Predictive study of metabolic pathways and biological processes induced by intestinal dysbiosis in weaned infants

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INTRODUCTION

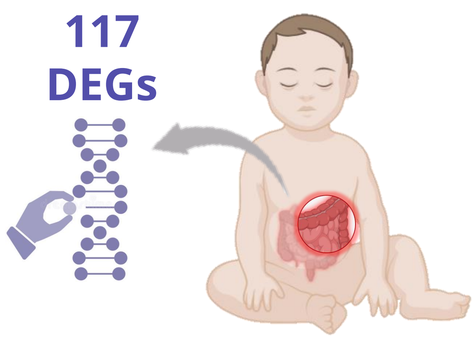
Weaning often leads to gastrointestinal problems, irritation and diarrhea in infants. Weaning influenced by various factors, involves complex interaction axes, in particular the gut-microbiota axis. Better understanding these responses and the underlying pathways may facilitate the development of targeted therapies to attenuate the intensity of dysbiosis and consequently gut inflammation in infants.

OBJECTIVE

The objective of this study is to introduce a new approach to visualize and understand the interactions between differentially expressed genes (DEGs) induced by dysbiosis and intestinal inflammation during the weaning period in infants, using bioinformatics methodologies.

MATERIAL AND METHODS

A set of 117 DEGs was collected from different bibliographic sources with a fold change >1 and p-value<0.05 adjusted. The analysis was performed in the Cytoscape platform (Version: 3.9.1 https://cytoscape.org/) through the different packages: GeneMANIA for gene function prediction from functional association networks, CytoHubba for the identification of hub genes, The Molecular Complex Detection (MCODE) for the determination of highly interconnected network region, and ShinyGO (version 0.65; http://bioinformatics.sdstate.edu/go/) to identify enrichments with the Gene Ontology (GO) domains and the curated pathway KEGG database.



Cytoscape

GeneMANIA

CytoHubba

MCODE

ShinyGO

RESULTS

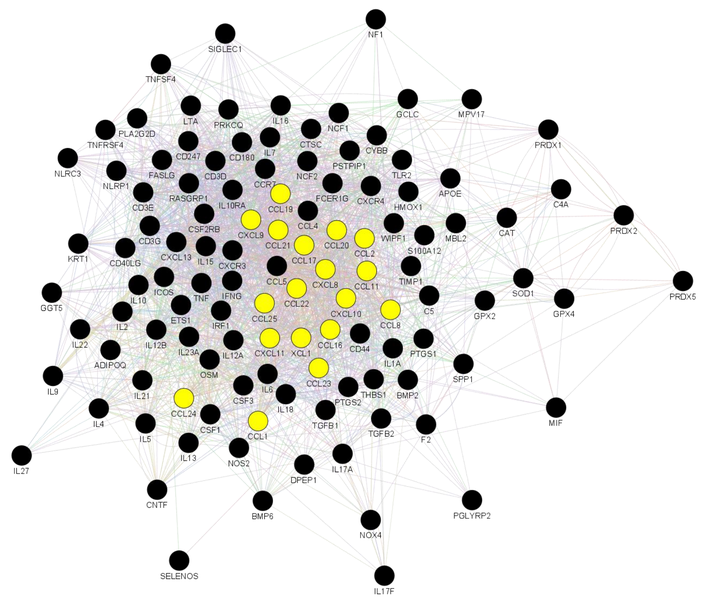


Fig 1. Functional association network of DEGs involved in intestinal inflammation due to weaning.

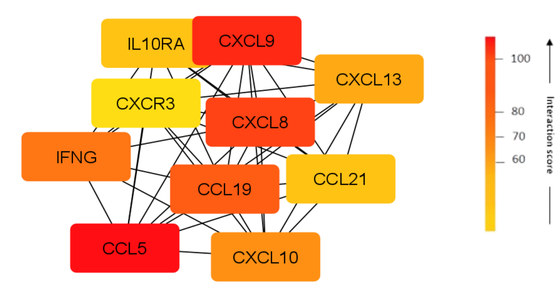


Fig 2. Interaction degree network of key genes involved intestinal inflammation after weaning.

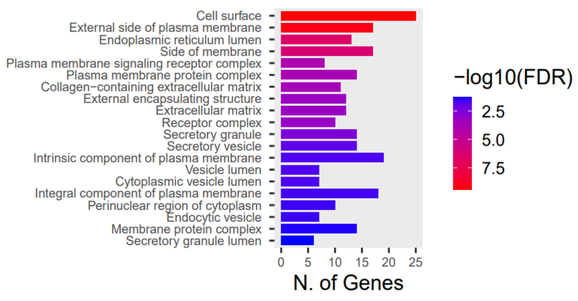


Fig 3. Cellular companant of DEG

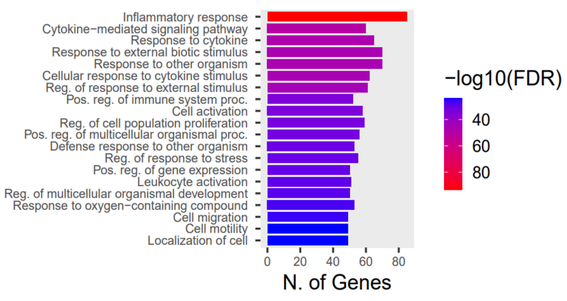


Fig 4. Biological process of DEG

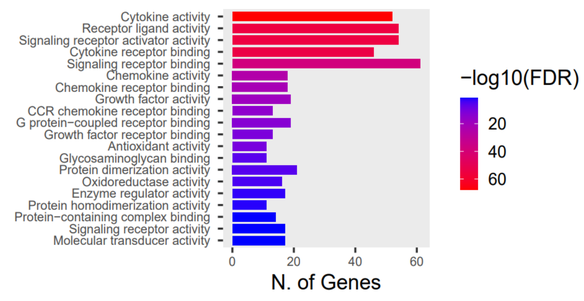


Fig 5. Molecular function of DEG

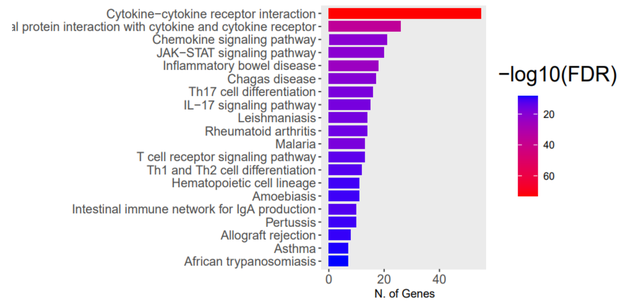


Fig 6. Signaling pathways involved in intestinal inflammation after weaning.

The findings unveiled the presence of six pivotal genes, namely **CCL19, CCL5, CXCL9, CXCL8, IFNG**, and **CXCL10**, which appear to play a role in the development and progression of intestinal inflammation in weaned infants. The identified biological processes of significant involvement included the **inflammatory response, response to external biotic stimulus, response to cytokine, and regulation of inflammatory response**. Additionally, the analysis revealed significant associations between these genes and pathways such as **cytokine-cytokine receptor interaction, inflammation mediated by chemokine, cytokine signaling pathway, inflammatory bowel disease, and chemokine signaling pathway.**

CONCLUSION

In conclusion, all the results obtained suggest that the balanced intestinal microbiota plays a crucial role in the intestinal homeostasis of infants during weaning. Thus, a diet rich in prebiotics and probiotics can be a very promising therapeutic alternative.

REFERENCES

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