Ultra-Processed Food Proxy Gene Signature Associated with Inflammation in Patients with Crohn's Disease

COLUMBIA | NEW YORK NUTRITION OBESITY RESEARCH CENTER IN THE DEPARTMENT OF MEDICINE

K Whyte, J Nye, J Kang, E Azizi, D Gallagher

Columbia University Medical Center, New York,

COLUMBIA | ENGINEERING The Fu Foundation School of Engineering and Applied Science

Introduction

Food processing is a relatively new feature used to measure diet quality and no consensus in ontology between disciplines exists. NOVA, developed by researchers from Sao Paolo University, defines ultra-processed food (UPF) as:

'Formulations of several ingredients, which besides salt, sugar, oils and fats, include food substances not used in culinary preparations, in particular, flavors, colors, sweeteners, emulsifiers, and other additives to imitate sensorial qualities of an unprocessed or minimally processed food and their culinary preparations or to disguise undesirable qualities in the final product.'[1]

Aim

UPF intake is associated with increased risk of suboptimal health outcomes across the lifespan, including inflammatory bowel disease (IBD). In the absence of cross-discipline collaboration, the tools to reveal underlying mechanisms remain unknown. Fortunately, the required information to create these tools exists across several databases. The purpose of this study was to

- Identify and annotate proxy gene markers related to UPF additives from these databases
- Investigate expression in patients with Crohn's disease.

Method

- Food additives identified using WHO/FAO Joint Expert Committee on Food Additives and published literature to create UPF gene list
- N=22 ileal biopsies from n=11 Crohn's patients[2] classified as inflamed (49,631 cells),or non-inflamed (40,033 cells)
- scRNAseq data preprocessed and clustering, scanpy score_genes function and Mann Whitney U used to determine significance
- Monocle 2 explored trajectory inference of UPF genes in inflamed and non-inflamed tissue

Results

Figure 1: kNN=15 Leiden cluster shows UPF coexpression with established inflammatory markers in cluster 9.

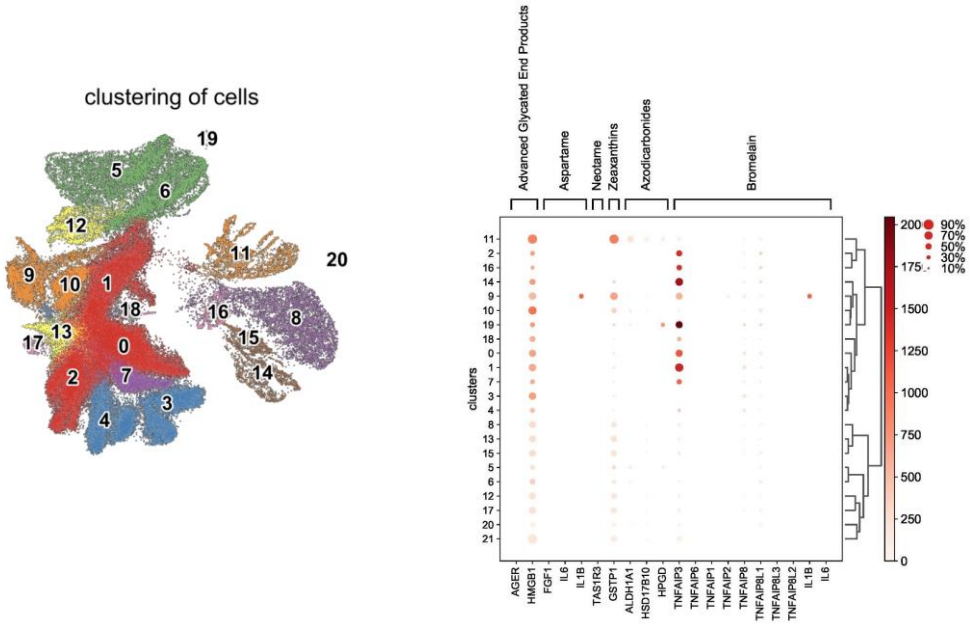


Figure 2: Median cell scores for inflamed (40.96) and non-inflamed (20.74) p<0.0001

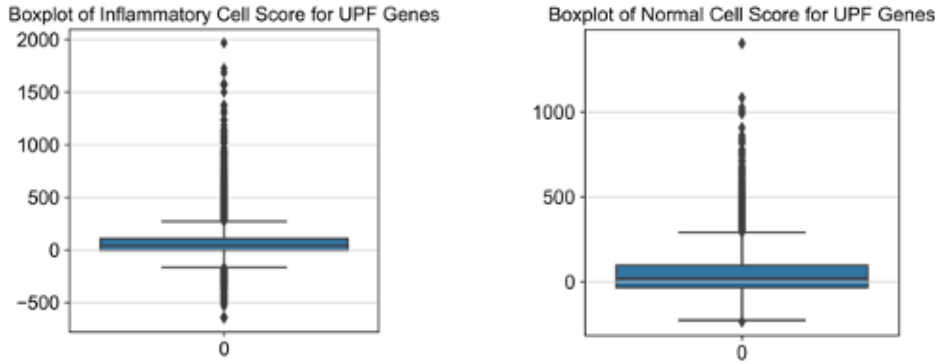
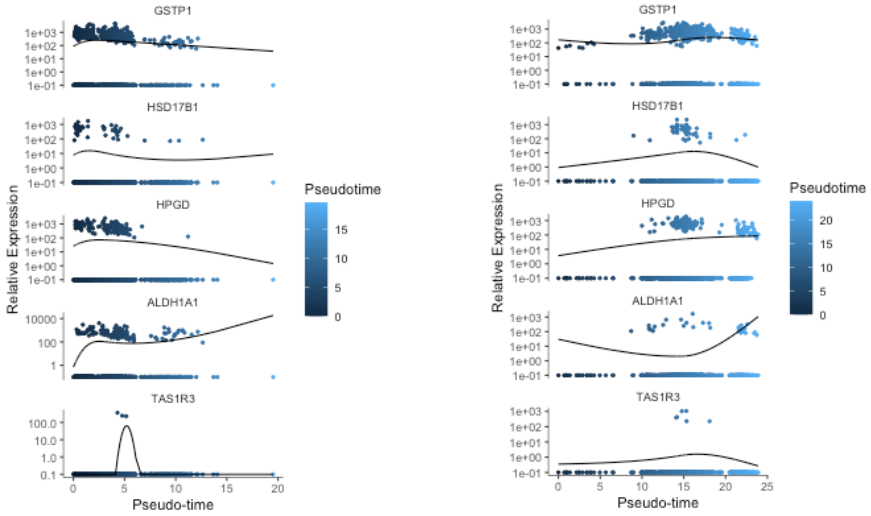


Figure 3: UPF gene expression patterns along pseudotime for inflamed and non inflamed



Conclusion

We observed coexpression with established inflammatory markers. Differences were observed between inflamed and non inflamed tissue. Consensus from experts in dietary assessment of UPF and bioinformatics would be required to establish validity and reliability of methods presented. Automation towards identifying this information would allow for translational clinical intervention studies to elucidate mechanisms for prediction algorithms to provide personalized recommendations related to individual UPF response

Acknowledgements

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[1] Monteiro C, Levy RB, Claro RM, de Castro IRR, Cannon G. A new classification of foods based on the extent and purpose of their processing. Cad Saude Publica. 2010;26(11):2039-2049.

[2] Martin JC, Chang C, Boschetti G, et al. Single-Cell Analysis of Crohn's Disease Lesions Identifies a Pathogenic Cellular Module Associated with Resistance to Anti-TNF Therapy. Cell. 2019 Sep;178(6):1493-1508.e20. DOI: 10.1016/j.cell.2019.08.008.