



BRAZILIAN JOURNAL OF MICROBIOLOGY

<http://www.bjmicrobiol.com.br/>



Environmental Microbiology

Variations in culturable bacterial communities and biochemical properties in the foreland of the retreating Tianshan No. 1 glacier

Xiukun Wu^{a,b}, Gaosen Zhang^{a,b}, Wei Zhang^{a,b}, Guangxiu Liu^{a,b,*}, Tuo Chen^{b,c}, Yun Wang^{a,b}, Haozhi Long^a, Xisheng Tai^a, Baogui Zhang^{a,b}, Zhongqin Li^c

^a Chinese Academy of Sciences, Northwest Institute of Eco-Environment and Resources, Key Laboratory of Desert and Desertification, Lanzhou, China

^b Key Laboratory of Extreme Environmental Microbial Resources and Engineering, Lanzhou, Gansu Province, China

^c Chinese Academy of Sciences, Northwest Institute of Eco-Environment and Resources, State Key Laboratory of Cryospheric Sciences, Lanzhou, China

ARTICLE INFO

Article history:

Received 4 June 2015

Accepted 24 October 2016

Available online xxx

Associate Editor: Iêda de Carvalho Mendes

Keywords:

Tianshan No. 1 glacier

Foreland

Culturable bacteria

Soil biochemical characteristics

ABSTRACT

As a glacier retreats, barren areas are exposed, and these barren areas are ideal sites to study microbial succession. In this study, we characterized the soil culturable bacterial communities and biochemical parameters of early successional soils from a receding glacier in the Tianshan Mountains. The total number of culturable bacteria ranged from 2.19×10^5 to 1.30×10^6 CFU g⁻¹ dw and from 9.33×10^5 to 2.53×10^6 CFU g⁻¹ dw at 4 °C and 25 °C, respectively. The number of culturable bacteria in the soil increased at 25 °C but decreased at 4 °C along the chronosequence. The total organic carbon, total nitrogen content, and enzymatic activity were relatively low in the glacier foreland. The number of culturable bacteria isolated at 25 °C was significantly positively correlated with the TOC and TN as well as the soil urease, protease, polyphenoloxidase, sucrose, catalase, and dehydrogenase activities. We obtained 358 isolates from the glacier foreland soils that clustered into 35 groups using amplified ribosomal DNA restriction analysis. These groups are affiliated with 20 genera that belong to six taxa, namely, Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, Actinobacteria, Bacteroides, and Deinococcus-Thermus, with a predominance of members of Actinobacteria and Proteobacteria in all of the samples. A redundancy analysis showed that the bacterial succession was divided into three periods, an early stage (10a), a middle stage (25–74a), and a late stage (100–130a), with the total number of culturable bacteria mainly being affected by the soil enzymatic activity, suggesting that the microbial succession correlated with the soil age along the foreland.

© 2018 Published by Elsevier Editora Ltda. on behalf of Sociedade Brasileira de Microbiologia. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

<https://doi.org/10.1016/j.bjm.2018.01.001>

1517-8382/© 2018 Published by Elsevier Editora Ltda. on behalf of Sociedade Brasileira de Microbiologia. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Introduction

Over the past 100 years, the average global temperature has increased by 0.74°C ,¹ and one consequence of this temperature increase is that glaciers are retreating in many mountainous areas of the world. As the glaciers retreat, the newly exposed land is a new habitat for microorganisms² derived from the air, clouds, snow, rain, and runoff waters from the glacier body in addition to autochthonous microorganisms.³ Bacterial communities may be key determinants of glacier foreland ecosystem stability and function because of their important roles in soil development, biogeochemical cycles and heterotrophic activities. Microbial communities change along the soil age gradient of a glacial foreland. Sigler et al.⁴ found that the number of dominant organism types and community evenness decreased with succession, but others found that the phylotype number, diversity, and evenness increased over time.^{2,5} However, most of those studies are focused on Polar and European mountain areas; therefore, studies on the bacterial community, soil biochemical properties and the correlation between bacteria and soil biochemical properties along chronosequences in such high Asian regions as the Tianshan Mountains are still needed.

The Tianshan No. 1 glacier is located in the Eastern Tianshan Mountains of Central Asia, mountains that are surrounded by desert.⁶ The climate in this area is a classical continental climate, and wind is an important climatic factor in the upper elevations of the mountains.⁷ The Tianshan No. 1 glacier has been studied intensively from a glaciological point of view since 1959,⁸⁻¹⁰ when the Tianshan Glaciological Station was built. Because of the availability of extensive glaciological data and detailed glacier retreat data, this area is an ideal location for the study of microbial distribution and growth related to both climatic and other environmental factors.^{11,12} Although the study of microorganisms in this area is very important, few studies have been performed. Bai et al.¹³ reported the bacterial diversity from permafrost in the Tianshan Mountains, and Yang et al.¹⁴ studied the permafrost bacterial and archaeal community structures in the same area. Sheng et al.¹⁵ first described the indigenous endophytic bacteria within subnival plants of the Tianshan Mountains. Wang et al.¹⁶ reported microbial biomass and soil enzyme activity variations along chronosequences, and Wu et al.¹¹ used pyrosequencing to analyze the bacterial diversity along chronosequences. However, studies regarding the variation of the culturable bacterial communities and biochemical characteristics along chronosequences in the Tianshan Mountains are not available, and thus fundamental knowledge on the culturable bacterial communities and biochemical characteristics in the Tianshan No. 1 glacier forelands is lacking.

In this study, we present data regarding the soil biochemical properties and diverse bacteria cultured using samples from the Tianshan No. 1 glacier forelands. The results could lead to a better understanding of the initial colonization and

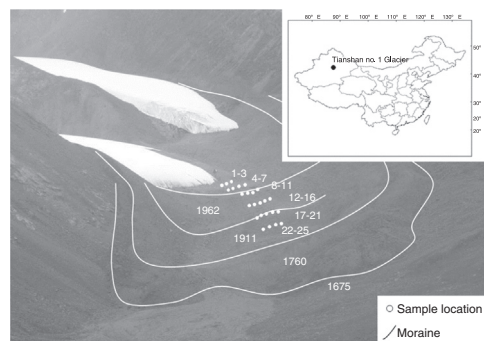


Fig. 1 – Map of sampling position.

succession patterns of microorganisms and soil development and the correlation between bacteria and soil biochemical properties along chronosequences in a high Asian region. Our aims were (1) to investigate the soil biochemical properties and culturable bacterial abundance variations along a chronosequence, (2) to determine the culturable bacterial community variations by using a low-nutrient medium cultured at 4°C and 25°C , and (3) to examine the correlations between the abundance of culturable bacteria and the soil biochemical properties with increasing soil age.

Materials and methods

Study site and sampling

The Tianshan Mountains extend through China, Kyrgyzstan and Kazakhstan in Central Asia and have 15,953 glaciers with a total area of $15,416\text{ km}^2$.¹⁷ The sample sites were located at Tianshan No. 1 glacier (N $43^{\circ}06'$, E $86^{\circ}48'$), 120 km southwest of Urumchi, China (Fig. 1). The top elevation at this glacier is 4486 m. The samples were collected at the east branch of Tianshan No. 1 glacier foreland along the chronosequence in front of the retreating glaciers. Twenty-five soil samples were collected in August 2010. These soil samples represent 6 periods: sites 1 to 3, sites 4 to 7, sites 8 to 11, sites 12 to 16, sites 17 to 21, and sites 22 to 25 represent 10a, 25a, 60a, 74a, 100a, and 130a, respectively. The succession time of every sampling site was determined using the annual glacier retreat observation data (from 1959 to 2010) from the Tianshan Glaciological Station (Chinese Academy of Sciences) and lichenometric chronology data (from 1958 to 1538).¹⁸ Each soil sample consisted of three subsample cores at a 5 cm depth collected at random in an area approximately $2\text{ m} \times 2\text{ m}$; the samples were mixed after the larger gravel had been removed. Pioneer plants appeared in the deglaciated soil within 10–100 years, and vegetation developed after 100 years of deglaciation. Successional species arriving within 10–100 years included *Cancrinia tianshanica*, *Bryophyta* spp., *Poa tianshanica*, *Draba nemorosa*, *Saxifraga hirculus* L., *Melandrium apricum*, *Leontopodium leptopodioides*, *Saussurea gnaphalodes*, *Crepis flexuosa*, *Rhodiola coccinea*, *Oxyria digyna*, and *Saussurea involucrata*, whereas *Senecio tianshanicus*, *Polygonum viviparum*, and *Pedicularis* spp. additionally appeared outside the glacier foreland. The soil samples were

* Corresponding author at: Key Laboratory of Desert and Desertification, Northwest Institute of Eco-Environment and Resources, Chinese Academy of Sciences, Donggang West Road No. 320, Lanzhou 730000, China.
E-mail: liugx@lzb.ac.cn (G. Liu).

Download English Version:

<https://daneshyari.com/en/article/8842464>

Download Persian Version:

<https://daneshyari.com/article/8842464>

[Daneshyari.com](https://daneshyari.com)