

GENETIC DIVERSITY OF MICROORGANISM ASSOCIATED WITH MAKEUP FOUNDATIONS AND APPLICATION TOOLS

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Decorative cosmetics, particularly makeup foundations and their application tools, are widely used in daily personal care routines and may serve as a source of microbial accumulation and transmission[1]. Microorganisms detected in these products may originate from the natural human skin microbiota as well as from environmental sources or improper usage practices, including potentially pathogenic species[2]. The genetic diversity of microorganisms in cosmetic products remains insufficiently explored, particularly in the context of long-term product use and repeated contact with the skin. Molecular analyses enabling the identification of bacterial genotypes are essential for understanding microbial diversity, tracking potential sources of contamination, and assessing possible health risks associated with cosmetic product use[3].

The aim of this study was to evaluate the genetic diversity of microorganisms found in makeup foundations and the application tools used with them.

Genomic DNA was extracted from bacterial isolates obtained from makeup foundation samples using the PureLink Genomic DNA Mini Kit according to the manufacturer's instructions. Bacterial identification was performed by PCR amplification of an approximately 1500 bp fragment of the 16S rRNA gene using universal primers 27F and 1541R, followed by agarose gel electrophoresis and visualization under UV light. Representative PCR products were purified, sequenced, and analyzed using MEGA X software, with sequence comparison performed against the GenBank database using NCBI BLAST.

A total of four microorganisms were identified in makeup foundations and their application tools, comprising two distinct fungal species and two bacterial species. The fungal species detected were *Aspergillus oryzae* and *Penicillium hordei*, while the bacterial species included *Priestia aryabhatai* and *Achromobacter xylosoxidans*. The presence of both fungal and bacterial taxa indicates mixed contamination patterns, likely influenced by repeated product use and environmental exposure.

The results of this study demonstrate the presence of both fungi and bacteria in makeup foundations and their application tools, which may contribute to the development of health-related issues, emphasizing the necessity for further research.

[1] M. Almukainzi, L. Alotaibi, A. Abdulwahab, N. Albukhary, and A. M. E. Mahdy, "Quality and safety investigation of commonly used topical cosmetic preparations," *Scientific Reports*, vol. 12, no. 1, p. 18299, Oct. 2022, doi: 10.1038/s41598-022-21771-7.

[2] I. K. Bedaida et al., "Makeup testers as reservoirs and transmission sources of antibiotic resistant bacteria," *Infection Disease & Health*, vol. 30, no. 3, pp. 211–216, Mar. 2025, doi: 10.1016/j.idh.2025.03.001.

[3] M. Ivashko, S. Burmei, L. Yusko, T. Chaikovska, and N. Boyko, "Microbiological diagnostics: From traditional to molecular genetic methods: A literature review," *Bulletin of Medical and Biological Research*, vol. 5, no. 4, pp. 34–41, Oct. 2023, doi: 10.61751/bmbr/4.2023.34.