

Illumina MiSeq Sequencing for Bacteria Identification on Audio-Visual Materials

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Abstract : Microbial deterioration threatens all objects of cultural heritage, including audio-visual materials. Fungi are commonly known to be the main factor in audio-visual material deterioration. However, although being neglected, bacteria also play a significant role. In addition to microbial contamination of materials, it is also essential to analyse air as a possible contamination source. This work aims to identify bacterial species in the archives of the Czech Republic that occur on audio-visual materials as well as in the air in the archives. For sampling purposes, the smears from the materials were taken by sterile polyurethane sponges, and the air was collected using a MAS-100 aeroscope. Metagenomic DNA from all collected samples was immediately isolated and stored at -20 °C. DNA library for the 16S rRNA gene was prepared using two-step PCR and specific primers and the concentration step was included due to meagre yields of the DNA. After that, the samples were sent to the University of Fairbanks, Alaska, for Illumina MiSeq sequencing. Subsequently, the analysis of the sequences was conducted in R software. The obtained sequences were assigned to the corresponding bacterial species using the DADA2 package. The impact of air contamination and the impact of different photosensitive layers that audio-visual materials were made of, such as gelatine, albumen, and collodion, were evaluated. As a next step, we will take a deeper focus on air contamination. We will select an appropriate culture-dependent approach along with a culture-independent approach to observe a metabolically active species in the air. Acknowledgment: This project is supported by grant no. DG18P02OVV062 of the Ministry of Culture of the Czech Republic.

Keywords : cultural heritage, Illumina MiSeq, metagenomics, microbial identification

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