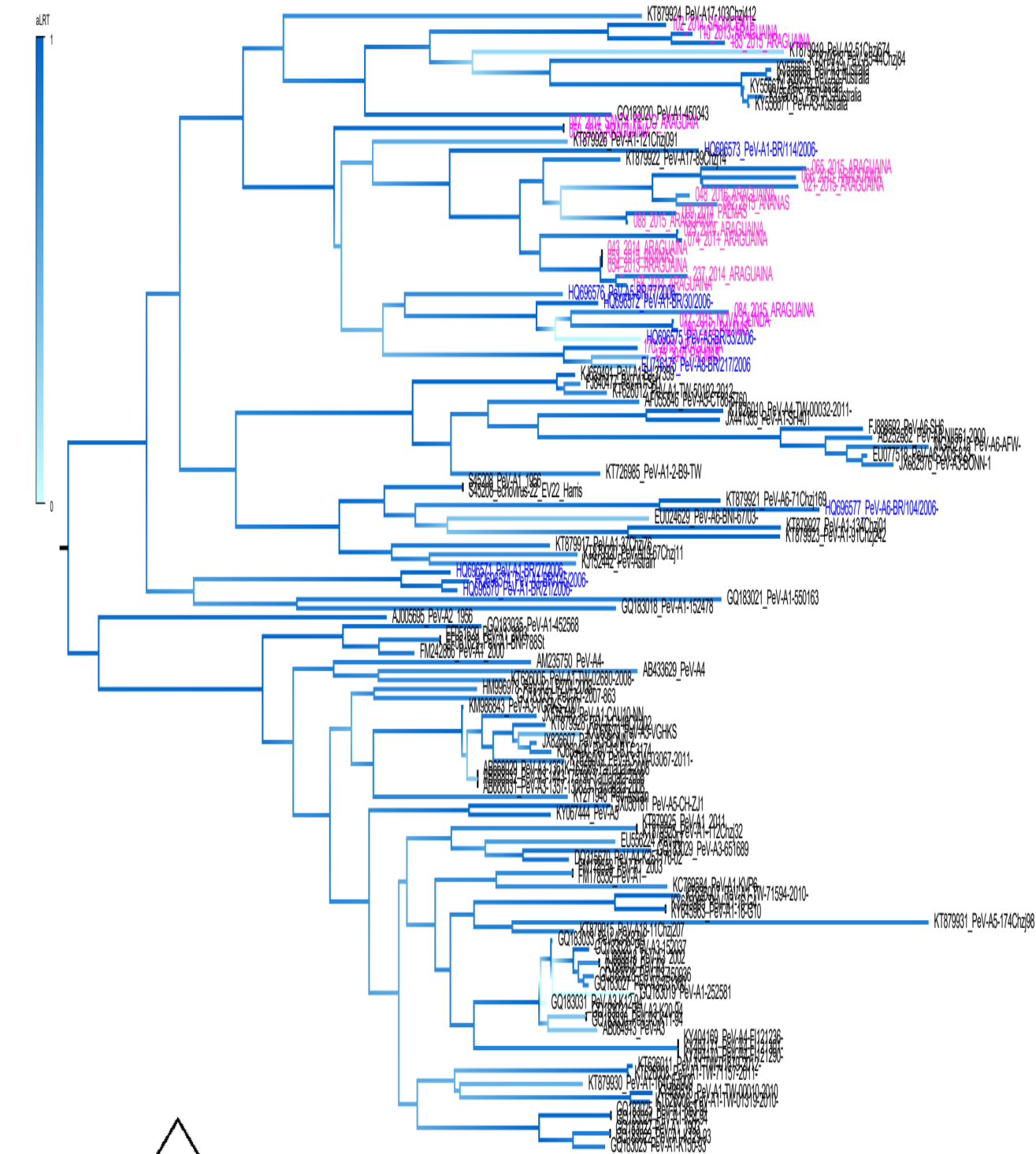


Figure S2. 3D tree of PeV

Maximum likelihood tree constructed using 3D gene region of PeVs.

Branch colors indicate the statistical support of each node that were calculated using aLRT. A colored scale indicating the aLRT values is also shown in the trees. Phylogenetic groups corresponding to the main genotypes are indicated by colored areas. Brazilian isolates were colored: blue indicate strains from Bahia and magenta indicate strains from Tocantins. The triangle in the base of tree is the likelihood map and it shows 47.4% of unresolved trees in the PeV genome alignment. Tree was constructed using maximum likelihood criteria implemented in the FastTree software¹, assuming GTR model plus gamma correction distributions and the proportions of variable sites in the alignment. Likelihood mapping was obtained using the software Tree-puzzle (version 5.3)²

Identification of sequences used in this study are in the Table 1S.

Figure S3 Genome tree of PeV and Mosaic map of PeV recombinant strains

Maximum likelihood tree constructed using near-complete genomes of PeVs.

Branch colors indicate the statistical support of each node that were calculated using the approximate likelihood ratio test (aLRT). A colored scale indicating the aLRT is also shown in the trees. Phylogenetic groups corresponding to the main genotypes are indicated by colored areas. The mosaic pattern of intergenotypes recombinant strains are indicated in the tree in diagrams next to each mosaic strain. Tree was constructed using maximum likelihood criteria implemented in the FastTree software¹, assuming GTR model plus gamma correction distributions and the proportions of variable sites in the alignment. Identification of sequences used in this study are in the Table 1S. Recombination analysis was performed using RDP software and the mosaic pattern showed in the figure is based on the bootscanning method.