FUNCTIONAL POTENTIAL OF THE GUT MICROBIOME IN NH BHUTANESE REFUGEE ADULTS WITH GLYCEMIC IMPAIRMENT

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BACKGROUND

- We and others have shown the gut microbiome is linked to metabolic health (Figure 1), but is highly population-specific[1,2]
- Refugee populations face higher risks of metabolic diseases, but are underrepresented in current research on the gut microbiome[3]

OBJECTIVES

- To identify differences in overall microbial communities (beta diversity) according to T2D
  <u>Hypothesis</u>: There is a difference in beta diversity according T2D status
- To assess the relationship between the functional richness of the fecal microbiota, diet, and glycemic status
  <u>Hypothesis</u>: UniProt richness is lower in T2D

METHODS

- Cross-sectional study of Bhutanese refugee adults (n=50) in NH from previous study (PI: Bigornia)
- Inflammatory and satiety markers via chemiluminescence assay
- Shallow shotgun sequencing utilized to characterize the gut microbiome via PALADIN pipeline
- Beta diversity (PERMANOVA, Bray-Curtis, Atchison)
- UniProt richness: Sum of unique number of UniProt IDs per sample
- Partial Spearman correlations of UniProt richness with compositional diversity and biomarkers
- UniProt richness compared according to T2D status (Wilcoxon rank sum)

COMPOSITIONAL RESULTS

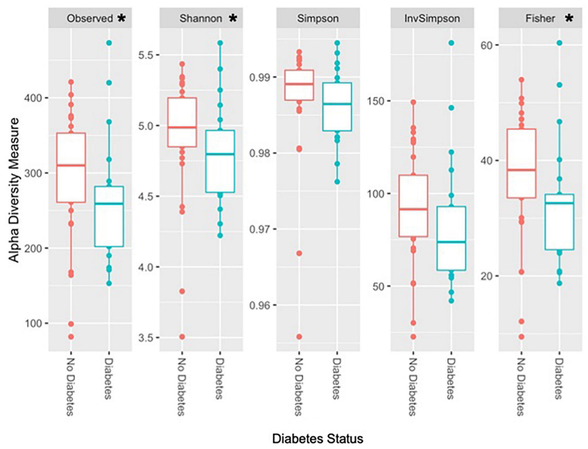

Figure 1. Richness and alpha diversity measures lower in T2D.*Significance level set at p=0.05. Previously published (Moser, et al. 2023)

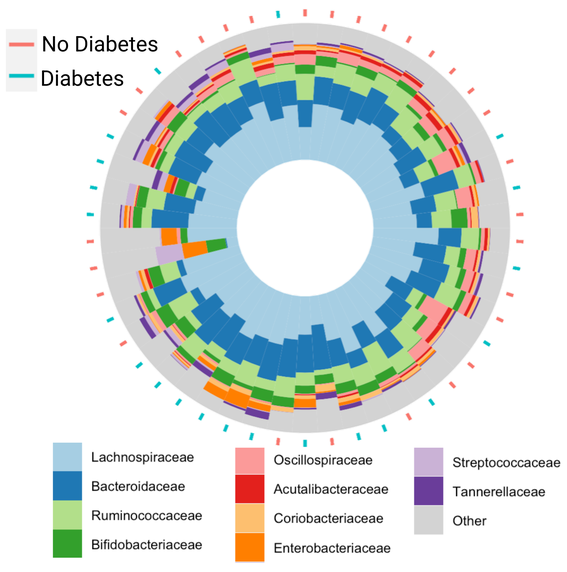

Figure 2. Centered log transformed family level taxonomic composition

Table 1. Beta diversity PERMANOVA indicating significant differences in microbial communities according to T2D status

	R^2	F	P-value
Bray-Curtis			
Family	0.05	2.71	0.019
Genus	0.04	1.78	0.063
Aitchison			
Family	0.06	3.12	<0.001
Genus	0.04	1.97	0.003

FUNCTIONAL RESULTS

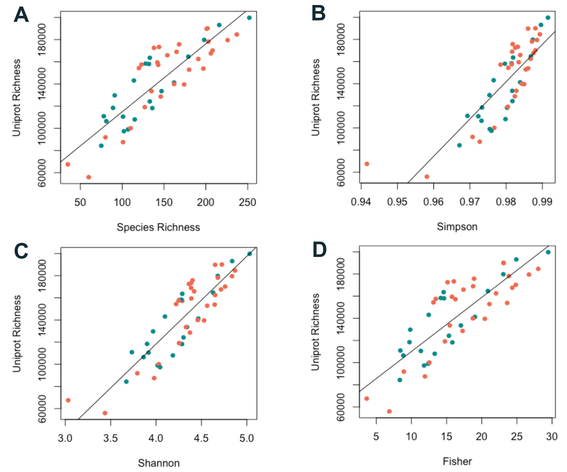

Figure 3. Significant partial spearman correlations of UniProt richness and compositional richness and diversity measures, adjusting for sequencing depth. A) UniProt richness vs Species Richness B) UniProt richness vs Simpson Diversity C) UniProt richness vs Shannon Diversity D) UniProt richness vs Fisher Diversity

Table 2. Nonsignificant partial spearman correlation, adjusting for age, of UniProt richness and markers of glycemic status, satiety, inflammation, and diet.

	n	Rho	p-value
Glycemic status			
Hemoglobin A1c	50	-0.08	0.573
Homeostatic Model Assessment for Insulin Resistance	50	0.06	0.705
Fasting Plasma Glucose	50	-0.18	0.214
Inflammatory Markers			
Lipopolysaccharide Binding Protein	50	-0.10	0.481
Satiety Hormones			
Leptin	50	0.25	0.083
Brain-Derived Neurotrophic Factor	50	-0.06	0.674
Dietary Intake			
Total Fiber	50	-0.23	0.111
Insoluble Fiber	50	-0.22	0.125
Soluble Fiber	50	-0.25	0.079
Diet Quality (HEI Score 2010)	47	0.12	0.437

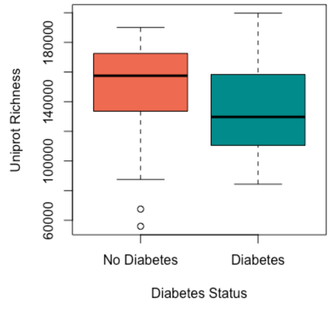

Figure 4. UniProt richness not significantly different according to T2D status. After excluding outliers, a significant difference in UniProt richness was observed according to diabetes status (p=0.043)

KEY FINDINGS

- Differences in microbial communities according to T2D
- Functional and compositional richness are correlated
- Functional richness was not statistically different according to diabetes status nor was it correlated with glycemic markers, inflammation, satiety, or diet

CONCLUSIONS

This study provides greater understanding of underlying mechanisms of the gut microbiota and glycemic impairment in an underrepresented population that experiences a large burden of chronic disease

FUTURE DIRECTIONS

Gene set enrichment to find specific functional characteristics or pathways that differ according to diabetes status

REFERENCES

1. Fan and Pedersen, PMID: 32887946
2. Moser, PMID: 36687728
3. Bhatta, PMID: 24849870

FUNDING

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