

Mass General

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meat and dark sources





Dietary and gut microbial determinants of fecal histidine-related metabolites

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More variation in the histidine-related metabolites was explained by the important gut microbiome species than by diet



The proportion of variation was represented by the mean R-squared values, which were computed through a total of 5 iterations of random forest regression models. Each random forest model included an 8:2 training/test split and a 5-fold cross validation.

Key correlation patterns

- with urocanic acid.
- p<0.0001 with urocanic acid).

Conclusion

We demonstrated the relative contributions of the microbiome and diet to histidine-related metabolites in the gut and identified key microbial species linked to these metabolites.

Our findings highlight the need to further explore the role of diet and the gut microbiome in histidine-related metabolic disturbances and health conditions.



Significant positive correlation (p=0.2, FDR-adjusted p=0.08) between liquor and 1-methylhistamine

Clostridiaceae members and R. gnavus were strongly positively correlated (p>0.2, FDR-adjusted p<0.05) with most histidine-related metabolites, except for a strong negative correlation (ρ <-0.4, FDR-adjusted p<0.0001)

Lachnospiraceae family displayed opposite correlation patterns with these metabolites (ρ <-0.2, FDR-adjusted p<0.0001 with most metabolites; p>0.2, FDR-adjusted