Systemic inflammation, tonsil microbiome, obstructive sleep apnea, and surgical outcome among children of different weight status

Hai-Hua Chuang[1], Jen-Fu Hsu[1], Li-Pang Chuang[1], Cheng-Hsun Chiu[1], Yen-Lin Huang [1], Hsueh-Yu Li[1], Ning-Hung Chen[1], Yu-Shu Huang[1], Chun-Wei Chuang[1], Hsin-Chih Lai [2], Chung-Guei Huang [1], and Li-Ang Lee[1]

[1]Chang Gung Memorial Hospital Linkou Main Branch
[2]Chang Gung University

October 13, 2020

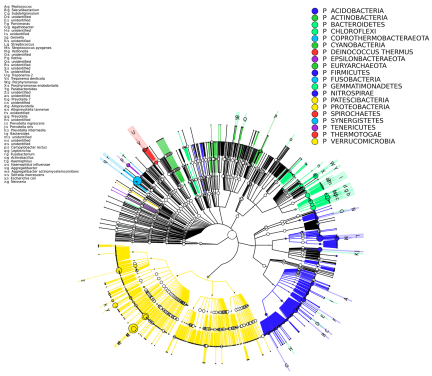
Abstract

Background: Systemic inflammation and tonsil microbiome have been linked to chronic intermittent hypoxia during sleep in children with obstructive sleep apnea (OSA). However, their relationships have not been comprehensively studied. Here, we investigated the associations between systemic inflammation, tonsil microbiome, OSA severity, and surgical outcome in pediatric OSA patients regarding different weight status. Methods: We recruited 33 children with OSA and non-healthy-weight (cases) and 33 children with OSA and healthy-weight (controls) were prospectively recruited and matched by the proportion of chronic tonsillitis. Each patient underwent adenotonsillectomy and received at least 3-month follow-ups. Systemic inflammatory biomarkers (interleukin [IL]-6, IL-10) were detected in the blood sampled in the morning. Tonsil microbiome was identified with 16S ribosomal RNA gene sequencing. OSA severity was assessed by standard whole-night polysomnography. Results: Differences in systemic inflammatory biomarkers, tonsil phyla, and apnea-hypopnea index were not statistically significant between both groups. After adenotonsillectomy, all OSA severity variables significantly improved; however, apnea-hypopnea index was significantly higher in the non-healthy-weight group and serum level of IL-6 significantly reduced in the healthy-weight group. The percentage changes in IL-6 and minimal pulse oxygen saturation were respectively associated with Deinococcus-Thermus and Eremiobacteraeota in the non-healthy-weight group, whereas the percentage change in IL-6 was associated with Patescibacteria and Cloacimonetes in the healthy-weight group. Furthermore, chronic tonsillitis was related to Chloroflexi, Acidobacteria, Euryarchaeota, Thermotogae, Hydrogenedentes, and Rokubacteria in the non-healthy-weight group. Conclusion: These preliminary findings are novel and provide insight for future research to understand the pathogenesis of the disease and to develop personalized treatments.

Hosted file

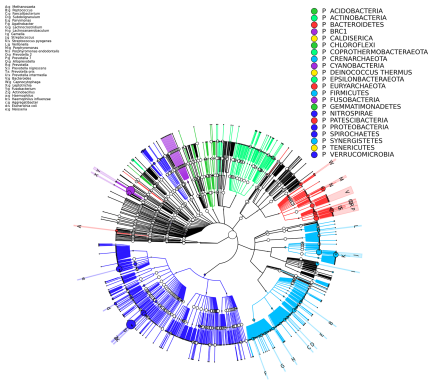
`Manuscript_PAI_20201012.pdf` available at https://authorea.com/users/363186/articles/486429-systemic-inflammation-tonsil-microbiome-obstructive-sleep-apnea-and-surgical-outcome-among-children-of-different-weight-status

OTU tree in the non-healthy-weight group



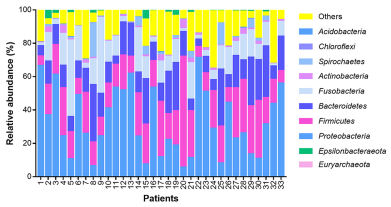
(A)

OTU tree in the healthy-weight group



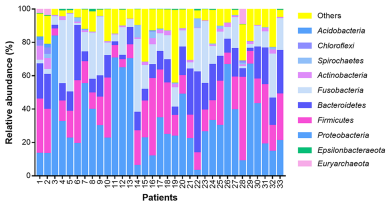
(B)

Top 10 tonsil phyla in the non-healthy-weight group



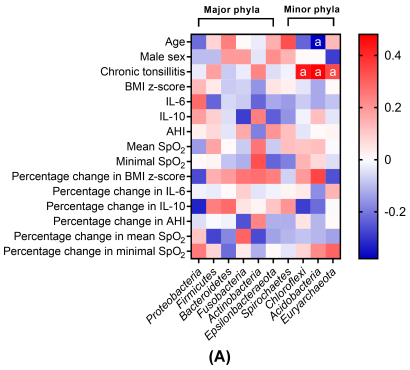
(C)

Top 10 tonsil phyla in the healthy-weight group



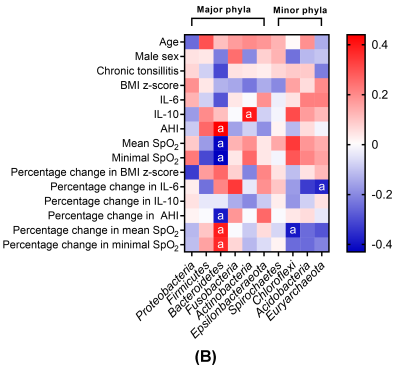
(D)

Non-healthy-weight group

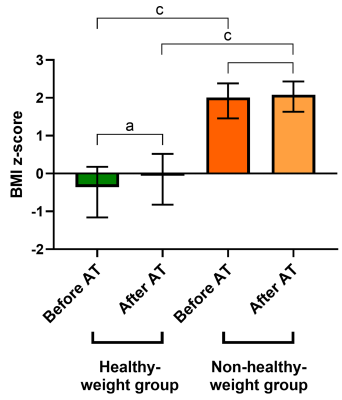


(A)

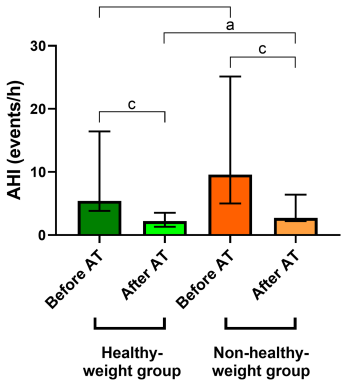
Healthy-weight group



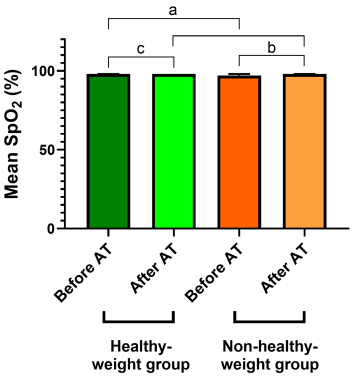
(B)



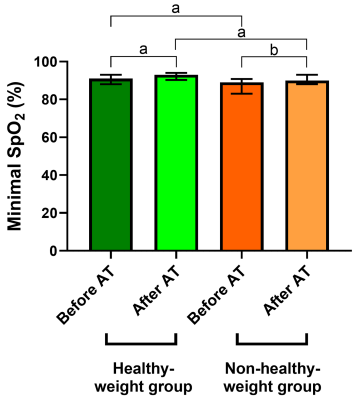
(A)



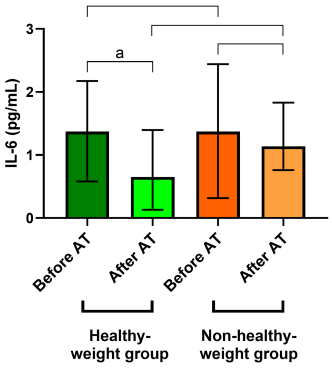
(B)



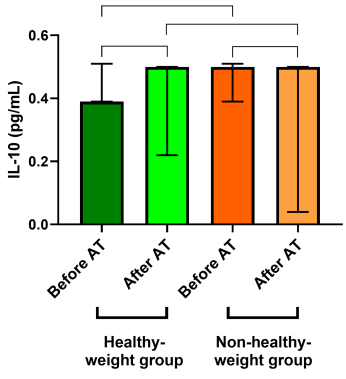
(C)



(D)



(E)



(F)