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Short Communication

Ocular Surface Microbiome in Chronic Conjunctivitis: Exploring New Frontiers in Diagnosis and Treatment

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DESCRIPTION

The human ocular surface, once considered a sterile environment, is now recognized as hosting a diverse and dynamic microbial community. Recent advances in metagenomics and next-generation sequencing have facilitated the characterization of the ocular surface microbiome, revealing its potential role in maintaining ocular health and contributing to disease pathogenesis. Among the disorders of interest, chronic conjunctivitis has emerged as a condition in which microbial dysbiosis may play a pivotal role, reshaping how clinicians understand and approach diagnosis and treatment [1].

Chronic conjunctivitis, defined as inflammation of the conjunctiva lasting more than four weeks, presents with persistent redness, discomfort, foreign body sensation, and discharge. It may be caused by a wide variety of agents, including bacterial, viral, chlamydial, allergic, and autoimmune factors. In many cases, conventional treatments such as antibiotics or antihistamines fail to provide sustained relief, raising the question of underlying microbial imbalance rather than a simple acute infection. The investigation into the ocular surface microbiome offers a promising new lens through which chronic conjunctivitis can be re-evaluated [2-4].

The normal ocular surface microbiome is composed primarily of commensal bacteria such as *Staphylococcus epidermidis*, *Corynebacterium spp.*, Propionibacterium acnes, and *Streptococcus spp*. These organisms are believed to contribute to ocular surface immunity by outcompeting pathogenic bacteria, modulating host immune responses, and maintaining barrier integrity. Factors such as age, environment, contact lens use, systemic disease, and antibiotic exposure can influence the diversity and composition of the ocular microbiota [5,6].

In patients with chronic conjunctivitis, studies have shown a reduced microbial diversity and an increase in potentially pathogenic species, a phenomenon known as dysbiosis. Common findings include an overrepresentation of *Staphylococcus aureus, Pseudomonas aeruginosa*, and in some cases, *Moraxella* and *Haemophilus* species. These alterations may provoke a sustained inflammatory response, perpetuating the cycle of redness, irritation, and tissue damage. Dysbiosis may also disrupt the mucin layer of the tear film, increasing ocular surface vulnerability and contributing to symptoms similar to dry eye disease [7-9].

Modern sequencing techniques, particularly 16S ribosomal RNA gene sequencing, have been instrumental in identifying microbial signatures associated with different forms of conjunctivitis. For example, allergic conjunctivitis may show shifts toward certain *actinobacteria*, while infectious cases show distinct clusters of gram-negative or gram-positive organisms. These insights have prompted researchers to explore microbiome profiling as a diagnostic tool, potentially allowing for more personalized and targeted therapies.

Therapeutic implications of the ocular microbiome are vast. Restoring a balanced microbial environment, rather than simply eliminating perceived pathogens, may be key to managing chronic conjunctivitis. Approaches such as topical probiotics, prebiotics, and microbiome-modulating agents are being explored to this end. For example, formulations containing beneficial strains of *Lactobacillus* and *Bifidobacterium* have shown promise in animal models in reducing ocular surface inflammation and pathogen colonization. The concept of microbial transplantation, akin to fecal transplants in gastrointestinal disease, has also been proposed for refractory ocular surface disorders, though clinical application remains in its infancy.

In addition to direct modulation, avoiding unnecessary disruption of the microbiome is essential. Overuse of broad-spectrum antibiotics, particularly in non-bacterial conjunctivitis, can lead to resistance and long-term alterations in ocular flora. Judicious use of antimicrobials, informed by culture or molecular diagnostic results, should be the standard of care. Likewise, preservative-free artificial tears and anti-inflammatory therapies may help support microbiome recovery in patients with non-infectious inflammation.

Beyond conjunctivitis, ocular surface microbiome research is extending into other domains such as blepharitis, dry eye disease, and post-surgical healing. In each case, a pattern of dysbiosis is emerging, suggesting that microbial balance is a unifying element of ocular surface homeostasis. Integration of microbiome screening into routine ophthalmic evaluation may ultimately become a reality, guiding clinical decisions and improving patient outcomes [10].

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