

Corrigendum

In the article 'Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes' (Chu *et al.*, 2010), the issue of uniqueness in soil bacterial community composition (endemism) among the study sites was not clearly addressed by the data presented in our original paper. We stated that '~ 55% of the sequences at each site were unique to that site' (page 3001), when in fact this value indicates the proportion of sequences within each soil that were classified into distinct phylotypes (sometimes several different sequences were classified into the same phylotype, since grouping was based on 97% sequence similarity). This error arose because the word 'unique' was incorrectly included in the y-axis legends of Figs 4A and 7A, when in fact the same phylotypes were often present in several soil samples. The correct y-axis legend for those figures should be 'Number of phylotypes (per 1000 sequences)'. Nevertheless, there was a very substantial amount of endemism within the study soils. We found 19 834 different phylotypes within the total of 46 003 detected phylotypes across all soils. The frequency distribution of the different phylotypes among the soils was typical of many ecological communities, with for example 13 196 phylotypes (67%) occurring only once and just 2 phylotypes (0.01%) occurring in all soils. These latter data demonstrate substantial endemism within the soil bacterial communities of the study sites, and better support our main conclusions.

Reference

Chu, H., Fierer, N., Lauber, C.L., Caporaso, J.G., Knight, R., and Grogan, P. (2010) Soil bacterial diversity in the Arctic is not fundamentally different from that found in other biomes. *Environ Microbiol* **12**: 2998–3006.