Effect of a Co-culture extract of Staphylococcus epidermidis and Escherichia coli on the growth rate of Escherichia coli

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Abstract

Background: Urinary tract infections (UTIs) are a major public health concern and among the most common infections. They are caused by various bacteria, including *Escherichia coli*, and in some cases, UTIs are polymicrobial. In polymicrobial infections, bacteria produce secondary metabolites that can either promote or inhibit one another's growth. This study investigates the effect of a co-culture extract from *Staphylococcus epidermidis* and *Escherichia coli* on the growth rate of *E. coli*.
Materials and methods: Standard strains of *Staphylococcus epidermidis* and *Escherichia coli* were co-cultured in Communal liquid medium. After centrifugation, the supernatant was collected and sequentially passed through a 0.22 µm syringe filter and a 10 kDa Amicon filter. Peptide fractions were then purified by HPLC. The effects of the co-culture extract and purified fractions on *E. coli* were subsequently evaluated using broth microdilution, colony and cell counting on agar plates, and flow cytometry.
Results: The MIC values of the crude extract, filtered co-culture extract, and peptide fraction F2 (RT 8.083) against *Escherichia coli* were >500 µg/mL. In the presence of the co-culture extract and peptide fraction F2, *E. coli* growth increased, with colony counts rising from 88.33×10^8 to 104.33×10^8 CFU/mL and from 180.33×10^5 to 230×10^5 CFU/mL, respectively. Flow cytometric analysis showed that more *Escherichia coli* cells remained viable when treated with peptide fraction F2 (RT 8.083) than with the unfractionated extract.
Conclusion: The crude co-culture extract, filtered extract, and peptide fraction F2 (RT 8.083) not only lacked antimicrobial activity against *Escherichia coli* but also promoted its growth—by approximately 18% for the crude and filtered extracts and 28% for fraction F2. The findings suggest that some components produced by coculture may stimulate the growth of *Escherichia coli* under laboratory conditions. Further research is needed to understand how this effect occurs and whether it has clinical significance.

Key words: Bacterial interactions, polymicrobial infections, Urinary tract infections, drug resistance, Staphylococcus epidermidis, Escherichia coli.

In Vitro Antileishmanial Activity of HESA-A against *Leishmania infantum* Promastigotes

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Abstract

Background and Objective: Visceral leishmaniasis is a potentially fatal parasitic disease, and available treatments may be associated with limitations such as toxicity, treatment failure, high costs, and drug resistance. This study aimed to investigate the in vitro antileishmanial activity of HESA-A against promastigotes of *Leishmania infantum* and compare the observed activity with that of meglumine antimoniate.
Materials and Methods: Stationary-phase promastigotes of *L. infantum* (MCAN/IR/96/LON49) were exposed to different concentrations of HESA-A (300, 150, 75, 35.5, 17.75, 8.87, and 4.43 µg/mL). Parasite viability was assessed using the MTT colorimetric assay after 24, 48, and 72 hours of exposure. The 50% inhibitory concentration (IC_{50}) was estimated using linear regression analysis. Morphological changes in treated promastigotes were also examined by light microscopy.
Results: A decrease in the IC_{50} values was observed as the exposure duration increased from 24 to 72 hours. The IC_{50} values of HESA-A at 24, 48, and 72 hours were 150 ± 2, 35.5 ± 4, and 8.87 ± 1 µg/mL, respectively. The corresponding IC_{50} values for meglumine antimoniate were 1,000 ± 2, 500 ± 3, and 250 ± 4 µg/mL, respectively. Under the experimental conditions of this study, HESA-A showed lower measured IC_{50} values than meglumine antimoniate at all three time points. Microscopic examination also revealed morphological changes, including apparent shrinkage and reduced or absent motility in treated promastigotes. These findings are limited to the promastigote stage of the parasite under in vitro conditions.
Conclusion: HESA-A inhibited *L. infantum* promastigotes in vitro and showed lower IC_{50} values than meglumine antimoniate. These preliminary findings are limited to the promastigote stage, and further studies involving intracellular amastigotes, mammalian cell cytotoxicity assessment, and in vivo models are required to evaluate the potential therapeutic value of HESA-A.
Keywords: HESA-A; Leishmania infantum; visceral leishmaniasis; antileishmanial activity; MTT assay; IC_{50}.

Macrophage Engineering and Functional Reprogramming: Emerging Biotechnological Strategies for Cancer and Infectious Diseases

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Abstract

This review discusses emerging biotechnological strategies for engineering and functionally reprogramming macrophages to modulate immune responses in infectious diseases and cancer. Macrophages exhibit remarkable functional plasticity, allowing them to adapt to tissue-specific and pathological signals and participate in antimicrobial defense, inflammatory regulation, tissue repair, and tumor progression. Although macrophage activation has traditionally been described using the M1/M2 classification, current evidence supports a broader spectrum of dynamic functional states shaped by the surrounding microenvironment. This plasticity provides an important rationale for therapeutic macrophage reprogramming.

The review first outlines the developmental origins, tissue specialization, and molecular mechanisms governing macrophage function. It then examines major biotechnological approaches for therapeutic modulation, including ex vivo genetic engineering and CAR-macrophage therapy, targeted mRNA delivery for in vivo reprogramming, nanoparticle-based delivery of nucleic acids and immunomodulatory agents, metabolic and signaling pathway modulation, and extracellular vesicle-based strategies. Selected preclinical and early clinical studies illustrate how these approaches may enhance macrophage-mediated antitumor activity, strengthen host defense against intracellular pathogens, or regulate excessive inflammation in conditions such as sepsis. The review also highlights the role of macrophage- and tumor-derived extracellular vesicles in intercellular communication and the regulation of the tumor immune microenvironment.

Finally, the translational challenges of macrophage engineering are discussed, including cellular heterogeneity, tissue-specific responses, targeted delivery, durability of therapeutic effects, long-term safety, manufacturing complexity, and the limited availability of clinical efficacy data. Overall, macrophage reprogramming represents a promising complementary therapeutic strategy for cancer and infectious diseases. Its successful clinical translation, however, will require disease-specific engineering approaches, precise targeting, functional assessment beyond conventional polarization markers, and rigorous evaluation of safety and therapeutic efficacy.

Keywords: Macrophage engineering; Macrophage reprogramming; Tumor-associated macrophages; Extracellular vesicles; Nanoparticle-mediated drug delivery.

Streptococcus pneumoniae Colonization in Families and Communities: Transmission Patterns, Serotype Sharing, and Epidemiological Implications

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Abstract

Streptococcus pneumoniae is an important cause of respiratory tract infections and invasive disease in humans. Asymptomatic nasopharyngeal colonization represents a key stage in the transmission cycle of this bacterium and may also precede the development of disease. Young children play an important role in pneumococcal circulation within the community because of their close contact with family members, attendance at daycare centers and schools, and characteristics of their developing immune systems. The family, as one of the major units of infectious disease transmission, provides an environment in which frequent and prolonged contact between children and adults may contribute to the acquisition, persistence, and spread of pneumococci. However, the identification of a shared serotype in two family members is, by itself, insufficient to establish direct transmission or determine the direction of transmission. Investigating colonization at the household level, alongside community-based studies, can provide valuable information on carriage prevalence, serotype diversity, concurrent colonization with multiple serotypes, and factors influencing transmission. This review examines the biological concepts underlying pneumococcal colonization, the role of families and communities, molecular detection methods, and the limitations of transmission inference. It also highlights the importance of longitudinal approaches and high-resolution molecular methods in improving our understanding of the epidemiology of *Streptococcus pneumoniae*.

Keywords: *Streptococcus pneumoniae*; nasopharyngeal colonization; carriage; household transmission; serotype; Co-colonization; molecular epidemiology.