

**Research Topic for the ParisTech/CSC PhD Program**  
*(one page maximum)*

**\*Field (cf. List of fields below):** Life and Health Science and Technology, Life Science and Engineering for Agriculture, Food and the Environment

**Subfield:** Life Science, OneHealth

**ParisTech School:** AgroParisTech

**Title:** Genetic variability of tick-borne viruses

**Advisor(s):** (name, email, website)

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[https://www6.inra.fr/bipar\\_eng/WHO-ARE-WE/Teams/VECTOTIQ/The-Team/](https://www6.inra.fr/bipar_eng/WHO-ARE-WE/Teams/VECTOTIQ/The-Team/)

**Short description of possible research topics for a PhD:**

Most arthropod-borne viruses (arboviruses) are RNA viruses, which are maintained in nature by replication cycles that alternate between arthropod and vertebrate hosts. Arboviruses appear to experience lower rates of evolution than RNA viruses that replicate only in a single host. This genetic stability is assumed to result from a fitness trade-off imposed by host alternation, which constrains arbovirus genome evolution. To test this hypothesis for tick-borne viruses, we will use 6 different viruses (from different viral families) that will be (1) maintain continuously in tick cell lines or mammalian cell lines and alternatively between tick and mammalian cell lines, (2) maintain continuously in ticks (*Ixodes ricinus* by artificial infection) and mice or alternatively between ticks and mice, (3) sequenced using high throughput sequencing (whole genome sequencing). Then genetic variability of those viral populations obtained in these different conditions will be assessed to identify viral compulsory genes implicated in tick and/or mammalian transmission. These data might give the opportunity to discover new antiviral strategies in tick vector and mammalian host, and will help to better predict arbovirus emergence and crossing species barriers.

**Required background of the student:**

We expect a highly motivated student with experience in virology and cell culture and/or molecular biology. Working Experience with arthropods and/or animal models will be highly appreciated. Good command of English and/or French is crucial.

**A list of 5 (max.) representative publications of the group:** (Related to the research topic)

- **Moutailler S** et al 2016. Co-infection of ticks: the rule rather than the exception. Plos Neglected Tropical Diseases. 2016 Mar 17;10(3):e0004539. doi:0.1371/journal.pntd.0004539.
- **Moutailler S**, et al 2016. Diversity of viruses in *Ixodes ricinus* and characterization of a neurotropic strain of Eyach virus. New microbes and new infections, 2016 Mar 5;11:71-81. doi: 10.1016/j.nmni.2016.02.012
- Michelet L, Delannoy S, Devillers E, Umhang G, Aspan A, Juremalm M, Chirico J, van der Wal FJ, Sprong H, Boye Pihl TP, Klitgaard K, Bodker R, Fach P, **Moutailler S**. 2014. High-throughput screening of tick-borne pathogens in Europe. Frontiers in Cellular and Infection Microbiology, 4:103. doi: 10.3389/fcimb.2014.00103.
- Arias-Goeta C, **Moutailler S**, et al 2014. Chikungunya virus adaptation to a mosquito vector correlates with only few point mutations in the viral envelope glycoprotein. Infection, Genetics and Evolution 24:116-26. doi: 10.1016/j.meegid.2014.03.015.
- **Moutailler S**, et al. 2011. Host alternation is necessary to maintain the genome stability of Rift Valley Fever Virus. PLoS Negl Trop Dis 5(5):e1156. doi: 10.1371/journal.pntd.0001156.