Check for updates

OPEN

Author Correction: Parkinson's disease and bacteriophages as its overlooked contributors

George Tetz , Stuart M. Brown , Yuhan Hao & Victor Tetz

Published online: 16 July 2020

This Article contains errors in Figures 3 and 5. Figure 3C incorrectly included a duplicate of Figure 3B. In Figure 5, the bacteriophage Streptococcus 7201, was omitted from the graph.

The correct Figures 3 and 5 appear below as Figures 1 and 2.

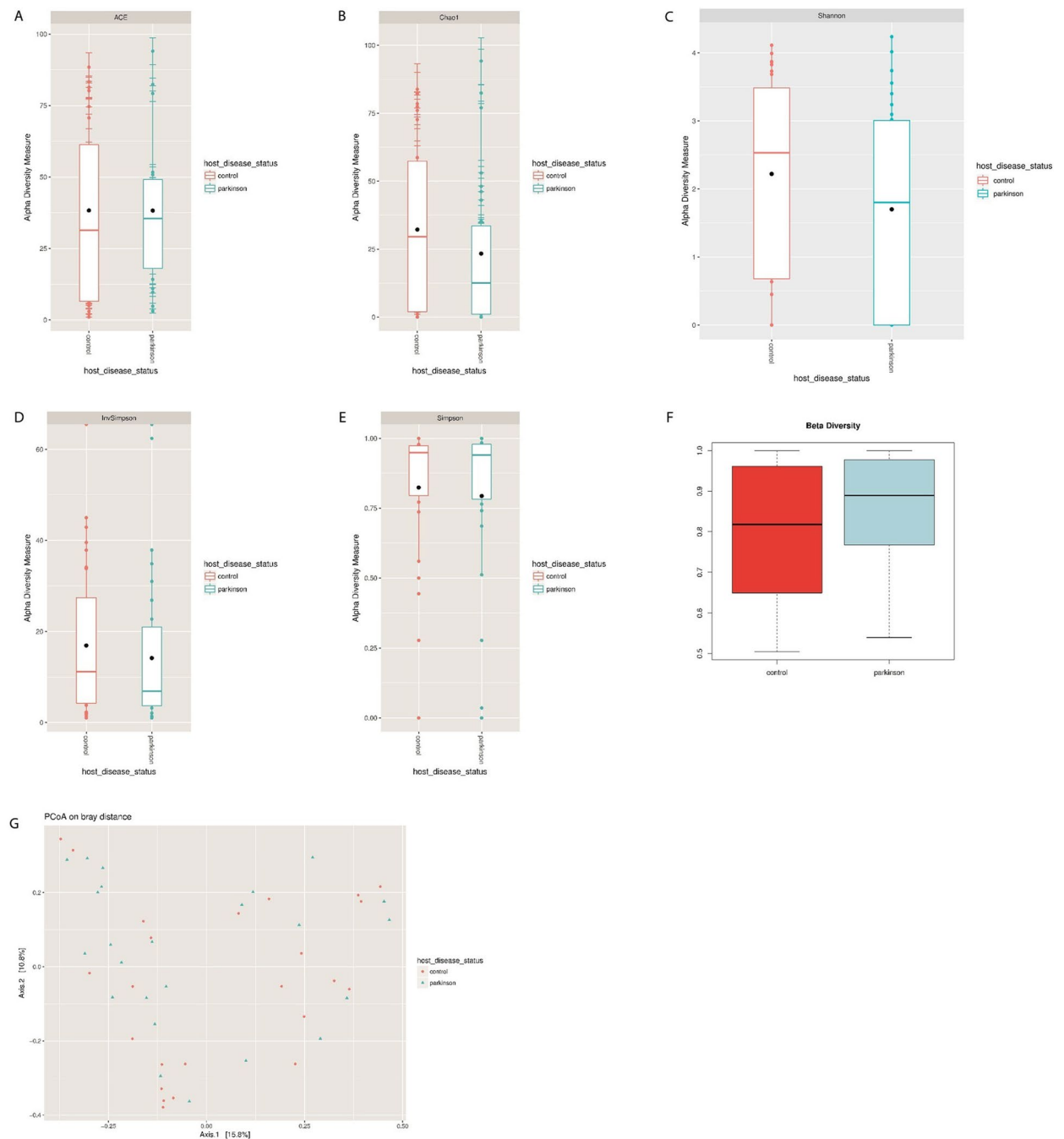**Figure 1.** Phagobiome richness in PD patients and healthy individuals. (**A**) ACE, (**B**) Chao1 and α-diversity, (**C**) Shannon, (**D**) Simpson, and (**E**) inverse Simpson indexes. Bacteriophage population diversity in PD patients and healthy individuals. (**F**) β-Diversity of phagobiota was measured using Spearman index. The X axis indicates samples and the Y axis shows Spearman index values: 0.5 means low difference and 1 means high difference (i.e., all species are different) in species diversity between samples. (**G**) PCoA plots of bacteriophage β-diversity based on Bray-Curtis dissimilarity analyses. Each dot represents a scaled measure of the composition of a given sample, colour- and shape-coded according to the group.
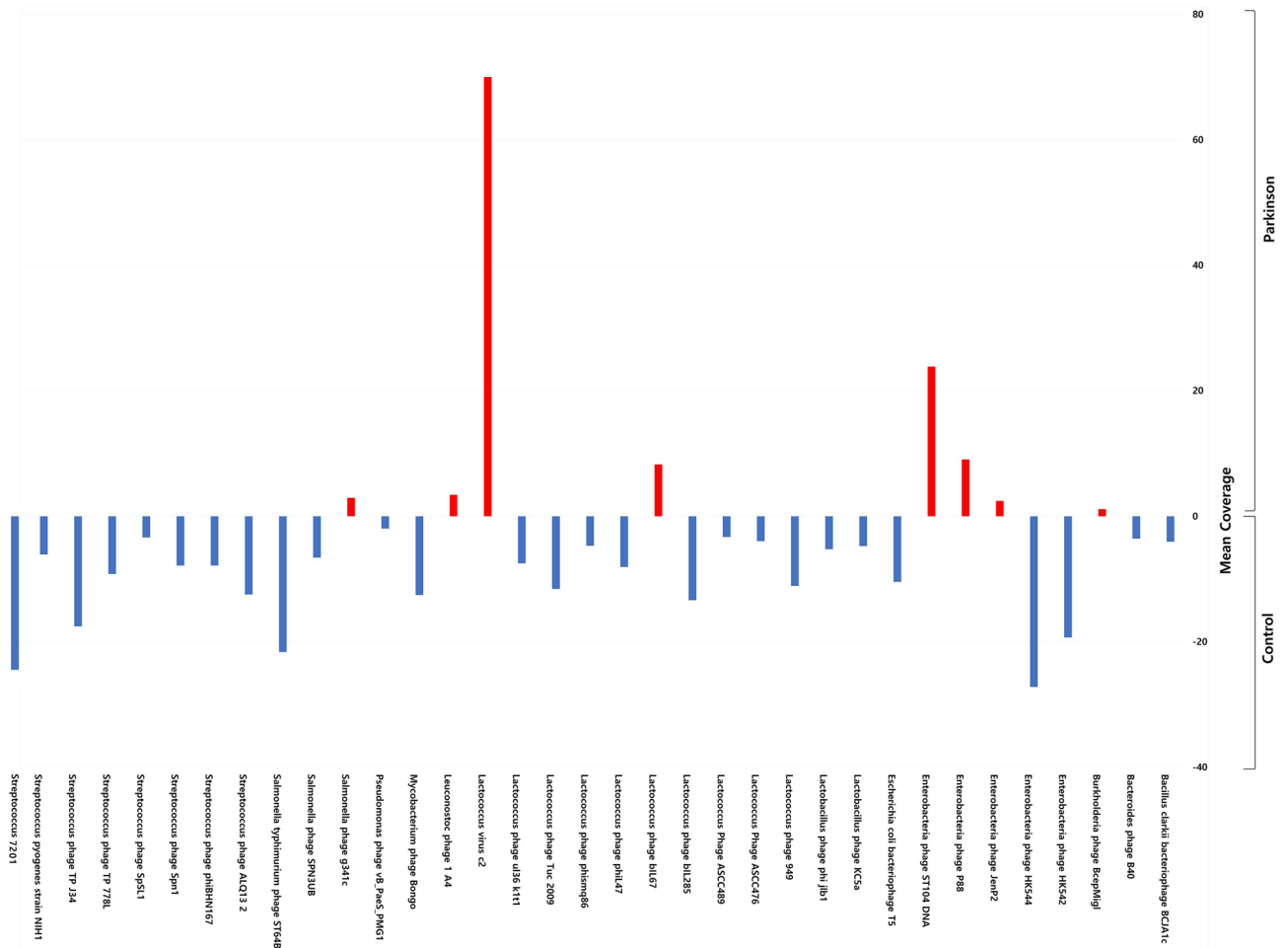
Figure 2. Exploration of bacteriophage diversity in PD patients and healthy participants. The bar graph shows bacteriophage abundance at the genus level in the PD or control group (relative abundance $\geq 0.01\%$ found in at least two samples per group).