

The 3rd International Electronic **Conference on Diversity**

15-17 October 2024 | Online

Exploring the interplay of the seminovaginal microbiome

Lucía Blanco-Rodríguez¹, Nerea M. Molina^{1,2}, Signe Altmäe^{1,2,3,4}

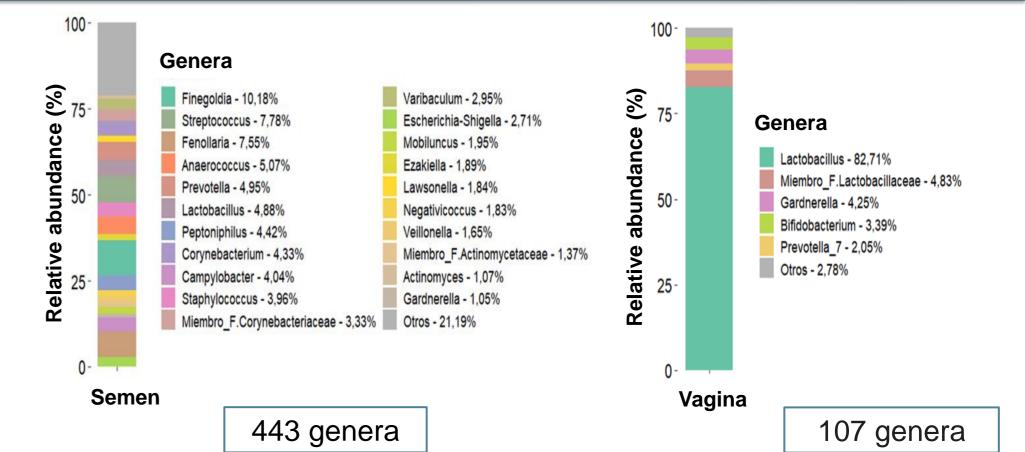
¹Department of Biochemistry and Molecular Biology, Faculty of Sciences, University of Granada, Granada, Spain. ²Instituto de Investigación Biosanitaria ibs.GRANADA, Granada, Spain. ³Division of Obstetrics and Gynecology, Department of Clinical Science, Intervention and Technology, Karolinska Institutet, Huddinge, Stockholm, Sweden. ⁴Department of Gynaecology and Reproductive Medicine, Karolinska University Hospital, Huddinge, Stockholm, Sweden.

Contact information: luciablancordr@correo.ugr.es

INTRODUCTION & AIM

The microbial communities inhabiting the reproductive tract play an important role in reproductive health. During unprotected sexual intercourse, the microorganisms present in the semen and vagina of heterosexual couples interact closely with each other. The concept of "seminovaginal microbiome" has recently emerged to refer to all microorganisms present in both environments. Each partner influences the microbial composition of the other, even sharing several bacterial taxa.

Therefore, to improve the understanding of this interaction, we aimed to analyse the microbial composition of semen and vagina samples from heterosexual couples and to assess their similarity in terms of composition and diversity.



RESULTS & DISCUSSION

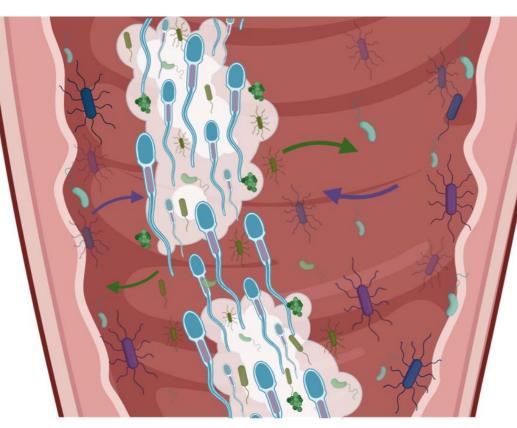


Figure 1. Interaction of the seminal and vaginal microbiome.

METHOD

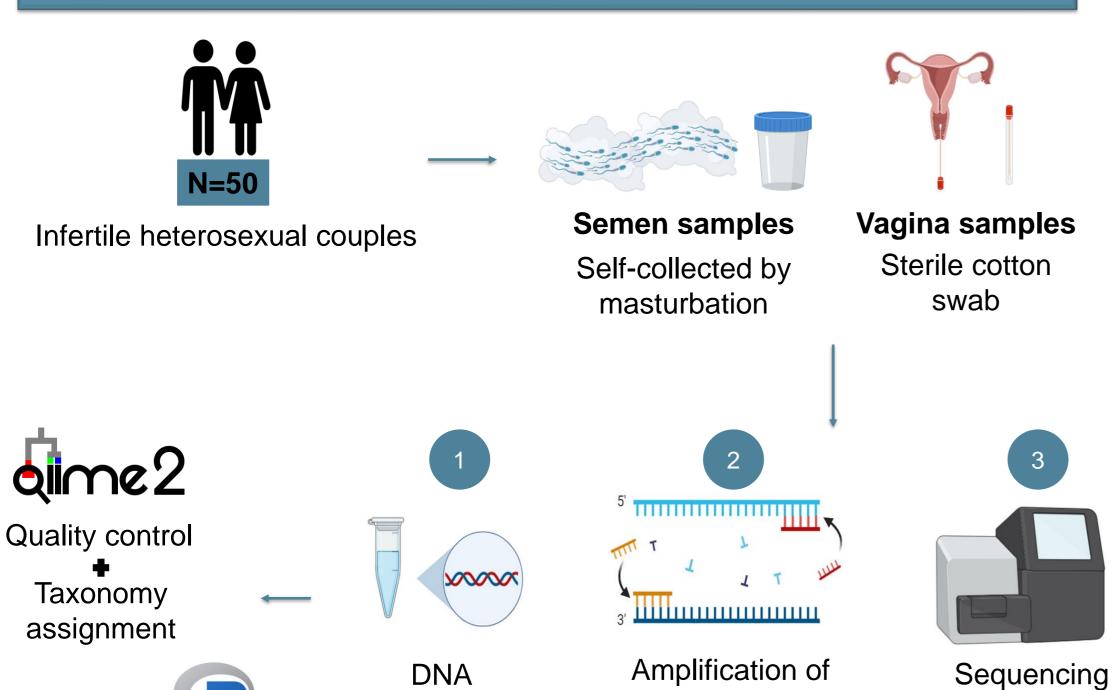


Figure 2. Graphic representation of the bacterial genera with the highest mean relative abundance in the semen and vagina samples.

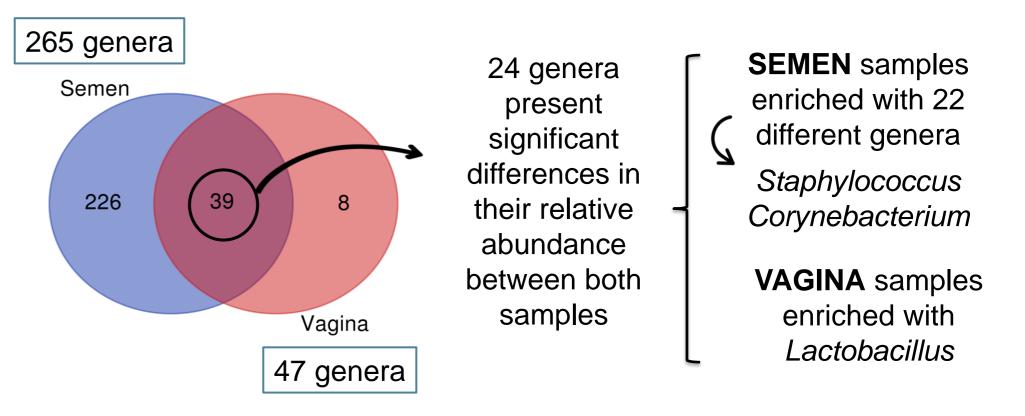


Figure 3. Venn diagram illustrating the number of genera specific to each sample type as well as those shared, after applying the 0.01% relative abundance filter.

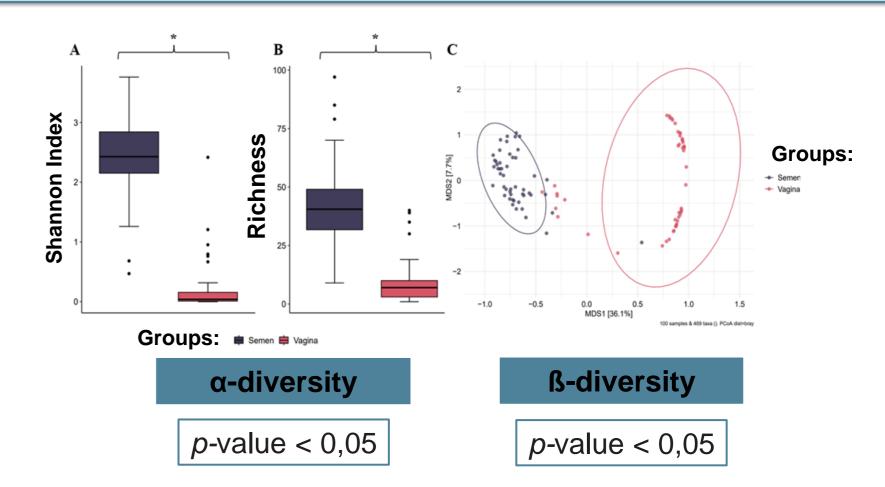


Figure 4. Comparative graphs of α -diversity and ß-diversity of the semen and vagina samples of the couples. A: Shannon-Weaver index. B: Richness. C: PCoA. "*" indicates that p-value<0.05.

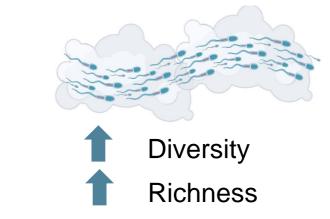


DNA extraction

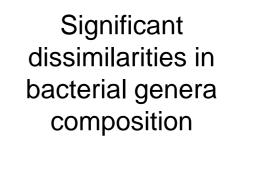
ibs.GRANADA

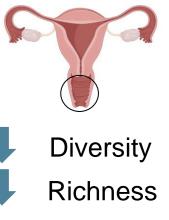
Statistical analysis

the V4 hypervariable region of the 16S rRNA gene



Junta de Andalucía



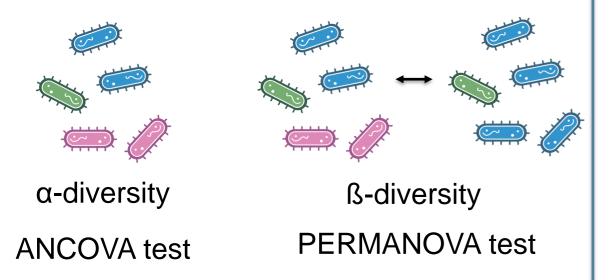


CONCLUSION

Microbial diversity analysis

UNIVERSIDAD

DE GRANADA



Differential abundance analysis

Illumina

MiSeq

0.01% relative abundance filter

Identifying those bacterial general significantly different between common genera to semen and vaginal samples

UNIÓN EUROPEA

There are significant differences in terms of diversity, richness and similarity of bacterial genera between semen and vaginal samples from couples who have unprotected sex.

There are different bacterial genera shared between both microbiomes.

□ Studying the couple's microbiome together provides a deeper understanding of their interaction.

FUTURE WORK / REFERENCES

Mändar, R., Punab, M., Borovkova, N., Lapp, E., Kiiker, R., Korrovits, P., Metspalu, A., Krjutškov, K., Nlvak, H., Preem, J. K., Oopkaup, K., Salumets, A., & Truu, J. (2015). Complementary seminovaginal microbiome in couples. Research in Microbiology, 166(5), 440-447. https://doi.org/10.1016/j.resmic.2015.03.009



IECD2024.sciforum.net