

Mosquito core viromes: do they exist?

Cassandra Koh, Maria-Carla Saleh

▶ To cite this version:

Cassandra Koh, Maria-Carla Saleh. Mosquito core viromes: do they exist?. Trends in Parasitology, 2024, 40 (3), pp.203-204. 10.1016/j.pt.2024.01.003 . pasteur-04874426

HAL Id: pasteur-04874426 https://pasteur.hal.science/pasteur-04874426v1

Submitted on 8 Jan 2025

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- **1** Mosquito core viromes: The importance of context
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- 3 Cassandra Koh^{1*} and Maria-Carla Saleh¹
- ⁴ ¹ Institut Pasteur, Université Paris Cité, CNRS UMR3569, Viruses and RNA Interference Unit, 75015
- 5 Paris, France
- 6 *Correspondence: cassandra.koh@pasteur.fr (C. Koh).
- 7 ORCID: 0000-0003-2466-6731 (C. Koh); 0000-0001-8593-4117 (M.C. Saleh)
- 8 Twitter: @koh_cassandra (C. Koh); @SalehLabParis (M.C. Saleh)
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10 Keywords: mosquito core virome, virome, mosquito-specific virus, disease ecology, virus
 11 metagenomics

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In response to our Opinion article on mosquito viromes and the paths towards implementable measures to counter the transmission of mosquito-borne viruses, De Coninck and Matthijnssens raise an important point on the definition of the increasingly used term 'core virome'. Across published mosquito virome studies, this term appears to have two usages with very different biological implications: to refer to the entire set of mosquito-infecting viruses, or to refer to a subset of common viruses found above a certain abundance or occurrence (i.e., prevalence) threshold. Here, we take advantage of this opportunity to add a little more to the discussion.

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De Coninckⁱ had previously presented how the microbiome research community view the term (core virome' and that the methodologies employed to assign 'core' status are varied and currently the subject of active debate [1,2]. It is generally agreed that core taxa must fulfil some criteria in terms of abundance or occurrence and therefore cannot comprise the entire virus community within a host given the high variability of virome composition across individuals and populations. We concur with this since viral taxa that occur with particularly high abundance or occurrence are more likely to have biological and ecological relevance. As such, defining core viromes is useful for refining future investigations and their analysis across populations permits insights into host-virus infection and transmission dynamics.

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31 In their letter, De Coninck and Matthijnssens posited that the concept of a core virome requires a 32 more nuanced understanding. In their very recent metagenomics study on single *Culex* 33 mosquitoes, no single virus species was shared among all individuals of the same mosquito species 34 from different sampling locations [3]. This new data, alongside previous studies in Aedes aegypti, 35 Ae. albopictus, Cx. quinquefasciatus, and Cx. pipiens, shows that the presence, in addition to the 36 composition, of core viromes are species-specific and may even be population-specific [3–6]. They 37 argued for caution and called for clear definitions in using the term 'core virome', which we 38 unreservedly echo. More precisely, the inclusion criteria or methodological details of assigning 39 core status should be well presented, and abundance or occurrence measures in single mosquitoes 40 should be aimed for.

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42 But not all core taxa are equally stable. A previous study from their group [5] made the distinction 43 between a vertically transmitted core virome and an environmentally derived core virome, which 44 emerges from comparisons between the viromes of lab-reared versus wild mosquito populations. 45 The viromes of wild populations often proved to be richer, due to a greater proportion of 46 environmentally derived viral taxa, and more diverse, as environmentally derived members may be 47 habitat-specific and may naturally fluctuate with time, climate, and other ecological factors [5,7]. It 48 follows that an environmentally derived core virome would be less stable than a vertically 49 transmitted one and must be interpreted within defined spatial and temporal scales. Hence, it 50 could be argued that 'core' status should be reserved for vertically transmitted viral taxa, which are

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51	more likely to have long-term coevolutionary relationships with their host. That said, the current
52	body of virus metagenomics studies in the same mosquito species across wide geographical scales
53	supports the alternative definition of "mosquito core virome" put forward in their letter, given that
54	single mosquito-specific virus species globally present in all tested populations, let alone
55	individuals, are seemingly rare [5,6,8,9].
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57	To summarise, we agree that viruses should not be granted 'core' status lightly and we encourage
58	researchers to consider the biological ecological implications of assigning candidate viral taxa into
59	core viromes. Research works from the group of De Coninck and Matthijnssens have significantly
60	shaped the mosquito virome zeitgeist and we look forward to following the data-informed
61	evolution of the 'core virome' concept.
62	
63	Acknowledgements and funding information
64	This work was supported by funding from the French Government's Investissement d'Avenir
65	program, Laboratoire d'Excellence Integrative Biology of Emerging Infectious Diseases (grant ANR-
66	10-LABX-62-IBEID to C.K. and M.C.S.), and by Fondation iXcore - iXlife - iXblue Pour La Recherche to
67	M.C.S.
68	
69	Declaration of interests
70	The authors declare no competing interests.
71	
72	Resources
73	ⁱ <u>http://disq.us/p/2vydkvk</u>
74	
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