Integrated multi-omics analysis reveals Lactobacillus anti-inflammatory process in vaginal tissue

A demonstration of Rmarkdown using Herman Bumpus' data

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December 17, 2020

$_{\scriptscriptstyle{5}}$ 1 Abstract

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2 Introduction

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- Introduction (2,3).
- Problem / question to answer

3 Results

35 Joint analysis of vaginal microbiome reveals distinct patient subgroups

- To understand the longitudinal and tissue-specific microbiome profile in vaginal samples, 113 adult female sex
- workers were enrolled in [...]. Among those, 14 were previously tested positive for HIV during the cohort's
- sampling procedure. [Describe here what was done and when, which samples, which tissues].
- 39 To be able to better undertand the differences in microbiome profile across all datasets collected, we performed
- 40 a joint graph-based clustering analysis in order to identify co-regulated bacterial communities (see "Methods"
- section for details). A total of 11 bacterial communities were identified.
- ⁴² Noticebly, bacterial community 11 consisted only of Lactobacillus species (Anaerococcus hydrogenalis,
- 43 Atopobium deltae, Bifidobacterium adolescentis, Bifidobacterium bifidum, Bifidobacterium longum/breve,
- 44 Brevibacterium paucivorans, Brevibacterium ravenspurgense, Campylobacter hominis, Chlamydia trachomatis,
- 45 Corynebacterium aurimucosum. Corynebacterium genitalium. Corynebacterium imitans. Corynebacterium
- 46 jeikeium, Corynebacterium pseudogenitalium, Corynebacterium simulans/striatum, Corynebacterium
- 47 sp/amycolatum, Corynebacterium spheniscorum, Corynebacterium sundsvallense/thomssenii, Dermabacter ho-
- 48 minis, Dorea formicigenerans, Enterococcus villorum/hirae/faecium/faecalis/canintestini/canis/dispar/durans,
- 49 Gemmiger formicilis, Lactobacillus coleohominis, Lactobacillus crispatus, Lactobacillus crispatus/acidophilus,
- 50 Lactobacillus gasseri/johnsonii/taiwanensis, Lactobacillus iners, Lactobacillus jensenii, Lactobacil-
- 51 lus mucosae, Lactobacillus reuteri, Lactobacillus reuteri/oris/frumenti/antri, Lactobacillus salivarius,
- 52 Megasphaera elsdenii, other Bacilli, other Bifidobacteriaceae, other Clostridia, other Corynebacterium,
- 53 other Ezakiella, other Gemella, other Gordonia, other Lactobacillales, other Lactobacillus, other
- 54 Listeria, other Mobiluncus, other Mogibacterium, other Murdochiella, other Nesterenkonia, other
- 55 Paraeggerthella, other Rhizobium, Peptoniphilus asaccharolyticus, Prevotella denticola, Staphylococcus
- 56 saccharolyticus/capitis/hominis/caprae/lugdunensis/epidermidis/simiae, Streptococcus dysgalactiae, Strep-
- 57 tococcus lutetiensis/equinus, Ureaplasma parvum, Brevundimonas mediterranea/intermedia/poindexterae,
- 58 Corynebacterium appendicis/imitans, Corynebacterium freneyi/sp/amycolatum, Enterococcus villo-
- 59 rum/hirae/faecium/faecalis/canintestini/canis/saccharolyticus/ratti/dispar/gallinarum/durans, other
- 60 Bacteroides, other Gammaproteobacteria).
- Patients were thus subdivided into 6 groups,
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44 Indentification of bacterial communities metabolic processes linked to Lactobacilli

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Indentification of bacterial communities metabolic processes linked to Lactobacilli

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146 4 Discussion

I have analysed data collected by Herman Bumpus³ on the relationship between sparrow (Passer domesticus) total length and surival following an unusually severe storm. I found that sparrows that died in the storm 148 were longer than sparrows that survived, which suggests that higher sparrow body length decreased survival. 149 Of course, it is not possible to definitively conclude a causal relationship between any aspect of body size and 150 sparrow survival, and even the available data collected by Bumpus would permit a more thoughtful analysis 151 than that conducted in this study (see Appendix Table 1). Overall, this document demonstrates how high quality, professional looking documents can be written using Rmarkdown. The underlying code for this manuscript is publicly available, along with accompanying notes 154 to understand how it was written. By using Rmarkdown to write manuscripts, authors can more easily use 155 version control (e.g., git) throughout the writing process. The ability to easily integrate citations though 156 BibTeX, LaTeX tools, and dynamic R code can also make writing much more efficient and more enjoyable. 157 Further, obtaining the benefits of using Rmarkdown does not need to come with the cost of isolating colleagues who prefer to work with Word or LaTeX because Rmarkdown can easily be converted to these formats (in 159 the case of Word, with the push of a button). By learning all of the tools used in this manuscript, readers 160 should have all of the necessary knowledge to get started writing and collaborating in Rmarkdown. 161

5 Methods

6 References

- 164 1. Johnston, R. F., Niles, D. M. & Rohwer, S. A. Hermon bumpus and natural selection in the house sparrow
- 165 Passer domesticus. Evolution 26, 20–31 (1972).
- 2. Darwin, C. The origin of species. 495 (Penguin, 1859).
- 3. Bumpus, H. C. Eleventh lecture. The elimination of the unfit as illustrated by the introduced sparrow,
- Passer domesticus. (A fourth contribution to the study of variation.). Biological Lectures: Woods Hole
- 169 Marine Biological Laboratory 209–225 (1898).

7 Appendix Table 1

An example table is shown below, which includes all of the variables collected by 3 for the first 10 measured sparrows. The full data set can be found online in GitHub.

¹⁷³ 8 FIGURES (MAIN)

8.1 Figure 1

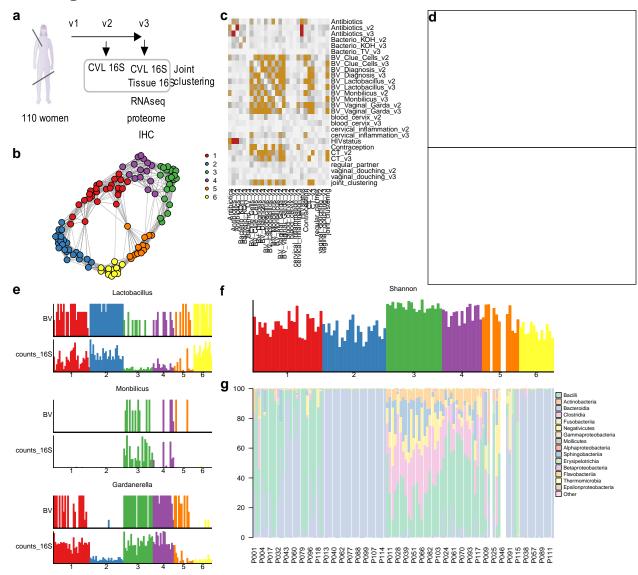


Figure 1. Identification of patient groups. (a) Schematic representation of #######. (b)

 $_{177}$ Schematic representation of ######### . (c) Schematic representation of ######### . (d)

Schematic representation of ##########.

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¹⁷⁹ 8.2 Figure 2

Figure 2. Identification and characterization of vaginal bacterial communities. (a) Schematic

representation of ########. (b) Schematic representation of ########. (c) Schematic

representation of ########. (d) Schematic representation of ########.

¹⁸³ 8.3 Figure 3

- Figure 1. Identification of patient groups. (a) Schematic representation of ######### . (b)
- Schematic representation of ########. (c) Schematic representation of ########. (d)
- Schematic representation of ##########.

9 FIGURES (SUPPL)

- 9.1 Figure S1
- 9.2 Figure S2
- 9.3 Figure S3
- 9.4 Figure S4
- 192 10 TABLES (MAIN)
- 193 **10.1** Table 1
- 194 10.2 Table 2
- 195 **10.3** Table 3
- 196 11 TABLES (SUPPL)
- 197 **11.1** Table S1
- 198 11.2 Table S2
- 199 11.3 Table S3