

微生物地理学のホットスポットとしての極域ハビタット

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Polar habitats as hot spots for microbio-geography

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“Everything is everywhere” (EiE) has long been an intriguing hypothesis, or a theorem or a debate, in microbial ecology. The original EiE hypothesis (Baas-Becking, 1934 *in de Wit and Bouvier*, 2006) is followed by another statement “but the environment selects”. As a whole, the hypothesis predicts that no biogeography would be established for microorganisms, *e.g.*, smaller than 1 mm (Finlay, 2002) but endemism may also be possible (*e.g.*, Martiny *et al.*, 2006). That is, a composition of easily detectable species microflora would be affected by environmental parameters such as temperature, salinity, pH, desiccation, UV radiation, light and/or nutrients availability, *etc.*

We have reported the occurrences of *cosmopolitans* that show no biogeography, and a typical cosmopolitan species was *Bacillus licheniformis* (Jadoon *et al.*, 2013). On the other hand, we have revealed non-cosmopolite (seemingly endemic) distributions for certain species/clones. Wider cosmopolite distributions were shown with lower grouping criteria, *e.g.*, >97% similarity of 16S rRNA gene sequences; however, higher criteria (*e.g.*, >99% similarity) resulted in narrower distributions (endemism) of certain Antarctic bacteria (Nakai *et al.*, 2013). That is, EiE emerges as a result of manipulated grouping criteria; this view is to be relatively readily tested in polar habitats where traditionally recognized cosmopolitans (often minor components of the corresponding microflora), and thus polar habitats would provide *hot* study opportunities.

Another *hot* opportunity comes from the aquatic (benthic) moss vegetation, *a.k.a.* moss pillars, thriving in association with a variety of microorganisms/moss, for which intensive genomic studies have been done (Nakai *et al.*, 2012 publications). Lichens and associated microflora in polar/alpine fellfields and peri-glaciers may also provide *hot* hints for microbio-geography. In addition, a brand new aspect of microbial biogeography is given from the newly established bacterial class *Oligoflexia* (Nakai, Nishijima, *et al.*, 2014). Not a few clones, along with a cultured species, have been reported from a large variety of habitats including an Alpine (German) glacier. Absence/presence of *Oligoflexia*-class species may shed light on previously unknown aspects of microbial biogeography.

References

- de Wit and Bouvier, ‘Everything is everywhere, but, the environment selects’; what did Baas Becking and Beijerinck really say? *Environmental Microbiology*, **8**, 755-758, 2006
- Jadoon, W.A., *et al.*, Biogeographical note on Antarctic microflora: Endemism and cosmopolitanism. *Geoscience Frontiers*, **4**, 633-646, 2013
- Finlay, B.J., Global dispersal of free-living microbial eukaryote species, *Science*, **296**, 1061-1063, 2002
- Martiny J.B.H., *et al.*, Microbial biogeography: putting microorganisms on the map, *Nature Reviews Microbiology*, **4**, 102-11, 2006
- Nakai, R., *et al.*, Microflora of aquatic moss pillars in a freshwater lake, East Antarctica, based on fatty acid and 16S rRNA gene analyses. *Polar Biology*, **35**, 425-433, 2012
- Nakai, R., *et al.*, Eukaryotic phylotypes in aquatic moss pillars inhabiting a freshwater lake in East Antarctica, based on 18S rRNA gene analysis. *Polar Biology*, **35**, 1495-1504, 2012
- Nakai, R., *et al.*, Diversity of RuBisCO gene responsible for CO₂ fixation in an Antarctic moss pillar. *Polar Biology*, **35**, 1641-1650, 2012
- Nakai, R., *et al.*, Phylogeographic analysis of nano bacteria with special reference to *Rhizobiales* strains that occur in cryospheric habitats. *Antarctic Science*, **25**, 219-228, 2013
- Nakai, R., Nishijima, M., *et al.*, *Oligoflexus tunisiensis* gen. nov., sp. nov., a Gram-negative, aerobic, filamentous bacterium of a novel proteobacterial lineage, and description of *Oligoflexaceae* fam. nov., *Oligoflexales* ord. nov. and *Oligoflexia* classis nov., *International Journal of Systematic and Evolutionary Microbiology*, **64**, 3353-3359, 2014.