

Metavirome characterization in *Anopheles darlingi* from three different geographical regions of Colombia

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INTRODUCTION

The association between *Anopheles* and viruses is relevant because its potential utility in biological vector control; in addition, it has implications for public health given that some *Anopheles* species might even spread viruses (1, 2). The recent emergence of metagenomics, driven by advances in massive sequencing technologies, has allowed virome characterization in different host types including mosquitoes (3). Despite its relevance, the viral component has been little explored in the Neotropical species of the *Anopheles* genus, including *Anopheles darlingi*, the principal malaria vector in the Neotropics and a primary vector in Colombia. Therefore, the aim of this study was to characterize the metavirome profile in *An. darlingi*, from important malaria-endemic regions of Colombia.

METHODOLOGY

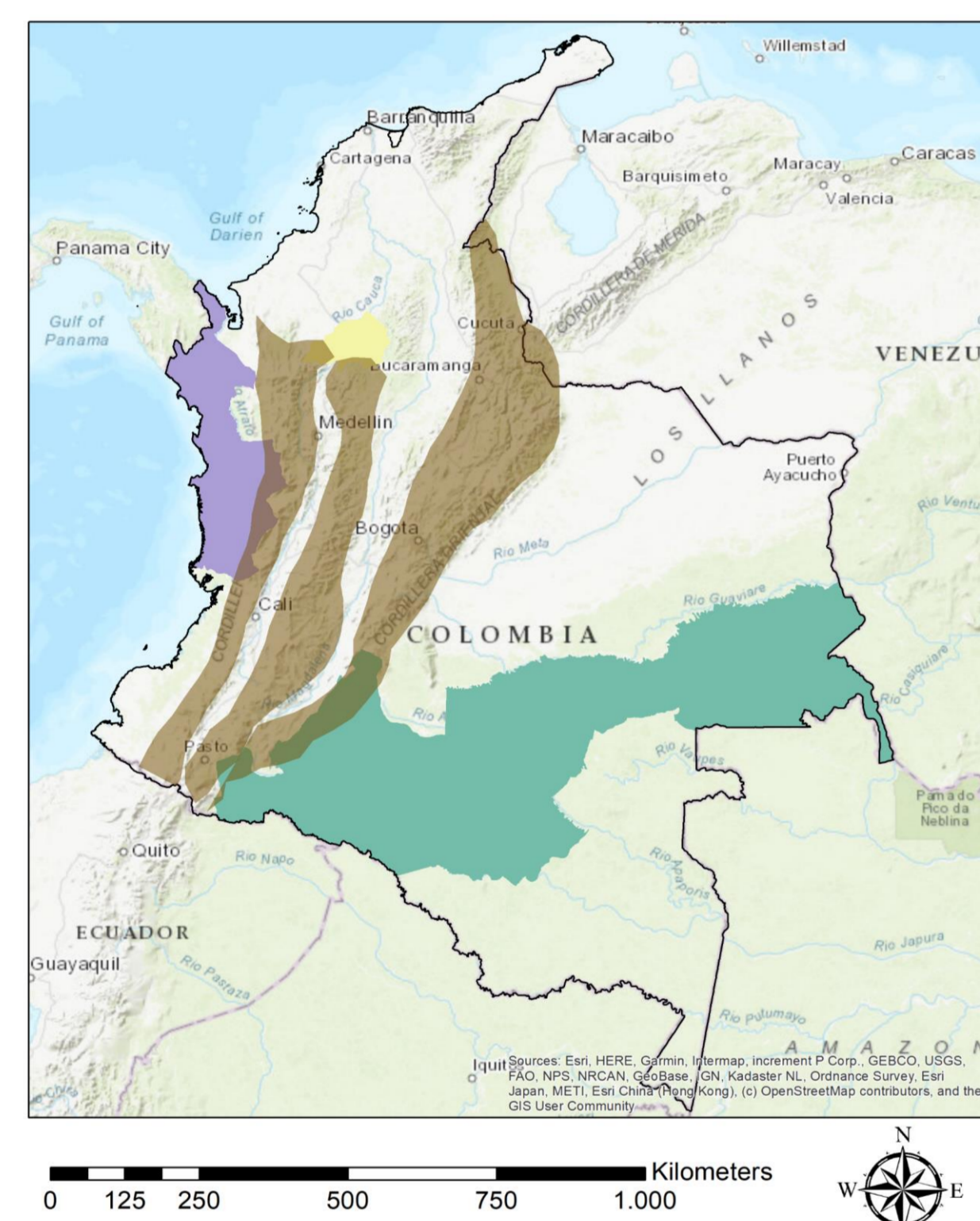
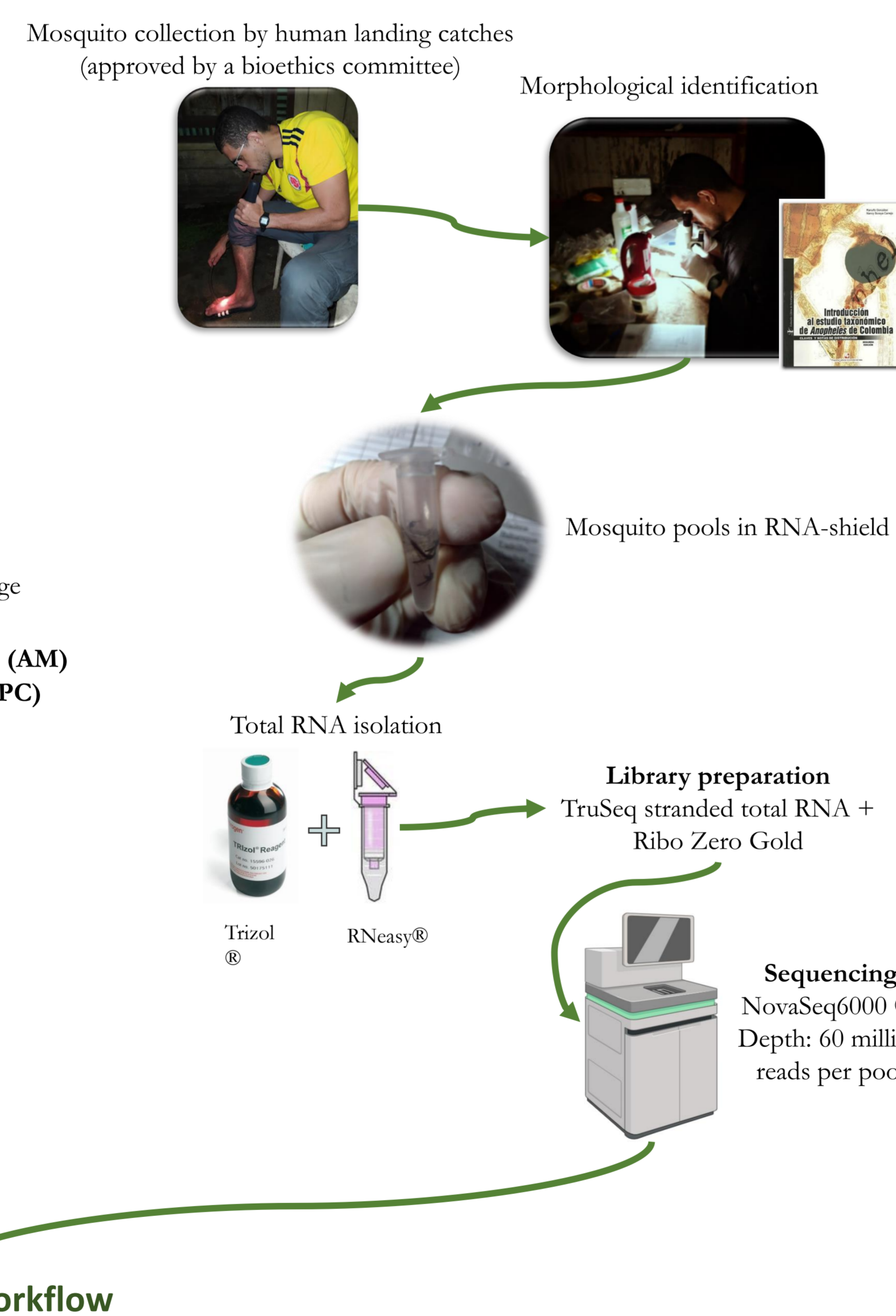
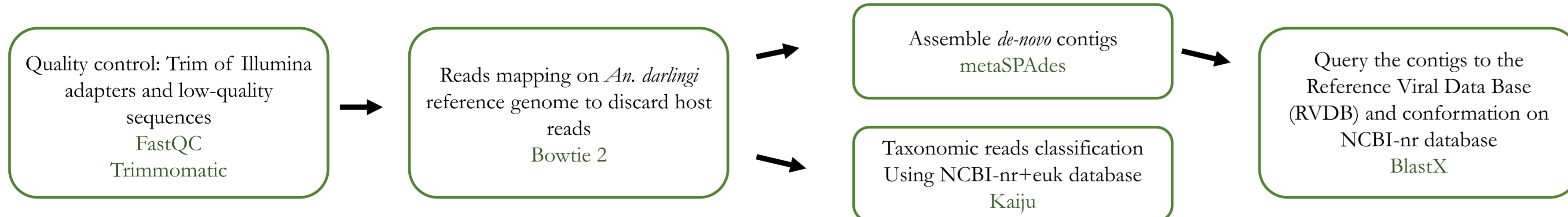


Figure 1. Map showing the Colombia malaria-endemic regions where mosquitoes were collected



Data were obtained from nine mosquito pools, all conformed of non-fed, non-pregnant females, except for the AdarPC3 sample which was the only sample made up of males that was possible to collect during the field trips.

Bioinformatic workflow



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RESULTS

A total of 357M PE-reads were obtained; 101700 PE-reads were classified as viral, distributed in 15 viral families and three unclassified viruses at the family level. A high proportion of reads was assigned to unclassified-*Ortervirales* (52%), *Chuviridae* (10%) and *Baculoviridae* (8%), followed by a group of “Unclassified Viruses” (6.9%) (Fig. 2). A similar viral composition was found in *An. darlingi* from all regions.

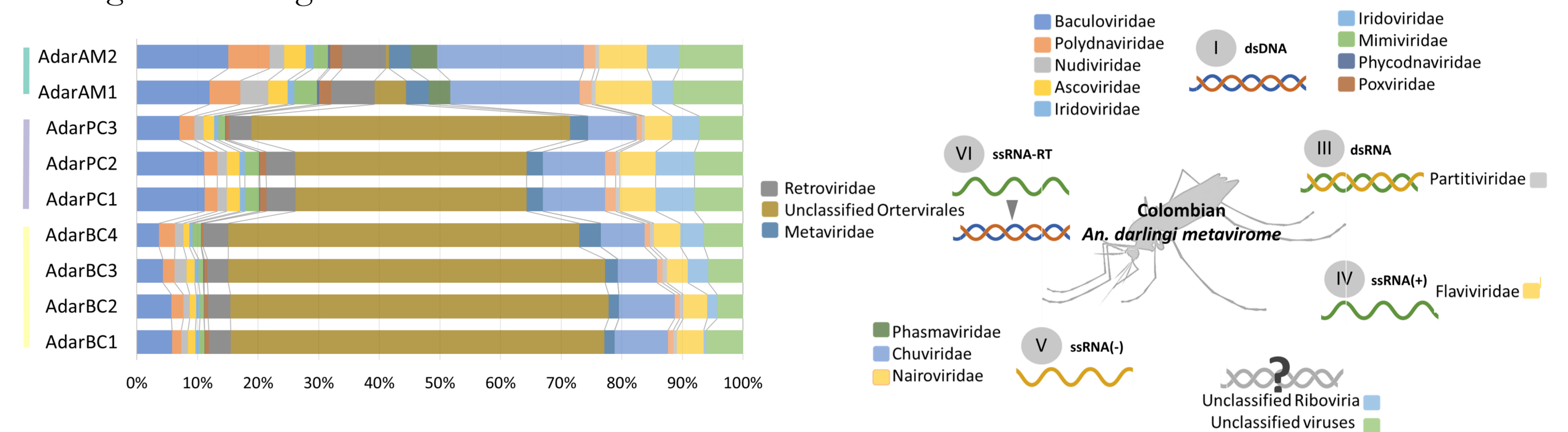


Figure 2. Viral reads annotated in the *Anopheles darlingi* pools. Each bar show the proportion of reads by viral family in each pool. The Baltimore classification for the identified viral families is indicated on the right figure.

Regarding the distribution of viral read counts by family, a high similarity was observed at the intra-region level (Bray Curtis > 0.84). Among endemic regions, a greater similarity was observed between the Pacífico and Bajo Cauca regions (Bray Curtis = 0.74) than between Bajo Cauca and Pacífico compared to the northern Amazon region (Bray Curtis = 0.41 and 0.43, respectively). The *An. darlingi* males pool from the Pacífico region (AdarPC3) showed greater similarity with females from the Bajo Cauca region (Bray Curtis = 0.85 and 0.92) than to the females from the same Pacífico region (Bray Curtis = 0.69 and 0.75) (Fig. 3).

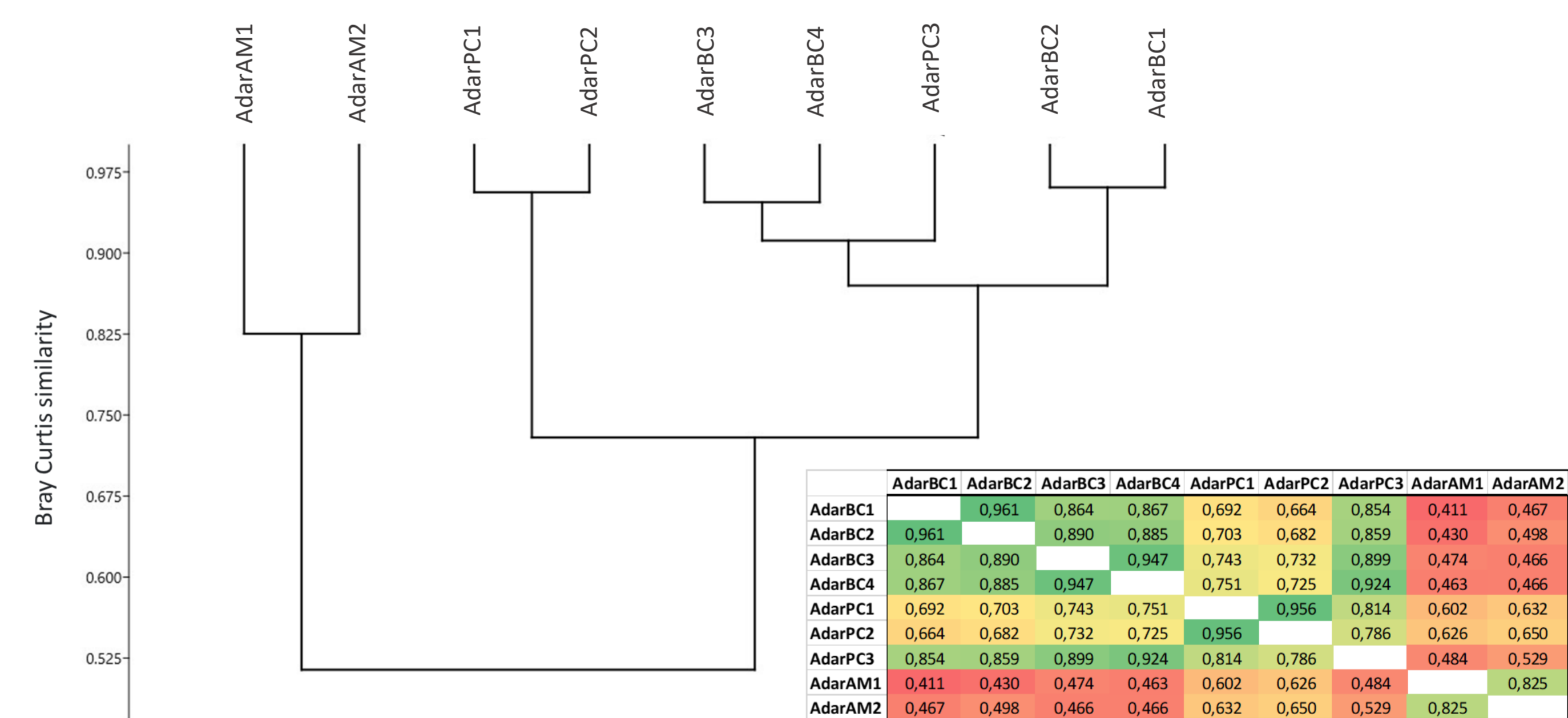


Figure 3. Distance analysis of viral read counts by family (normalized) based on the Bray-Curtis similarity index.

CONCLUSION

The similarity found in the *An. darlingi* virome composition between Bajo Cauca and Pacifico regions and the difference with the northern Amazonas region may be due to the Andes; this mountain range acts as a geographical barrier separating *An. darlingi* population from northwest and northeast Colombia (4, 5). In addition, environmental-specific conditions of each region may be contributing to the differences observed. This work contributes knowledge on the *Anopheles* virome composition.

ACKNOWLEDGMENTS

- This study was developed under a project funded by Escuela de Microbiología, code No. 2021-41851 and received support from Colciencias (Now Minciencias), project code No. 753-2018.
- To members of the Molecular Microbiology Group, University of Antioquia and Entomology Unit “Secretaría de Salud” of Guaviare Department.