

Aerobiology and cultural heritage: some reflections and future challenges

Cesareo Saiz-Jimenez · Juan M. Gonzalez

Received: 18 April 2007 / Accepted: 25 April 2007
© Springer Science+Business Media B.V. 2007

Aerobiology is focused on the study of passive transport of organisms and particles of biological origin in the atmosphere (Mandrioli and Ariatti 2001). During the last decades, a strong correlation between aerobiology and biodeterioration of works of art has been claimed, due to the fact that the air is the main vehicle for the dispersion of microorganisms (Sorlini 1993). Several lists of airborne microorganisms and their counterparts in works of art have been published (e.g., Nugari et al. 1993; Montacutelli et al. 2000; Monte and Ferrari 2000; Valentin 2003). Generally, airborne microorganisms were similar or identical to those isolated from biodeteriorated works of art (mural paintings, museum collections, etc.) and, in many cases, a direct effect was inferred.

So far, studies on bacterial and fungal communities in indoor environments (caves, tombs, hypogean monuments, buildings, etc.) have mainly been based on cultivation techniques. Recently, the detection of ribosomal RNA gene sequences through the use of molecular methods has become a powerful tool for investigating microbial communities. Results have revealed a significantly broader diversity than cultivation-based studies (Schabereiter-Gurtner et al. 2003; Zimmermann et al. 2005). For example, Laiz et al. (2003) showed clear differences between the

bacteria isolated from the walls of the Altamira cave and those determined by DNA analysis.

While DNA-based molecular analysis of microbial communities allows the detection of microorganisms present in a sample, only a portion of the microorganisms in an environment present detectable physiological activity. The use of RNA-based molecular analysis of environmental samples allows the detection of metabolically active members of the microbial communities since the amount of RNA per cell is proportional to its metabolic activity (Molin and Givskov 1999). The results obtained from comparative analyses based on DNA and RNA have showed differences in the microorganisms that are generally detected by these strategies (Gonzalez et al. 2006; M.C. Portillo, J.M. Gonzalez, and C. Saiz-Jimenez, unpublished data), suggesting distinct perceptions of the microbial communities under study.

A recently published paper by Brodie et al. (2007) described a method that could help to solve these questions. They designed a custom high-density DNA microarray for the comprehensive identification of both bacterial (8,434 Bacteria taxa) and archaeal (307 Archaea taxa) organisms approaching the broad range of microbial diversity dispersed in the air. The authors detected and monitored airborne microorganisms from two cities, Austin and San Antonio, USA, over 17 weeks. At least 1,800 different microorganisms were detected, including the phyla Acidobacteria, Bacteroidetes, Chloroflexi, Cyanobacteria, Firmicutes, Nitrospira,

C. Saiz-Jimenez (✉) · J. M. Gonzalez
Instituto de Recursos Naturales y Agrobiología, CSIC,
Apartado 1052, 41080 Sevilla, Spain
e-mail: saiz@irnase.csic.es

Verrucomicrobia, Proteobacteria, and the candidate bacterial divisions OP3 and TM7. This microbial diversity may be equivalent to that recently observed in some biodeteriorated sites (M.C. Portillo, J.M. Gonzalez, and C. Saiz-Jimenez, unpublished data).

In the near future, modern molecular tools will considerably expand our knowledge of the diversity of airborne microorganisms by enabling the detection of a wide range of so far uncultured microorganisms. Implementing these techniques into classical sampling procedures used in aerobiology will be one of the first requirements to be met.

Acknowledgements The authors acknowledge funding from the Ministry of Education and Science, project CGL2006-07424.

References

- Brodie, E. L., DeSantis, T. Z., Parker, J. P. M., Zubietta, I. X., Piceno, Y. M., & Andersen, G. L. (2007). Urban aerosols harbor diverse and dynamic bacterial populations. *Proceedings of the National Academy of Sciences of the United States of America*, 104, 299–304.
- Gonzalez, J. M., Portillo, M. C., & Saiz-Jimenez, C. (2006). Metabolically active Crenarchaeota in Altamira cave. *Naturwissenschaften*, 93, 42–45.
- Laiz, L., Gonzalez, J. M., & Saiz-Jimenez C. (2003). Microbial communities in caves: Ecology, physiology, effects on paleolithic paintings. In R. J. Koestler, V. R. Koestler, A. E. Carola, & F. E. Nieto-Fernandez (Eds.), *Art, biology, and conservation: Biodeterioration of works of art* (pp. 210–225). New York: The Metropolitan Museum of Art.
- Mandrioli, P., & Ariatti, A. (2001). Aerobiology: Future course of action. *Aerobiologia*, 17, 1–10.
- Montacutelli, R., Maggi, O., Tarsitani, G., & Gabrielli, N. (2000). Aerobiological monitoring of the “Sistine Chapel”: Airborne bacteria and microfungi trends. *Aerobiologia*, 16, 441–448.
- Monte, M., & Ferrari, R. (2000). Airborne microorganisms in a subterranean archaeological area of the basilica of San Lorenzo in Lucina (Rome). *Aerobiologia*, 16, 435–439.
- Molin, S., & Givskov, M. (1999). Application of molecular tools for in situ monitoring of bacterial growth activity. *Environmental Microbiology*, 1, 383–391.
- Nugari, M. P., Realini, M., & Roccardi, A. (1993). Contamination of mural paintings by indoor airborne fungal spores. *Aerobiologia*, 9, 131–139.
- Schabereiter-Gurtner, C., Piñar, G., Lubitz, W., Rolke, S., & Saiz-Jimenez, C. (2003). Acidobacteria in Paleolithic painting caves. In C. Saiz-Jimenez (Ed.), *Molecular biology and cultural heritage* (pp. 15–21). Lisse: Balkema Pub.
- Sorlini, C. (1993). Aerobiology: General and applied aspects on the conservation of art works. *Aerobiologia*, 9, 109–115.
- Valentin, N. (2003). Microbial contamination in museums collections: organic materials. In C. Saiz-Jimenez (Ed.), *Molecular biology and cultural heritage* (pp. 85–91). Lisse: Balkema Pub.
- Zimmermann, J., Gonzalez, J. M., Saiz-Jimenez, C., & Ludwig, W. (2005). Detection and phylogenetic relationships of highly diverse uncultured acidobacterial community on paleolithic paintings in Altamira cave using 23S rRNA sequence analyses. *GeomicrobiologyJournal*, 22, 379–388.