Culturable Fungal Diversity in Topsoil of Degraded Wild Fruit Forests in Ili (Postprint)

Authors: By Chen Jie, WU Nan, Zhang Bingchang, Rong Xiaoying, Hu Wenge, Zhang Yuanming

Date: 2018-06-28T00:00:00+00:00

Abstract

To understand the diversity of culturable fungi in the surface soil under degraded wild fruit forests in the Ili region, the dilution plate method was used to isolate different species of culturable soil fungi from the surface soil of healthy fruit tree coverage areas (H soil) and diseased fruit tree coverage areas (D soil). Based on alignment of culturable fungal ITS gene sequences with sequences in the NCBI GenBank database, reference strain sequences with the highest similarity were selected, and a phylogenetic tree was constructed. The results showed that 25 fungal strains were isolated from the surface soil of the degraded wild fruit forest, belonging to 3 subphyla, 6 classes, 8 orders, 11 families, and 11 genera. The dominant genus of soil fungi isolated from H soil was Penicillium, while the dominant genera in D soil were Penicillium and Fusarium; Clonostachys and Purpureocillium were found only in H soil, whereas Phoma and Leptosphaeria existed only in D soil. The Shannon-Wiener diversity index of culturable fungi in H soil (2.10) was greater than that in D soil (1.98), and the evenness index of H soil (0.91) was also higher than that of D soil (0.79). Thus, a comprehensive understanding of the distribution of fungal communities in wild fruit forests can help guide pest and disease control efforts in fruit forests.

Full Text

Studies on the Topsoil Culture-dependent Fungal Diversity of the Degraded Wild Apple Forests in Yili

CHEN Jie-zuo[1],[2], WU Nan[1], ZHANG Bin-chang[1], RONG Xiao-ying[1], HU Wen-ge[3], ZHANG Yuan-ming[1]

[1]Key Laboratory of Biogeography and Bioresource in Arid Land, Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences, Xinjiang, China, 830011

[2]State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China, 100101
[3]College of Life Science, Shihezi University, Shihezi, China, 832000

Abstract

The Tianshan wild fruit forest in Xinjiang represents one of the world' s origins of cultivated deciduous fruit trees, featuring the largest area and most pristine dense distribution across Eurasia. In recent years, large-scale human development has severely damaged this ecosystem, causing not only extensive harm to the fruit trees themselves but also a significant decline in species diversity. Current research on wild fruit ecosystems has primarily focused on aboveground components, with microbial communities in the soil receiving little attention.

The objective of this study was to evaluate the diversity of culturable fungi isolated from the topsoil of healthy fruit trees (Hsoil) and diseased fruit trees (Dsoil) in degraded wild fruit forests. Using dilution plate techniques and 18S rDNA sequence analysis, we obtained sequences from 25 distinct colonies isolated from the degraded wild fruit forest. These sequences were subsequently submitted to GenBank and compared with known sequences to construct a phylogenetic tree. Results revealed that: (1) the strains clustered into 3 phyla, 6 classes, 8 orders, 11 families, and 11 genera; (2) *Penicillium* was the dominant genus in Hsoil, while both *Penicillium* and *Fusarium* were dominant in Dsoil, with *Clonostachys* and *Purpureocillium* being endemic to Hsoil, and *Phoma* and *Leptosphaeria* occurring exclusively in Dsoil; (3) the Shannon-Wiener diversity index of Hsoil was 2.10, greater than that of Dsoil (1.98), and the evenness index of Hsoil was 0.91, higher than Dsoil (0.79). The biological characteristics of these culturable fungi isolated from the wild fruit forest require further investigation to better inform soil pest control strategies in wild apple forests.

Keywords: degraded wild fruit forests; upper soil; culturable fungi; diversity

Note: Figure translations are in progress. See original paper for figures.

Source: ChinaXiv —Machine translation. Verify with original.