Characterizing Post-Coital Vaginal and Penile Microbial Transfer and Persistence

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INTRODUCTION

Conventional forensic DNA screening in sexual assault cases relies on the detection of spermatozoa to identify male contributors. However, this approach is ineffective when spermatozoa are absent. With the growing accessibility of next-generation sequencing, analyzing genital microbiota presents a promising alternative[1]. Microbial DNA offers potential advantages such as persistence and resistance to degradation[2].

This study examines the transfer and persistence of penile and vaginal microbiota. Pre- and post-coital swabs were collected from four couples to assess microbial transfer, with persistence evaluated through comparison of post-coital swabs collected before and after showering. Bacterial libraries targeting the V3–V4 regions of the 16S rRNA gene were sequenced to characterize inter-individual differences and identify the presence of shared or persistent bacterial genera.

MATERIALS & METHODS

Pre-Coital Swab → Coitus → Post-Coital Swab

Pre-Coital Swab → Coitus → **Post-Coital Shower** → Post-Coital Swab

Sampling

(n = 4 couples, 6 coital events per couple)
Minimum 72 hours abstinence prior

Microbiome Extraction

PureLink™ Microbiome DNA Purification Kit

Illumina 16S Metagenomic Library Prep & Sequencing

Illumina MiSeqFGx™

Bioinformatic Processing

DADA2 (SILVA v132 and NCBI BLAST)

Statistical Analysis

R (4.1.1) and RStudio (v1.4)

RESULTS & DISCUSSION

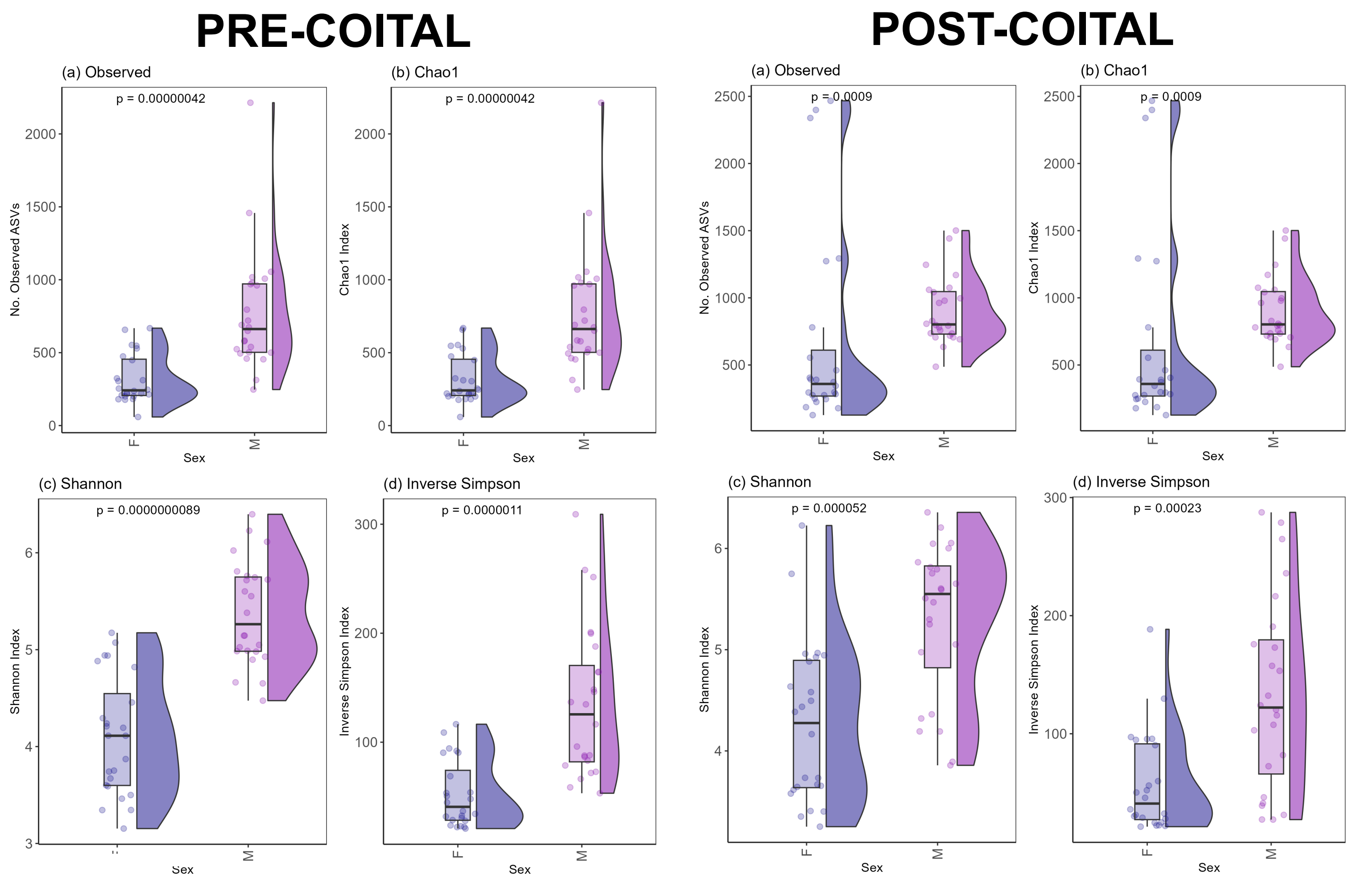

Figure 1. Differences in alpha diversity observed between vaginal and penile microbiomes.
Pre-coital penile microbiomes are more diverse than vaginal microbiomes in (a) observed, (b) Chao1, (c) Shannon, and (d) Inverse Simpson diversity measures. However, vaginal microbiomes are more diverse in post-coital samples.

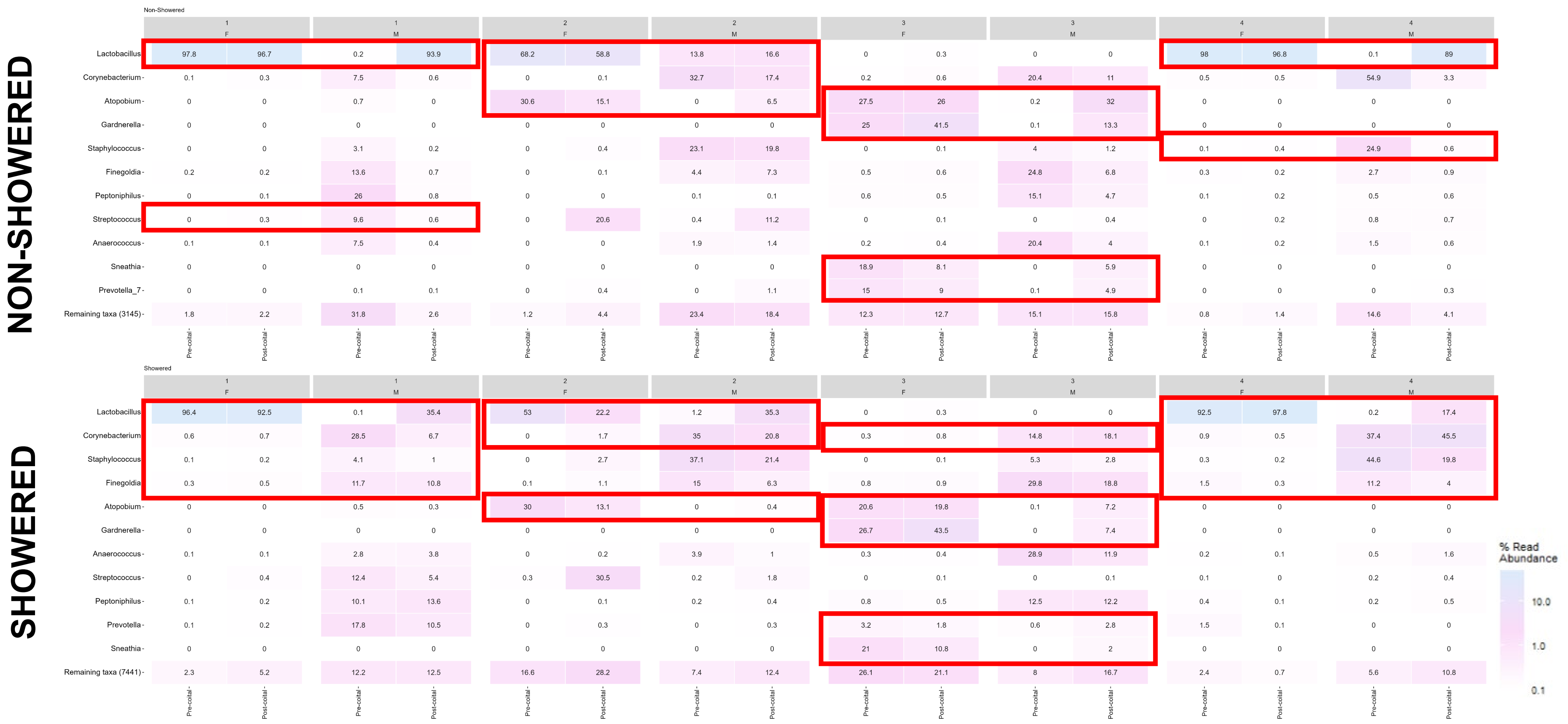

Figure 2. Taxonomic heat map of relative differences between showered and non-showered coital events in vaginal and penile microbiomes.
Different transfer events were observed in the changes of taxonomic distribution in both pre- and post-coital microbiomes across all four couples. Instances of taxonomic changes due to transfer or persistence through showering are noted in red.

- Pre-coital penile microbial diversity was significantly greater than vaginal microbiomes. Following intercourse, vaginal microbial diversity increased while penile microbial diversity decreased.
- In couples 1 and 4, transfer of *Lactobacillus*-dominant vaginal microbiomes to penile microbiomes persisted through showering.
- The female participant of couple 2 had a *Lactobacillus* and *Atopobium*-dominant vaginal microbiome. Transfer of both genera to the penile microbiome persisted through showering.
- In couple 3, the transfer of the four dominant genera (*Atopobium*, *Gardnerella*, *Sneathia*, and *Prevotella*) from the vaginal microbiome to the penile microbiome also persisted through showering.
- While transfer of penile microbial genera to vaginal microbiomes represented a smaller portion of the taxonomic changes, these transfers also persisted through showering.

CONCLUSIONS

- Post-coital increase in vaginal microbial diversity and loss of penile diversity observed across all couples (**Figure 1**).
- Transfer was observed in post-coital vaginal and penile microbial genera (**Figure 2**).
- Variable levels of post-showering persistence observed across donor couples.

ACKNOWLEDGEMENTS

Samples were collected from living donors using Sam Houston State University Institutional Review Board approved protocol 2020-166. This research was supported by the Forensic Sciences Foundation Douglas M. Lucas Grant.

REFERENCES

[1] R. Dixon, S. Egan, S. Hughes, B. Chapman, The Sexome - A proof of concept study into microbial transfer between heterosexual couples after sexual intercourse, Forensic Science International 348 (2023) 111711. https://doi.org/10.1016/j.forsciint.2023.111711.

[2] T. Nguyen-Hieu, G. Aboudharam, M. Drancourt, Heat degradation of eukaryotic and bacterial DNA: an experimental model for paleomicrobiology, BMC Research Notes 5 (2012) 528. https://doi.org/10.1186/1756-0500-5-528.

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