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Unraveling the triad: interplay between prenatal depression, inflammation and the gut microbiota - Integrative analysis

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Introduction

- **The gut-brain axis (GBA)** links the gut and brain through various systems, influencing emotions, cognition, and gut health. The gut microbiota plays a key role, with imbalances potentially leading to **systemic inflammation** and **depressive symptoms**. Genetic and environmental factors also contribute to depression by disrupting the gut barrier and neurotransmitter balance. During the perinatal period, hormonal changes and inflammation may impact **maternal mental health** via the GBA. Alterations in maternal gut microbiota during pregnancy can affect both maternal and infant health.

- This study explores the **role of microbiota and immunity in pregnancy-related depression**, focusing on key genes and pathways involved in gut-brain communication and neuroinflammation.

Methods

- **PPI:** The protein-protein interactions network
- **GO:** Gene Ontology

Expressed genes datasets — 219 GENES

PubMed

ReGEO Restructured GEO

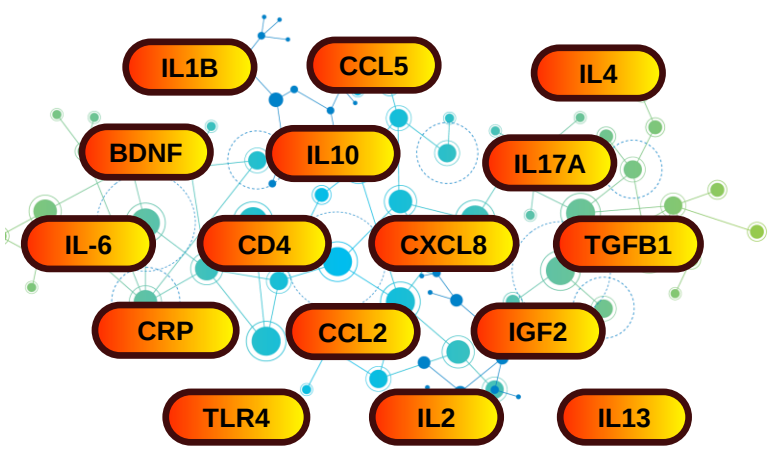
PPI — StringApp

GO Analysis — R SRPLOT

Metabolomic analysis — MetaboAnalyst 6.0 Metabo Analyst

Results & Discussion

1. Protein-protein interaction networks



The protein-protein interaction networks of DEGs obtained are determined **16 main genes** involved in various signalling pathways linked to **prenatal depression** and **neuroinflammation**

2. Enrichment analysis GO and KEGG

Genes were enriched in bacterial response, MAPK cascade regulation, and inflammation **(Figure 1). Molecular functions** included cytokine and neurotrophin receptor binding. **Cell components** focused on vesicles, synapses, and membrane rafts. Overall, these DEGs are mainly associated with **inflammation** and **neuroinflammation**

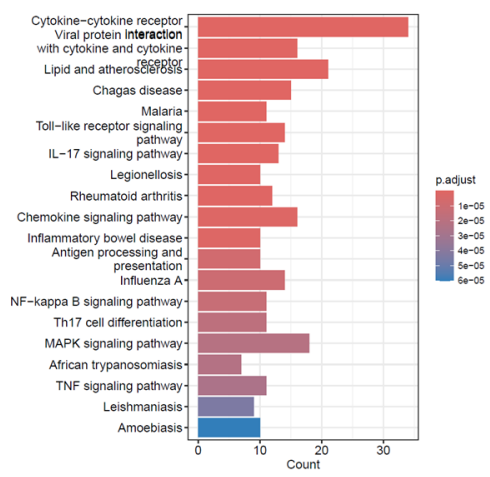
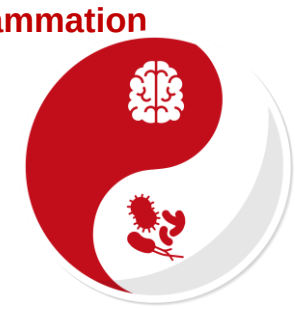


Figure 2: KEGG pathway enrichment analysis of the selected DEGs (P < 1e-5)



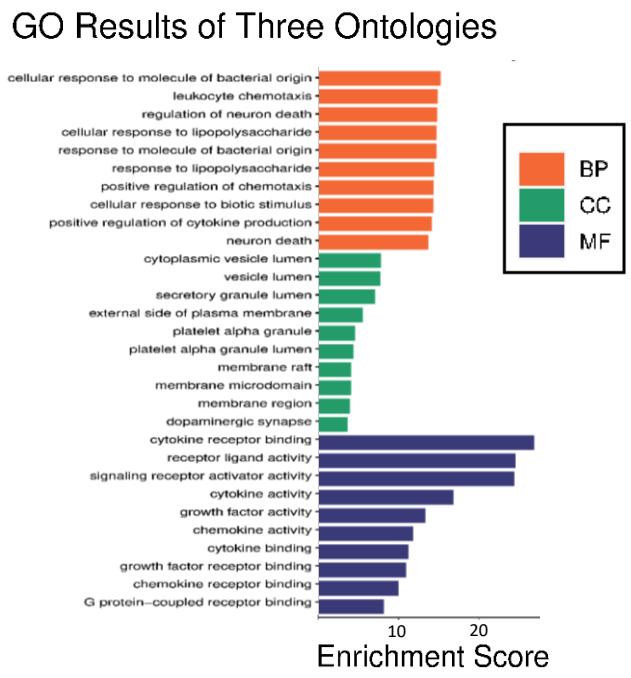
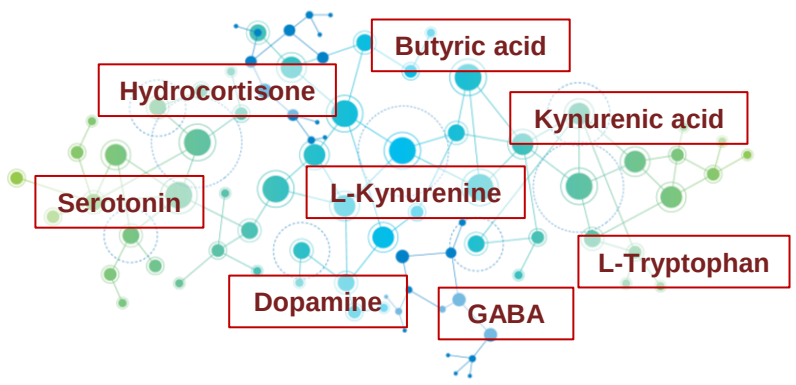


Figure1: The top 10 enrichment score in the GO enrichment analysis of the selected genes; molecular functions for DEGs (P value ≤ 6 e-9).

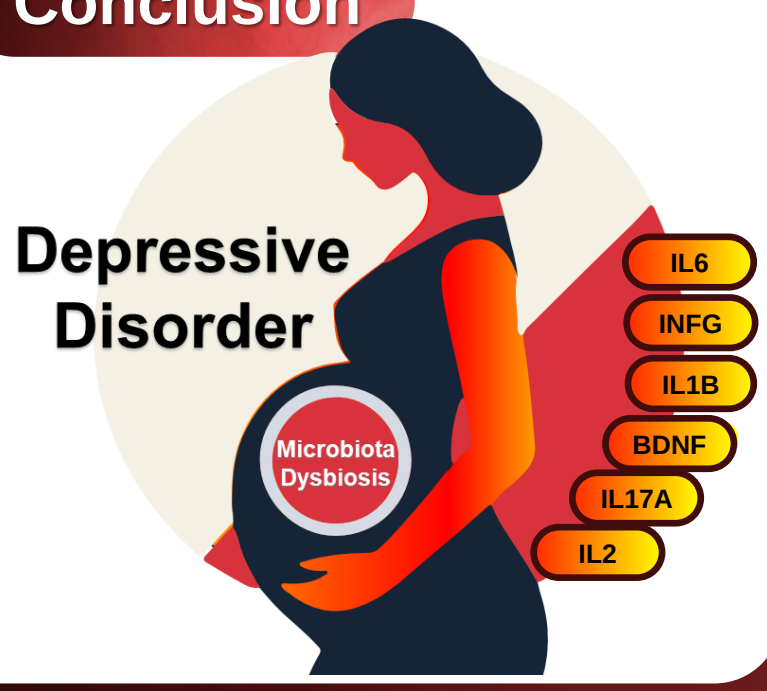
The most significantly enriched pathways of the DEGs were subjected to **KEGG analysis (Figure 2).** The signalling pathways of the DEGs were mainly enriched in Signalling molecules and interaction, Inflammatory bowel disease, Endocrine and metabolic diseases, IL-17 signalling pathway and Neurotrophin signalling pathway. ClusterProfiler's GO enrichment and KEGG pathway results support SRplot's findings

3. MetaboAnalyst anlysis

To establish the link between our genes, the pathways, neuroinflammation and perinatal depression, we employed the network analysis module. The metabolites most involved in the pathways identified were **Cortisol, serotonin, dopamine, gamma-aminobutyric acid (GABA), tryptophan, butyric acid and kynurenic acid**.



Conclusion



brain sciences

MDPI