Niche analysis of microbial community reveals the South-to-North water diversion impacts in Miyun Reservoir

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Abstract. The South-to-North water diversion impacts on microbial community niche were investigated in the water receiving area. In this paper, the community structure, niche breadth and overlap of the dominant genus were determined to approach the distribution features of microbes and the community changes in Miyun Reservoir. Our results showed that before water transfer, the main bacteria phylum was Proteobacteria, Bacteroidetes, Cyanobacteria, Firmicutes and Actinobacteria. The niche breadth range (OMI value) of dominate bacteria genus was 0.01~0.54, and the tolerance value range was 0.55~4.56. After water transfer, Proteobacteria, Cyanobacteria, Actinobacteria, Bacteroidetes and Verrucomicrobia were the dominate phylum. The niche breadth range of dominate bacteria genus was 0.00~0.38, and the tolerance value range was 0.55~4.56. It indicated that after water diversion, the relative abundance of the Proteobacteria and Verrucomicrobia increased significantly (p<0.05), and the ecological niche of the genus Candidatus Methylacidiphilum, Chitinophagaceae and OM27 clade was significantly differentiate (p<0.05). The niche overlap results suggested that the inter-species niche competition becomes more intense after the water transfer, which reflected the different utilization ability of each bacteria genus in the new aquatic environment of the Miyun Reservoir.

1. Introduction
Microbes are an important part of the food web of aquatic ecosystem, which play a crucial role in the process of the energy and material circulation and water quality regulations[1]. Microbial community structure can directly reflect the feature of environment, which diversity is also affect the ecosystem function change[2].Bacterial is very sensitive to environmental stresses. Environmental stresses can promote rapid evolution of bacterial community to adapt to the new environment [3].Therefore, the strong adaptability of the microbial community can ensure the rapid restoration of stability in the changing environment[4].

Ecological niche plays an important role in understanding community structure and function, inter-species relationship among species, biodiversity, dynamic succession of communities and population evolution [5]–[7]. Ecological niche measure is based on the calculation of niche breadth and niche overlap. Niche breadth refers to the sum of various resources utilized by a population in a community, which reflects the utilization status of the population. Niche overlap will occur when two species
jointly possess a certain resource, such as nutrient composition and space. The two indicators jointly reflect the utilization ability of the population and the adaptability to the environment[8].

Mayan reservoir (latitude 40°19'–41°31', longitude 115°25'–117°33') is the final water receiving area of the middle route of South-to-North water transfer project[9],[10]. The evolution and development of the aquatic ecosystem in this reservoir is not only related to ecological environment health, but also to the urban water supply security in Beijing[11],[12]. However, there is still lack of knowledge about microbial community niche changes in such huge project. Therefore, in this study, we sought to determine the changes in community structure, niche breadth and overlap after water transfer. Our result will provide more information about microbial community structure and function adapt to environmental stress resistance and resilience of South-to-North water diversion project and assist in the assessment and management of the drinking water reservoir.

2. Materials and Methods

2.1. Sampling sites
The Mayan reservoir is the largest drinking water supply reservoir in Beijing. At the end of October 2015, South-to-North water diversion project started. By the end of 2016, the storage capacity of Mayan reservoir reached 1.65 billion cubic meters from 0.8 billion cubic meters in 2014. Nine typical sites (BHB, CHB, CHK, BHK, JG, YL, DGZ, WY and KZX) were chosen for water sampling at October 4, 2014 and October 15, 2016 represented for before and after water transfer samples, respectively.

2.2. DNA Extraction, PCR Amplification and Sequencing
DNA isolation, PCR amplification and Illumina Miser PE 250 sequencing were carried out in Shanghai Major Bio Bio-pharm Technology C., Ltd. The OTUs (operational taxonomic units) were calculated in Mother. Bio information analysis was performed using R package software.

2.3. Estimating the niche of microbial taxonomic units
The niche breadth of each taxonomic unit was characterized by Outlying Mean Index (OMI) analysis[13]. A tolerance index is also provided by the analysis, representing the variability of the environment used by the taxonomic unit. Niche overlap between taxonomic units were calculated by R package software[14].

3. Results

3.1. Microbial community composition
High throughput sequencing found that before the water diversion (Fig.1(A)), Proteobacteria, Bacteroidetes, Cyanobacteria, Formicutes and Actinobacteria were the dominate phylum bacteria, accounting for 19.3%, 18.8%, 16.7%, 15.2% and 8.7% of the total sequence, respectively. While Proteobacteria (30.6%), Cyanobacteria (18.75%), Actinobacteria(18.67%), Bacteroidetes(14.15%) and Verrucomicrobia (10.6%) were the most phylum in the after water transfer samples (Fig.1(B)). The results showed that the relative abundance of the bacteria of Proteobacteria and Verrucomicrobia were significantly increased (p<0.05) after water diversion.
3.2. Niche breadth and tolerance of taxonomic units

Before the water diversion, the niche breadth range (OMI value) of dominate bacteria genus was 0.01–0.54, and the tolerance value range was 0.55–4.56. The highest OMI value in the genus of Planktothricoides and Pseudomonas was 0.54 and 0.47, respectively. The lowest OMI value was the same in the genus of hgcl_clade, Candidatus_Methylophilum and CL500.29_marine_group (Fig.3 (A), Table.1). After water transfer, the niche breadth range of dominate bacteria genus was 0.00–0.38, and the tolerance valve range was 0.55–4.56. Our results showed that there were no significant niche differentiation before water transfer (P>0.05). However, Candidatus.Methylophilum,Chitinophagaceae and OM27.clade have a high tolerance to the environmental variables defined in this analysis after water transfer (Table 1). The significant test showed that the marginality of these three genus were different from that expected by chance (P < 0.05).
Figure 3. The distribution of dominant genus on environmental gradients in before (A) and after (B) water transfer samples using the OMI analysis.

Table 1. Niche parameters for top 20 genus in the water column of Mayan Reservoir. The inertia (total variability), Outlying Mean Index (OMI) and tolerance index (Tol) were computed for each to dominate genus. Species in bold show significant deviation from the origin indicating marginal niches.

| Taxon                        | Before water transfer | MNI | OM | Tol | PValue |
|------------------------------|-----------------------|-----|----|-----|--------|
| Cyanobacteria                | B1                    | 7.88| 0.0| 1.5 | 0.762  |
| Lactococcus                  | B2                    | 8.78| 0.2| 1.4 | 0.476  |
| CL500.3                      | B3                    | 7.61| 0.0| 1.6 | 0.714  |
| hgcI.clade                   | B4                    | 8.18| 0.0| 1.4 | 0.619  |
| NS11.12_marine_group         | B5                    | 8.02| 0.0| 1.7 | 0.571  |
| Roseiflexus                  | B6                    | 8.07| 0.2| 1.5 | 0.810  |
| Enterococcus                 | B7                    | 8.39| 0.2| 2.0 | 0.429  |
| Synechococcus                | B8                    | 8.17| 0.0| 2.3 | 0.143  |
| OPB56                        | B9                    | 8.00| 0.0| 1.4 | 0.476  |
| Pseudomonas                  | B1                    | 8.94| 0.4| 1.6 | 0.381  |
| Candidatus_Methylacidip      | B1                    | 7.77| 0.5| 1.7 | 0.381  |
| Candidatus_Aquirestis        | B3                    | 8.17| 0.1| 1.8 | 0.476  |
| CL500.29_marine_group        | B1                    | 8.13| 0.0| 0.8 | 0.905  |
| Fluviicola                   | B1                    | 8.00| 0.0| 1.8 | 0.286  |
| env.OPS_17                   | B1                    | 7.98| 0.0| 1.9 | 0.857  |
| Planktothricoides            | B1                    | 6.52| 0.5| 1.6 | 0.667  |
| Limnobacter                  | B1                    | 7.84| 0.0| 1.3 | 0.524  |
| Bacillus                     | B1                    | 8.38| 0.1| 1.7 | 0.571  |
| OM27.clade                   | B2                    | 7.86| 0.0| 2.2 | 0.714  |

| Taxon                        | After water transfer  |
|------------------------------|-----------------------|
| Cyanobacteria                | A1                    |
| Lactococcus                  | A2                    |
| CL500.29.marine.group        | A2                    |
| Candidatus_Aquirestis        | A3                    |
| Flavobacterium               | A4                    |
| Limnohabitans                | A5                    |
| Dinophysis.acuminata         | A6                    |
| Comamonadaceae               | A7                    |
| Candidatus.Methylacidip      | A8                    |
| Chthoniobacter                | A9                    |
| Virgulinella.fragilis        | A1                    |
| Synechococcus                | A1                    |
| Limnobacter                  | A1                    |
| Chitinophagaceae             | A1                    |
| GKS98.freshwater.group       | A1                    |
| Fluviicola                   | A1                    |
| Sediminibacterium            | A1                    |
| Verrucomicrobiaceae          | A1                    |
| Polynucleobacter             | A1                    |
| OM27.clade                   | A2                    |
3.3. Niche overlap

As showed in Table 2, the range of niche overlap value was 0.897~1.000 before the water transfer. The smallest value of niche overlap was 0.897 in the B10 (Pseudomonas) and B14 (CL500.29_marine_group), while B4 (hgcI_clade) and B10 (Pseudomonas) groups had the highest overlap value. After water transfer, the range of niche overlap values of the dominant species was 0.987~1.000. The results showed that A1 (hgcI.clade), A2 (CL500.29. Marine. Group), A5 (Limnohabitans) and A7 (Comamonadaceae) had more overlap relationship with the other dominant species. It is suggested that the inter-species niche competition becomes more intense after the water transfer, which reflected the different utilization ability of each bacteria genus in the new aquatic environment of the Miyun Reservoir.

Table 2 Niche overlaps among dominant genus in before and after water transfer samples

| No. | A14  | A13  | A12  | A11  | A10  | A9   | A8   | A7   | A6   | A5   | A4   | A3   | A2   | A1   |
|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
|     | 0.997| 0.995| 0.995| 0.997| 0.992| 0.995| 0.993| 0.998| 0.999| 0.999| 0.994| 0.986| 0.997| 0.998|
| B1  | 0.996| 0.968| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.998| 0.991| 1.000| 1.000| 1.000|
| B2  | 0.997| 0.962| 0.996| 0.997| 0.997| 0.997| 0.999| 0.999| 0.999| 0.998| 0.992| 1.000| 1.000| 1.000|
| B3  | 0.997| 0.962| 0.996| 0.997| 0.996| 0.999| 0.999| 0.999| 0.998| 0.997| 0.989| 0.998| 0.998| 0.998|
| B4  | 0.996| 0.968| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 1.000| 1.000| 1.000|
| B5  | 0.997| 0.966| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999|
| B6  | 0.996| 0.976| 0.998| 1.000| 0.999| 1.000| 0.999| 1.000| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999|
| B7  | 0.993| 0.974| 0.999| 1.000| 1.000| 0.997| 0.998| 1.000| 0.997| 0.997| 0.997| 0.997| 0.997| 0.997|
| B8  | 0.998| 0.963| 0.998| 0.999| 0.998| 0.997| 0.999| 1.000| 0.994| 0.987| 0.987| 0.987| 0.987| 0.987|
| B9  | 0.997| 0.968| 0.999| 0.999| 0.999| 0.997| 0.986| 0.996| 0.995| 0.988| 0.998| 0.998| 0.998| 0.998|
| B10 | 0.994| 1.000| 0.993| 1.000| 1.000| 1.000| 0.999| 0.996| 1.000| 0.999| 0.988| 0.989| 1.000| 1.000|
| B11 | 0.996| 0.966| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 1.000| 0.999| 1.000|
| B12 | 0.996| 0.962| 1.000| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 1.000| 1.000| 1.000|
| B13 | 0.995| 0.973| 0.999| 1.000| 1.000| 1.000| 0.997| 0.996| 0.995| 0.995| 0.996| 0.996| 0.996| 0.996|
| B14 | 0.997| 0.966| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 1.000| 1.000|
|     | 0.998| 0.967| 0.998| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999| 0.999|

4. Discussion

Ecological niche theory has been widely used in the research of inter-species relation, community structure and population evolution, which reflects the relationship between living organisms and habitat conditions [8], [15], [16]. Our results showed the niche characteristic of different bacteria at each sampling sites in Miyun Reservoir the relationship with microbial community and the distribution of species in the habitat. The microbial community composition at genus level showed that the proportion of Cyanobacteria occupied obviously higher at most sampling sites such as estuary area (CHK, BHK) and shallow water area (YL and WY) (Fig 2 (A)), but the distribution is not uniform which made the ecological breadth was narrower (Table 1). Niche breadth depends on the size of the species of the utilization of resources and the ability to adapt to the environment. Under the same habitat conditions, the wider niche breadth, the narrower the degree of specialization. In this situation, we called the species was generalized species. On the contrary, the narrower niche breadth, the higher the degree of specialization. Such species called specialized species. When narrowing the scope of environmental resources, the generalization species tend to expand its ecological niche, and specialized species contract its ecological niche. For example, both the genus Planktothricoides and Pseudomonas had the higher OMI values (Table 1) indicated that they were the generalized species before the water transfer. However, the niche breadth of them obviously narrowed after the water transfer, their ecological niche were also occupied by the other dominate species. Another example was hgcI_clade had a higher proportion of microbial community composition in the before and after...
water transfer samples, but OMI value was also lower after water transfer, indicating that the species niche position may differentiation in the future.

Due to the water diversion make the change of the water environment in Miyun Reservoir, the ecological niche differentiation of the genus Candidatus. Methylacidiphilum, Chitinophagaceae and OM27 clade were evident from the spatial distribution along environmental gradients (p<0.05). The genus Candidatus Methylacidiphilum OMI value was 0.01 before the water transfer, but its value increased to 0.05 after water transfer. The ecological niche differentiation was significant (p<0.05) indicated that the water resource utilization capacity of the species was enhanced after the water transfer (Table.1). The habitat conditions change lead to niche position differentiation and also make the degree of niche overlap change between species[17].Niche overlap reflects strong correspondence between two species and the intensity of their competition by shared resources. Species are thus characterized in terms of their similarity in resource use or their niche overlap [18],[19], [20]. Niche overlap response to ecological environmental change and the competition between inter-species in Mayan Reservoir. For example, Pseudomonas and CL500.29_marine_group had the lowest niche overlap value, indicating that these two genera are not competitive in resource utilization before the water transfer. However, the higher niche overlap values between his clade, CL500.29. Marine. Group, Limnohabitans, Comamonadaceae and other dominant species, suggesting that these genera with other species in the fierce competition on the resource utilization, which has significant influence on microbial community structure and reservoir distribution.

The impact of South-to-North water diversion on the water environment is complex due to human regulation and disturbance. Microbial community distribution in Mayan Reservoir regulated by the many factors such as temperature, water source input (Danjiangkou Reservoir) and physicochemical and biological factors. Due to the large habitat difference between the water source and water receiving area, the dynamic of microbial community caused niche difference at different diversion stage. This study reveals microbial community niche position and overlap at preliminarily diversion stage. In the future, we will need to explore the relationship with different environmental factors and various species niche at different diversion stage.

5. Conclusion
The niche analysis of microbial community in Mayan Reservoir reveals the water diversion impacts on ecological environment. The analysis of niche position and niche overlap revealed the species niche distribution and differences under a certain environmental gradients. However, water diversion projects make local habitat environment change. Therefore, species traits, environmental factors and some other important ecological factors should be coupled with the current data for ecological assessment in the further study.

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