

Analysis of Conjunctival Sac Microbiome in Meibomian Gland Dysfunction and Mixed Dry Eye Patients

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Abstract

Purpose: Ocular surface microbiome changes can affect meibomian gland dysfunction (MGD) development. This study aimed to observe the differences in the microbial community of the conjunctival sac between patients with MGD and with aqueous-deficient dry eye (ADDE). *Patients and methods:* Conjunctival sac swabs were collected from 15 eyes with meibomian gland dysfunction and 13 eyes with mixed dry eye (MGD with ADDE). Isolated bacterial DNA from conjunctival sac swabs were analyzed with 16S ribosomal RNA (rRNA) gene amplicon sequencing. Alpha diversity analysis of microbial community diversity was performed by Chao1 index, Shannon index and Simpson index. Beta diversity was validated with principal coordinate analysis (PcoA) and bioinformatic analysis of relative abundances and their functional annotations was performed at the genus levels. *Results:* There was no significant difference in alpha diversity between the two groups of dry eye patients (chao1 index, $P=0.245$; Shannon index, $P=0.570$; Simpson index, $P=0.582$), but there was a difference in beta diversity ($P=0.001$). *Ralstonia*, *Corynebacterium*, *Burkholderia-Caballeronia-Paraburkholderia*, *Thiothrix* and *Cutibacterium* were the top 5 genus, *Ralstonia* and *Corynebacterium* were significantly different between the two groups. At the species level, the infection rate and abundance of bacteria including *Comamonas denitrificans* (MGD v.s. Mixed, 100% v.s. 0%, $P=0.002$), *Raoultella planticola* (100% v.s. 0%, $P=0.002$), *Pseudomonas mosselii* (100% v.s. 40%, $P=0.011$) and *Pseudomonas aeruginosa* (70% v.s. 0%, $P=0.017$) were significantly different between the two groups. Functional annotation showed that differences in the microbial pattern of the conjunctival sac between the two groups were accompanied by differences in the expression levels of genes controlling carbohydrate metabolism and histidine kinases, which were higher in the mixed dry eye group. *Conclusion:* The microbial community structure of the MGD dry eye group was similar to that of the Mixed dry eye group, but there were differences in the relative abundance and infection-positive rate of partial specific microorganisms, accompanied by differences in carbohydrate metabolism and histidine kinase expression. *Corynebacterium*, and *Ralstonia* may play important roles in the pathogenesis of MGD and mixed dry eye.

Keywords

Meibomian Gland Dysfunction, Aqueous-Deficient Dry Eye, Ocular Surface, Microbiome, Conjunctival Sac