RES-062

Gut Microbiota Sugnatures Predict Antihistamine Efficacy in Burn-Related Pruritus

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Background

Post-burn pruritus (PBP) is a frequent and distressing complication of burn injury. Antihistamines are commonly prescribed, yet their efficacy varies among patients. Recent evidence suggests that gut microbiota can modulate immune responses and influence drug effectiveness. However, their role in mediating antihistamine response in PBP remains poorly understood.

Methods

Fifty-six male burn patients were categorized into three groups: no pruritus (NP), histamine-responsive (HR), and histamine-nonresponsive (HNR). Fecal samples were collected at baseline and 8 weeks after antihistamine administration. Microbiota composition was analyzed via 16S rRNA gene sequencing. Functional predictions were generated using PICRUSt2.

Results

Alpha and beta diversity did not differ significantly between groups. However, genus-level analysis identified group-specific patterns: Sutterella was enriched in the HR group, while Faecalimonas, Ligilactobacillus, and Catenibacillus were more abundant in HNR patients. Post-treatment, the HR group showed increased microbial richness and upregulated proteolytic and antioxidant pathways. In contrast, the HNR group demonstrated enrichment of amino acid and fatty acid metabolism with reduced redox-related functions.

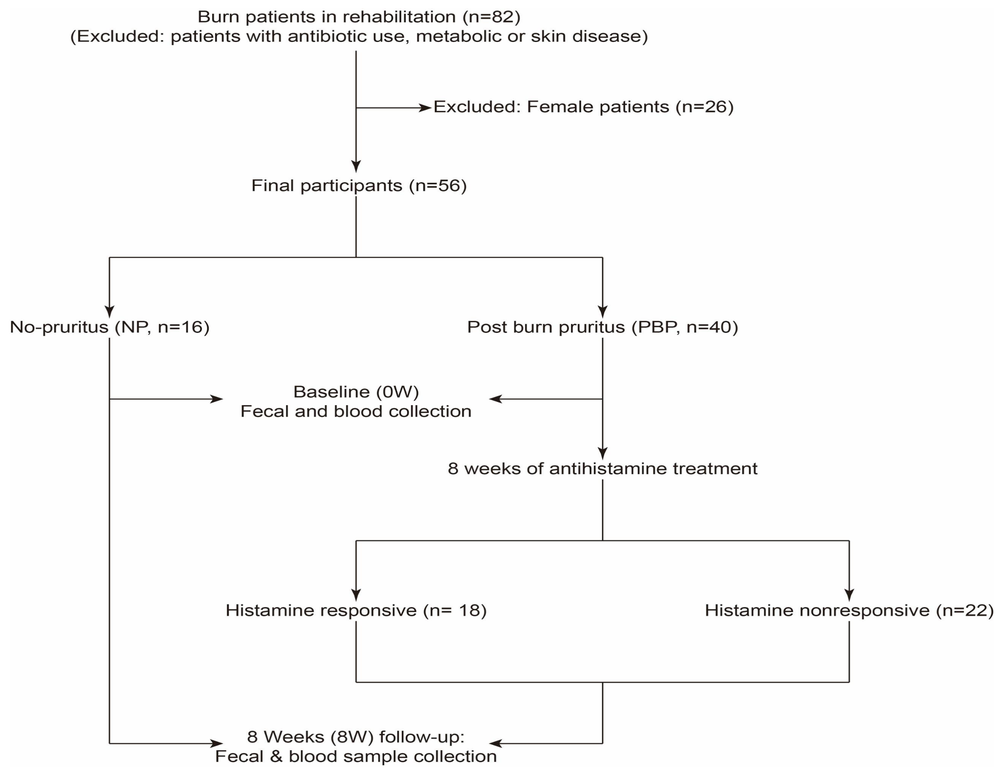

Figure 1. Study design and participants' flow chart

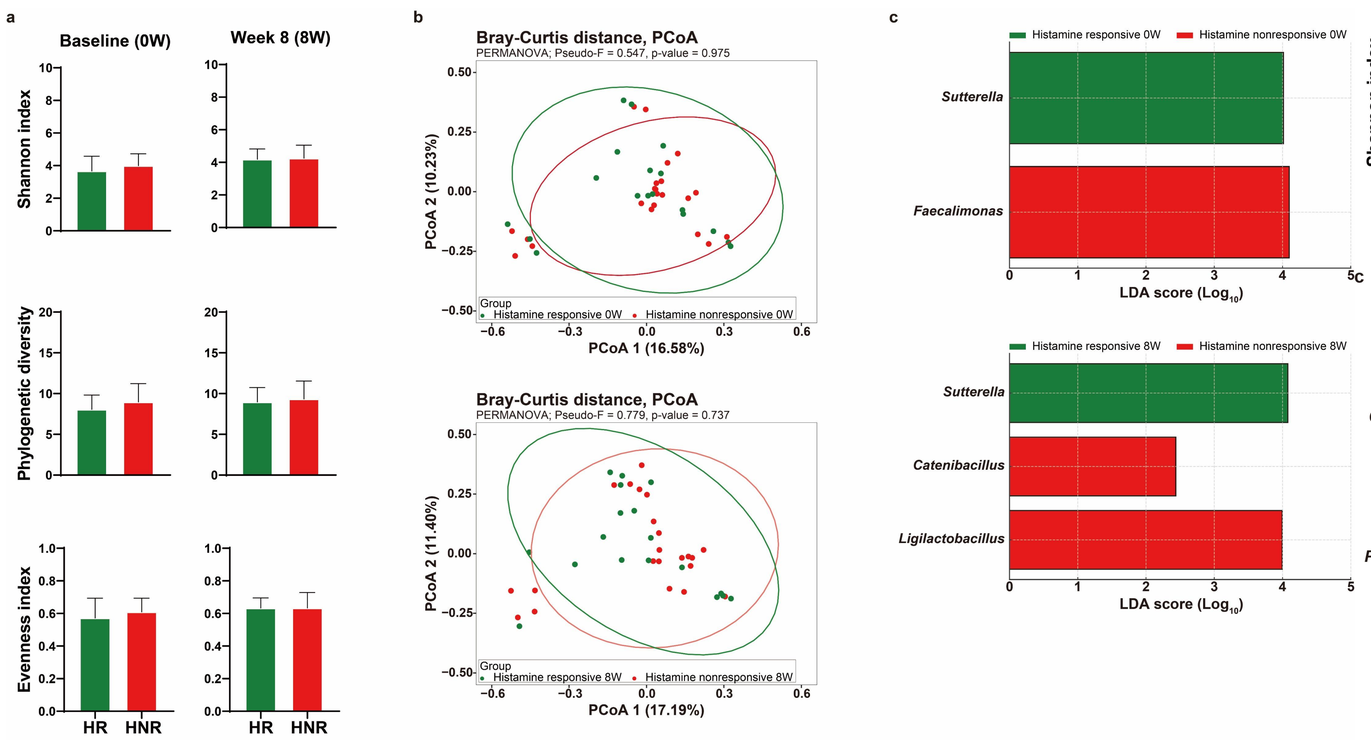

Figure 2. Diversity and taxonomic differences between HR and HNR groups. Diversity and taxonomic differences between HR and HNR groups. (a) Alpha diversity metrics showing no significant differences between groups ($p > 0.05$). (b) Bray–Curtis-based PCoA showing no significant clustering (PERMANOVA, $p > 0.05$). (c) LEfSe analysis revealing *Sutterella* and *Faecalimonas* as enriched in the HR and HNR groups, respectively, at baseline. At Week 8, *Sutterella* remained enriched in the HR group, whereas *Ligilactobacillus* and *Catenibacillus* were enriched in the HNR group ($p < 0.05$).

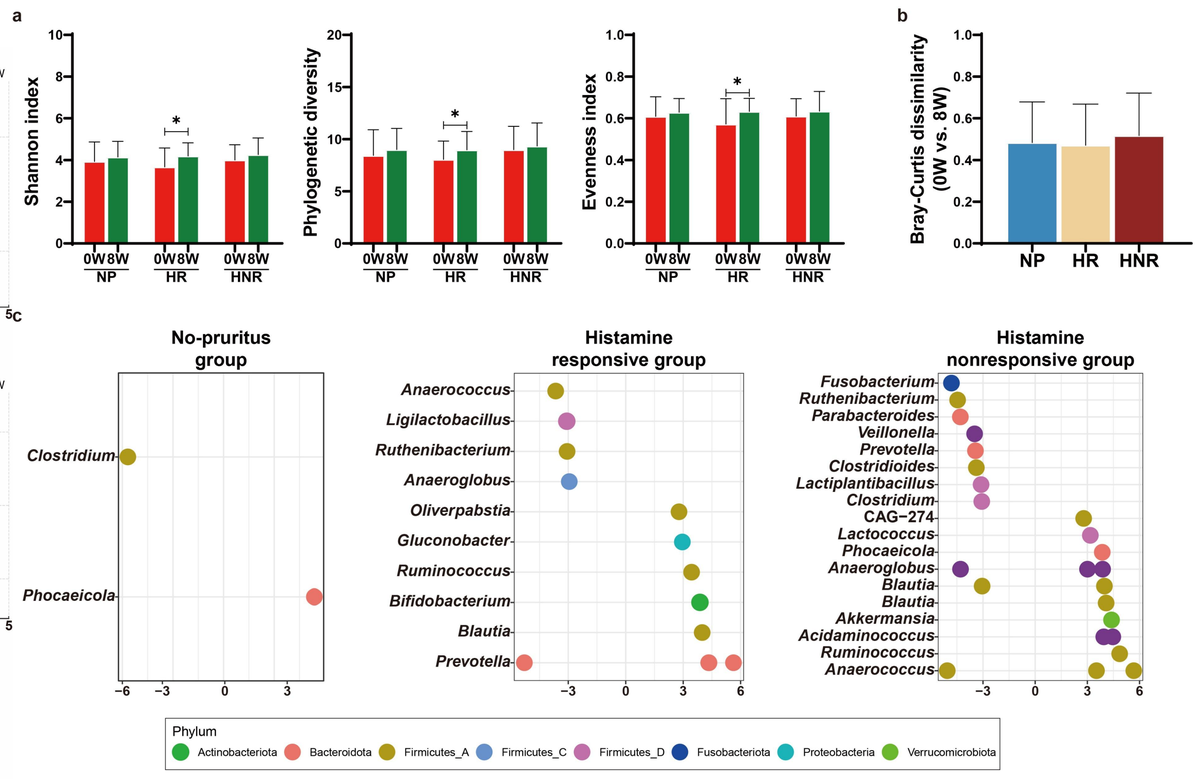

Figure 3. Longitudinal changes in gut microbiota composition in NP, HR, and HNR groups. Longitudinal changes in gut microbiota composition in NP, HR, and HNR groups. (a) Significantly increased alpha diversity in the HR group alone at Week 8 ($p < 0.05$). (b) Bray–Curtis dissimilarity between paired samples (0W vs. 8W) showing no significant changes within any group. (c) edgeR analysis revealing minor changes in the NP group (2 ASVs), with the HR and HNR groups exhibiting more substantial taxonomic shifts. The most significantly altered genera are highlighted.

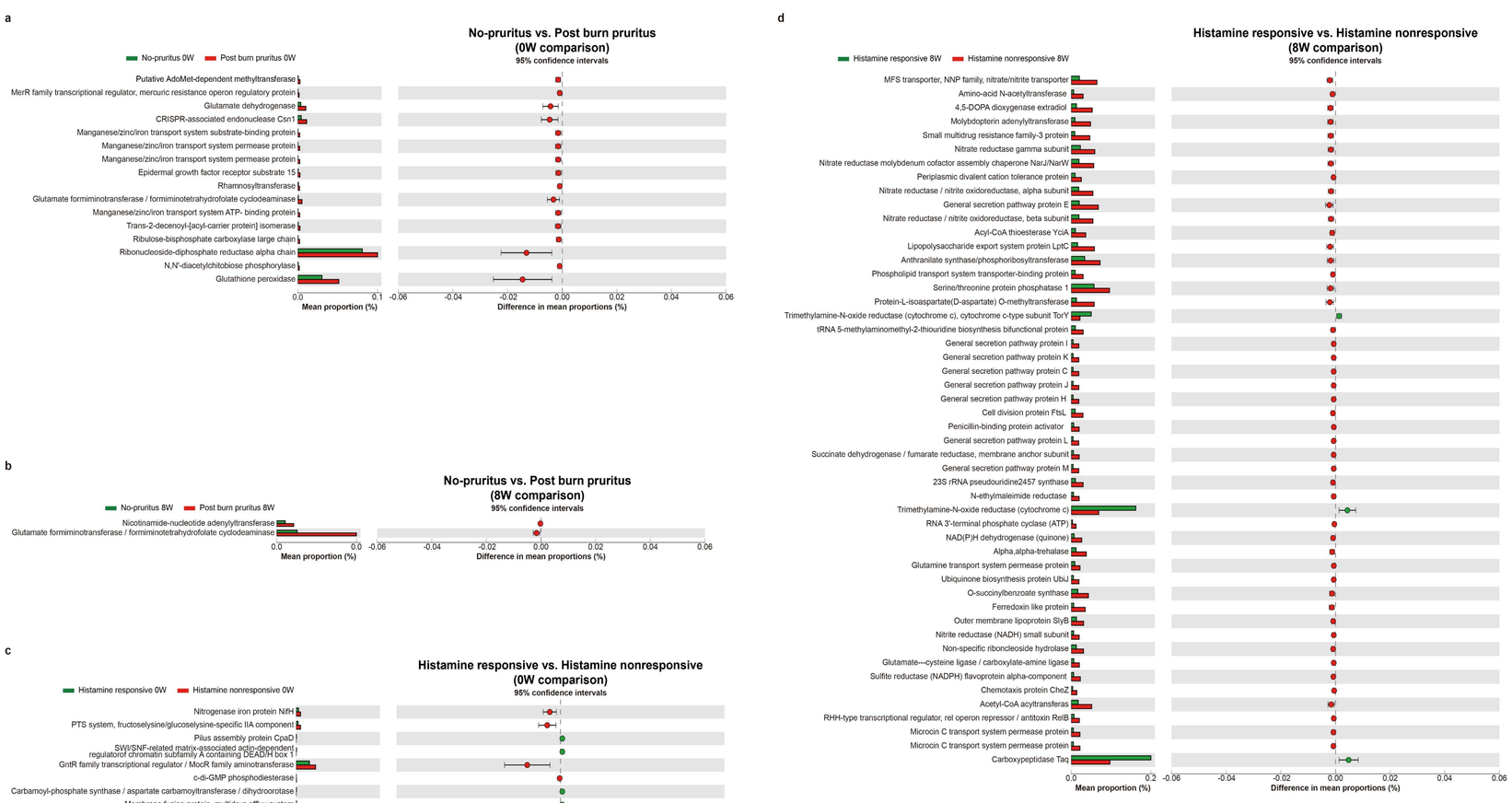

Figure 4. Functional differences in predicted microbial pathways based on PICRUSt2. Functional differences in predicted microbial pathways based on PICRUSt2. (a & b) Comparison between NP and PBP groups at baseline and Week 8. (c & d) Comparison between HR and HNR groups at baseline and Week 8. STAMP analysis identified differentially abundant KEGG orthologs (KOs); only functions showing $p < 0.001$ are presented. Error bars indicate 95% confidence intervals.

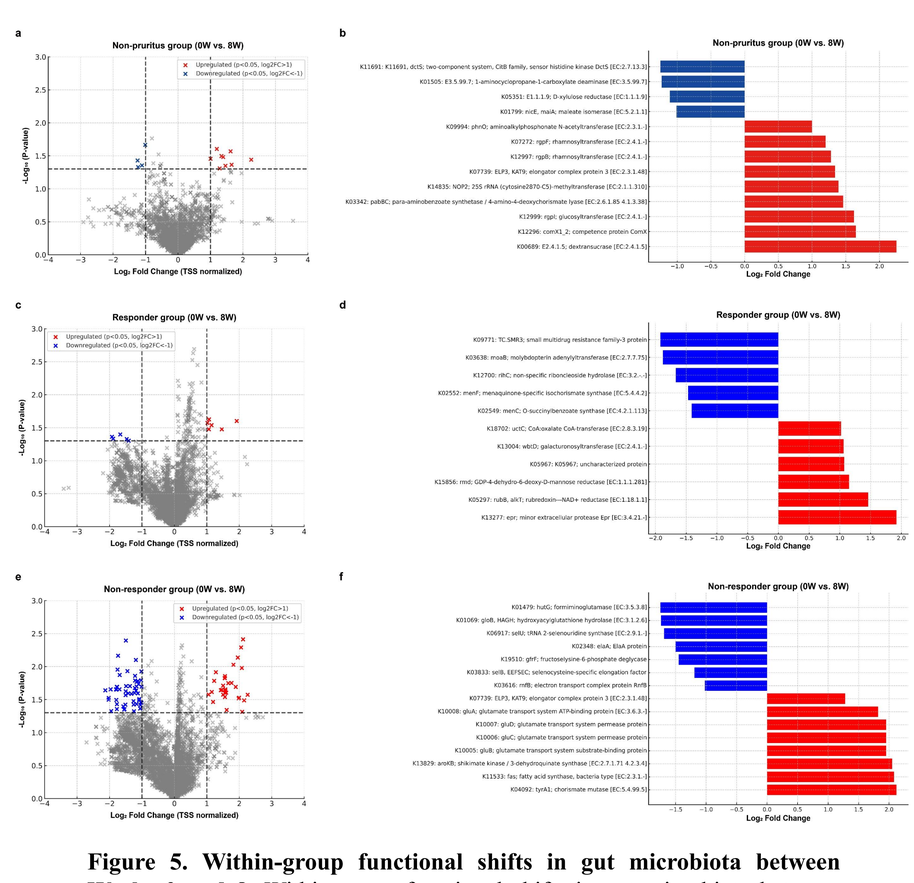

Figure 5. Within-group functional shifts in gut microbiota between Weeks 0 and 8. Within-group functional shifts in gut microbiota between Weeks 0 and 8. Predicted KO functions were analyzed using PICRUSt2 and visualized via volcano plots (log2 FC vs. –log10 *p*-value) and bar charts. (a & b) NP group: moderate functional shifts with limited KO changes. (c & d) HR group: increase in proteolytic and redox-related functions. (e & f) HNR group: the most extensive functional alterations, including activation of amino acid and fatty acid metabolism and downregulation of antioxidant pathways. Only the top 15 significantly altered KOs are shown in the HNR bar chart.

Conclusion

Distinct gut microbiota signatures and functional traits are associated with antihistamine efficacy in burn-related pruritus. These findings highlight the potential of gut microbial profiling as a predictive tool for personalized management of post-burn pruritus.

Acknowledgments

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