S18-1
Environmental change and its affect on microbial ecosystems

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環境改変と微生物生態系
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Key word: Microbial ecosystem, Environmental change, Infectious disease, Aquatic environment

Humans have changed their environment to survive and to achieve a safer and more comfortable life. For example, drinking water and wastewater infrastructures are indispensable for civilized societies to prevent water-borne infectious diseases. We install new systems in our house such as air conditioning or circulating bath for comfortable life. However, excessive loading on environments might disturb microbial ecosystems, resulting in outbreaks of pathogenic microbes and the expansion of infectious diseases. Clarifying the relationship between environmental alterations and changes in microbial ecosystems is thus important to prevent further outbreaks of infectious diseases. In this symposium, we aim to understand the links between the following factors: environmental changes; ecosystem disturbance and the occurrence of infectious disease; and impact on society. We focus on Legionella, nontuberculous mycobacteria and Koi herpesvirus (KHV) from the viewpoint of their environmental linkage.

S18-2
Dynamics of Mycobacterium avium in healthy volunteers' residences

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居・住環境における非結核性抗酸菌の動態解明
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Key word: Nontuberculosis mycobacteria, environmental disease, quantitative, physiological activity

Mycobacterium avium complex (MAC) which consists of Mycobacterium avium and M. intracellulare is the major clinical isolate of nontuberculous mycobacteria, and occasionally causes lung diseases but not tuberculosis. MAC infection is thought to be associated with exposure to aerosol generated in residential environments, but its infectious route and source remain unknown because of the lack of knowledge about dynamics of MAC. In this study, we determined the abundance and evaluated physiological activity of Mycobacterium spp. and MAC in biofilm formed in residences with culture-independent approaches. In each residence (46 healthy volunteers), we collected biofilms from 4 points including the surfaces of showerhead, kitchen drain and bathroom drain and the inside of the bathtub inlet pipe. By using 16S rRNA gene targeted quantitative PCR, Mycobacterium spp. were found in 2% of showerhead samples, 52% of kitchen drain samples, 78% of bathroom drain samples and 45% of bathtub inlet pipe samples. M. avium was detected in five bathtub inlet pipes (10^3-10^4 cells/cm²). Respiratory active mycobacteria were frequently detected in the drain samples with Auramine O-CTC staining. In conclusion, drains can be the niches of Mycobacterium spp., but bathtub inlet pipe could be rather suitable environment for survival of M. avium. These findings may contribute to prevent infection with MAC.