

sensitive detection of an arbovirus in wild-caught vectors.

Gil Patricia^{1,2*}, Virginie Dupuy^{1,2}, Rachid Koual^{1,2}, Assane Gueye Fall³, Biram Biteye³, Geoffrey Gimmonneau^{1,2}, Albane Marie⁴, Benoit Frances⁴, Grégory Lambert⁴, Ignace Rakotoarivony^{1,2}, Laetitia Gardes^{1,2}, Thomas Balenghien^{1,2}, Claire Garros^{1,2}, Serafin Gutiérrez^{1,2}

¹CIRAD, UMR ASTRE, F-34398 Montpellier, France.

²ASTRE, Univ Montpellier, CIRAD, INRA, Montpellier, France.

³ISRA, BP 3120 Dakar, Senegal.

⁴EID Méditerranée Montpellier, France.

* patricia.gil@cirad.fr

The study of viral communities has recently been boosted by the use of the so-called high-throughput sequencing (HTS) technologies. Coupled with random amplification of nucleic acids, HTS allows the identification of viral species present in a given sample without a-priori knowledge on their identity but their resemblance to known viruses. The huge interest of this approach for virus ecology and diagnostics has triggered several technical improvements in most steps required in virus metagenomics, from nucleic-acid extraction to bioinformatics analysis of sequencing results. Surprisingly, there is yet a key step that has received little attention, that of library preparation. Here, we describe a library preparation for exploring viral diversity in a large number of samples with the use of high-throughput sequencing. This method uses custom adaptors that are PCR ligated, allowing low cost, high multiplexing and fully exploitable read lengths. After validation of our method with artificial viral communities, we have tested it with two samples set from wild-caught arthropod vectors showing that our approach allows to identify an arbovirus in highly-degraded samples with a relatively high sensitivity.

Keywords: Metagenomics; arbovirus; arthropod vectors.

P15. Conserved virome diversity and structure in the mosquito vector *Culex pipiens*.

Gil Patricia^{1,2}, Rakotoarivony Ignace^{1,2}, Loire Etienne^{1,2}, Marie Albane³, Francès Benoit³, L'Ambert Grégory³, Busquets-Martí Núria⁴, Birnberg Lotty⁴, Sandra Talavera⁴, Carlos Aranda⁴, Bessat Mohamed⁵; Otify Yehia⁵; Mansini Giuseppe⁶; Goffredo Maria⁷, Ayari Emna⁷, Mejri Selma⁷, Muth Erika⁸, Cheval Justine⁸, De Visser Louise⁸, Lamany Arnaud⁸, Cabannes Eric⁸, Hebert Charles⁸, Eloit Marc⁹, Gutierrez Serafin^{1,2*}

¹CIRAD, UMR ASTRE, F-34398 Montpellier, France.

²ASTRE, Univ Montpellier, CIRAD, INRA, Montpellier, France.

³EID Méditerranée Montpellier, France.

⁴CreSA-IRTA, Transboundary infections Subprogram Campus de la Universitat Autònoma de Barcelona, Edifici CReSA s/n 08193 Bellaterra, Barcelona, Spain.

⁵Department of Parasitology, Alexandria University. Edfina, Rasheed-Line, Behaira, PO 22758, Egypt;

⁶Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Via Campo Boario, 64100 Teramo, Italy.

⁷Laboratory of Clinical Virology, Institut Pasteur de Tunis, Tunisia.

⁸PathoQuest, 25 Rue du Dr Roux, 75015 Paris, France.

⁹Pathogen Discovery Laboratory, Biology of Infection Unit, Inserm U1117, Institut Pasteur, Paris, France.

* serafin.gutierrez@cirad.fr

Recent epidemics caused by different mosquito-borne viruses underline the viral diversity associated to mosquitoes. However, beyond human viral pathogens, we know little on other viruses of the

mosquito virome. This unexplored diversity probably influences vector competence and other aspects of the mosquito biology, as shown for the mosquito bacteriome. We have analysed the virome of *Culex pipiens*, a mosquito vector of important arboviruses like Rift Valley fever virus or West Nile fever virus. To this end, we have coupled a metagenomics approach with a large sampling campaign involving different countries and habitats around the Mediterranean basin. Our results show for the first time conserved patterns in virus diversity among mosquito populations, as well as specificities probably linked to different environmental conditions. The discovery of a ubiquitous group of viruses strongly supports the existence of a core virome in *Culex pipiens* that is likely to influence mosquito physiology.

Keywords: virome, arbovirus, mosquito, vector

P16. Epichloë endophyte effects on leaf blotch pathogen (*Rhynchosporium* sp.) of tall fescue vary among grass origin and environmental conditions.

Miia Kauppinen*, Irma Saloniemi, Kari Saikkonen, Marjo Helander

Natural Resources Institute Finland (Luke), Itäinen Pitkätatu 3, 20520 Turku, Finland.

* miia.kauppinen@utu.fi

Systemic Epichloë endophytes are common fungal symbionts of many cool-season grasses. They are known for their capability of increasing host plant tolerance against biotic and abiotic stressors, including grass pathogens. However, results on endophyte-mediated disease resistance have been ambiguous, and the underlying mechanisms of disease resistance remain unknown. We studied how Epichloë endophytes affect naturally occurring leaf blotch (*Rhynchosporium* sp.) pathogen infections of wild and cultivated tall fescues (*Schedonorus phoenix*). Endophyte-infected and uninfected tall fescues were grown in a common garden experiment in southern Finland for eight growing seasons. The experimental plants were subjected to nutrient and water treatments. Our preliminary results show that the effects of endophytes on leaf blotch infection incidences varied among plant origins under different environmental conditions. Overall, American cultivars had lower pathogen infections than the Nordic wild grasses. American manipulatively endophyte-free plants had considerably higher pathogen levels compared to their endophytic counterparts under some treatments. Endophytic wild plants from Åland, Finland, exhibited higher leaf blotch incidences than naturally or manipulatively endophyte-free plants, whereas with plants from Gotland, Sweden, the case was opposite. These results indicate that Epichloë endophytes may either suppress or increase pathogen *Rhynchosporium* infections in tall fescues, depending on grass origin and environmental conditions.

Keywords: Leaf blotch, *Rhynchosporium*, *Epichloë*, Fungal endophytes, Grasses

P17. Immune response in relation to bovine mammary gland microbiome during transition to once-a-day milking.

Lucie Rault¹, Jocelyne Guinard-Flament², Pierre-Alexandre Lévêque^{1,2}, Sarah Barbey³, Frederic Launay³, Pierre Germon⁴, Yves Le Loir^{1*}, Sergine Even¹

¹UMR 1253 INRA-Agrocampus Ouest STLO, Rennes, France.

²UMR 1348 INRA-Agrocampus Ouest PEGASE, Rennes, France.

³UE INRA du Pin-au-Haras, Exmes, France.

⁴UMR 1282 INRA-Université François Rabelais ISP, Tours, France.

* yves.le-loir@inra.fr

Bovine mastitis is an inflammatory disease of the mammary gland, often due to bacterial infections. We have recently established a link between bovine teat microbiome and history of animal with regard to mastitis, suggesting a link between teat microbiota and health. In an attempt to further explore this



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