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Effect of pulque-derived microbiota with probiotic potential on metabolism and gut microbiota composition in a murine model

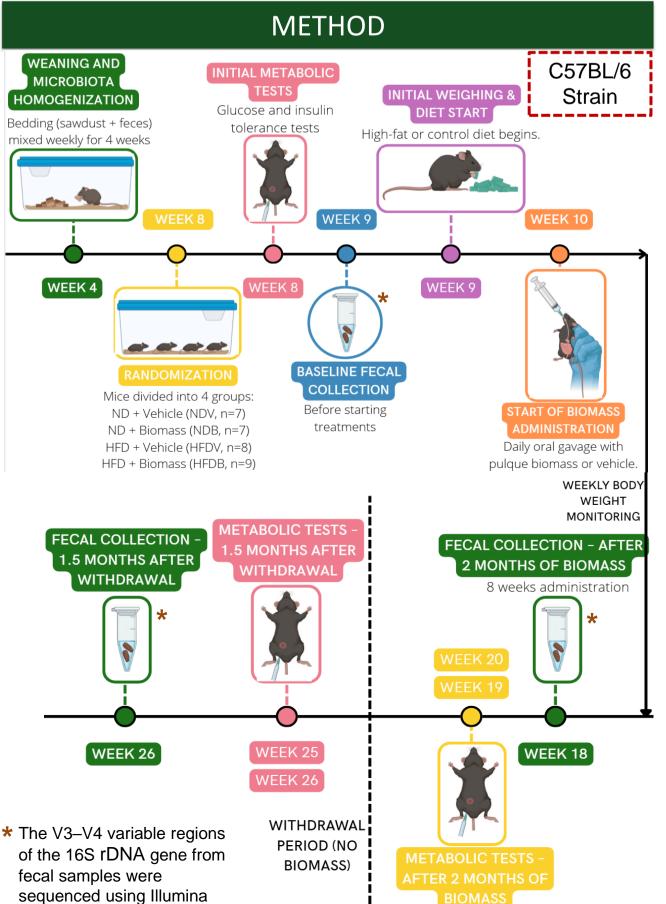
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INTRODUCTION & AIM Lactiplantiba-Leuconostoc cillus mesenteroides plantarum P45 P46 **Probiotic** potential of pulquederived strains Lactobacillus Lactobacillus sanfrancisbrevis Lb9H Lactobacilli censis & Saccharomyces Leuconostoc cerevisiae & Sastric acid resistence **Zymomonas Antimicrobial activity** Acetobacter Lactic mobilis **Bile salt resistence** Reduces intestinal fermentation permeability Gluconobactei Alcoholic Anti-infective activity (A) Reduces inflamation fermentation against salmonella Acetic Hepatic protective effect fermentation by reducing LPS-induced lipid peroxidation

The aim of this study is to evaluate how pulque microbiota administration influences metabolic responses and gut microbial composition in high-fat-diet (HFD) mice



NovaSeq 6000

RESULTS & DISCUSSION

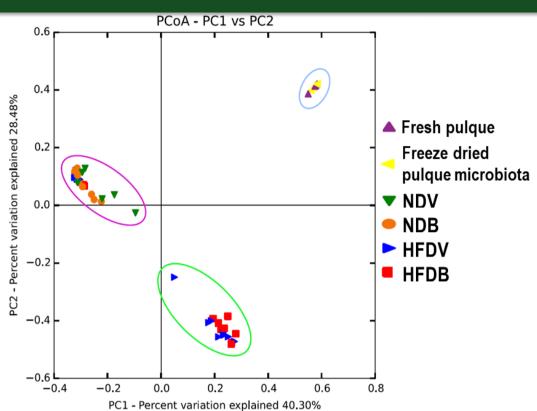


Fig 1. PCoA (Bray–Curtis) of bacterial beta diversity in pulque, lyophilizates, and feces. NDV, NDB, HFDV, HFDB as indicated in method.

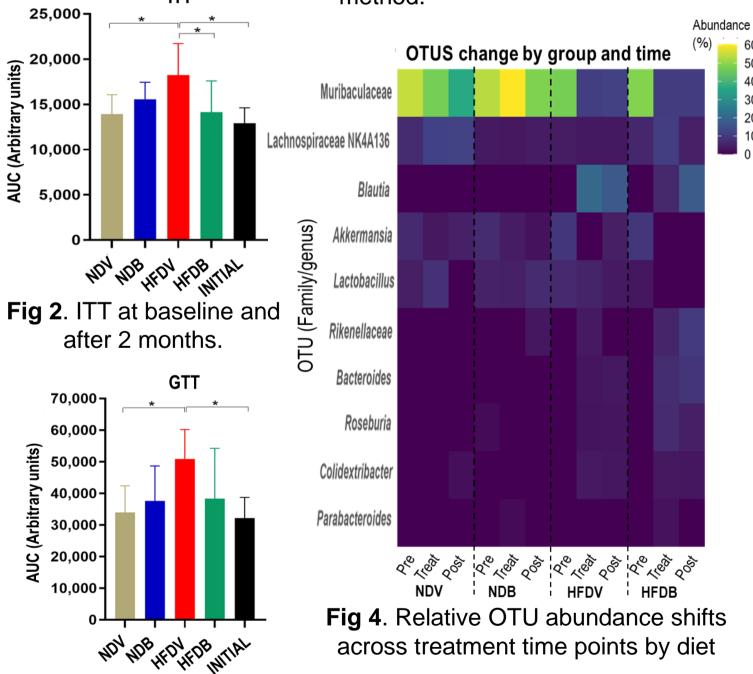


Fig 3. GTT at baseline and after 2 months.

CONCLUSION

Diet shaped the gut microbiome; pulque biomass finetuned it, improving insulin sensitivity in high-fat-fed mice.

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Acknowledgments

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