

Metagenomic Analysis of Human Lens Microbiota Associated with Ophthalmic Diseases

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Abstract

© 2016, Springer Science+Business Media New York. Keratoconus is an ophthalmological pathology which is manifested in noninflammatory conical protrusion of the central part of the cornea. Its etiology is still unknown and pathogenesis is poorly explored. There are number of reports supporting either genetic, metabolic, immunological, endocrinological, or ecological theories with several evidences of its association to other diseases. Nevertheless, the underlying reason of keratoconus development remains unknown. In this study, we applied next-generation sequencing approach for establishing a pipeline for analysis of potential involvement of microorganisms in the development of keratoconus. To assess the variability of lens microbiota, we performed 454 pyrosequencing of 16S rRNA gene. We compared bacterial community from 12 patients with keratoconus, keratoconjunctivitis, and myopia. Proteobacteria was the most dominant phylum (90 %), which were present in every sample. We also found the presence of phyla Actinobacteria and Firmicutes in each lens sample. On the species level, we were able to detect more than 150 bacterial strains, belonging to Enterobacteriales (52.7 %); Pseudomonadales (25 %), Burkholderiales (5.4 %), Sphingomonadales (5.1 %), Rhizobiales (4.4 %), Lactobacillales (1.3 %), Actinomycetales (1.2 %), Caulobacteriales (1.2 %), and Bacillales (1 %).

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Keywords

16S rRNA, Contact lenses, Keratoconjunctivitis, Keratoconus, Metagenomics

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