環境制限と分散が大陸性南極における菌類群集の組成に果たす役割

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Role of environmental selections and dispersal in the composition of fungal communities in continental Antarctica

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Ice-free regions of continental Antarctica, comprising only about 2% of the continent, are not only cold and arid but also remote and isolated, imposing strong selection pressures and dispersal limitations on the establishment of organisms. Despite the harsh environment, previous studies reported the occurrence of free-living fungi in soils and in association with bryophytes in coastal outcrops of continental Antarctica (Hirose et al. 2013). However, few studies have examined whether the geographic distribution of fungal community in continental Antarctica are related to environmental conditions or whether the similarity of community composition diminishes simply with increasing geographic distance, which is mainly caused by a dispersal limitation. The purpose of the present study was to investigate the relative role of niche related (environmental) and non-niche related (spatial) processes for the spatial variations of microfungal community associated with moss in Lützow-Holm Bay area, East Antarctica. Samples were collected at 41 locations in five ice-free regions of Lützow-Holm Bay area (East Ongul Island, Langhovde, Skallen, Skarvsnes, and Breidvågnipa) and in one region of Mt. Riiser-Larsen area in East Antarctica, during JARE51 from December 2009 to February 2010. Five moss blocks (2 × 2 × 2 cm) were collected at each location, making a total of 205 blocks for fungal isolation. Fungi were isolated from one moss stem (2 cm in length) from each moss block with a modified washing method, DNA of fungal isolates was extracted from mycelia, and the rDNA ITS and 28S regions were amplified. The isolates were grouped into molecular operational taxonomic units (MOTUs) according to BLAST search and phylogenetic analyses. Fungi were isolated from 185 (90%) out of the 205 samples tested for isolation. A total of 290 isolates were obtained, zero to five isolates (1.4 isolates on average) per sample, which were classified into 24 MOTUs. We then used variation partitioning based on the distance-based redundancy analysis (db-RDA) to quantify the contribution of the environmental and spatial variables to the community structure of microfungi. The relative weight of each fraction (purely and shared fractions and unknown fractions) was estimated following the methodology described by Peres-Neto et al. (2006). Presence/absence data of MOTUs for each moss sample were converted into a dissimilarity matrix using the Simpson's index. We conducted the differentiation of total dissimilarities into turnover and nestedness components. The equation was: 0.985 (β_{SOR}) = 0.970 (β_{SIM}) + 0.015 (β_{NES}), indicating that the turnover was responsible for most of the dissimilarity. Moss species, water content, electric conductivity, and nitrogen content of moss tissues were selected as environmental factors. The percentages explained by the environmental and spatial fractions were 15.9% an 1.4%, respectively, indicating niche related fractions explained the variation of microfungal community more than non-niche related fractions. Shared fraction between environmental and spatial variables was 2.6%. In total, 19.8% of the community variation was explained and the remaining 80.2% were unexplained. When the data of Mt. Riiser-Larsen area were excluded from the analysis, which is located > 500 km away from Lützow-Holm Bay area, the percentages explained by the spatial and shared fractions increased to 4.7% and 9.0%, respectively, suggesting a dispersal limitation of microfungi in Lützow-Holm Bay area.

References

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