

Identification and Characterization of *Burkholderia cepacia* Complex Species Isolated from Clinical and Environmental Samples

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The *Burkholderia cepacia* complex (Bcc) comprises Gram-negative bacteria known to be significant causes of nosocomial and opportunistic infections, particularly in patients with compromised immune systems and those suffering from cystic fibrosis. This group of bacteria is characterized by a high level of antimicrobial resistance and widespread environmental distribution, making them potentially dangerous pathogens in both clinical and environmental settings.

The aim of this study was the isolation and identification of Bcc bacteria from clinical and environmental samples, including species-level differentiation based on phenotypic and molecular-biological characteristics. Additionally, the study evaluated the antibiotic and bacteriophage susceptibility of the identified Bcc strains.

For the isolation and identification of Bcc from clinical and environmental samples, a range of microbiological methods was employed. These included selective and differential culture media, various biochemical tests (e.g., API 20 NE), and advanced approaches such as matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS), polymerase chain reaction (PCR), *recA* gene detection, and ERIC-PCR for genetic profiling of the isolates. These techniques enabled in-depth identification and characterization of Bcc representatives.

The identified Bcc isolates demonstrated species diversity—seven distinct Bcc species were detected—and ERIC-PCR revealed notable genetic variability among strains within the same species. These findings indicate substantial species- and strain-level diversity of Bcc in both clinical and environmental samples.

Antibiotic susceptibility testing showed high resistance rates to chloramphenicol (40.7%) and ticarcillin-clavulanate (95%), while susceptibility to meropenem and trimethoprim-sulfamethoxazole was observed, suggesting these antibiotics as potential treatment options for Bcc infections. Furthermore, the study confirmed the presence of Bcc in environmental sources, highlighting potential reservoirs that may contribute to the transmission of infections.

In conclusion, the findings of this study offer valuable insights into the epidemiology and antimicrobial resistance patterns of Bcc in Georgia, where data on the prevalence and distribution of this pathogen remain scarce. The results may contribute significantly to improving infection control strategies and epidemiological surveillance of Bcc-related infections in the region.