

Phylogenetic and molecular analyses of more prevalent HCV1b subtype in the Calabria Region, Southern Italy.

Nadia Marascio^{*1a}, Angela Costantino^{2a}, Stefania Taffon², Alessandra Lo Presti², Michele Equestre³, Roberto Bruni², Giulio Pisani⁴, Giorgio Settimo Barreca¹, Angela Quirino¹, Enrico Maria Treccarichi⁵, Chiara Costa⁵, Maria Mazzitelli⁵, Francesca Serapide⁵, Giovanni Matera¹, Carlo Torti⁵, Maria Carla Liberto¹, Anna Rita Ciccaglione².

¹ Department of Health Sciences, Institute of Microbiology, "Magna Graecia" University of Catanzaro, Catanzaro, Italy.

² Department of Infectious, Parasitic and Immune-Mediated Diseases, Istituto Superiore di Sanità, Rome, Italy.

³ Department of Cell Biology and Neuroscience, Department of Cell Biology and Neuroscience

⁴ Center for Immunobiologicals Research and Evaluation, Istituto Superiore di Sanità, Rome, Italy

⁵ Department of Medical and Surgical Sciences, Unit of Infectious and Tropical Diseases, Magna Graecia University, Catanzaro, Italy.

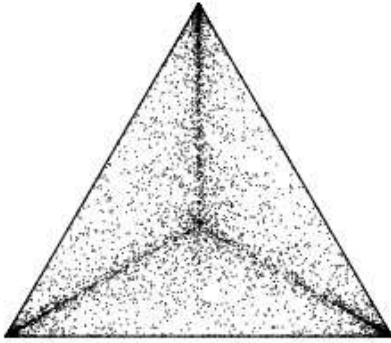
*Correspondence: Nadia Marascio, PhD, "Magna Graecia" University, Viale Europa – Loc. Germaneto, 88100 Catanzaro, Italy. E-mail: nadiamarascio@gmail.com, phone: +39-09613697742, fax: +39-09613697760.

a: contributed equally

Figure legend

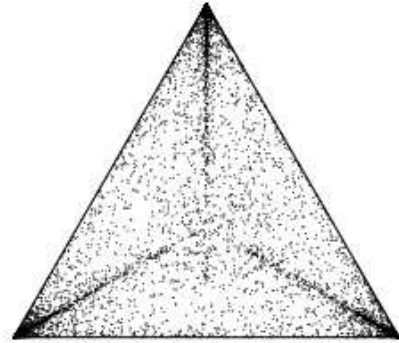
Figure S1. Likelihood mapping of HCV NS5B first (a) and second (b) dataset. The dots inside the triangles represent the posterior probabilities of the possible unrooted topologies for each quartet. Numbers indicate the percentage of dots in the centre of the triangle corresponding to phylogenetic noise (star-like trees).

a)



13.2%

b)



7.5 %