Airborne microbiology in enclosed spaces through molecular approach

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Airborne microbiology in enclosed spaces through molecular approach

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Air is an effective vector for microorganisms but its microbial content is still few describe. However, airborne microorganisms are common microbial contaminants in indoor environments making microbial quality of air a particularly relevant matter. Indeed, airborne microorganisms are involved in some respiratory symptoms, allergies or infections among occupants.

Traditionally, most studies use culture methods which do not describe the full microbial diversity. Indeed, only among 1% of environmental microorganisms are cultivable (Amann *et al.*, 1995) and microbial aerosols appear to be particularly subject to non-cultivability because of stresses related to collection methods (Radosevich *et al.*, 2002 ; Wang *et al.*, 2001). Molecular tools, although rarely used in such studies, could provide a better description of airborne microbiology.

This work aims to use molecular tools in order to consider airborne microbial diversity and load. Such study could provide a better description of indoor airborne microbiology.

Air samples were obtained using an experimental high volume bioaerosol collector located in two different places (a museum and an open space office). The overall load of fungi and bacteria was assessed by Quantitative Real time PCR (qPCR). A qualitative view of the diversity was made using a molecular fingerprints tool, the SSCP (Single Strand Conformation Polymorphism).

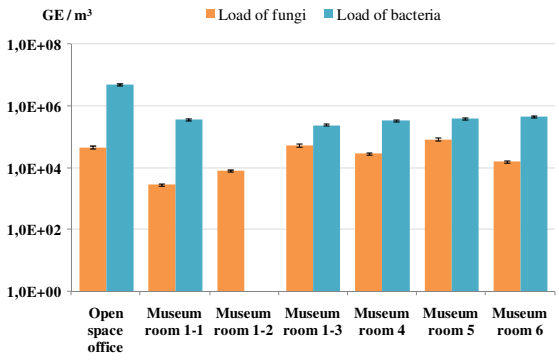

Figure 1. Load of fungi and bacteria obtained in two enclosed spaces by qPCR.

The first results show a load of fungi comprised between $2{,}89.10^3$ and $8{,}57.10^4$ GE/m^3 of air and a load of bacteria comprised between $2{,}46.10^5$ and $4{,}60.10^5$ GE/m^3 of air in the museum. In the office bacterial concentration reach $4{,}90.10^6$ GE/m^3 due to high confinement while fungal concentration observed match with those found in the museum.

The Single Strand Conformation Polymorphism (SSCP) analysis show a high diversity in indoor air and a relative stability of the bacterial community structure in a same place during a short time (several hours). As for eukaryotes, disparities exist in the community structure over a short period of time.

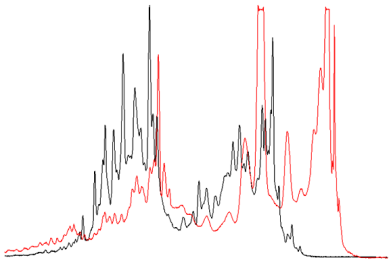

Figure 2. Bacterial SSCP fingerprint of two different sites (the museum in red and the office in black)

Bacterial and eukaryotes SSCP fingerprint were not similar in the two enclosed spaces studied.

Molecular analysis represent a powerful tool to picture the microbial diversity in enclosed spaces. Monitoring microbial communities variations could bring some elements about spatial and temporal diversity.

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