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Phylogenetic Diversity of Wetlands at the Source of the Qin River

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Abstract [**Objectives**] To explore the phylogenetic diversity of wetlands at the source of the Qin River and provide data reference for future research. [**Methods**] Taking survey data (July, 2016) of plants in wetlands at the source of Qin River as research object, this study utilizes Phylocom 4.2 to construct plant (in wetlands at the source of Qin River) genealogical tree for 72 non-angiosperm species within research area, besides, the paper adopts Pedigree diversity index (PD), community pedigree structure index (net Relatedness index, NRI and Nearest Taxon Index, NTI) to analyze pedigree diversity and pedigree structure of plants in wetlands at the source of Qin River. This paper is going to explain the scientific question: pedigree diversity, pedigree β diversity, and pedigree structure of plants in wetlands at the source of Qin River, in order to study on relatedness and stability of community. [**Results**] The effect of habitat filtration will result in similar species adaptation and close genetic relationships in the community, manifesting as genealogy aggregation. On the contrary, the effect of competitive exclusion can lead to distant species' genetic relationships in the community, manifesting as genealogy divergence. In this study, there was a tendency of aggregation among the species in sample plot S5, which indicated that the effect of habitat filtration was dominant in this plot, and in S2 and S6 the species had a decentralized trend. The NRI and NTI values in other plots were different in the positive and negative. [**Conclusions**] This research serves as an initial exploration of the phylogenetic diversity and community assembly mechanisms in the wetlands at the source of Qin River. Further studies incorporating environmental factors and human activities could provide deeper insights into community ecology phenomena and assembly mechanisms.

Key words Qin River source, Genealogical tree, Pedigree diversity, Wetland

0 Introduction

Biodiversity serves as a crucial indicator for describing community assembly and ecosystem functions, closely linked to ecological processes such as community and ecosystem formation, productivity, and stability[1]. Therefore, diversity can be considered the core issue in ecology[2]. Biodiversity encompasses not only species diversity but also phylogenetic diversity and functional diversity[3]. In fact, species diversity may even be the least informative among all these dimensions of biodiversity, whereas phylogenetic diversity and functional diversity can better reveal the construction, maintenance, and functioning of communities and ecosystems in comparison. Research indicates that regions with identical species diversity may exhibit varying levels of phylogenetic and functional diversity, while areas with differing species diversity can demonstrate similar degrees of phylogenetic and functional diversity[2,4–6].

1 Overview of research area

The Qin River is located in Shanxi Province, China. It flows through the Qinlu Plateau and the Taihang Mountains, then traverses the plains at Wulongkou in Jiyuan. The elevation at the basin's edge reaches 1 500 m, while the mountainous central section averages around 1 000 m. Over half of the Qin River basin consists of rocky forested areas, one-third comprises loess-rock hills, and nearly one-tenth is wetlands. As one of Shanxi's eight major rivers, the Qin ranks second in length, surpassed only by the Fen River basin, with a total drainage area of approximately 2 000 km^2. Serving as the mother river of Qinyuan County, it originates from six to seven source regions, with Hedi Village being the primary source, hence recognized as the river's origin. The source region features diverse wetland types, unique cultural and wetland landscapes, along with abundant flora and fauna. The Qin River's wetland ecosystem represents a distinctive and exemplary model of loess hilly riverine sources. The wetland boasts rich biodiversity within a delicate yet complex ecosystem. The river's historical and cultural diversity, coupled with its continuity, demonstrates irreplaceable uniqueness, particularly highlighting its distinctive regional cultural significance (Shanxi Qin River Source National Wetland Park). The wetlands at the source of Qin Rivers are situated in Qinyuan County's Hanhong Township, with elevations ranging from 1 600 to 2 200 m, located in the heart of the Taiyue Mountains in northwestern Qinyuan County, Changzhi City.

2 Research methods

2.1 Preparation of species list Since Flora of China, *etc.* do not adopt the APG III classification system, some plant family delineations differ from APG III. The APG III system currently best reflects phylogenetic relationships among plants and must therefore be applied. To batch-query plant families under APG III, the R package plant list (by Zhang Jinlong) was used to generate taxonomic lists of families, genera, and species.

2.2 Plot settings This paper focuses on the wetland at the source of the Qin River. Mainly, random sampling and typical sampling methods were employed to establish plots at six different elevations: 1 600, 1 800, 1 900, 2 000, 2 100, and 2 200 m. Each elevation served as a sampling site, with six 1 × 1 plots set

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perpendicular to the river channel on both sides. The number of plots within each site was determined based on the existing vegetation types. Detailed records were made for plant coverage, height, species name, and abundance within each plot. Additionally, relevant conditions such as habitat characteristics outside the plot, latitude and longitude, elevation, slope aspect, gradient, and vegetation were documented.

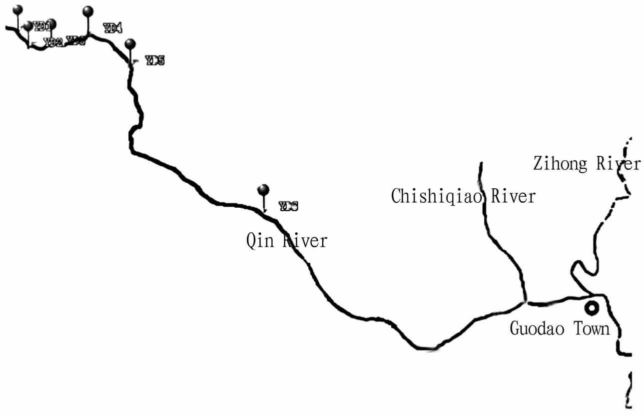

Fig. 1 Map of the Qin River

2.3 Calculation of phylogenetic indices

2.3.1 Phylogenetic diversity. The phylogenetic diversity (PD) of each sampling site was calculated using the pd module in the Phylocom software.

2.3.2 Community Phylogenetic Structure. Each sampling site's plant community was analyzed for its phylogenetic structure using the net relatedness index (NRI) and the nearest taxon index (NTI).

NRI was calculated using the following formula:

$$NRI_{\text{sample}} = -1 \times \frac{MPD_{\text{sample}} - MPD_{\text{randsample}}}{Sd\ (MPD_{\text{randsample}})}$$

NTI was calculated using the following formula:

$$NTI_{\text{sample}} = -1 \times \frac{MNTD_{\text{sample}} - MNTD_{\text{randsample}}}{Sd\ (MNTD_{\text{randsample}})}$$

where NRI_{sample}, NTI_{sample}, $MPD_{\text{randsample}}$, and $MNTD_{\text{randsample}}$ represent the actual observed values in the community, while MPDrandsample and MNTDrandsample represent the mean values obtained from 999 random combinations of species on the constructed phylogenetic tree. Sd denotes the standard deviation. MPD (Mean Phylogenetic Distance) is the average evolutionary distance between all species pairs in the community, while MNTD (Mean Nearest Taxon Distance) represents the average evolutionary distance between any species and its closest relative in the community. The above formulas indicate that the closer the phylogenetic relationship between species, the smaller their values will be.

When the NRI and NTI indicators are greater than 0, the species in the quadrat exhibit higher phylogenetic clustering than communities randomly assembled from the species pool, indicating a tendency for closely related species to co-occur. Conversely, when the NRI and NTI indices are less than 0, the phylogenetic relationships among species are more dispersed than randomly assembled communities, suggesting a tendency for distantly related species to co-occur. When the NRI and NTI indices are equal to 0, the community phylogenetic structure is random. It can be observed that NRI reflects the overall similarity among all species, while NTI captures the influence of the most similar species.

2.4 Construction of the phylogenetic tree The Phylomatic online tool was used to generate an evolutionary tree based on the Angiosperm Phylogeny Group III (APG III) classification system.

3 Results and Analysis

3.1 Phylogenetic tree of plants in the source wetland of the Qin River Using the Phylocom 4.2 software package, a phylogenetic tree was constructed for 72 non-angiosperm species in the research area, and Figtree v1.4.3 was employed to visualize the tree (Fig. 2).

3.2 Phylogenetic diversity of plants in the source wetland of the Qin River The phylogenetic diversity results for six plots in the source wetland of the Qin River are presented in Table 1, where ntaxa denotes the number of species, and PD refers to the sum of all branch lengths in the phylogenetic tree that includes and is limited to the species in the community. The phylogenetic diversity indices for the six plots ranged from 647.814 to 1 065.619, with PD values in descending order: S1 > S2 > S5 > S4 > S6 > S3. As shown in the table, a higher number of species exhibited larger PD values. For instance, s1 had the highest species count (85) and the largest PD value, whereas s3 had the fewest species and the smallest PD value.

Table 1 Phylogenetic diversity of plants in the source wetland of the Qin River

Sample	Ntaxa	PD
S1	85	1 065.619
S2	83	882.087
S3	61	647.814
S4	62	691.338
S5	75	757.17
S6	58	681.932

3.3 Phylogenetic β-diversity Table 2 presents the phylogenetic β-diversity results for six plots in the source wetland of the Qin River, representing the pairwise phylogenetic distances among 13 plots, *i.e.*, the length of shared evolutionary history among species pools from different plots.

Table 2 Phylogenetic β-diversity of plants in the source wetland of the Qin River

Sample	S1	S2	S3	S4	S5
S1					
S2	270.913 8				
S3	258.257 8	273.176 9			
S4	277.712 9	284.052 6	278.516 7		
S5	260.578 6	275.221 6	262.231 9	280.532 8	
S6	269.334 0	280.364 3	270.949 1	283.482 5	273.014 5

The results indicate that the range of phylogenetic β-diversity indices among the sample plots is 258.257 8 – 284.052 6. Four pairs

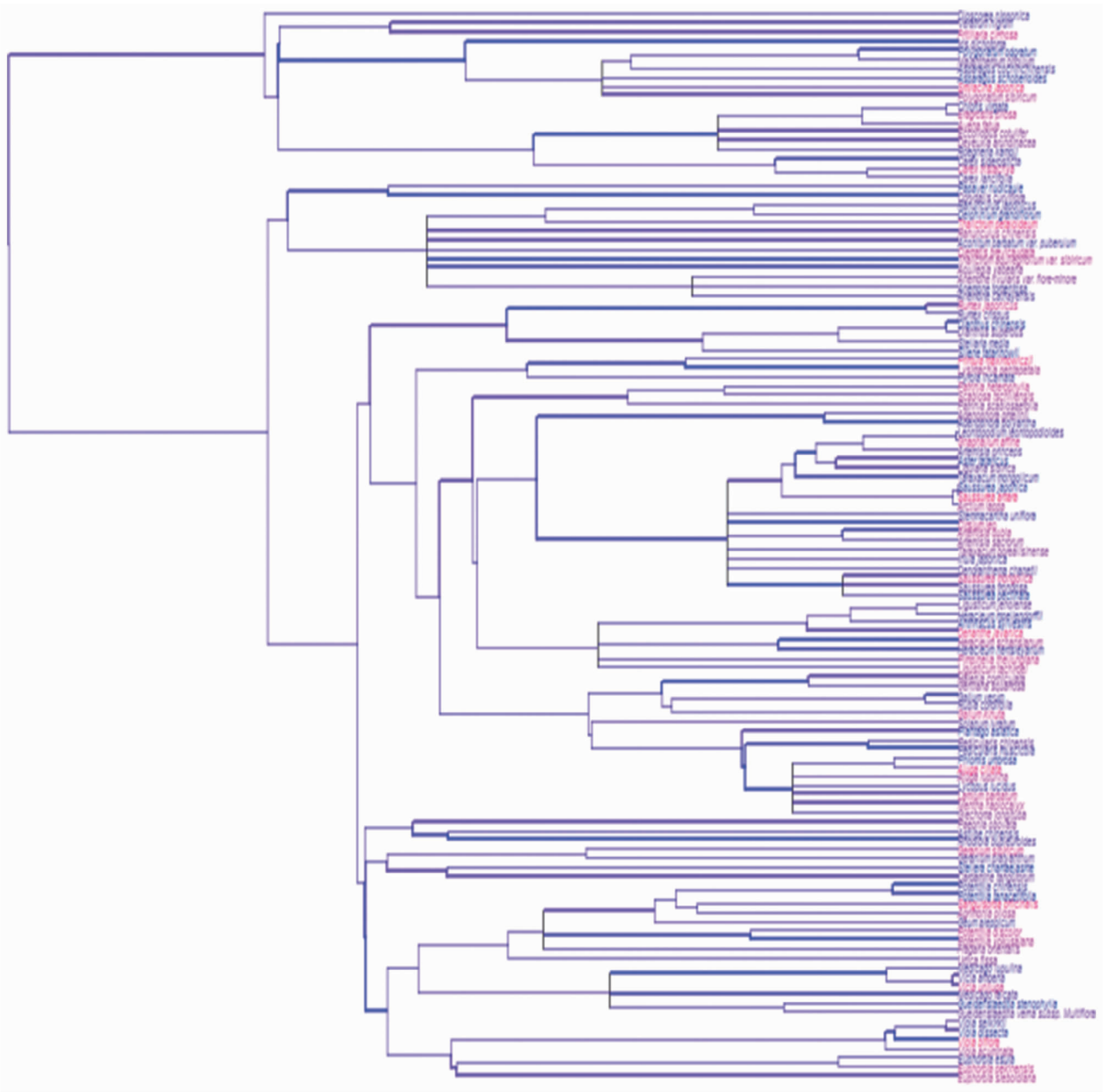

Fig. 2 **Construction of the phylogenetic tree for plants in the source wetland of the Qin River**

of plots have β-diversity indices exceeding 280: plots S2 and S4, S2 and S6, S4 and S5, and S4 and S6, suggesting significant taxonomic differences between these plots. Among them, the phylogenetic distance between plots S2 and S4 is the greatest, with the highest phylogenetic β-diversity index of 284.052 6. The dominant plant families in plot S2 are Rosaceae and *Ranunculaceae*, including species such as Potentilla yokusaiana, *Aquilegia yabeana*, and *Sanguisorba officinalis*. Plot S4 is primarily dominated by *Cyperaceae*, such as *Carex lancifolia* and *Carex tristachya*. Only one pair of plots, S1 and S3, has a β-diversity index below 260, indicating relatively minor taxonomic differences between them. Eleven shared species were found in these two plots, including *C. lancifolia*, *Thalictrum petaloideum*, and *Fragaria orientalis*. The number of shared species accounts for 28.94% and 25.58% of the total species in the two plots, respectively.

3.4 Phylogenetic structure of plant communities in the source wetland of the Qin River In the six sample plots of the wetlands at the source of Qin River, distinct phylogenetic structures were identified (Tables 3 and 4). In plots S2, S5, and S6, the mean pairwise phylogenetic distance (MPD) between species was 286.223 7, 268.343 9, and 287.215 3 million years, respectively, while the mean nearest taxon distance (MNTD) was 210.920 1, 204.477 2, and 243.920 1 million years, respectively. Analysis revealed that the observed MPD and MNTD were smaller than the random phylogenetic distances and random nearest taxon distances, respectively, resulting in net relatedness index (NRI) and nearest taxon index (NTI) values greater than 0. This indicates a clustered phylogenetic structure in plot S5, suggesting a tendency for species aggregation. In contrast, plots S2 and S6 exhibited divergent patterns, with both MPD and MNTD values below 0. For the remaining plots, inconsistent signs of NRI and NTI indices made it impossible to determine whether the phylogenetic structure was clustered or divergent.

The phylogenetic diversity results for the six sample plots in the wetlands at the source of Qin River are as follows: ntaxa represents the number of species, and PD refers to the sum of all branch lengths in the phylogenetic tree that includes and is limited to the species in the community. The phylogenetic diversity indices for the six plots ranged from 647.814 to 1065.619, with PD values in descending order: s1 > s2 > s5 > s4 > s6 > s3. As shown in the table, a higher number of species exhibited larger PD values. For instance, s1 had the highest species count (85) and the largest PD value, whereas s3 had the fewest species and the smallest PD value.

Table 3 Mean pairwise phylogenetic distance, random phylogenetic distance, standard deviation of random phylogenetic distance, and net relatedness index for plant species in the source wetland of Qin River

Plot	MPD	MPD. rnd	MPD. sd	NRI
S1	257.097 7	267.679 2	32.404 0	0.305 3
S2	286.223 7	267.512 7	33.988 8	−0.583 9
S3	266.473 1	267.428 0	41.701 9	0.062 2
S4	287.220 1	267.393 7	40.280 0	−0.786 3
S5	268.343 9	267.652 3	35.841 6	0.074 1
S6	287.215 3	287.215 4	40.966 5	−0.422 2

NOTE The units for mean pairwise phylogenetic distance, random phylogenetic distance, and standard deviation of random phylogenetic distance are all million years.

Table 4 Mean nearest taxon distance, random nearest taxon distance, standard deviation of random nearest taxon distance, and nearest taxon index for plant species in the source wetland of Qin River

Plot	MNTD	MNTD. rnd	MNTD. sd	NTI
S1	210.145 1	198.012 4	32.620 2	−0.417 7
S2	210.920 1	199.721 6	34.063 0	−0.333 3
S3	205.071 4	214.091 3	40.342 6	−0.241 4
S4	209.158 6	212.053 3	39.287 6	0.123 8
S5	204.477 2	204.472 2	35.720 4	0.131 8
S6	243.920 1	215.178 7	39.837 2	−0.706 7

The range of phylogenetic β-diversity indices among sample plots was 258.257 8 − 284.052 6. Four pairs of plots have β-diversity indices exceeding 280: plots S2 and S4, S2 and S6, S4 and S5, and S4 and S6, suggesting significant taxonomic differences between these plots. Among them, the phylogenetic distance between plots S2 and S4 is the greatest, with the highest phylogenetic β-diversity index of 284.052 6. Plot S2 was predominantly vegetated with Rosaceae and Ranunculaceae species such as *Potentilla yokusaiana*, *A. yabeana*, and *S. officinalis*, whereas Plot S4 was dominated by Cyperaceae species including *Carex lancifolia* and *Carex tristachya*. Only one pair of plots, S1 and S3, has a β-diversity index below 260, indicating relatively minor taxonomic differences between them. Eleven shared species were found in these two plots, including *C. lancifolia*, *T. petaloideum*, and *F. orientalis*.

Species in Plot S5 exhibited clustering tendencies, indicating habitat filtering as the dominant ecological process. In contrast, species in Plots S2 and S6 showed dispersal patterns. The NRI and NTI values were inconsistently signed (positive/negative) across other plots, aligning with existing research demonstrating that discordance between NRI and NTI indices is biologically plausible.

4 Conclusions and discussion

Research indicates that habitat filtering leads to similar adaptive capacities and closer phylogenetic relationships among species within a community, manifesting as phylogenetic clustering. Conversely, competitive exclusion results in more distant phylogenetic relationships among species, presenting as phylogenetic overdispersion[7]. In this research, the species in plot S5 exhibited a clustering trend, suggesting that habitat filtering dominates in this plot. In contrast, plots S2 and S6 showed a dispersal trend among species. The NRI and NTI values in other plots were inconsistent in their positive and negative signs. Existing studies have found that discrepancies between NRI and NTI indices are possible. This phenomenon is related to the health and stability of the community; the disappearance of vulnerable species within a community can lead to a decline in its ecosystem functions[8]. This research focuses on investigating the diversity of wetland plants at the source of the Qin River from a phylogenetic perspective. Wetland plants are influenced by the unique hydrological and soil conditions of wetlands. This research serves as an initial exploration of the phylogenetic diversity and community assembly mechanisms in the wetlands at the source of Qin River. Further studies incorporating environmental factors and human activities could provide deeper insights into community ecology phenomena and assembly mechanisms[9].

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