

## Supplementary Data: Provenance and geographic spread of St. Louis encephalitis virus

Anne Kopp<sup>1</sup>, Thomas R. Gillespie<sup>2,3</sup>, Daniel Hobelsberger<sup>4</sup>, Alejandro Estrada<sup>5</sup>, James M. Harper<sup>6</sup>, Richard A. Miller<sup>6</sup>, Isabella Eckerle<sup>1</sup>, Marcel A. Müller<sup>1</sup>, Lars Podsiadlowski<sup>7</sup>, Fabian H. Leendertz<sup>4</sup>, Christian Drosten<sup>1#</sup>, Sandra Junglen<sup>1#</sup>

<sup>1</sup> Institute of Virology, University of Bonn Medical Centre, Bonn, Germany

<sup>2</sup> Department of Environmental Studies and Program in Population Biology, Ecology and Evolution, Emory University, Atlanta, USA

<sup>3</sup> Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, USA

<sup>4</sup> Robert Koch Institute, Berlin, Germany

<sup>5</sup> Estación de Biología Tropical Los Tuxtlas, Instituto de Biología, Universidad Nacional Autónoma de México, Mexico

<sup>6</sup> Department of Pathology, University of Michigan, Ann Arbor, MI 48109-2200, USA

<sup>7</sup> Institute of Evolutionary Biology and Ecology, University of Bonn, Germany

# Address for correspondence:

Sandra Junglen, Institute of Virology, University of Bonn Medical Centre, Sigmund Freud Str. 25, 53127 Bonn, Germany, Tel.: +49-228-287-13064, Fax: +49-228-287-19144, e-mail:

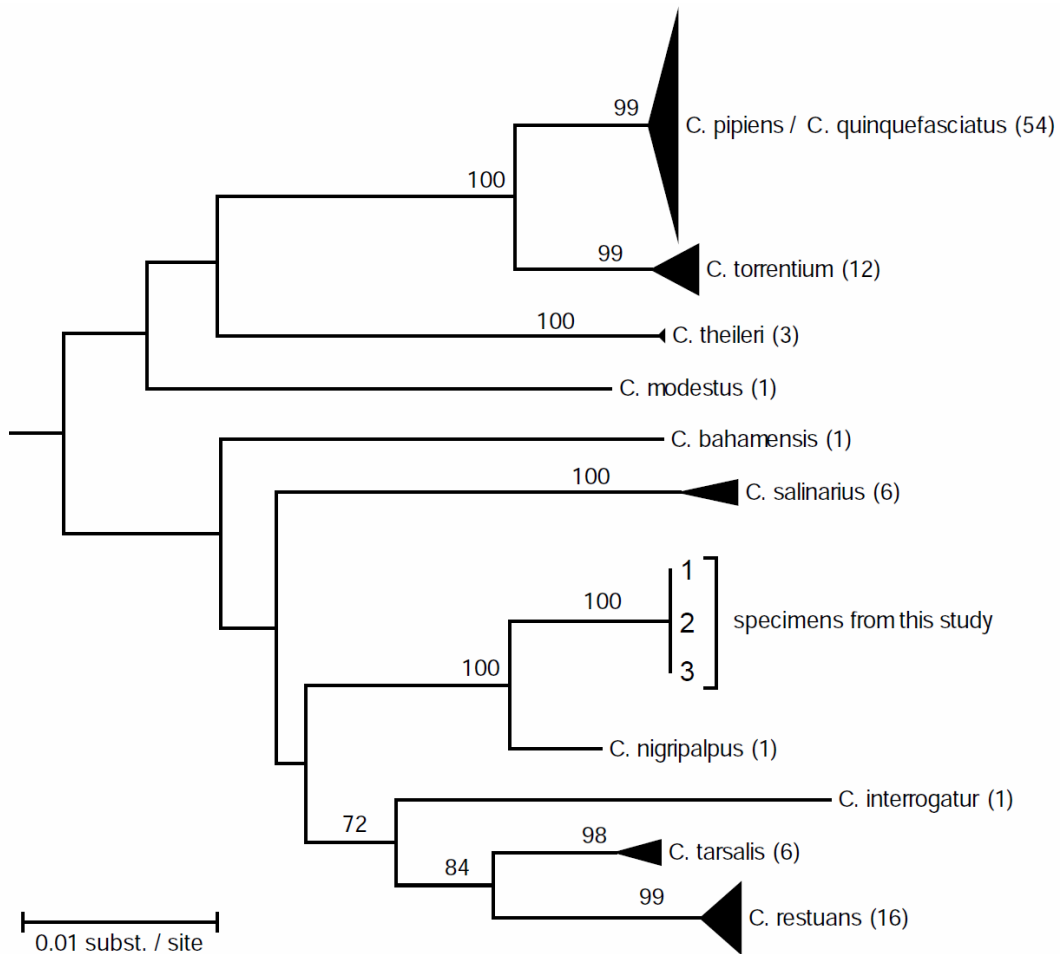
[junglen@virology-bonn.de](mailto:junglen@virology-bonn.de)

Christian Drosten, Institute of Virology, University of Bonn Medical Centre, Sigmund Freud Str. 25, 53127 Bonn, Germany, Tel.: +49-228-287-11055, Fax: +49-228-287-19144, e-mail:

[drosten@virology-bonn.de](mailto:drosten@virology-bonn.de)

### ***Dataset S1: Mosquito species***

Female mosquitoes were identified using identification keys of Darsie [70], Carpenter [71], and Clark-Gil [72]. Identification of mosquito species was confirmed by barcoding based on cytochrome C oxidase I gene using the primers LCO1490 5'-GGTCAACAAATCATAAAGATATTGG and HCO2198 5'-TAAACTTCAGGGTGACCAAAAAATCA [73]. Tree-based species determination was done with a dataset of 1890 culicid records from GenBank. Alignment was done with MAFFT v.6, FFT-NS-1 [74], NJ analysis with bootstrapping under K2P model was performed with MEGA 5 [75].



**Figure S1. Tree-based species identification of mosquito specimens.** COI sequences from three specimens were compared with 1890 culicid records from GenBank. Alignment was done with MAFFT v.6, parameter set FFT-NS-1 (Katoh & Toh 2008), neighbour joining distance analysis (K2P model and 100 bootstrap pseudoreplicates) was performed with MEGA5 (Tamura et al 2011). Only that part of the tree with the unknown specimens and their closest relatives is shown. Monophyletic species clusters were collapsed. Numbers after species names denote the number of individual sequences in the tree; numbers above branches are bootstrap percentages (only shows when support exceeds 50%). Sequences of the three new specimens are identical. Sequence similarity to their nearest neighbour (*C. nigripalpus*) is 98,48%.

Katoh K, Toh H (2008). Recent developments in the MAFFT multiple sequence alignment program. *Brief Bioinform* 9, 286-298.

Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S. (2011). MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Mol Biol Evol* 28: 2731-9.