Investigating the oral microbiome for biomarker discovery in cancer using data from the Canadian Partnership for Tomorrow's Health

Jacob T. Nearing PhD Candidate Dalhousie University



Canadian Partnership for Tomorrow's Health

The Human Microbiome

You are never alone...



KATERYNA KON/SCIENCE PHOTO LIBRARY, via Getty Images









Objectives

1) What anthropometric, dietary and lifestyle factors are associated with the oral microbiome?

2) Determine the presence of oral microbiome biomarkers in breast, prostate, and colon cancer

Analysis of the healthy oral microbiome





Nearing et al., 2020, msphere

41 Variables

- Geography - Demographics

- Body Composition
- Diet



Factors related to oral microbiome composition





Multiple oral microbiome genera are associated to daily life factors

	Corynebacteriaceae Corynebacterium
	Propionibacteriaceae Pseudopropionibacterium
	Paludibacteraceae F0058
	Porphyromonadaceae Porphyromonas
	Prevotellaceae Prevotella 2
	Prevotellaceae Prevotella 6
	Prevotellaceae Prevotella 7
	Tannerellaceae Tannerella
	Flavobacteriaceae Capnocytophaga
	Weeksellaceae Bergeyella
	Bacillaceae Bacillus
	Family XI Gemella
	Carnobacteriaceae Granulicatella
	Lactobacillaceae Lactobacillus
	Streptococcaceae Streptococcus
	Defluviitaleaceae Defluviitaleaceae UCG-011
	Family XI Parvimonas
	Family XIII Mogibacterium
	Lachnospiraceae Lachnoanaerobaculum
	Lachnospiraceae Oribacterium
	Lachnospiraceae Stomatobaculum
	Lachnospiraceae uncultured
	Ruminococcaceae Ruminococcaceae UCG-01
	Veillonellaceae Dialister
	Veillonellaceae Megasphaera
	Veillonellaceae Selenomonas
	Veillonellaceae Veillonella
	Veillonellaceae uncultured
	Veillonellaceae unclassified
	Leptotrichiaceae Leptotrichia
	Burkholderiaceae Lautropia
	Neisseriaceae Kingella
	Neisseriaceae Neisseria
	Neisseriaceae unclassified
	Cardiobacteriaceae Cardiobacterium
	Pasteurellaceae Aggregatibacter
	Pasteurellaceae Haemophilus
	Pseudomonadaceae Pseudomonas
	Spirochaetaceae Treponema 2
	Synergistaceae Fretibacterium
	Mollicutes uncultured
	Mycoplasmataceae Mycoplasma
	Color Key
tier 90, 910, 900, 900, Moi tab. 950 911, 90, 900, 900, Moi ee, 191	
of Mor Hers cervin cervin in User spoen ist Sice Inc. Wers cervin cervin in Ray had in the	
ree sed 3- an 3- Sai ther Way Nast ice 5 ble Stigt Hir Denne	-1 -0.5 0 0.5 1
White of Crit of Live Body Jun detail Man Last	
Nr the office to Ves	



Multiple predicted oral microbiome pathways are associated to daily life factors

ubiquinol-7 biosynthesis (prokaryotic) ubiquinor- y biosynthesis (brokaryotic) ubiquinol-9 biosynthesis (brokaryotic) ubiquinol-10 biosynthesis (knowaryouc) ubiquinol-10 biosynthesis (knowaryotic) ubiquinoi- to unosynanesia (monenyouo) ubiquinoi-8 biosynthesis (prokaryotic) Uperpainway or uniquinor o orosyntresis (proveryour) L-arginine blosynthesis III (via N-acetyl-L-citrulline) TCA cycle VIII (helicobacter) myo-, chiro- and scillo-inositol degradation nitrate reduction I (denitrification) TCA cycle VII (acetate-producers) superpathway of glucose and xylose degradation Superpatriway or glucose and sylose degradation TCA cycle V (2-oxoglutarate:ferredoxin oxidoreductase) reductive TCA cycle A (2-oxoglutarate) Superpathway of heme biosynthesis from uroporphyrinogen-11 Superpathway of heme blosynthesis from glycine sunate reduction ، (dssimilatory) superpathway of pyridoxal 5'-phosphate biosynthesis and salvage سمرسه hirevonthasis کی superpathway of sulfate assimilation and cysteine biosyntnessis i Nichine hinocynthesis المنظر المروسية 8-amino-7-oxononanoate biosynthesis i Superpathway of L-methionine biosynthesis (by sulfhydrylation) thiazole biosynthesis II (Bacillus) UDP-N-acetylglucosamine-derived O- L-tytosme degradatuon i - 2 ²-dianatamida- 2 2-didanavi-alaha- - D-manata bidok bidosmittesis UDP-N-acety/glucosamine-genveg U-antigen block blosyfutilesib P-2,3-diacetamido-2,3-dideoxy-alpha;-D-mannuronale blosyfutilesib h-utini formoniation to lantata formata ethanni and acetata خلفانانانات ج، ٢- تانافانات العالية الم hexitol fermentation to lactate, formate, ethanol and acetate ممانية مراييم المراييم De retrinerinarion to raciale, for marce, et rarion and accetate Peptidoglycan biosynthesis IV (Enterococcus faecium) peptidglycan biosynthesis II (staphylococci) superpartway or (K, K)-putaneolor plosymmesis peptidoglycan biosynthesis V (β-lactam resistance) tointroin and contractive constitutions attended Superpathway of (R,R)-butanediol biosynthesis leichoic acid (poly-glycerol) biosynthesis L-rhamnose degradation | superpathway of 2,3-butanedial biosynthesis Gerany/gerany/diphosphate biosynthesis / via mevalonate) annhin raeniration / (nimbromediate) aerobic respiration / (via movies (via movies)) superpathway of phylloquinol biosynthesis aure, paumo v mynodumo uosymuesis 1,4-dihydroxy-2-naphthoate biosynthesis I ADP-L-glycero-&beta:-D-manno-heptose biosynthesis i //Ilburinate a ~-diamide biosynthesis / cashi and i ineartian AUr-L-glycero-β-U-manno-nepiose olosyntresis cob(II)yrinate a.c-diamide biosynthesis I (early cobalt insertion) ermarnathway of menanuinnl-& binevnthesis II Superpathway of menaquinol-8 biosynthesis II 1,4-dihydroxy-6-naphthoate biosynthesis in CDP-D-glycero-&alpha:-D-manno-heptose biosynthesis Ur-U-Siycero-α-U-manno-heptose biosynthesis superpathway of sulfur oxidation (Acidianus ambivalens)



Refined Grain Servings Steeping Light Exposure Vegetable Servings Waist Hip Ratio Fat Free Mass



Refined Grain Servings is predicted to be associated with changes in carbon metabolism

L

ubiquinol-7 biosynthesis (prokaryotic) ubiquinol-9 biosynthesis (prokaryotic) ubiquinol-10 biosynthesis (prokaryotic) superpathway of ubiquinol-8 biosynthesis (prokaryotic) L-arginine biosynthesis III (via N-acetyl-L-citrulline) TCA cycle VIII (helicobacter) myo-, chiro- and scillo-inositol degradation TCA cycle VII (acetate-producers) superpathway of glucose and xylose degradation TCA Cycle V (2-oxoglutarate:ferredoxin oxidoreductase) superpathway of heme biosynthesis from uroporphyrinogen-III superpathway of heme biosynthesis from glycine superpathway of pyridoxal 5'-phosphate biosynthesis and salvage Superpathway of sulfate assimilation and cysteine biosynthesis superpathway of L-methionine biosynthesis (by sulfhydrylation) thiazole biosynthesis II (Bacillus) Pyridoxal 5'-phosphate biosynthesis (2-methylcitrate cycle II L-tyrosine degradation (

	Color Key							
		-0.2	 -0.1 oį	l 0 g odd	0.1 s	0.2		
								_
Refined	Vegetable Salt Usage Grain Servings	W _{ais}	Ster Ste	^{3eping} atio	Male*	Heigi		



Summary

1) Anthropometric, dietary factors, and some demographics are associated with the oral microbiome

2) Each factor explains relatively low amount of variation

3) Refined grain usage is linked to potential metabolic changes in oral microbiome





Objectives

1) What anthropometric, dietary and lifestyle factors are associated with the oral microbiome?

2) Determine the presence of oral microbiome biomarkers in breast, prostate, and colon cancer

Exploring associations between the oral microbiome and cancer

- Cancer free at collection
- Diagnosis from follow-up or cancer registry
- 1:1 case control matched
 - Sex
 - Age (+/- 2 years)
 - Smoking

Sample Counts



Expected Results/Future Directions

- 1) Oral microbiome risk factors for breast, prostate and colon cancer
- 2) Classify individuals that go on to develop cancer based oral microbiome signature
- 3) Connect oral microbiome data with other CanPath data:

WWWWWW

1) Heavy metals from toe nails

2) Blood metabolites

3) Genetic Signatures





Thank You



Committee Members: Dr. Nikhil Thomas Dr. Zhenyu Cheng Dr. Ketan Kulkarni











researchNS





