

BITS :: Call for Abstracts 2021 - Oral communication

Type	Oral communication
Session	Multimomics and Single Cell Analysis
Title	An integrated analysis on stool microRNA and microbial content in subjects with different dietary regimes
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Affiliation

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Motivation

Gastrointestinal disorders are the result of a complex molecular interaction between individual genetic background, transcriptional and epigenetic regulatory mechanisms, and environmental factors, including a specific nutritional regime and the gut microbial content. By integrative analysis of small RNA-Seq and metagenomic data, our group demonstrated that a combined signature of human stool microRNAs (miRNAs) and bacterial species is able to accurately discriminate colorectal cancer patients from subjects with precancerous lesions or healthy individuals. To further characterize the small RNA-mediated host-microbial interactions and their dependence on a specific dietary regime, stool small RNA-Seq, metagenomic data, and dietary information was collected for healthy subjects following an omnivorous, vegetarian, or vegan diet or celiac patients following a gluten-free diet.

Methods

Human and bacterial small RNA-Seq data were analyzed using the Docker-based pipeline developed by our group in the frame of the Reproducible Bioinformatic Project. Shotgun metagenomic data were analyzed using MetaPhlan3 to estimate the microbial relative abundances and with SIAMCAT to identify species characterizing each sample class. The daily nutrient intake was estimated based on a validated self-administered food-frequency questionnaire.

The R package mixOmics was applied for the integration of the three datasets (taxonomic profiles, miRNA expression profiles, and dietary information), using the Data Integration Analysis for Biomarker discovery using Latent cOMponents (DIABLO) model. Classification accuracy of the features identified by the DIABLO analysis was performed using a 10-fold cross-validation approach with the Random Forest classifier implemented in Weka.

miRNA target functional enrichment analysis was performed using RBiomirGS.

Results

Differential expression analysis revealed 49 miRNAs whose stool levels differentiate vegetarian/vegan from omnivorous subjects. Conversely, 100 stool miRNAs were observed to be differentially abundant in celiac individuals following a gluten-free diet with respect to omnivorous subjects. In parallel metagenomic data analysis highlighted different microbial species whose abundance was specifically associated with a dietary regime.

Integrative analysis of stool small RNA, microbial species, and nutritional information highlight a subset of features significantly associated and able to accurately discriminate the different dietary regimes. In particular, folate and lipid metabolism emerged as a target of features characterizing a plant-based diet while the regulation of inflammatory response features related to the gluten-free diet.

Finally, the features were explored in a comparison between patients with colorectal cancer or adenomas with respect to healthy individuals to verify their dysregulation in a disease context.

Info

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Figure

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<i>Availability</i>	-
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