亜北極ツンドラの植物リターにおける菌類多様性の調査

大園享司 [1]、田中香穂 [1]、松岡俊将 [2]、北川涼 [3]、増本翔太 [3]、西澤啓太 [3]、長谷川元洋 [4]、内田雅己 [5]、森章 [3]
[1] 同志社大学理工学部
[2] 兵庫県立大学大学院シミュレーション学研究科
[3] 横浜国立大学大学院環境情報研究院
[4] 森林総合研究所四国支所
[5] 国立極地研究所

Assessment of fungal diversity on plant litter in a subarctic tundra

Takashi Osono[1], Kaho Tanaka[1], Shunsuke Matsuoka[2], Ryo Kitagawa[3], Shota Masumoto[3],
Keita Nishizawa[3], Motohiro Hasegawa[4], Masaki Uchida[5], Akira S Mori[3]
[1]*Faculty of Science and Engineering, Doshisha University*
[2]*Graduate School of Simulation Studies, University of Hyogo*
[3]*Environment and Information Sciences, Yokohama National University*
[4]*Forestry and Forest Products Research Institute, Shikoku Research Center*
[5]*National Institute of Polar Research*

The taxonomic diversity of fungi associated with plant litter was investigated Kuujjuarapik-Whapmagoostui (55°31'N, 77°75'W), Quebec, Canada. A total of 91 litter samples of two dominant plant species were collected during the fieldwork in July 2016, including 48 samples of dead tissues of *Racomitrium lanuginosum* and 43 samples of dead needles of *Picea glauca*. DNA was extracted from litter, and fungal rDNA ITS1 regions were amplified with PCR and sequenced with a MiSeq sequencer (Osono 2014). A total of 2,521,434 sequences were obtained from 40 and 22 samples of *R. lanuginosum* and *P. glauca*, respectively, and after removing chimera, short, and low-quality sequences and pyrosequencing errors the remaining 1,183,631 sequences were assembled into 969 operational taxonomic units (OTUs) with a 97% similarity criterion. A pipeline Clident was used to systematically annotate the taxonomy of the OTUs (Tanabe and Toju 2013), resulting in the detection of 551 fungal OTUs of which 228 OTUs (41% of 551) were identified to family, 183 OTUs (33%) to genus, and 100 OTUs (18%) to species. Of 87 fungal families identified, Herpotrichiellaceae was the most OTU-rich family, including 28 OTUs, followed by Mortierellaceae (13 OTUs), Aspergillaceae (9 OTUs), and Orbiliaceae (8 OTUs). The most frequent OTUs were Dothideomycetes sp. (OTU_534) and Fungi sp. (OTU_614) both of which were found in 32% of the 62 samples, followed by *Trichdoerma* sp. (OTU_121, 31%), Helotiales sp. (OTU_577, 31%), and *Malassezia restricta* (OTU_130, 27%). OF 551 OTUs, 401 and 264 OTUs were detected on *R. lanuginosum* and *P. glauca*, respectively, of which 114 OTUs were common to two plant species. The mean numbers ± s.e. of OTUs were 24.5 ± 2.0 and 23.3 ± 2.0 on *R. lanuginosum* and *P. glauca*, respectively, and were not significantly different at 5% level by t-test, indicating that the low number of OTUs in *P. glauca* was attributable to the low number of samples examined. The mean OTU number on *R. lanuginosum* was significantly and negatively correlated with the height of moss colonies (Pearson's $r = -0.319$, $P<0.05$), suggesting that the growth of moss colonies influenced the fungal colonization. No such significant correlation was found for *P. glauca* needle litter. The mean OTU number of neither *R. lanuginosum* nor *P. glauca* was significantly correlated with C/N ratio of litter.

References

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