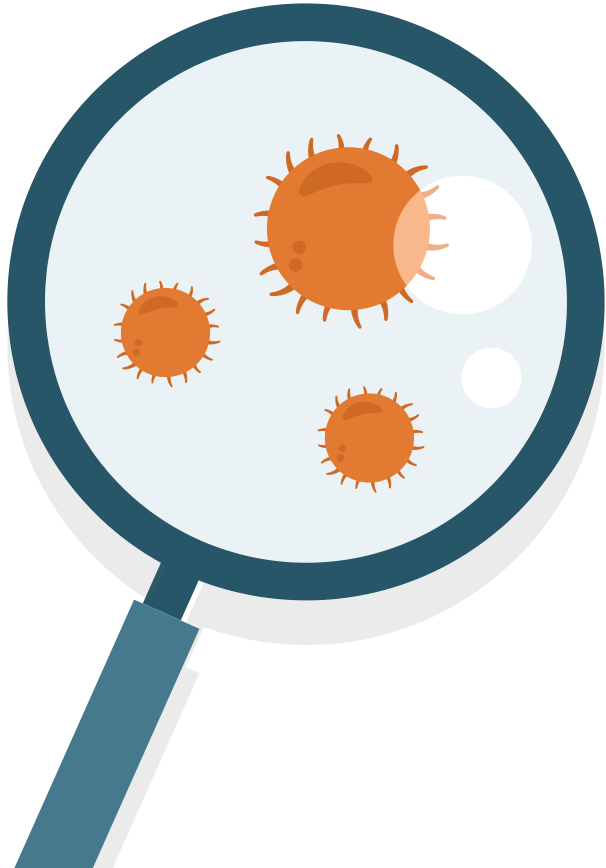


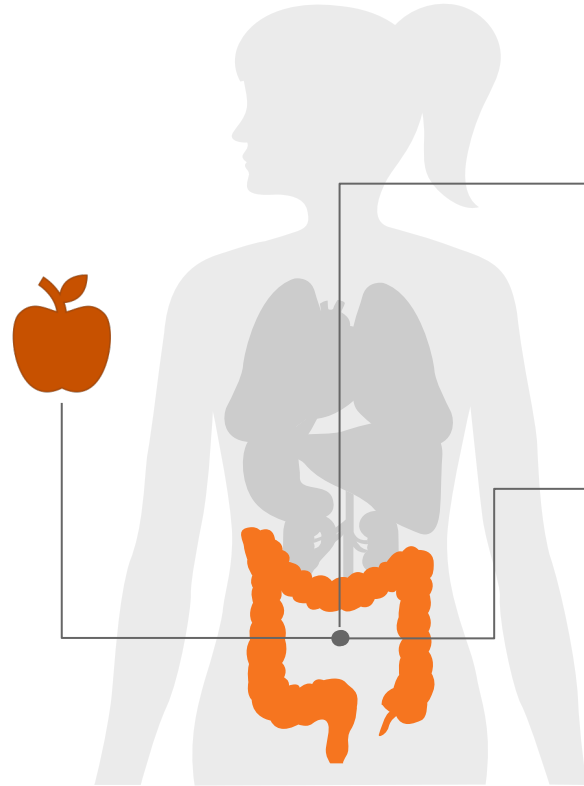
Functional Potential of the Gut Microbiome in NH Bhutanese Refugee Adults with Glycemic Impairment

Presented by Brandy Moser BS BA
UNH Graduate Research Conference 4/10/23

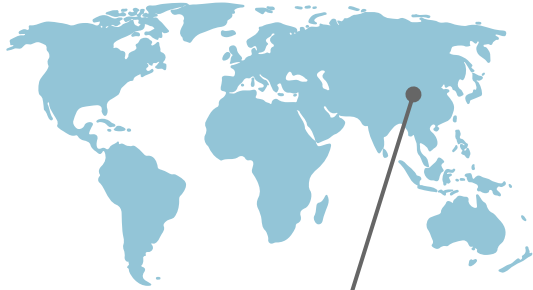
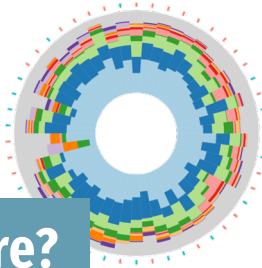
Presentation Outline



01	Background
02	Objectives
03	Methods
04	Results: Compositional Diversity & Functional Richness
05	Conclusions
06	Acknowledgements



Who is there?



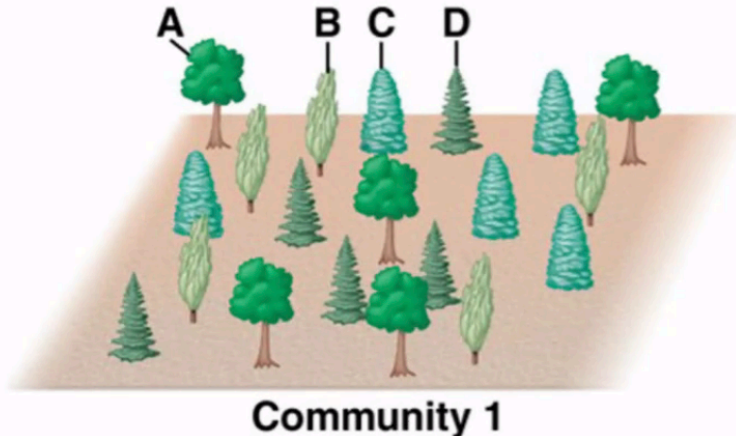
Bhutan

What do they have the potential to do?



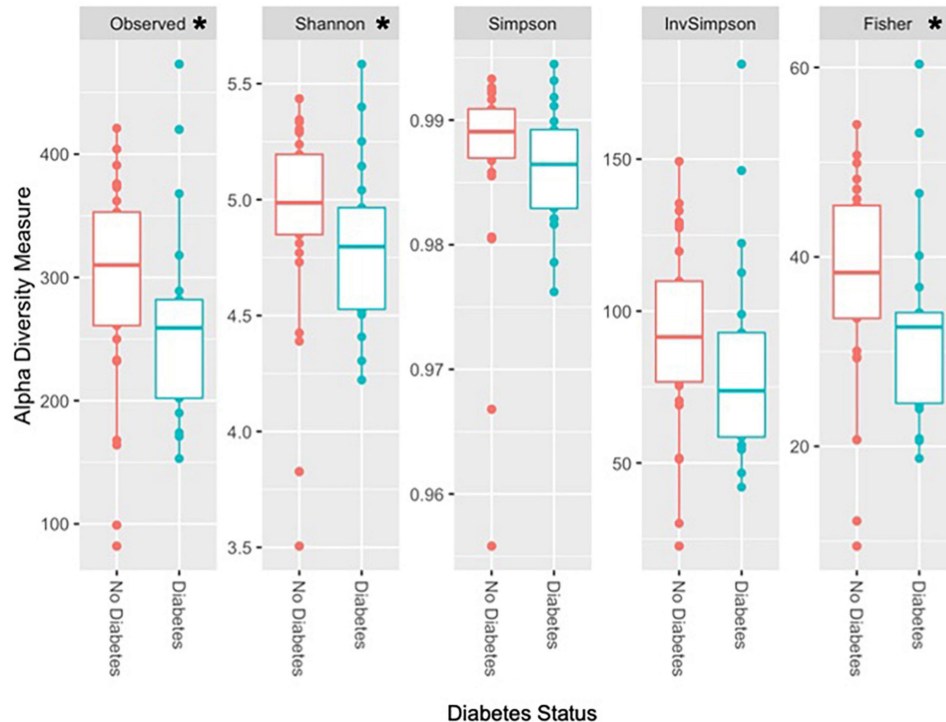
Richness: Number of unique trees within each forest

Alpha Diversity: Number and distribution of trees within each forest



Richness: Number of unique species within each group

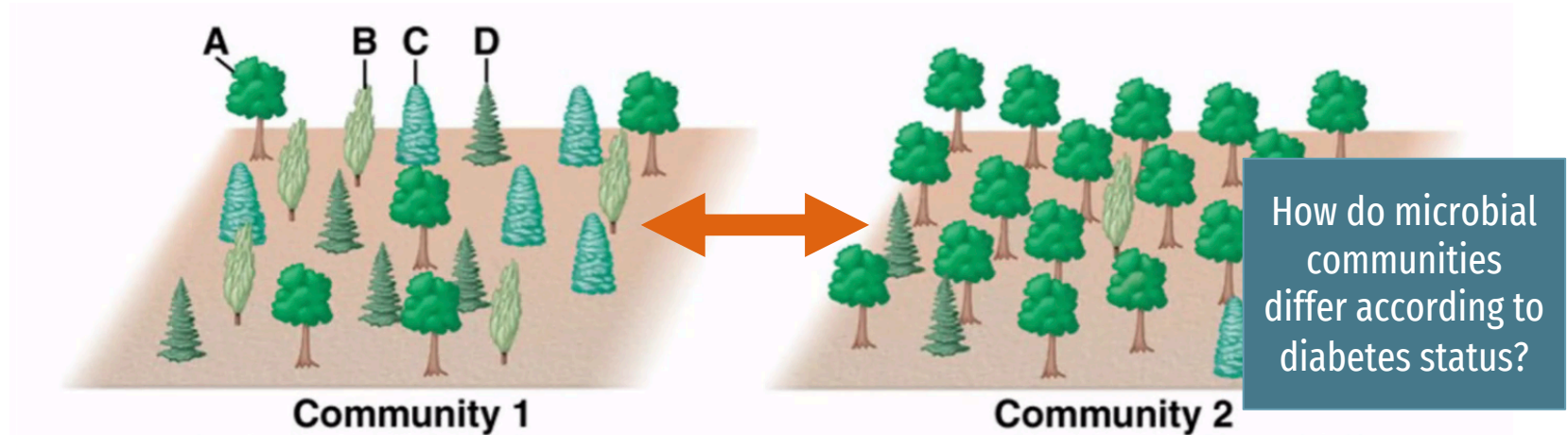
Alpha Diversity: Number and distribution of species within each group



How is functional richness different according to diabetes status?

Richness: Number of unique trees within each forest

Alpha Diversity: Number and distribution of trees within each forest



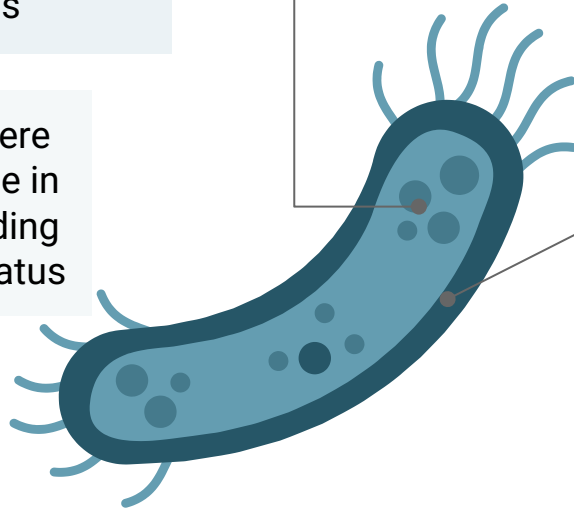
Beta Diversity: Differences in trees between communities

Objectives

Who is there?

To identify differences in overall microbial communities (beta diversity) according to type 2 diabetes status

We hypothesized there would be a difference in beta diversity according to type 2 diabetes status



What do they have the potential to do?

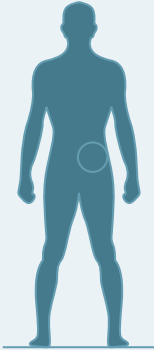
To assess the relationship between the functional richness of the fecal microbiota, diet, and glycemic status

We hypothesized that UniProt richness would be lower in type 2 diabetes

Methods

Cross-sectional study of Bhutanese refugee adults (n=50) in NH

01



Sample Demographics

Previously Conducted

02



Glycemic Status & Inflammation

Previously Conducted

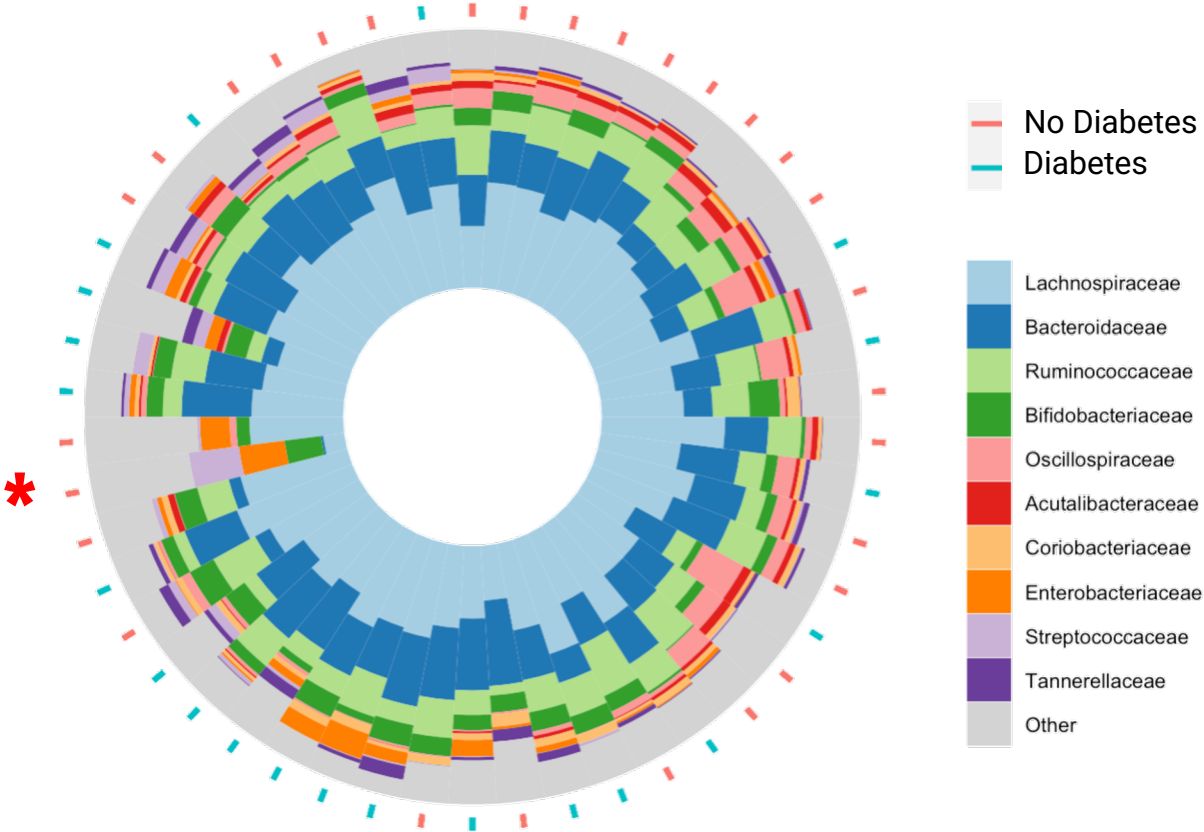
03



Microbiome Analysis

Composition &
Function

Family Level Microbial Composition



Beta Diversity

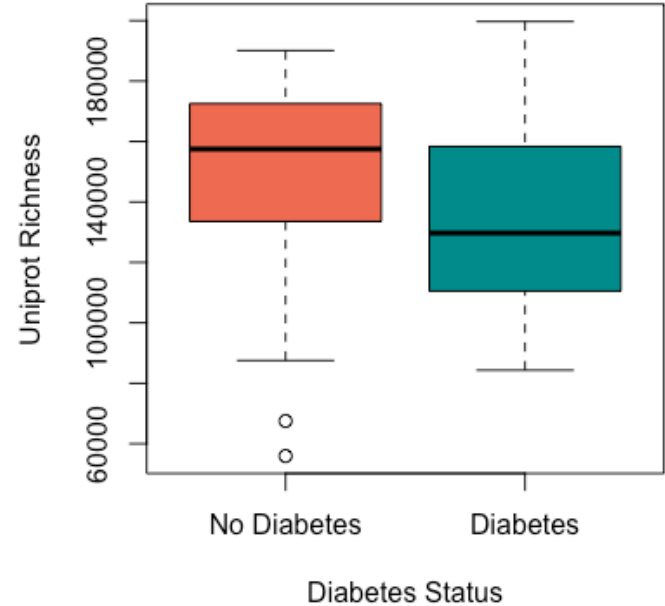
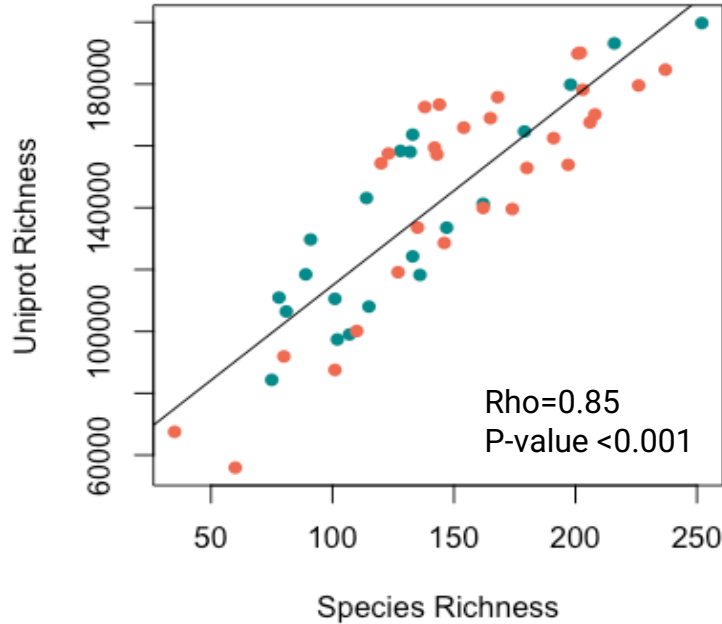
Beta diversity PERMANOVA according to diabetes status

	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

Differences in the microbial communities according to diabetes status

Functional Richness

UniProt Richness: Number of unique UniProt proteins in a metagenomic sample



Functional and compositional richness are correlated

Functional Richness

Partial spearman correlations of UniProt richness and biomarkers

	Partial Spearman ¹		
	n	Rho	P-value
Glucose Measures			
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
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

¹Partial spearman correlation adjusting for age

Functional richness is not correlated to glycemic status or inflammation

Conclusions

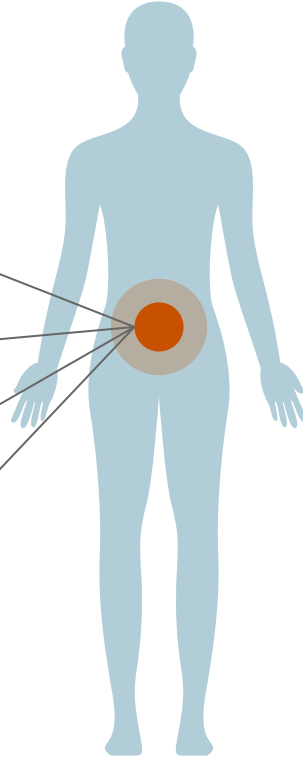
Key Findings

✓ **Beta Diversity vs Diabetes Status**

✓ **UniProt Richness vs Composition**

× **UniProt Richness vs Diabetes Status**

× **UniProt Richness vs Glycemic Status**



Importance

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

Next Steps

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

ACKNOWLEDGMENTS

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Thesis Committee

Maria Carlota Dao, Ph.D., Sherman Bigornia, Ph.D., & Kelley Thomas, Ph.D



Thank you!



Any Questions?

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