Meta-analysis of the mosquito microbiome uncovers new targets for vector control and highlights ecological drivers of the microbiota

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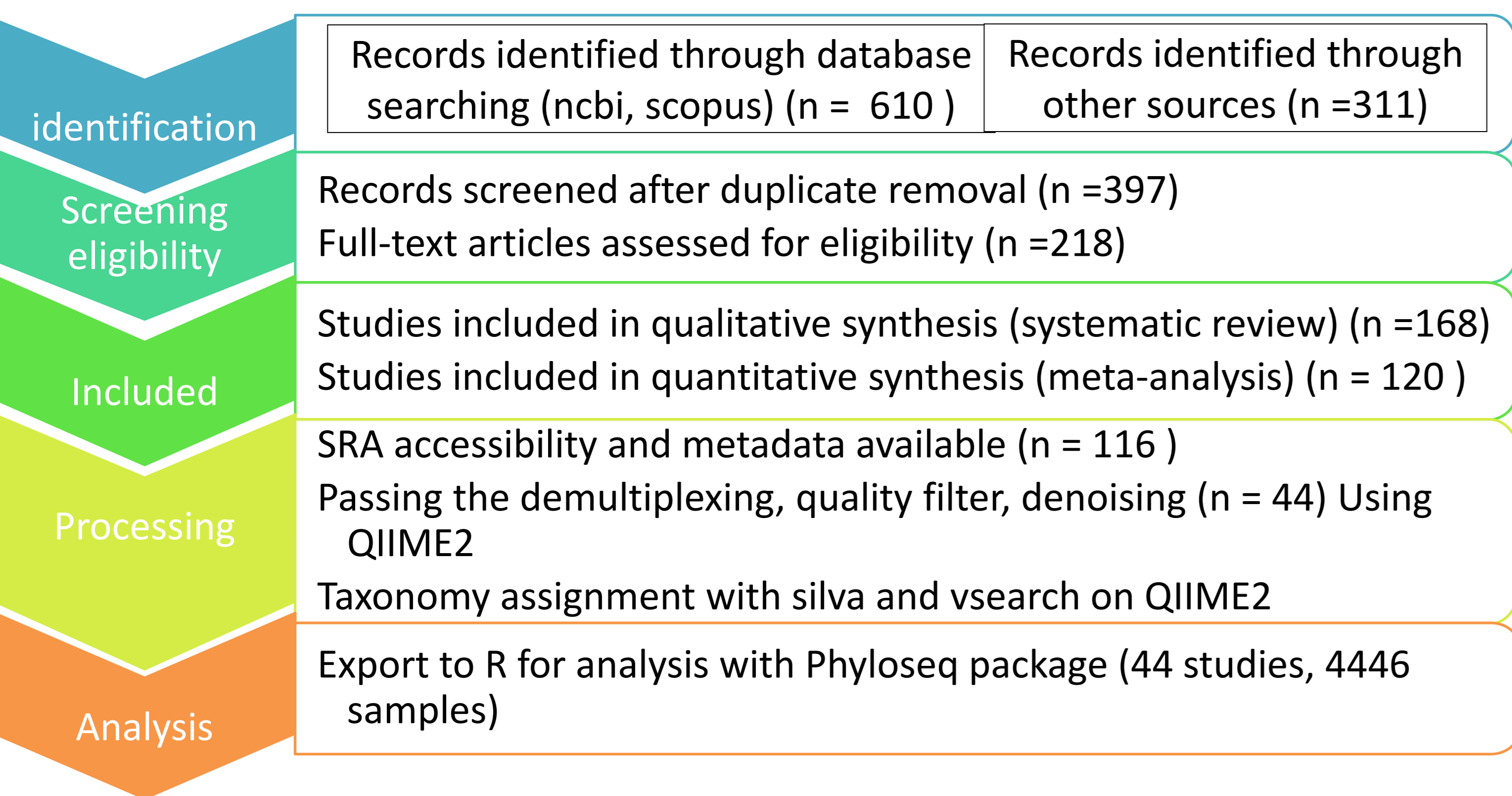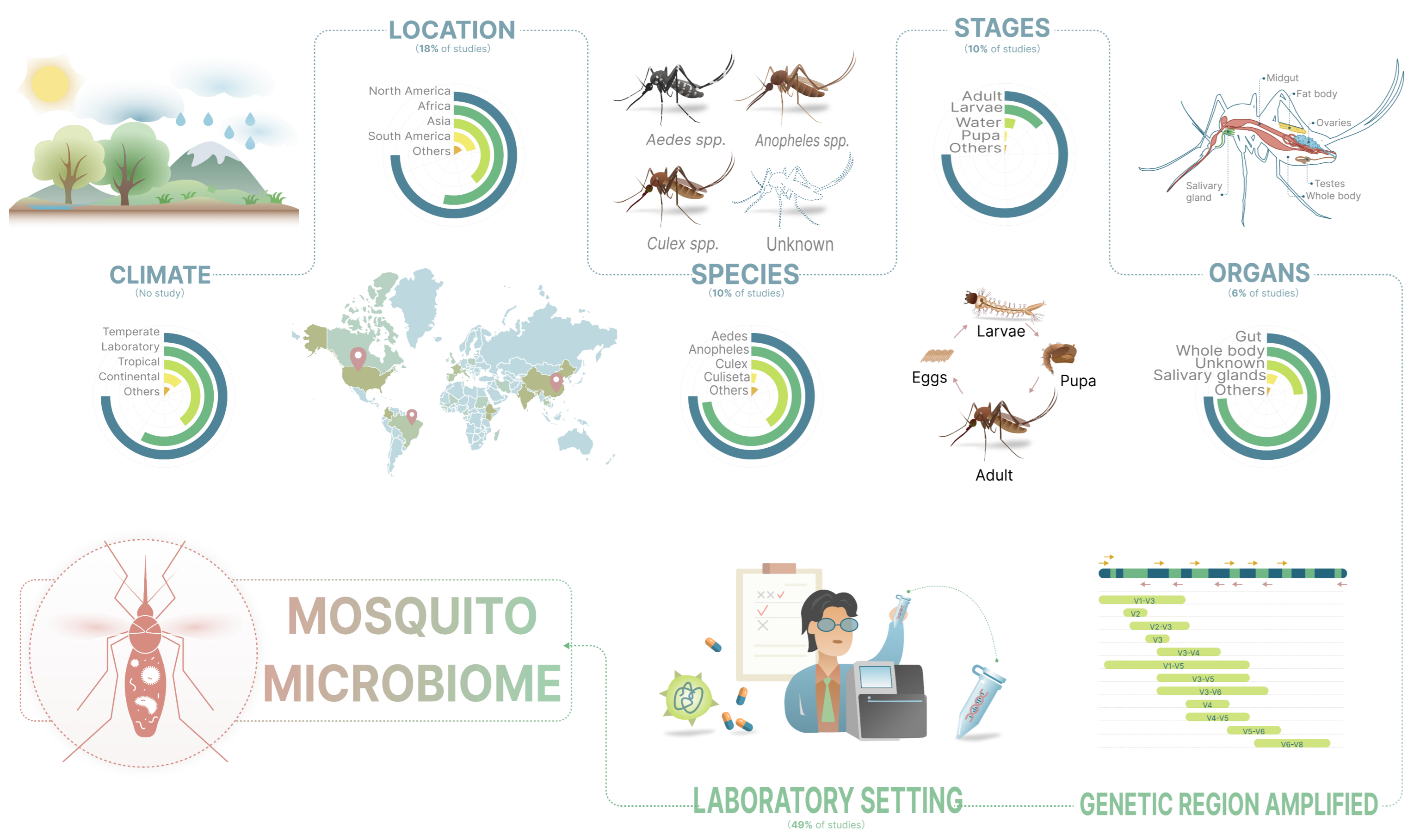
Context

Mosquito-Environment interactions include microbiota
Mosquito microbiome studies are usually highly focused
Disparities in sampling and analysis make comparing difficult
Finding targets for Bacteria Mediated Vector control is challenging
We are lacking :
➢ Oversight of global sampling trends
➢ Which environmental criteria matters the most
➢ Major components of microbiota
➢ How prevalent and abundant they are
➢ Easy access to global mosquito microbiome data

Methods

identification
Records identified through database searching (ncbi, scopus) (n = 610) | Records identified through other sources (n =311)

Screening eligibility
Records screened after duplicate removal (n =397)
Full-text articles assessed for eligibility (n =218)

Included
Studies included in qualitative synthesis (systematic review) (n =168)
Studies included in quantitative synthesis (meta-analysis) (n = 120)

Processing
SRA accessibility and metadata available (n = 116)
Passing the demultiplexing, quality filter, denoising (n = 44) Using QIIME2
Taxonomy assignment with silva and vsearch on QIIME2

Analysis
Export to R for analysis with Phyloseq package (44 studies, 4446 samples)

Results : Repartition of the studies and factors at play in shaping the microbiome

Knowing how people have designed their studies allows us to highlight both research gaps but also what researchers consider important factors to consider. For mosquito genera, focus has been made on genera that are most famous, highlighting the need to understand other, lesser-known bridge vectors.

Data availability

The data table of prevalence and abundance for each mosquito, as well as their presence in the groups described in the Venn diagram, is available and will help mosquito researchers find suitable targets for their studies.

References

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, K., Brejnrod, A., Brislawn, C. J., Brown, C. T., Callahan, B. J., Caraballo-Rodríguez, A. M., Chase, J., … Caporaso, J. G. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, 37(8), 852–857. https://doi.org/10.1038/s41587-019-0209-9

Bascuñán, P., Niño-Garcia, J. P., Galeano-Castañeda, Y., Serre, D., & Correa, M. M. (2018). Factors shaping the gut bacterial community assembly in two main Colombian malaria vectors. *Microbiome*, 6(1), 1–12. https://doi.org/10.1186/s40168-018-0528-y

Results : Venn diagram of the study

Figure 1 Venn diagram of the bacteria genera grouped by (a) continent (b) stage and (c) mosquito genus
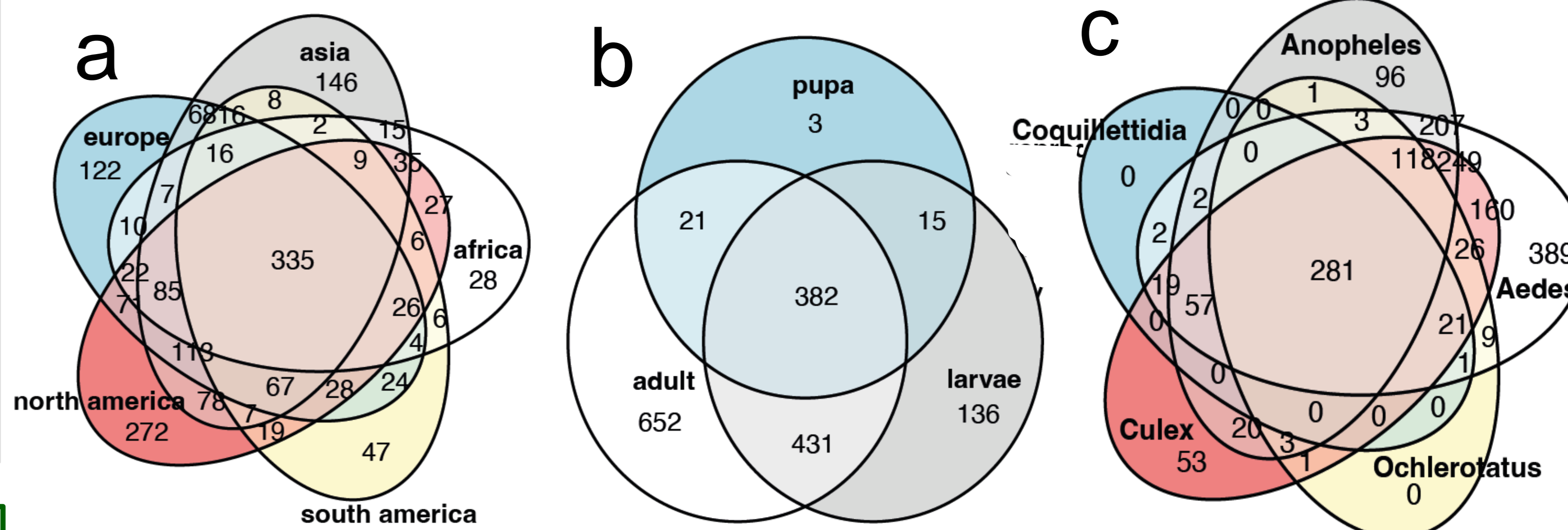
The Venn diagrams highlight a much smaller number of genera detected in the lab, highlighting the huge lack of diversity from lab samples as opposed to field ones.
It also allows to find a bacteria that could be present across all stages of a mosquito.

Results : Inventory bacteria found in the study

Table 1: General table of all bacteria present in our study (total length 1733)

Genus ID	abundance	prevalence
Wolbachia	20.10%	55.03%
Enterobacter	1.67%	53.98%
Coxiella	24.41%	53.76%
Herbaspirillum	1.36%	51.73%
Halomonas	13.11%	43.59%
Diaphorobacter	0.54%	34.69%
Neoasaia	7.52%	25.65%
Tepidicella	0.31%	24.39%
Succinivibrio[..]	20.84%	23.78%
Bacillus	0.37%	21.48%

Table 2 : Bacteria genera present across all categories studies (total length 86)

Genus ID	abundance	prevalence
Enterobacter	1.67%	53.98%
Bacillus	0.37%	21.48%
Delftia	2.22%	19.84%
Kocuria	8.44%	6.34%
Micrococcus	0.21%	3.49%
Corynebacterium	0.99%	1.74%
Tepidimonas	0.44%	1.72%
Roseomonas	0.48%	1.53%
Comamonas	22.81%	0.92%
Rhodococcus	8.47%	0.74%

Some bacteria are very prevalent but at low abundance so they could be hidden in smaller studies. Some bacteria are very present across groups but with both a low prevalence and a low abundance like Tepidimonas or Rhodococcus.

Herbaspirillum is very prevalent but not very abundant, maybe it is a good target that was unnoticed. Inventoring the bacteria found in each category helps us define targets that are widespread, or on the contrary if you are looking for a highly specific target.

Results : Differential abundance

Figure 5 ANCOM differential abundance plots between lab and field and between gut vs other organs combined
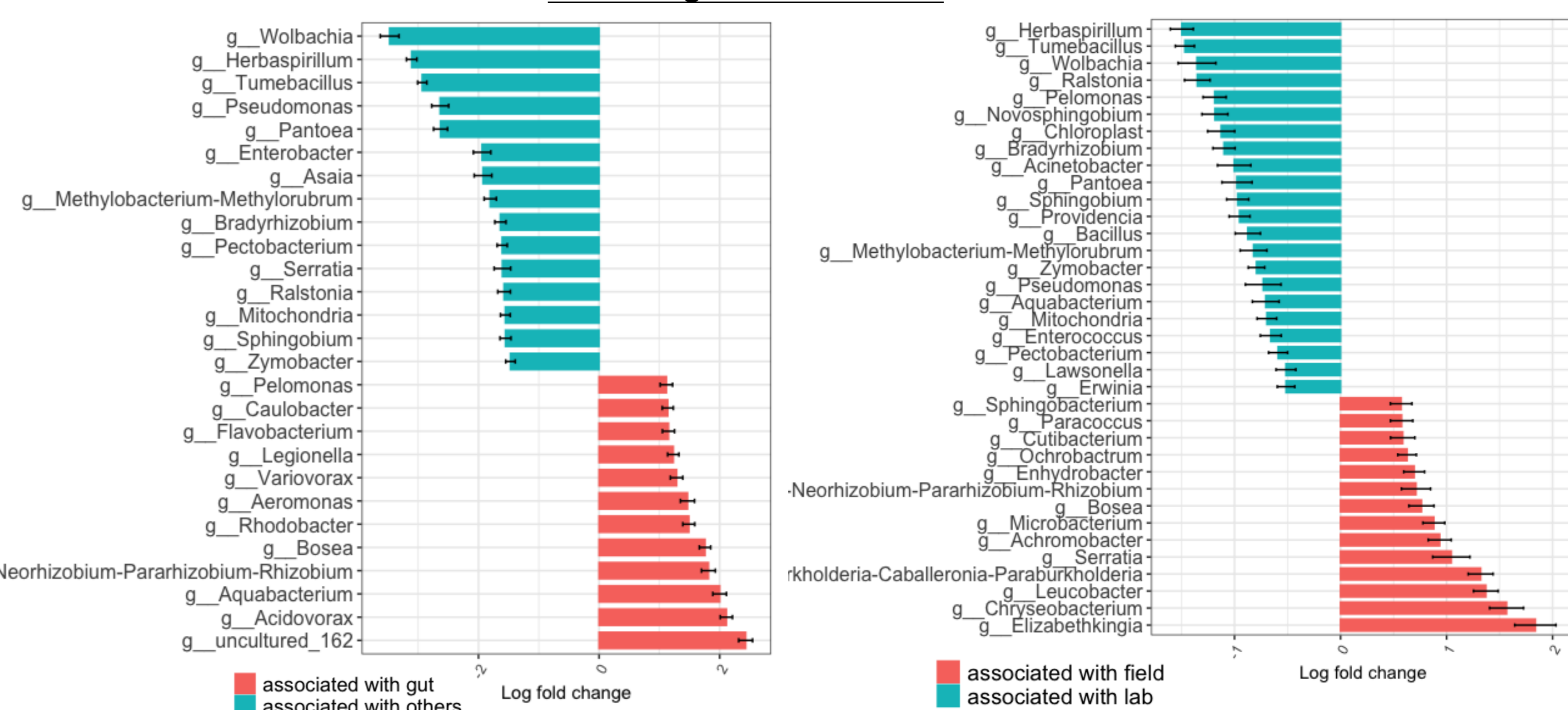
Bacteria previously overlooked like Tumebacillus and Herbaspirillum are positively associated with the gut, making them possible targets for control of the midgut.
Some bacteria highlighted by the study are "uncultured", highlighting the need for studies which culture bacteria from field collected mosquitoes.
Wolbachia is always highlighted as a very important bacteria

Conclusion

This study allows to identify high-prevalence and low abundance bacteria, helping to select targets for further investigation.
The actors at play in shaping the microbiome are complex and need further analysis to determine the leading factor.s.

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