

## Letter

Mosquito core viromes:  
do they exist?Cassandra Koh <sup>1,\*,@</sup> and  
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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 [1], De Coninck and Matthijnsens raise an important point on the definition of the increasingly used term ‘core virome’ [2]. Here, we add a little more food for thought and offer our speculation on the existence of a global mosquito core virome.

Across published mosquito virome studies, this term appears to have two usages with very different biological implications: to refer to (i) the entire set of mosquito-infecting viruses, or to (ii) a subset of common viruses found above a certain abundance or occurrence (i.e., prevalence) threshold.

De Coninck had previously presented how the microbiome research community view the term ‘core virome’ and how the methodologies employed to assign ‘core’ status are varied and currently the subject of active debate [3,4]. It is generally agreed that core taxa must fulfil some criteria in terms of abundance and/or occurrence and therefore cannot comprise the entire virus community within a host given the high variability of virome composition across individuals, populations, and species. As core viral taxa are likely to have biological and ecological relevance, characterising core viromes is useful for refining future investigations, and their analysis across populations permits insights into host-virus infection and transmission dynamics.

In their letter, De Coninck and Matthijnsens posited that the concept of a mosquito core virome requires a more nuanced

understanding [2]. In their very recent metagenomics study on single *Culex* mosquitoes, no single virus species was shared among all individuals of the same mosquito species from different sampling locations [5]. These new data, in juxtaposition to previous studies in *Aedes aegypti*, *Ae. albopictus*, *Culex quinquefasciatus*, and *Cx. pipiens*, show that the presence, in addition to the composition, of core viromes is species-specific and may even be population-specific [5–8]. They argued for caution and called for clear definitions in using the term ‘core virome’, which we unreservedly echo. More precisely, the inclusion criteria or methodological details of assigning core status should be well presented, and abundance and occurrence measures in single mosquitoes should be aimed for.

But not all core taxa are equally stable. A previous study from their group [7] made the distinction between a vertically transmitted core virome and an environmentally derived core virome, which emerges from comparisons between the viromes of laboratory-reared versus natural mosquito populations. The viromes of natural populations often prove to be richer, due to a greater proportion of environmentally derived viral taxa, and more diverse, as environmentally derived members may be habitat-specific and may naturally fluctuate with time, climate, and other ecological factors [7,9]. It follows that an environmentally derived core virome would be less stable than a vertically transmitted one and must be interpreted within defined spatial and temporal scales. It could even be argued that ‘core’ status is more applicable to vertically transmitted viral taxa, which are more likely to produce persistent and transgenerational infections and have long-term coevolutionary relationships with their host. That said, environmentally derived taxa could be considered ‘core’ for a population if they are consistently found associated with the host species across large temporal scales.

To finish, although we agree that we are still at the beginning of the mosquito core virome debate, virus metagenomics studies in the same mosquito host across wide geographical scales are already showing that it is rare to find a single mosquito-specific virus species, vertically transmitted or not, that is present in all tested populations [7,8,10,11]. This suggests that a global core virus, and therefore a global core virome, is unlikely to exist, at least in the mosquito species investigated. Mosquito core viromes may therefore be valid only for specific populations, and further research using appropriate numbers of individual mosquitoes will reveal whether any taxa are capable of reaching 100% occurrence. Our guess is no.

Research works from the group of De Coninck and Matthijnsens have been shaping the mosquito virome *zeitgeist* by providing evidence for the presence and absence of core viromes within several host species [5–7]. We look forward to following the data-informed evolution of the ‘core virome’ concept in mosquitoes.

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**Declaration of interests**

The authors declare no competing interests.

**Resources**

<http://disq.us/p/2vydkvk>

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