Study on Soil Microbial Community Structure of River Wetland in Tumen River Basin

Fengyang Hong¹, Yuge Chang ¹, Zhiyu Fan², Weihong Zhu¹, Mingji Jin²*

¹Department of Physical geography, Yanbian University, Yanji, Jilin, 133002, P.R. China
²Department of Agricultural Resources and Environment, Yanji, Jilin, 133002, P.R. China

*Corresponding author’s e-mail: jinmingji@ybu.edu.cn

Abstract. This study explored the relationship between soil microbial community structure and soil environmental factors in river wetlands of Tumen River Basin by analyzing the soil microbial community structure and combining soil environmental factors. As a result, there were significant differences in microbial community diversity among river wetlands in the Tumen River Basin. Proteobacteria and Actinobacteria were the abundant dominant phylum of microbial, moreover, Actinobacteria and Alphaproteobacteria were the dominant class of microbial. Soil environmental factors such as soil organic matter, soil total nitrogen and soil total potassium are the main factors affecting the change of microbial community structure in river wetlands of Tumen River Basin.

1. Introduction
The response of microorganisms to environmental changes has been the subject of constant attention in ecosystem research [1-3]. Soil microbial community structure is closely related to vegetation and environmental factors in wetland system. Therefore, this study attempts to explore the relationship between soil microbial community structure and soil environmental factors in river wetlands of Tumen River Basin by analyzing the microbial community structure and combining soil environmental factors. This paper will provide a basis for effective protection of wetland ecosystems.

2. Material and methods

2.1 Sample collection
Samples were collected from the Tumen River basin wetlands in August 2017. Tumen River is located on the border of China, North Korea and Russia in the southeast of Jilin Province, China. It is an important international river. Its total length is 505.4km and its watershed area is 33168.4 km². As shown in Figure 1, in this study, the Tumen River Basin was divided into two major areas: the main stream and the tributaries. A total of seven sampling sites were set. They were the TRU, TRM and TRD sampling sites on the upper, middle and lower reaches of the Tumen River, and the HR, BR and GR sampling sites on the Hailan River, the Buerhatong River and the Gaya River in the Tumen River tributaries. FR on Fengwu Reservoir of Wangqing River, a secondary tributary. The soil samples were collected from the top 0-20cm from sample sites.
2.2 Measurement indicators and methods
The microbial analysis in this study used 16S rRNA Miseq high-throughput sequencing. The physicochemical properties were determined by soil bulk density (BD), soil pH, soil organic matter (SOM), soil total nitrogen (TN), soil total phosphorus (TP) and total potassium (TK), were determined by reference to Chinese standard analytical methods[4].

3. Results and discussion

3.1 Soil physicochemical properties
It can be seen from Table 1 that the other five indicators except TP in the soil physicochemical properties are significantly different (p<0.05), the BD amplitude is 1.09~1.71 g/cm³, and the pH is 6.49 ~7.87, SOM ranged from 10.61 to 79.78 g/kg, TN ranged from 1.48 to 2.37 g/kg, and TK ranged from 6.95 to 29.46 g/kg. The highest of SOM, TN and TK in 7 sample sites were presented in TRU, followed by FR and lowest in HR. The TP ranged from 0.27 to 0.68 g/kg, and the difference between the sample sites was not significant (p>0.05).

Table 1. Soil physicochemical properties

| Sampless | BD(g/cm³) | pH    | SOM (g/kg) | TN (g/kg) | TP (g/kg) | TK (g/kg) |
|----------|-----------|-------|------------|-----------|-----------|-----------|
| TRU      | 1.09±0.03 | 7.08±0.89 | 79.78±19.12 | 2.37±0.18 | 0.53±0.30 | 29.46±2.23 |
| TRM      | 1.53±0.22 | 7.87±0.19 | 17.06±4.09  | 1.68±0.11 | 0.68±0.07 | 7.78±0.14  |
| TRD      | 1.57±0.05 | 6.73±0.19 | 16.90±1.66  | 1.63±0.12 | 0.44±0.07 | 8.29±0.20  |
| HR       | 1.42±0.11 | 7.73±0.13 | 10.61±0.90  | 1.48±0.16 | 0.27±0.01 | 6.95±0.15  |
| BR       | 1.33±0.18 | 6.51±0.06 | 25.18±0.56  | 1.75±0.17 | 0.35±0.01 | 7.59±0.18  |
| GR       | 1.39±0.21 | 6.92±0.71 | 14.99±0.71  | 1.78±0.12 | 0.29±0.01 | 7.34±0.05  |
| FR       | 1.71±0.14 | 6.49±1.05 | 37.89±10.26 | 1.94±0.23 | 0.34±0.00 | 10.26±1.14 |
3.2 Microbial community structure

It can be seen from Table 2 that the microbial community evenness (Simpson and Shannon) and the richness (Chao 1 and ACE) in the seven sample sites were all presented in TRD, and the lowest presented in FR. The microbial community diversity of the seven samples was TRD>TRU>BR>HR>TRM>GR>FR, and the difference between the sample sites was significant (p<0.01).

Table 2. Microbial community diversity index

| Samples | OTUs  | Simpson | Shannon | Chao1       | ACE       |
|---------|-------|---------|---------|-------------|-----------|
| TRU     | 29910 | 0.998   | 10.18   | 2898.49     | 3100.20   |
| TRM     | 48529 | 0.996   | 10.01   | 2668.06     | 2842.45   |
| TRD     | 30914 | 0.998   | 10.29   | 3096.29     | 3365.87   |
| HR      | 48018 | 0.996   | 10.02   | 2676.33     | 2890.55   |
| BR      | 15404 | 0.999   | 10.13   | 2842.40     | 2951.87   |
| GR      | 32937 | 0.996   | 9.98    | 2670.25     | 2885.35   |
| FR      | 12171 | 0.993   | 9.77    | 1850.00     | 1850.00   |

As shown in Figure 2, the dominant phyla in all samples were Proteobacteria, Actinobacteria, Acidobacteria and Chloroflexi. The relative abundances of the four dominant phyla in each sample were greater than 81%, of which Proteobacteria was the highest among the five samples including TRU, TRM, TRD, HR and FR. Actinobacteria was the most abundant in BR and GR samples. It was reported that Actinobacteria is negatively correlated with pH [6], while the pH monitoring results of BR and GR samples are neutral partial acid, which may be the main cause of the highest enrichment of Actinobacteria.

As shown in Figure 3, the dominant classes in all samples were Actinobacteria, Alphaproteobacteria, Gammaproteobacteria and Betaproteobacteria. The relative abundances of the four dominant classes were more than 41%. Among them, Actinobacteria was the highest abundances in HR, BR, FR and GR samples in tributaries, and Alphaproteobacteria was the highest abundances in TRU, TRM and TRD samples in main stream.

As shown in Figure 4, the Principal component analysis (PCA) method was used to analyze the results of the OTU composition between the samples. The TRM, HR, BR and GR samples in the Tumen River Basin were clustered into one group, and the microbial community structure was similar among the four samples. TRU and TRD were clustered into another group, and FR was clustered separately, which had a large difference in microbial community structure from other samples.
3.3 Influence of environmental factors on microbial community structure

The microbial community structure in the wetland system is not only affected by vegetation, but also affected by environmental factors such as abiotic factors[7-9]. Therefore, in order to understand the influence of environmental factors on microbial community structure, Redundancy analysis (RDA) of microbial community structure and soil physicochemical properties were carried out in this study. The results were shown in Figure 5, in the river wetlands of the Tumen River Basin, SOM (p<0.01), TN (p<0.05) and TK (p<0.05) were significant for the changes of microbial community structure. Previous studies have also reported that SOM, TN and TK are highly correlated with microbial community structure. Landa et al. [10] considered that the increase of SOM was not only increases the diversity of microbial community structure, but also increases the gene abundance of microbial community structure; Zhang et al. [11] and Cai et al. [12] considered that the distribution of nutrients such as TN and TK was one of the important factors affected the diversity and function of microbial communities.
4. Conclusion
There were significant differences in microbial community diversity among river wetlands in the Tumen River Basin, but the TRM, HR, BR and GR microbial community structures in the midstream were similar. Proteobacteria and Actinobacteria were the most abundant dominant phyla in all samples, and Actinobacteria and Alphaproteobacteria were the most abundant dominant classes. Combined with soil environmental factors, soil environmental factors such as SOM, TN and TK have significant effects on the changes of microbial community structure in river wetlands of Tumen River Basin.

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