

Evolutionary Dynamics of the Human Oral Microbiome

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BACKGROUND:

Populations of the human microbiota, which are continually and rapidly evolving, are possibly under selective pressure for manipulation capacities: any genetic mutation that enables individual microbes to shift host behavior toward improved survival and reproductive success should be favored by natural selection [1-6]). Bacteria that metabolize host foods are expected to increase their access to these substances by evolving to exploit the mechanisms of food intake of their hosts [2, 6]. For oral bacteria, such as *Streptococcus mutans*, mutations that enable shifts in the mechanisms governing food intake should favor those variants that increase the intake of dietary sugar.

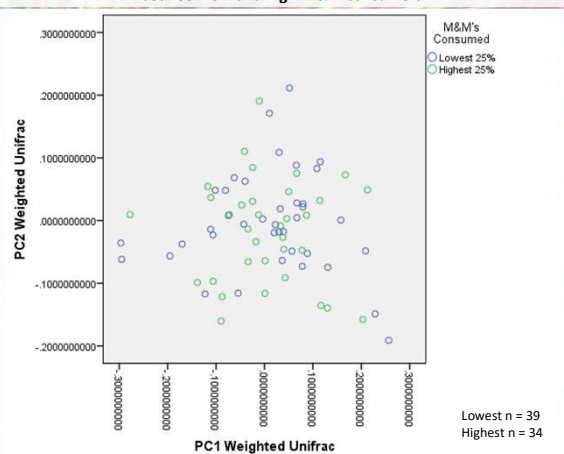
METHODS: We conducted an association study to test for relationships between 1) food intake in the lab and 2) microbiome data, with controls for 3) recent food intake and oral hygiene behavior. Saliva was stimulated and expectorated into a 50mL tube following chewing a piece of unflavored, unsweetened mastic gum for a period of 1 minute. Participants were then given access to 100 grams of M&M's and told to consume as many as they wanted.

HYPOTHESIS: Positive association between abundance of saccharolytic (sugar-degrading) oral bacteria and increased intake of sugar (M&M's).

SUMMARY OF RESULTS FOR EATING MANIPULATION HYPOTHESIS:

To date, we do not find evidence to support this hypothesis, using beta diversity metrics, alpha diversity metrics, or genera abundances.

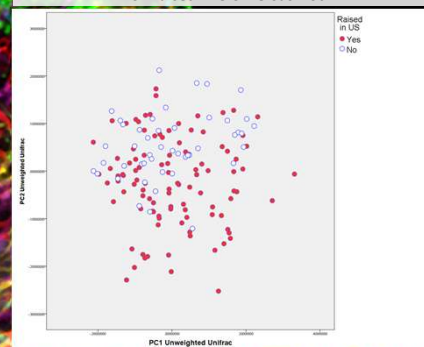
No significant differences in phylogenetic diversity between low and high M&M consumers:



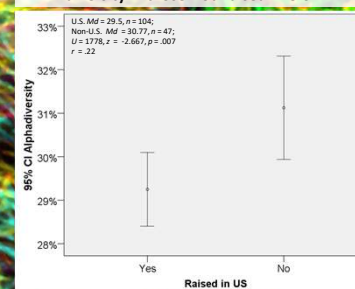
OTHER RESULTS OF INTEREST:

Participants raised in the U.S., versus those not, show significant differences for measures of alpha diversity, beat diversity, oral hygiene, eating behavior, and relative proportions of genus *Veillonella*:

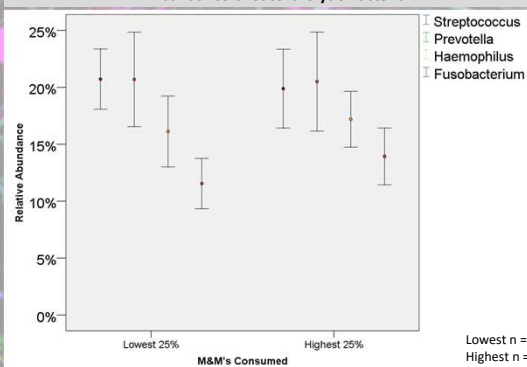
Some evidence of community clustering (beta diversity) for Raised in U.S. versus Not:



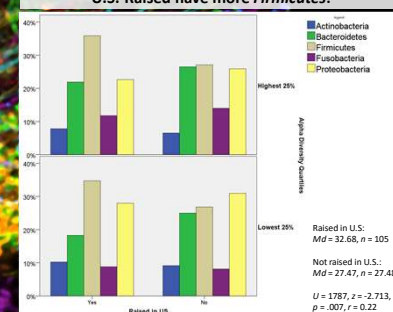
Higher within-subjects' (alpha) taxonomic diversity in those Not Raised in U.S.:



No Significant Differences in M&M Consumed by Abundance of Saccharolytic Bacteria:



U.S.-Raised have more Firmicutes:



Study design:

PART I, AT HOME:

Survey 1	SURVEY 1	
	• Weight/Height (BMI) • Dietary restraint	• Ethnicity • Raised in U.S.?

PART II, IN LAB:

1) Saliva sample	Oral microbiome 16s rRNA)		
	SURVEY 2		
	Intake: • Hunger level • Liking for M&M's • Diet	Oral hygiene: • Tooth brushing • Mouthwash use • How often? • When last?	Last food: • When? • Sugary foods?
2) Survey 2	Food access: grams of M&M consumed		
3) Food			

CONCLUSIONS: Our initial analyses do not support a role for common saccharolytic genera in changing oral intake of M&M candy provided during testing. We plan to continue testing this hypothesis using unstructured abundance data from the salivary microbiome results. In the next phase of our work, we will investigate specific mechanisms for possible oral bacteria manipulation of the components of eating behavior. We plan to experimentally manipulate the microbiome using anti-microbial mouthwash, testing for pre- and post-treatment effects on sweet taste perception.

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Works cited: 1) Alcock, J., C.C. Makiy, and C.A. Aktipis. Is eating behavior manipulated by the gut-microbial ecosystem? Evolutionary pressures and potential mechanisms. *Biological Reviews*, 2014, 89(10) p. 940-943.
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