



## **Mineralogical influence on the structure and diversity of bacterial communities associated with silicate minerals**

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The understanding of the mineralogical influences on surface and subsurface microbial community structure and diversity is greatly enhanced by the use of culture-independent molecular techniques both *in situ* and in laboratory experiments. Gleeson et al [2, 3] found significant correlations between certain species of bacteria and fungi and whole-rock geochemistry within a pegmatitic granite. Little is known however about the microbial populations associated with particular silicate minerals, or the extent to which the chemistry of the mineral and the surrounding micro-environment influences the structure of microbial populations. In this study, the biofilm formed on sterile mineral crystals was used to assess the microbial colonization pattern on different silicate minerals during colonization by microorganisms present in a river water during a period of 8 and 12 weeks. Upon retrieval from the river of submerged perforated plastic tubes containing mineral particles (1-2 mm) of albite, biotite, muscovite, quartz and microcline the structure and diversity of the microbial community associated with each type of mineral was evaluated using DNA and ARN-based community fingerprinting approaches (automated ribosomal intergenic spacer analysis – ARISA). The molecular biology approach was combined with multivariate statistics: multidimensional scaling (MDS), and canonical analysis of principal coordinates (CAP) to identify how mineralogical differences influence the microbial community structure

formed on the silicate minerals “incubated” in Liffey River, Ireland. SEM analyses showed variable degrees of colonization on the mineral surfaces. The different substrata selected for different subdivisions of bacteria within the Proteobacteria and statistical analyses suggested a strong mineralogical influence on the structure and composition of the solid phase-associated community with distinct ribotypes being selected on each type of silicate mineral. The results suggest that mineralogical heterogeneity is responsible for the differences in the microbial community structure and diversity of the biofilm formed on the analysed mineral surfaces.

### **References**

[1] Gleeson, D.B., Clipson, N., Melville, K., Gadd, G.M., and McDermott, F. (2005) *Microb. Ecol.* **50**(3), 360-368.

[2] Gleeson D.B., Kennedy N.M., Clipson, N., Melville, K., Gadd, G.M. and McDermott, F.P. (2006) *Microb. Ecol.* **51**(4), 526-534.