

Virome characterization of *Culex pipiens* in France through metagenomics analysis: a new virus discovered

Gil Patricia¹, Rakotoarivony Ignace¹, L'Ambert Grégory², Marie Albane², Francés Benoit², Koual Rachid¹, Loire Etienne¹, Albina Emmanuel³, Gutierrez Serafin¹

1. CIRAD, UMR CMAEE, Montpellier, France; 2. EID Méditerranée, Montpellier, France; 3. CIRAD, UMR CMAEE, Petit-Bourg, Guadeloupe, France

CONTEXT

Culex pipiens is a mosquito vector of West Nile Virus (WNV), a flavivirus causing sporadic disease outbreaks affecting human and animal populations. WNV epidemics have taken place in France, mainly in French Camargue. We are interested in characterising the virome of *C. pipiens* to identify insect-specific viruses which could play a role in WNV epidemiology or could be used as bio-insecticides. Moreover, we also study the impact of human activity on virome composition. Here we present the first results of the virome of *C. pipiens* having led to the identification on a new insect-specific virus.

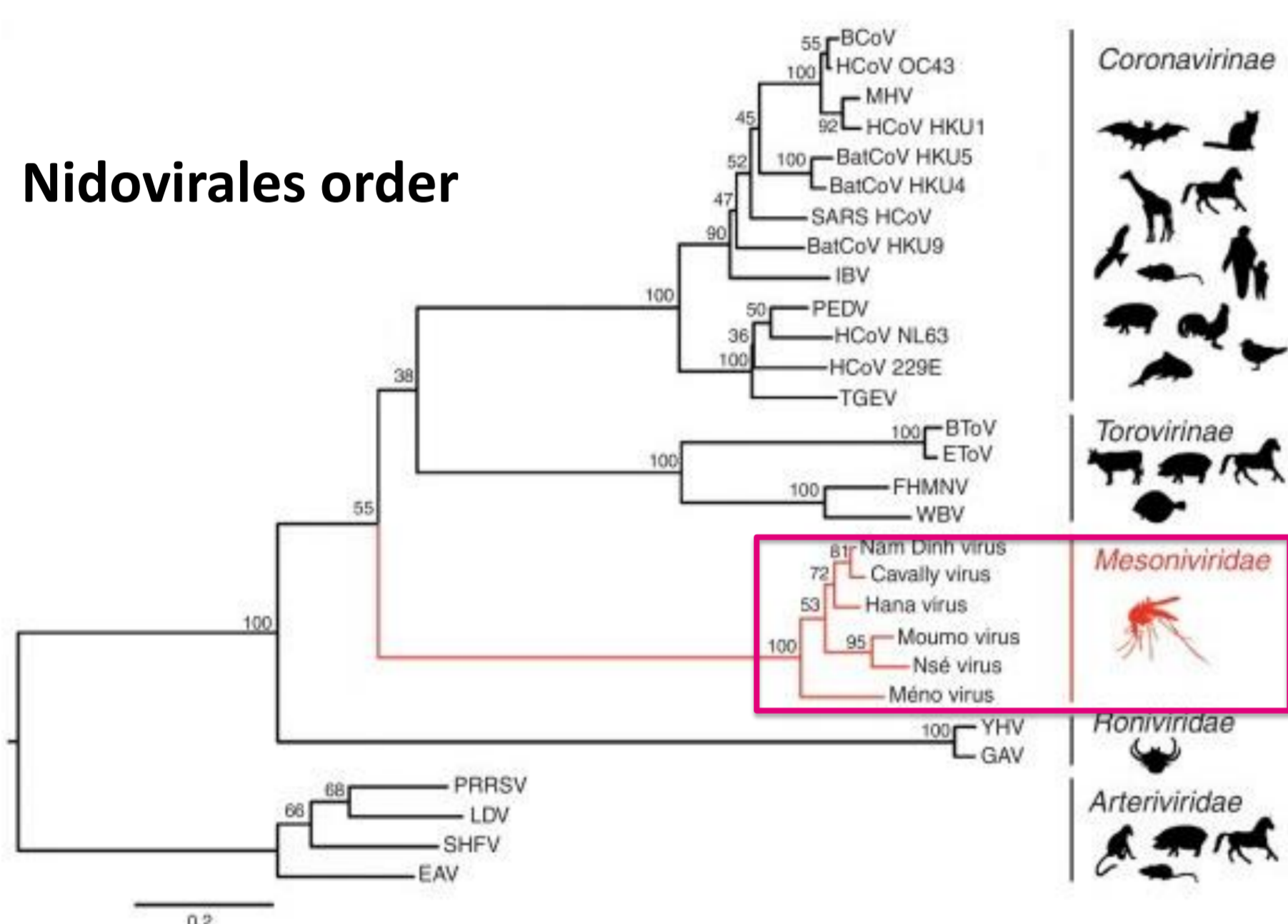
RESULTS

Sampling in 6 sites in French Camargue (4 periurban and 2 rural sites) once per month along 4 months

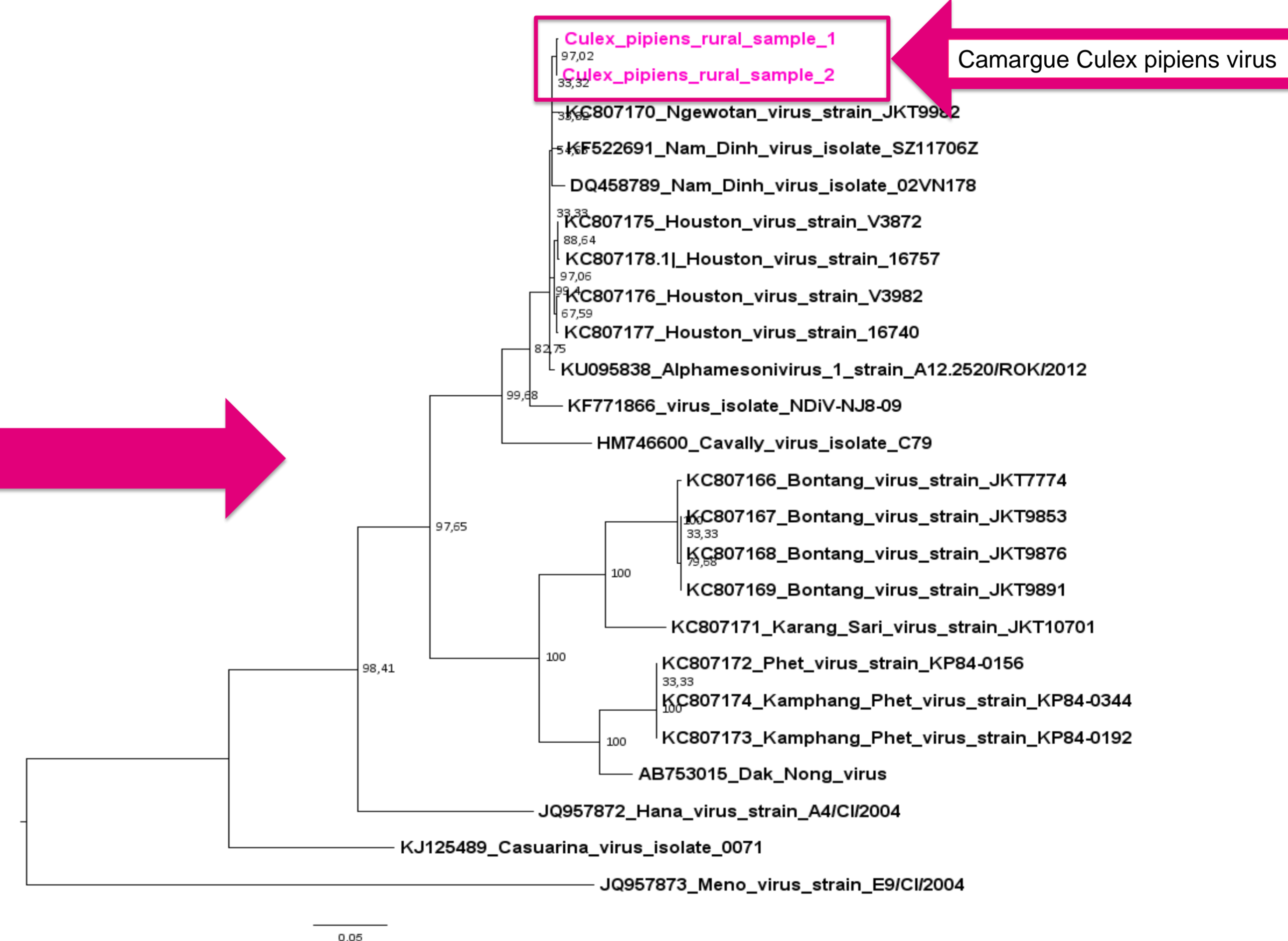


A metagenomic approach allowed the discovery of a Mesonivirus: Camargue *Culex pipiens* virus?

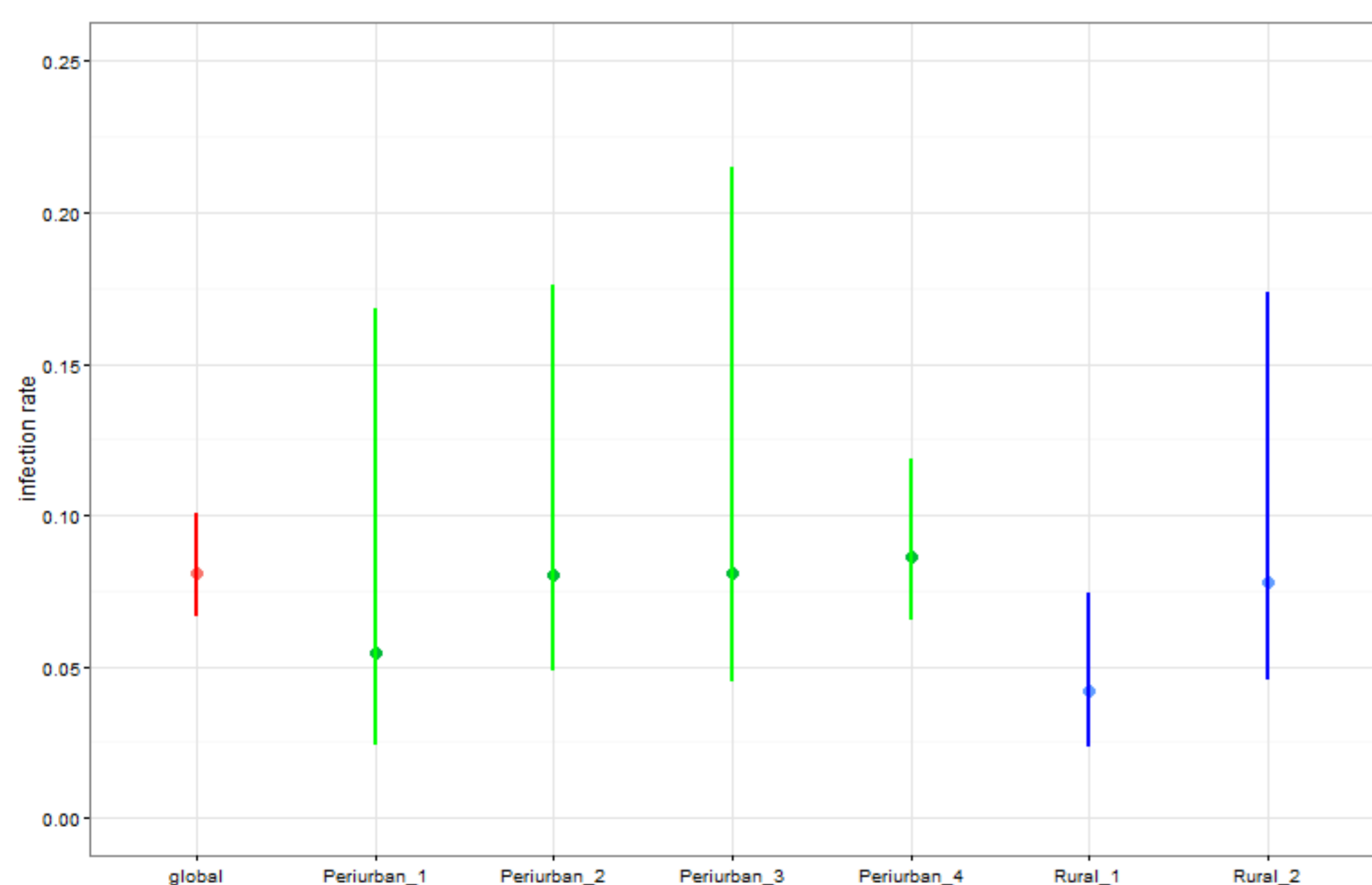
Maximum likelihood phylogeny of the Nidovirales from Junglen et al 2013.



Maximum likelihood phylogeny of the full ORF1a gene from Mesoniviruses

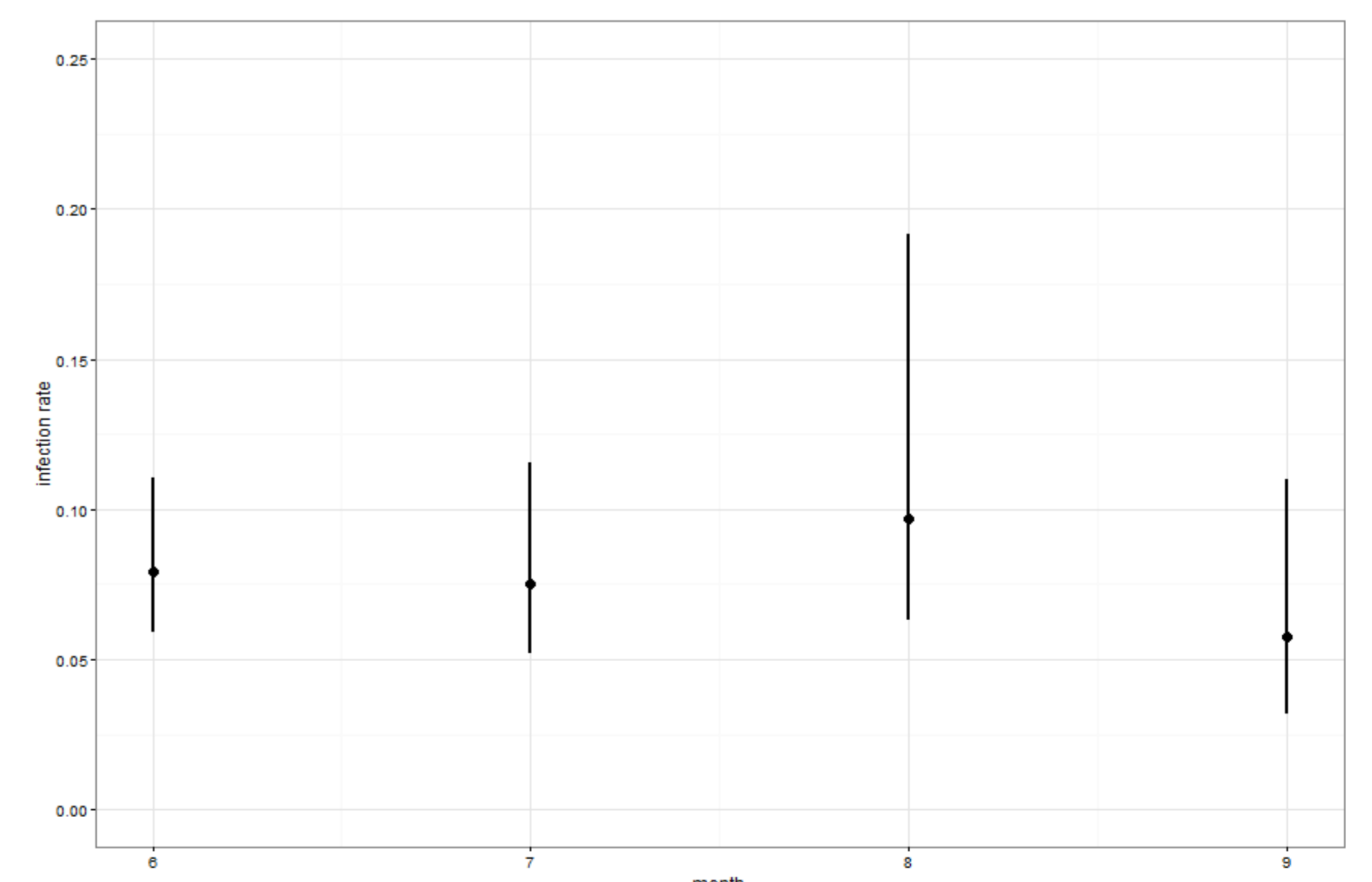


Prevalence of Camargue *Culex pipiens* virus in *C. pipiens*



No effect of the human impact on the prevalence

No effect of the time point on the prevalence



CONCLUSION AND PERSPECTIVE

- First Mesonivirus discovered in Europe.
- High prevalence of the virus in all sites during summer 2015 regardless antropisation level.
- Virus isolation on C3/36 cells succeeded.
- Perspectives: study the impact of mesonivirus on mosquito fitness and on WNV competence.