

Exercise-induced modulation of gut microbiota in rats with metabolic syndromes

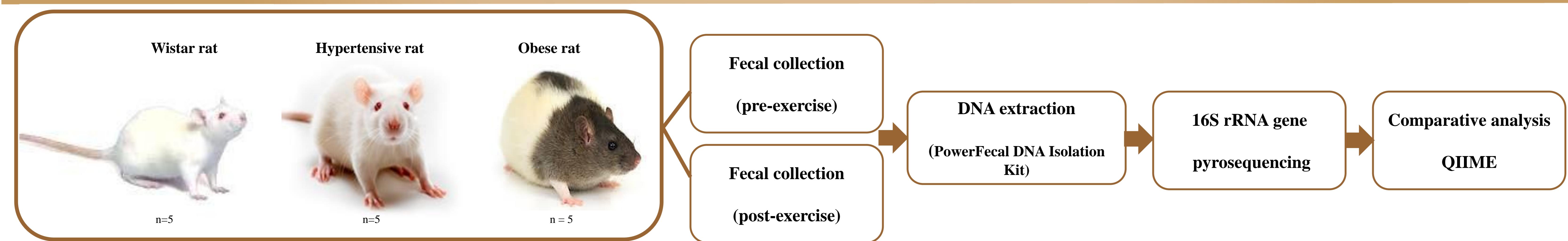
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Introduction

Obesity and diabetes mellitus are multifactor diseases associated to cardiovascular disorders that affect huge proportion of our society. Growing evidence suggests that gut microbes contribute to several pathological conditions as well as the exercise is a well-known agent used for numerous pathologies treatments, such as obesity and hypertension. As only a small fraction of the bacterial communities present in the gut can be in vitro cultured, barcode 16S rRNA gene pyrosequencing from fecal samples collected before and after exercise training was used for to access the relationship between controlled exercise training and gut microbiota composition in the obese (OB), non-obese rats (WISTAR) and spontaneously hypertensive rats (SHR). The central hypothesis of this study was that controlled exercise would lead to significant changes in the composition of gut microbial communities.

Materials and Methods



Results

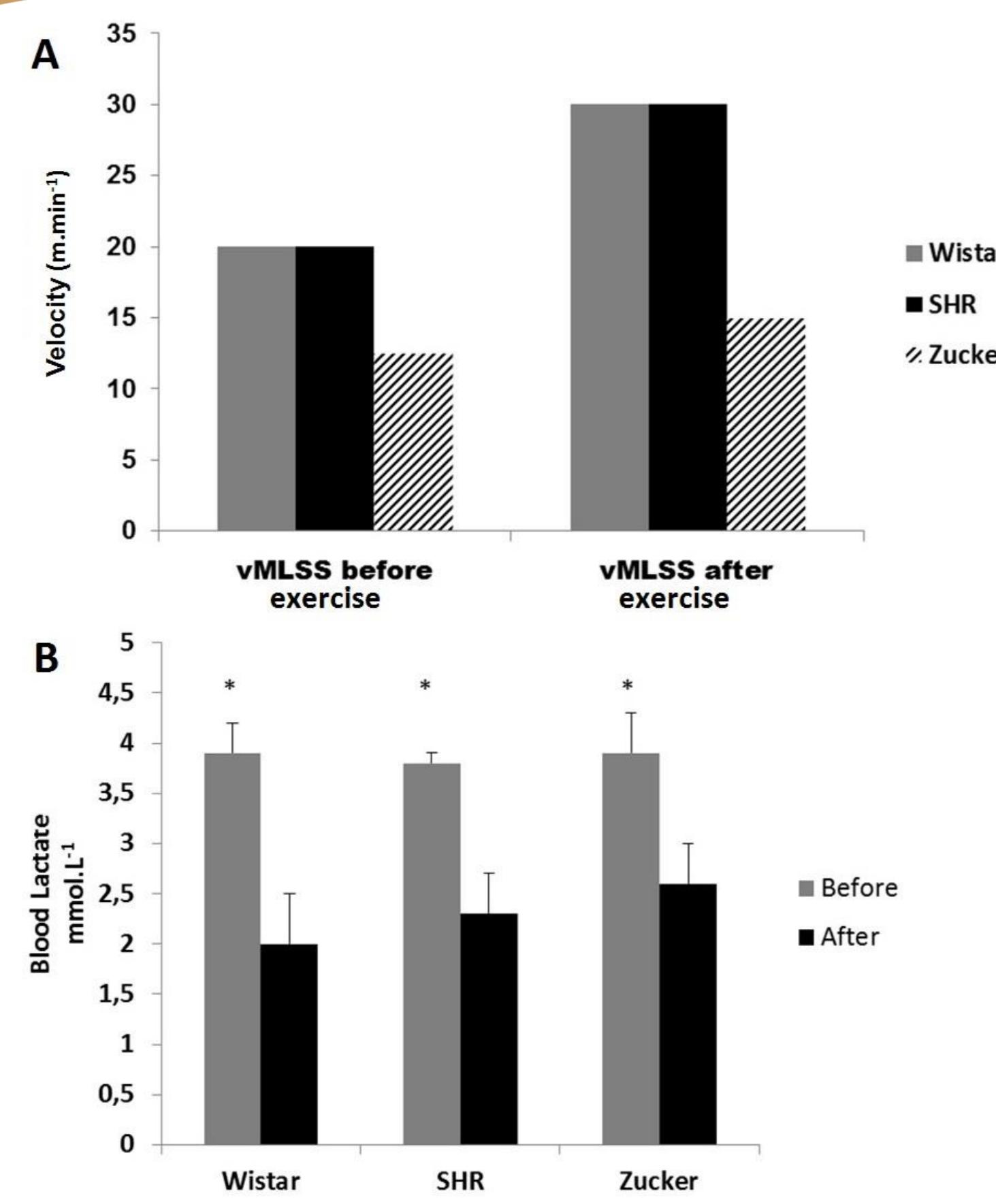


Figure 1 Training parameters. (A): Comparison between exercise training velocity from MLSS. (B): When the initial and final velocity of exercise training was compared, a significant reduction was evidenced in BLC.

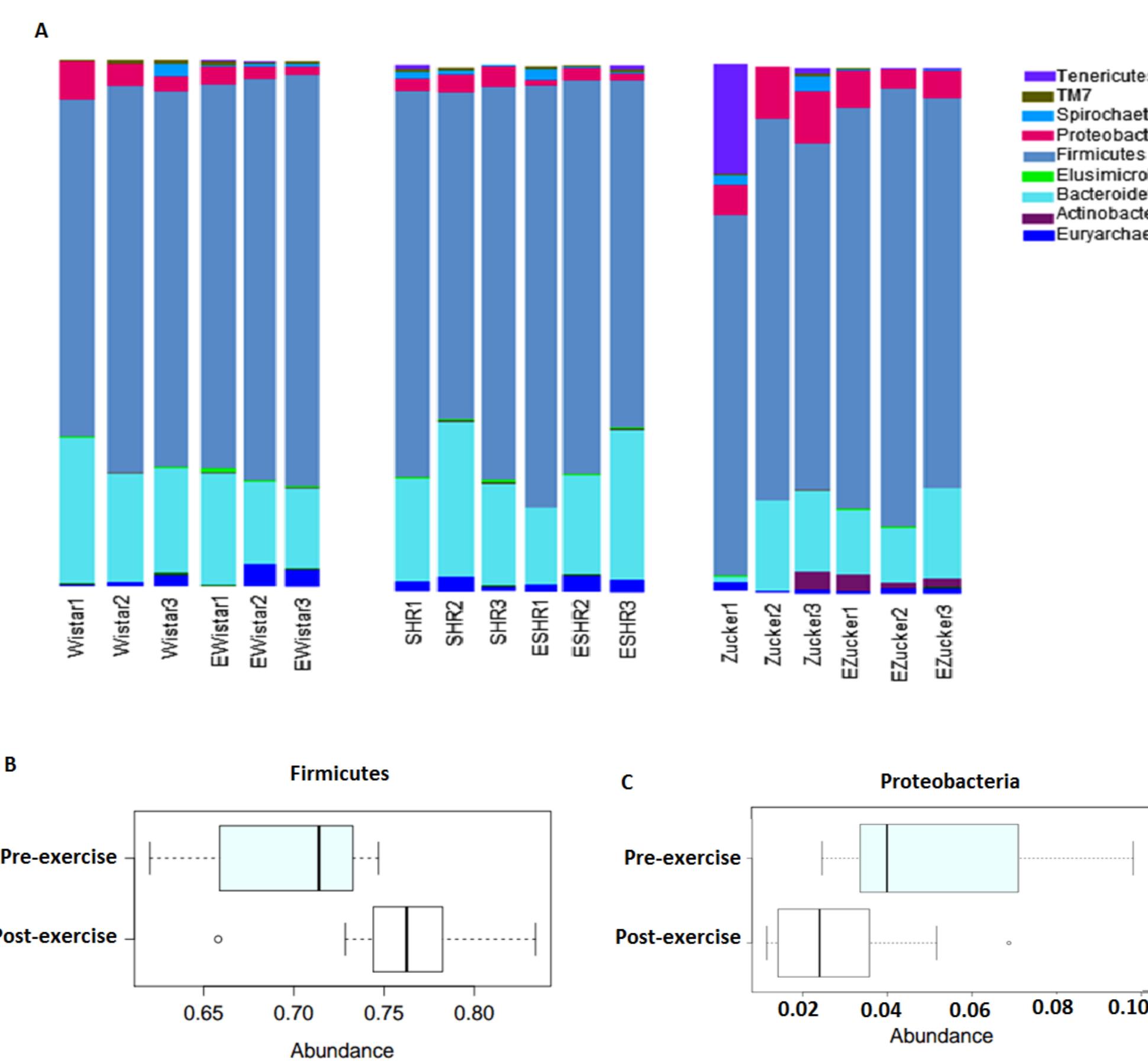


Figure 2: Bacterial distribution. Evaluated at the main phylum taxonomical level in fecal samples from Wistar, SHR and Zucker collected from triplicate rats before and after four weeks training.

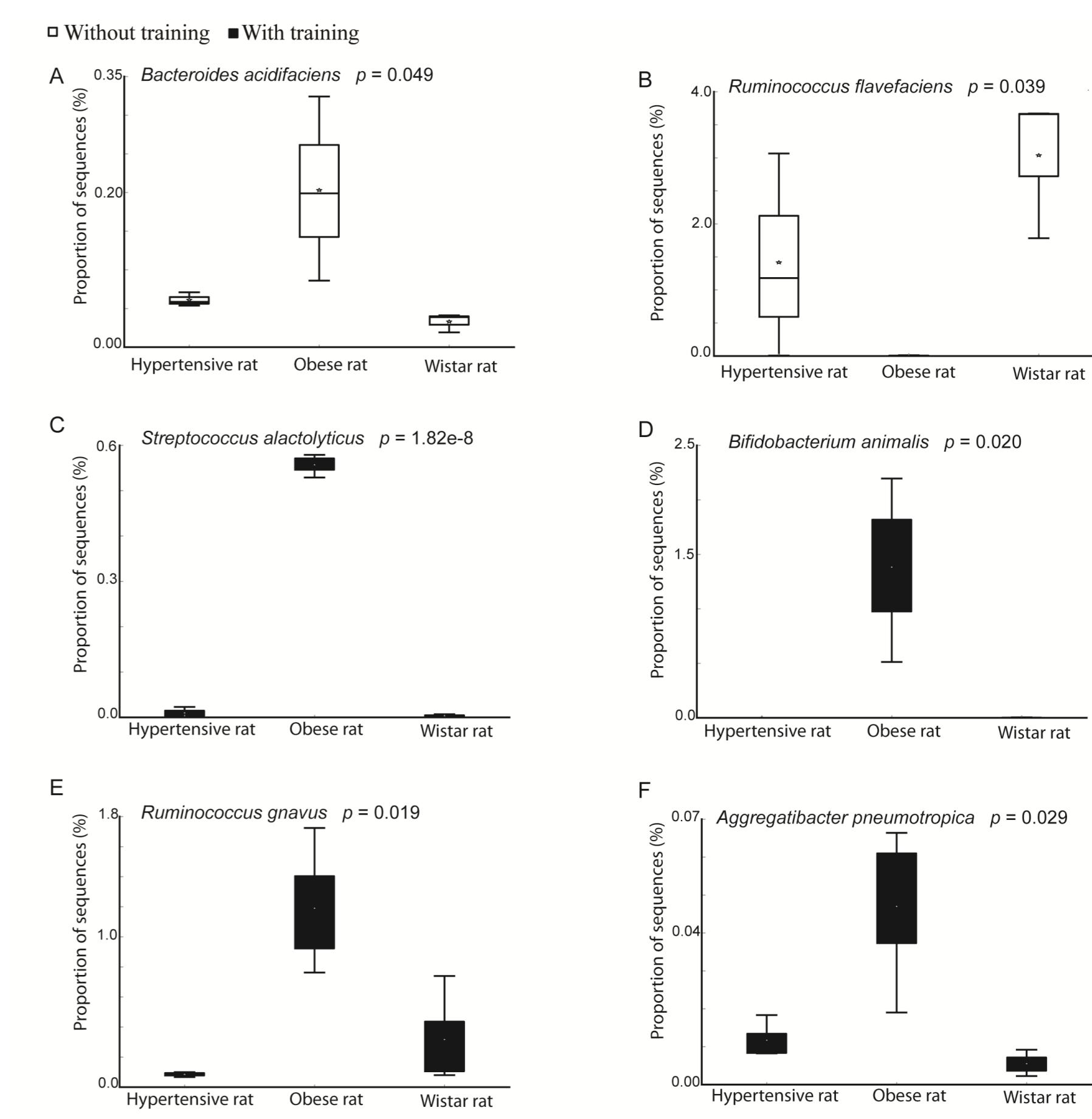


Figure 3: Species abundance profile of fecal sample before and after exercise training. Box plot showing the distribution in the proportion of sequences (%) of main species of each rat lineage.

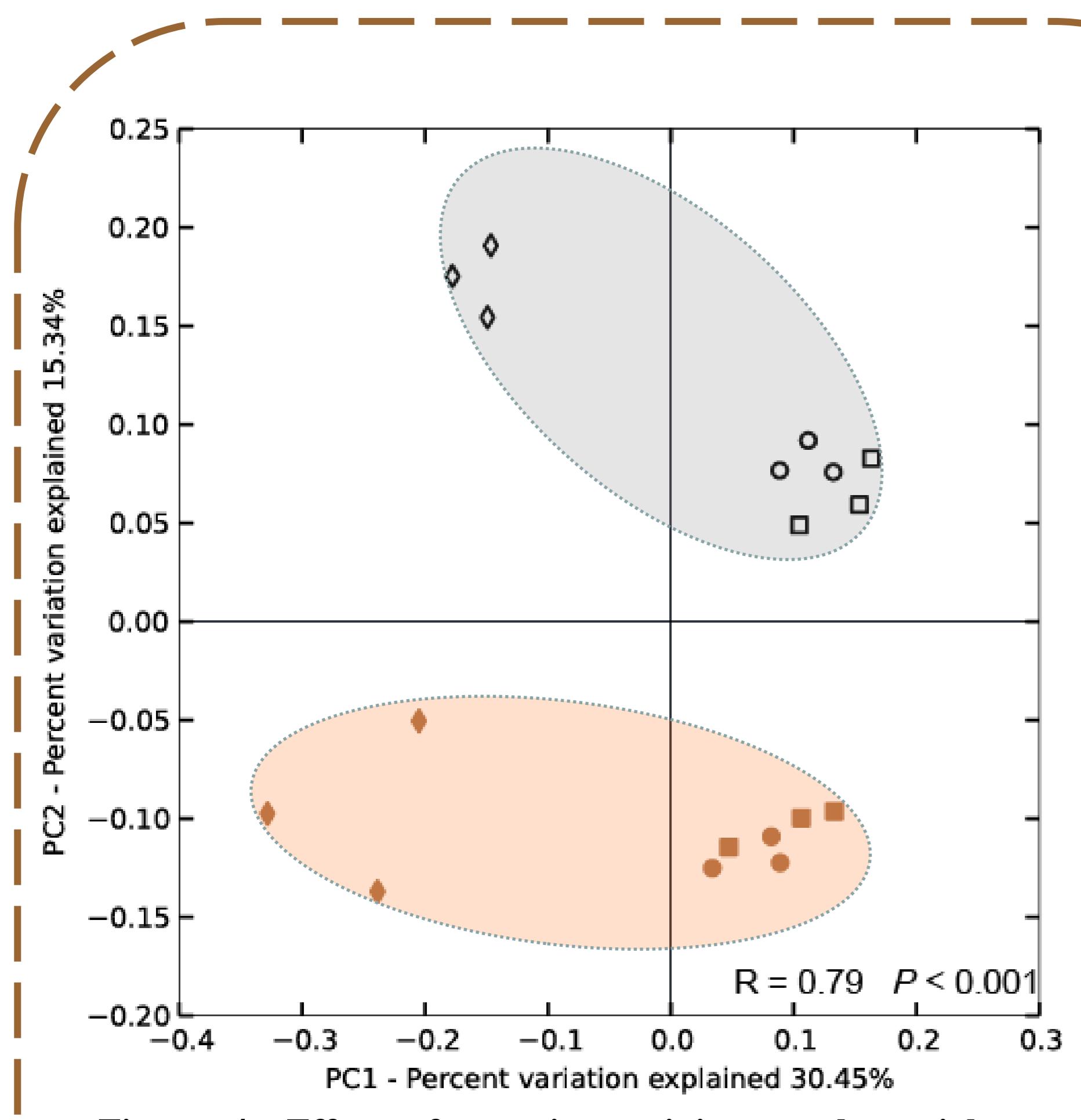


Figure 4: Effect of exercise training on bacterial community. Principal coordinates analysis (PCoA) of unweighted UniFrac distances generated from fecal samples collected from triplicate rats without exercise training (brown symbols) and with exercise training (white symbols). The result of the ANOSIM similarity analyses confirmed that samples harbor a distinct bacterial community.

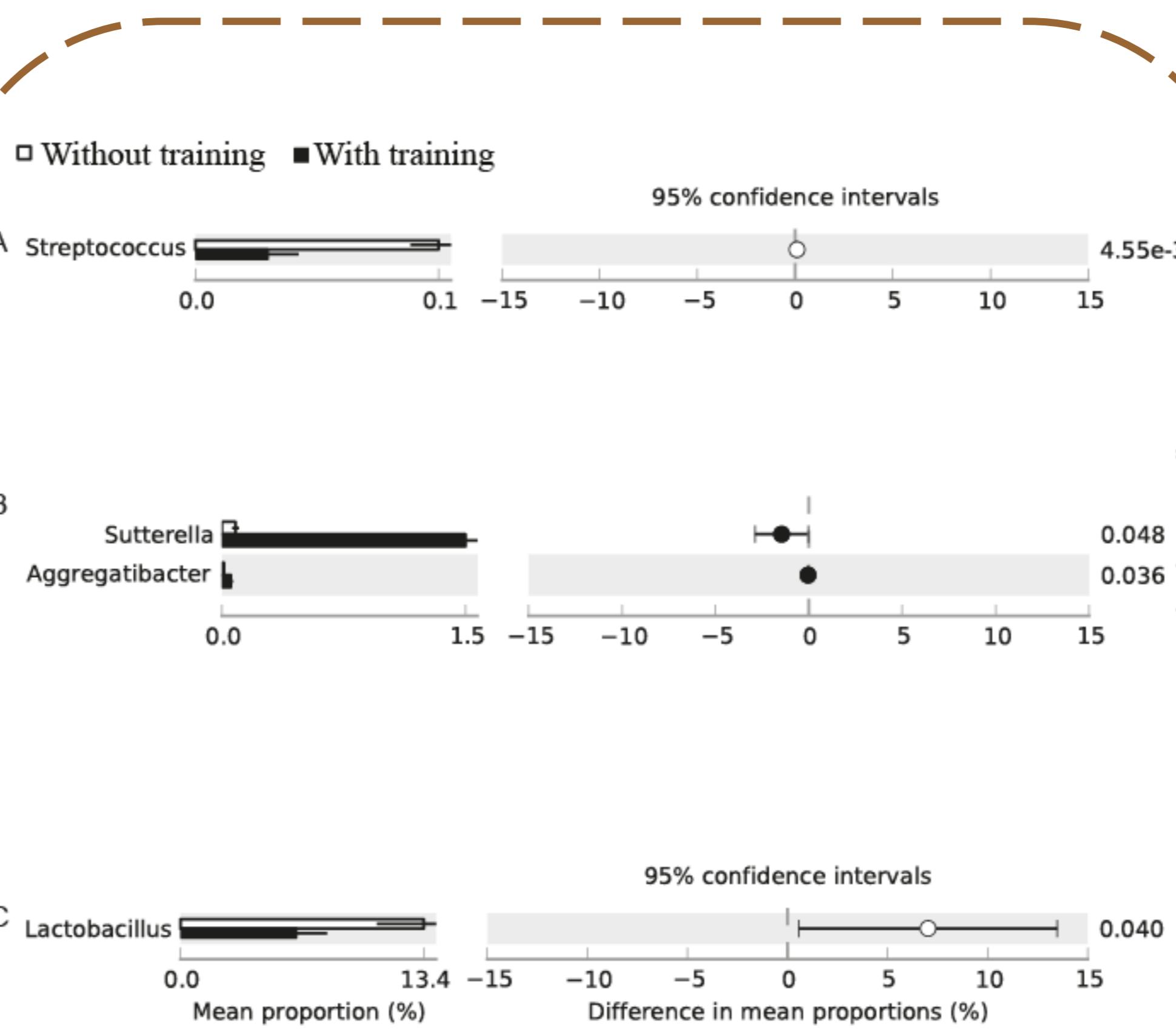


Figure 5: Effect of exercise on Genus relative abundance. Proportion of relative abundance for the statistical analyses of Genus level profiles distributed in Wistar rats (A), Hypertensive rats (B) and Obese rats (C). Features with a α -value of $p < 0.05$ were considered significant.

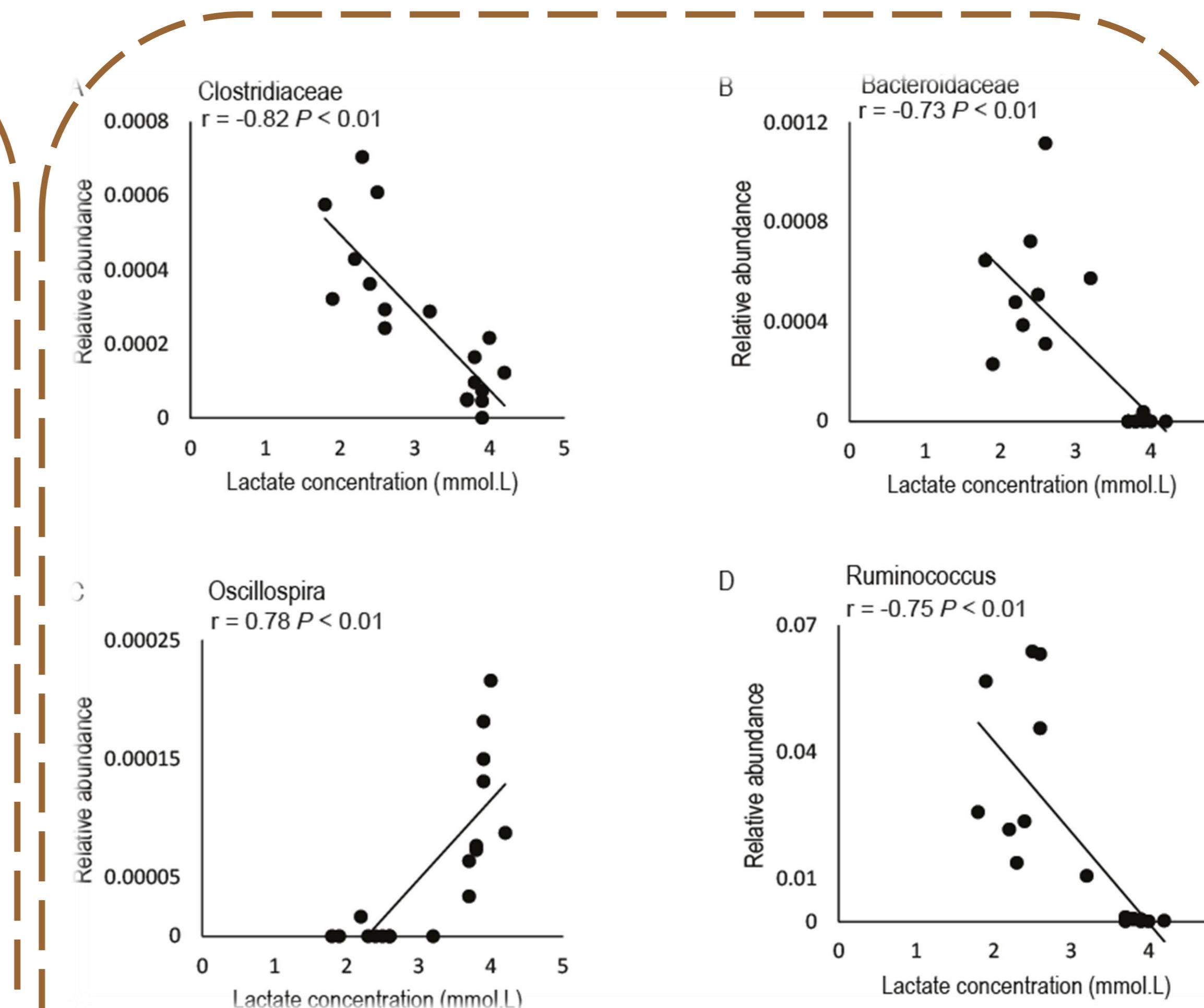


Figure 6: Microbial abundance and blood lactate concentration correlation. Correlations between the relative abundances of the bacterial communities (OTUs) and blood lactate concentration ($\text{mmol} \cdot \text{L}^{-1}$). Pearson correlation coefficients (r) are shown for each taxon, with the associated FDR-corrected P values.