A Distinct Brain-Gut Microbiome Profile Exists for Obese Females with Food Addiction

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INTRODUCTION

- The obesity epidemic continues to be a major public health problem both in the United States (US) and globally.¹
- Obesity has a complex and multifactorial etiology, and the limited progress in obesity treatments can in large part be attributed to the failure to apply a systems biology-based approach to understand its pathophysiology and to develop individualized strategies to achieve sustained weight loss and prevention.¹⁻³
- A growing body of literature has demonstrated bidirectional signaling between the gut microbiome and the brain, mediated via neural, metabolic, endocrine, and immune-related signaling mechanisms.^{4,5}
- Perturbations at any level of this system resulting in compromised inhibitory mechanisms that normally regulate food intake, can bias ingestive behaviors towards predominant hedonic ingestion (food addiction), cravings, and overeating.^{2,6,7}
- AIM: To explore the relationship between food addiction and the brain-gut microbiome using a multi'omics approach in order to show that food addiction is related to alterations in neural communications that are associated with gut microbial and metabolite changes.

METHODS

- Subject: N=105 healthy female subjects.
- Fecal samples were stored at -80 C and shipped to Metabolon for processing and analysis using mass spectrometry and their global metabolomics and bioinformatics platform, focusing on Tryptophan-related metabolites.
- 16S rRNA gene sequencing was performed on all fecal samples using Illumina HiSeq platform.
- Structural and diffusion weighted magnetic resonance imaging was conducted at UCLA using a Siemens 3T MRI scanner.
 - <u>Reward networks</u>: caudate, putamen, globus pallidus, amygdala, hippocampus, nucleus accumbens, medial orbital frontal gyrus
- The Yale Food Addiction Scale (YFAS) was administered, and food addiction was defined as a score>3⁸

Results: Table 1

	Low YFAS (n=82)	High YFAS (n=23)	p-value
Age (mean +/- SD) (yrs)	32.95 + 10.02	30.26 + 10.53	0.26
BMI (mean +/- SD)	29.2 + 5.6	34.3 + 5.6	0.0001
Normal Weight (n=16) %	19.5	0.0	
Overweight (n=38) %	39.0	26.1	
Obese (n=51) %	41.5	73.9	0.01
Race/Ethnicity			
Hispanic (n=41) %	37.80	43.48	
Caucasian (n=28) %	24.39	34.78	
African American (n=13) %	13.41	8.70	
Asian (n=21) %	21.95	13.04	
Other (n=2) %	2.44	0.00	0.75





CNSR



Results: FA is Associated with Changes in the Brain-Gut-Microbiome



Results: Brain-Gut-Microbiome Axis Changes Accurately Identifies FA





✓ Akkermansia
✓ Eubacterium biforme
↑ Megamonas



Conclusion

- Overall, food addiction behaviors in females were associated with a distinct microbial profile, increase signaling between the intraparietal sulcus/transverse parietal sulcus, brainstem and the putamen of the reward center of the brain, and a decrease in indoleproprionate, a tryptophan derived microbial metabolite.
- Using the significant findings on brain imaging, fecal metabolite, and DESEq2 analysis of the fecal microbiome, a random forest classifier was created with a high accuracy for predicting patients with food addiction behaviors.
- This data suggests that food addiction behavior may be mediated via effects of the gut microbiome and their metabolites on the reward centers of the brain.
- This suggests the possibility of targeting the brain-gut microbiome axis to combat food addiction behavior and obesity.

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