Integrated omics-based analysis reveals distinct microbial-metabolite interaction networks in eosinophilic and non-eosinophilic CRSwNP in a Chinese population

14
Eosinophilic (Eos) CRSwNP

7
Non-eopsinophilic (NonEos) CRSwNP

14
Healthy controls

16S rRNA gene sequencing

Untargeted metabolomics

Microbial diversity

Taxonomic differences

Metabolic alterations

Eosinophilic (Eos) CRSwNP

⇊ Microbial diversity

⇈ *Staphylococcus*
⇈ *Corynebacterium*

⇈ Fumaric acid
⇈ Linoleic acid
⇈ Arachidonic acid

Linked to
- oxidative stress
- lipid-mediated inflammation

Non-eopsinophilic (NonEos) CRSwNP

↓ Microbial diversity

↑ *Streptococcus*
↑ *Anaerococcus*
↑ *Clostridium XIVa*

⇈ Glutamine
⇈ Taurine
⇈ Ethanolamine phosphate

Shifts in amino acid and nitrate metabolism

Correlation analysis

↔

Phenotype-specific networks connect core microbial genera and metabolites

Distinct inflammatory microenvironments between subtypes

- **Divergent microbial and metabolic signatures in Eos and nonEos CRSwNP**

Mechanistic insights into subtype-specific disease processes

May guide development of targeted diagnostic and therapeutic strategies

Zhang H, Zi X, Li X, et al. Rhinology 2026. https://doi.org/10.4193/Rhin25.166

ISSN 0300-0729
RHINOLOGY
Official Journal of the European and International Societies