Supplementary material

Modulation of the gut microbiota modulation by galactooligosaccharide protects against heavy metal lead accumulation in mice

Qixiao Zhai^{1,2,4}, Jing Wang^{1,2}, Shi Cen^{1,2}, Jianxin Zhao^{1,2}, Hao Zhang^{1,2,3}, Fengwei Tian^{1,2,4*}, Wei Chen^{1,2,3,5}

¹State Key Laboratory of Food Science and Technology, Jiangnan University, Wuxi, Jiangsu 214122, China

²School of Food Science and Technology, Jiangnan University, Wuxi, Jiangsu 214122, China.

³National Engineering Research Centre for Functional Food, Wuxi, Jiangsu 214122, China

⁴International Joint Research Laboratory for Probiotics at Jiangnan University, Wuxi, Jiangsu 214122, China

⁵Beijing Innovation Centre of Food Nutrition and Human Health, Beijing Technology and Business University (BTBU), Beijing 100048, China

*Corresponding author:

Fengwei Tian, State Key Laboratory of Food Science and Technology, Jiangnan University, Wuxi, Jiangsu 214122, China. E-mail: fwtian@jiangnan.edu.cn, Phone: (86)510-85912155

Materials and Methods

The evaluate the efficacy of the antibiotic treatment on microbiota depletion of mice

Individual fecal samples of mice were taken at the end of antibiotic treatment. Samples were incubated in brain heart infusion and in thioglycolate broths for at least 3 days at 37°C and bacterial growth was monitored daily by turbidity assessment.¹ Compared to other reported antibiotic treatments that lasted for more than 4 weeks,^{1,2} the antibiotic treatment used in the present study was in a shorter time, but sometimes failed to establish a gnotobiotic mouse model.³ Only mice without cultivable gut microbiota were selected for further studies.

Figures

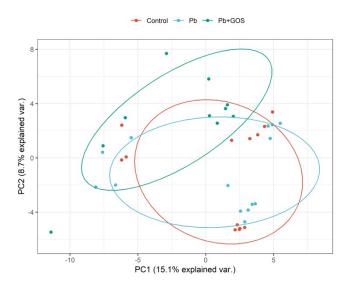


Fig. S1 Principal component analysis (PCA) plot for the genera of gut microbiota of mice in Control, Pb, and Pb+GOS groups. The ellipse represents the confidence region for each group.

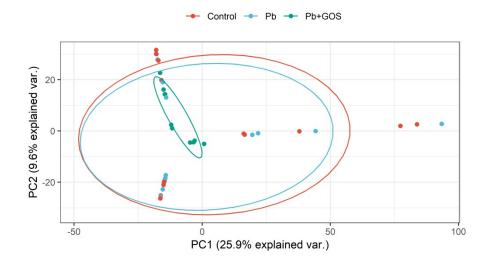


Fig. S2 Principal component analysis (PCA) plot based on OTU relative abundance of gut microbiota of mice in Control, Pb, and Pb+GOS groups. The ellipse represents the

confidence region for each group.

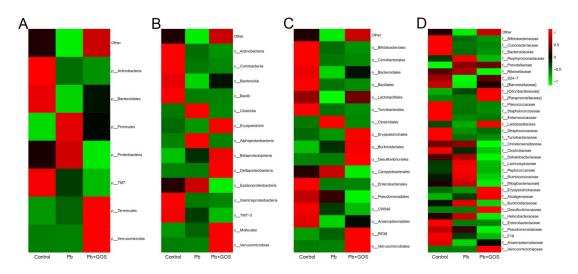


Fig. S3 Heatmap of the microbiota composition for the phylum (A), class (B), order (C) and family (D) of mice. Red indicates increased genera and green indicates decreased genera.

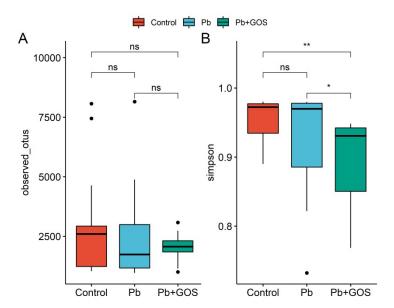


Fig. S4 Boxplots of the Observed_otus (A) and Simpson index (B) for the gut microbiota of mice. The upper and lower lines represent the 25% and 75% quantile values, respectively. * and ** indicate significant differences (P < 0.05 and P < 0.01)

between groups. n.s. indicates no significant differences (P > 0.05) between groups.

References

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