

## NEWS AND VIEWS

## PERSPECTIVE

**The rich and the sensitive: diverse fungal communities change functionally with the warming Arctic**

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Fungi are very abundant and functionally pivotal in Arctic terrestrial ecosystems. Yet, our understanding of their community composition, diversity and particularly their environmental drivers is superficial at the very best. In this issue of *Molecular Ecology*, Timling *et al.* (2014) describe perhaps one of the most comprehensive and geographically ambitious molecular studies on Arctic fungal communities to date. The results highlight the potential sensitivity of the fungal communities to plant communities, environmental conditions and therefore to environmental change. Thus, these studies lay a foundation to educated speculation on the fungal community migration northwards as a result of predicted climate change.

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Timling *et al.* (2014) take advantage of the North American Arctic Transect (NAAT) and include five bioclimatic subzones in the Arctic. Further, the study pairs the cryoturbated patches (see Kade *et al.* 2005 for further information) with the intermediate noncryoturbated patches, exploring thus both the impacts of disturbance in small scales and the broad geographical perspective. The inclusion of these cryoturbated, patterned ground features elegantly incorporates an abundant and important element of Arctic systems (Walker *et al.* 2008), that is, the disturbance resulting from frequent and repeated frost upheaval.

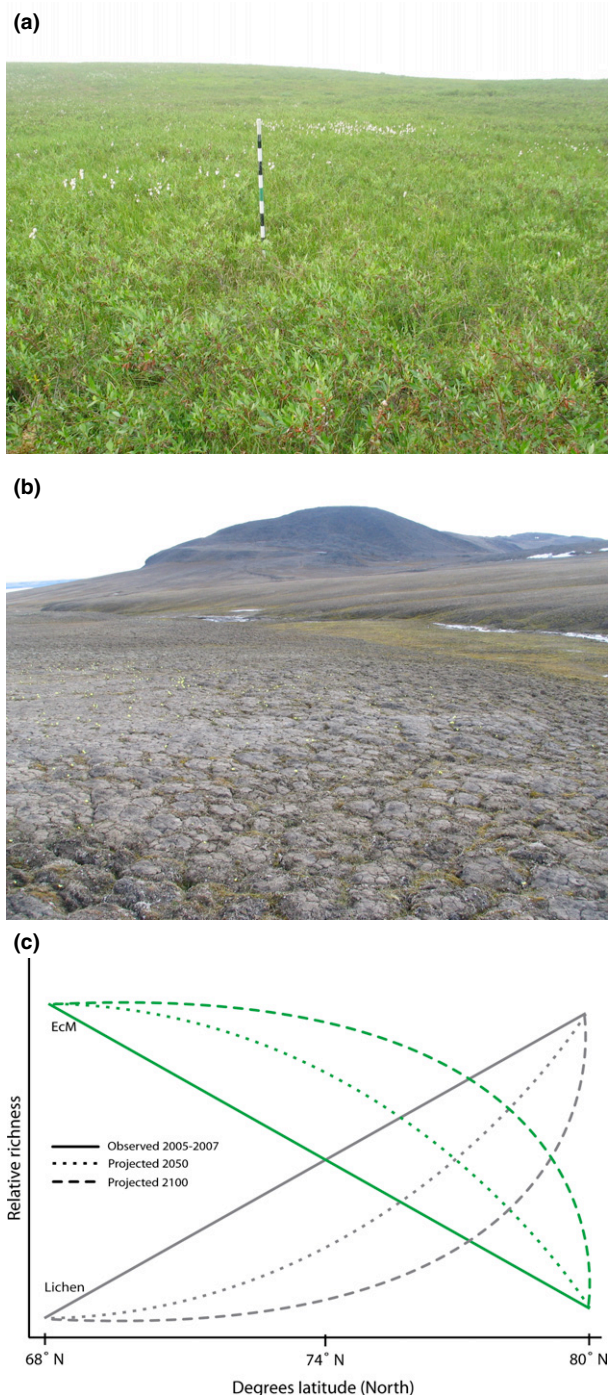
While some of the observations may seem expected – such as the replacement of mycorrhizal taxa by lichenized taxa – the results include some great surprises. We often highlight how extreme, unique and exceptional the Arctic environments must be, because of their short growing seasons, low mean temperatures and frequent frost upheaval that disturbs the soil systems. Yet, a majority of the

detected taxa in the Arctic seem widely distributed cosmopolitans, while only few seem to be Arctic endemics, contrasting with previous suggestions about dispersal limitations for some fungi (Taylor 2008; Peay *et al.* 2010). These studies also highlight the importance of the host–fungus–environment interactions. Current climate change predictions suggest shifts in the environmental conditions that facilitate a northward migration of vegetation (Normand *et al.* 2013) and consequently accompanying migration of associated fungal communities (Fig. 1). We utilized the projected ectomycorrhizal host expansion in the Arctic (Normand *et al.* 2013) and extrapolated Timling *et al.* (2014) observations on the decline of the root symbionts and their replacement by the lichenized fungi in higher latitudes. Based simply on the predicted future outer ranges of the woody shrub expansion, we speculate that the fringe where the lichenized taxa dominate in the Arctic will grow thinner. The importance of this is beyond taxon replacement: the two fungal groups are functionally distinct and their contributions to global biogeochemistry probably extremely different.

It is this environmental change angle that makes broad studies of this kind particularly valuable. The strong responses of common shrubs and the concomitant shifts in the associated fungal communities strongly signal that broad surveys of the Arctic fungi are timely. This study establishes an important benchmark in the face of predicted environmental change and the resultant woody encroachment in the Arctic. Many earlier molecular studies on the fungal communities in the Arctic focus exclusively on mycorrhizal fungi (e.g. Walker *et al.* 2011; Blaaid *et al.* 2012). Those that focus on environmental change have reported large shifts in fungal communities associated with common and dominant shrubs as exemplified by the dramatic increase in Cortinariaceae associated with *Betula nana* after two decades of climate manipulations (Deslippe *et al.* 2011). While Timling *et al.*'s (2014) study is observational and includes no manipulation of the environmental conditions, the broad targeting of soil-inhabiting fungi and the broad geographical coverage highlight the potential for functional shifts in the dominant fungal communities. One of the primary drivers for the changes in the fungal communities across the Arctic may indeed be the migration of shrubs that host a variety of root-associated fungi. It is also important to bear in mind that analyses of soil fungi serve as a good proxy for mycorrhizal communities inhabiting the substrates (Coince *et al.* 2013), even in the absence of specific targeting of the mycorrhizal or other root-associated communities.

The vast areas of the Arctic encompass a variety of climatic conditions, each with distinct vegetation types. This is highlighted by the distinct NAAT bioclimatic subzones

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analysed by Timling *et al.* (2014). The fungal communities inhabiting these subzones were also distinct and correlated with soil pH, climate and/or vegetation. On a more general note, the analyses of correlations between the fungal communities and their environmental drivers contribute to the general observation that it is often the soil (or substrate) pH that may be among the strongest drivers for fungal and/or bacterial community assembly (Rousk *et al.* 2010). The changes in communities that were correlated

**Fig. 1** Timling *et al.* (2014) report shifts in the relative richness of ectomycorrhizal (EcM) and lichenized fungi along a latitudinal gradient spanning across five Arctic climatic subzones (see fig. 3b in Timling *et al.* 2014). (a) Arctic tundra vegetation in the warmest and most southern subzone E. Note the high abundance of mycorrhizal host plants as indicated by *Salix* spp. in the foreground. (b) Patterned ground at a mesic site of the coldest and most northern subzone A. The figure shows the absence of shrubs, although the mainly crustose lichens are less obvious in the photograph (Ina Timling, Personal Communication). (c) We extrapolated from the observations (solid lines) by Timling *et al.* (2014) based on projected changes in climatically suitable areas and plant migration rates (see fig. 2 and Appendix S5 in Normand *et al.* 2013) in 2050 and 2100 (dashed lines). We speculate that as shrubs migrate north in the warming Arctic, so do their fungal symbionts, resulting in taxon and functional group replacement over time. Photographs (Fig. 1a and b) were kindly provided by Donald 'Skip' Walker.

with vegetation or climate may not be unexpected as a result of the very extensive distances between the study sites included into the study.

Timling *et al.* (2014) cloned and Sanger-sequenced nearly 8000 full-length ITS/partial LSU reads representing a large increase in the sequence information available for Arctic fungal communities. Most other current high-throughput sequencing studies suffer from short read lengths that limit the potential ecological/taxonomic inference that can be drawn from the data. While the ITS and LSU reads do often provide congruent views of the fungal communities (Brown *et al.* 2014; Porras-Alfaro *et al.* 2014), one of the great benefits of this study is the partial sequencing of the conserved LSU coupled with the more variable, full-length ITS read. The longer reads used here allow for a greater confidence in OTU assignment to taxa, while shorter reads derived from the so-called next-generation platforms may inflate richness estimators. We currently struggle with the molecular taxon concepts and poorly understand the structure of data acquired from many, if not most, high-throughput sequencing platforms. Further, phylogenetic taxon assignments of fungi may be elusive because we do not fully understand how these relate to reproductively isolated groups of individuals. Although the sequencing depth in this study is by no means enormous by present day data standards, the high-quality ITS/LSU Sanger sequences cover nearly half of the fungal richness recorded in the entire Arctic thus far. These data clearly highlight the importance of the Arctic fungal communities, their sensitivity to environmental change and the need for deeper exploration of these understudied ecosystems. It is perhaps good and important to point out that the molecular data in this case are in agreement with the observations on sporocarp and plant community responses aboveground. It is gratifying to see that the multiple data acquisition methods provide congruent results as well as support predictions afforded by modelling studies.

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