



Article Seasonal Variations in Plant Species Diversity and Phylogenetic Diversity in Abandoned Farmland of China's Huang–Huai Plain

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Abstract: Amidst urbanization and industrialization in China, abandoned farmland plays a crucial role in safeguarding plant diversity within agricultural landscapes. This study aimed to examine the patterns of seasonal variation in plant diversity within abandoned farmland habitats in the Huang–Huai Plain region. Nonparametric tests were employed to analyze plant species diversity and phylogenetic diversity across seasons. Redundancy analysis and linear regression were conducted to examine the associations between plant species composition, species diversity, phylogenetic diversity, and soil environmental factors. Our results showed that plant species diversity, richness, and phylogenetic diversity were highest in spring, followed by summer, and lowest in autumn. The phylogenetic structure of plant communities demonstrated a tendency to diverge in spring, become random in summer, and cluster in autumn. Soil available potassium and soil organic matter emerged as important factors influencing plant species composition. The content of soil organic matter and ammonium nitrogen level exhibited a significantly positive correlation with the species diversity and phylogenetic diversity of plants. This study underscores the significance of considering seasonal and temporal scales when investigating plant diversity and provides a theoretical basis for biodiversity conservation in agricultural landscapes.

Keywords: agricultural landscapes; abandoned farmland; biodiversity; species diversity; phylogenetic diversity; seasonal variations; soil environmental factors

1. Introduction

The agricultural landscape is one of the most significant types of land cover on Earth's terrestrial surface, and biodiversity plays a crucial role in the ecological functions, processes, and services of agricultural landscapes [1–3]. Globally, the increasing food demand of the growing population, the continuous expansion of agricultural land, and the encroachment on natural and seminatural habitats have led to the fragmentation of regional landscape patterns and the loss of biodiversity [3,4]. Moreover, agricultural intensification and the widespread use of chemical fertilizers, pesticides, and herbicides further threaten farmland biodiversity [5–7]. In this context, the residual natural and seminatural habitats in agricultural landscapes, such as abandoned farmlands, wooded areas, hedges, and ditches, are crucial biological shelters that can significantly increase the variety of plants, surface animals, birds, microorganisms, and other organisms, as well as the availability of ecosystem services [8–11]. Therefore, the existence of nonagricultural habitats such as abandoned farmland plays an important role in conserving biological diversity in agricultural landscapes.



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Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). As a result of urbanization and industrialization, the loss of the rural population often leads to a large-scale abandonment of land [12]. Human disturbance drastically diminished after the farmland was abandoned, and the plant community gradually regenerated. A large number of studies have shown that the abandonment of arable land promotes the increase in plant diversity, and the rise in plant diversity is conducive to the growth and stability of agricultural yield, the increase in pollinators, the decrease in weeds, and the decrease in insect pests [13]. As a result, abandoned farmland is crucial for sustaining biodiversity, increasing agricultural productivity, and providing habitat for species as well as other ecosystem services [14]. In China, abandoned farmland accounts for approximately 20% of the total arable land [15], and the extent and degree of abandonment are increasing [16], underscoring the importance of studying plant diversity in abandoned farmland.

Plant species diversity can directly reflect the composition and changing of plants in a community. However, plant diversity is not limited to species diversity alone; it also encompasses functional diversity and phylogenetic diversity [17]. Phylogenetic diversity, which considers evolutionary relationships among species, has been increasingly employed to investigate plant diversity in recent years [18]. Phylogenetic diversity provides supplementary information and different perspectives for understanding species coexistence and spatial distribution patterns from the perspectives of ecology and evolution [19,20]. Additionally, the phylogenetic structure can reflect the interspecific relationships and driving forces of community construction, making it especially suitable for studying the early succession period of community recovery [21,22].

Climate, soil, and other environmental factors vary significantly across seasons [23–25], and these seasonal changes affect soil fertility, plant growth, plant reproduction, and plant community structure [26,27]. Therefore, studying the seasonal variation in plant species diversity and phylogenetic diversity is important for maintaining ecosystem stability and protecting biodiversity. Previous studies on plant diversity have mainly focused on different habitats [28,29], spatial scales [30–33], gradients (water, soil nutrients, elevation, etc.) [34,35], and human disturbances [36,37]. The seasonal variation in plant diversity remains underexplored.

The Huang–Huai Plain in China is a critical grain-producing area, characterized by four distinct seasons and a long history of farming tradition. However, the region's ecological environment security and biodiversity protection are currently under significant pressure due to the need for food security and supply. As an agricultural landscape nonagricultural habitat, abandoned farmland has much plant diversity. Natural and seminatural habitats, including abandoned farmland, can support agricultural production and the preservation of biodiversity. However, despite the potential significance of abandoned farmland in ecological conservation, limited research has been conducted on the seasonal changes in plant diversity of such areas, with existing studies primarily focusing on the changes in plant diversity over different years of abandonment [38–40].

In the Huang–Huai Plain, a primarily agricultural region characterized by significant variations in temperature, rainfall, and soil environmental factors across seasons, human activities have varying degrees of impact during different periods. Given these contextual factors, our study aims to investigate two hypotheses: (1) distinct differences exist in the plant community structure and plant diversity characteristics across abandoned farmland in different seasons, and (2) soil environmental factors are significantly correlated with the plant species diversity and phylogenetic diversity of abandoned farmland.

To investigate these hypotheses, we conducted plant surveys and collected soil samples to analyze changes in plant diversity and the relationship between plant diversity and soil environmental factors. Our study aimed to address the following questions: (1) What is the structure of the plant community in abandoned farmland in the Huang–Huai Plain, and how does it change across seasons? (2) What are the seasonal changes in plant diversity, and is there a correlation between species diversity and phylogenetic diversity? (3) What is the relationship between the plant community and soil environmental factors in abandoned farmland?

2. Materials and Methods

The study area is located at the Agricultural Ecological Experimental Station of Henan University, in Kaifeng City, Henan Province, China (114°18'12" E, 34°52'06" N). Prior to 2017, this experimental station was abandoned farmland, which was subsequently restored into an ecological farm for the cultivation of various vegetables, pumpkins, tubers, legumes, and other crops. Starting from September 2020, all cultivated crops were cleared, and the farmland was abandoned. Within the experimental station, a total of 12 plots of abandoned farmland were established, covering a total area of 276 square meters (23 m \times 12 m). Each abandoned plot had a rectangular shape with an area of 15 square meters (3 m \times 5 m) and was demarcated with 50 cm high partition boards. There was a 50 cm buffer zone between the plots, and weed cloth was laid to prevent interference from plants outside the plots. The research area is situated on China's Huang–Huai Plain, which has a monsoon climate of medium latitudes. The average annual temperature in the study area is 14.4 °C, with an annual precipitation of 631 mm. The soil texture of the study area is predominantly composed of the Yellow River sediment and sandy soil, with a soil pH of 8.66. In the agricultural landscape of the Huang–Huai Plain, nonagricultural habitats were primarily in the early stage of community succession. The community was mainly composed of functional groups of annual and monocotyledon plants, with a simple community structure and apparent dominant populations [41].

2.1. Plant Surveys

To assess the plant communities, surveys were conducted in 12 plots during the growing season, which occurred between spring and autumn in 2022. Specifically, the surveys were carried out in the spring (March to May), summer (June to August), and autumn (September to November) when the plants were actively growing in the area under study. The surveys were conducted twice during each season to capture any potential changes in plant growth, resulting in a total of six surveys per plot. During each survey, data were collected on the average height, coverage, and the total number of plants for each species present in the plot. Five individuals of each species were randomly measured using a steel ruler to calculate their average height. Coverage was estimated by visually assessing the proportion of each species' coverage area to the total plot area. The plant data for each season represent the average of the two surveys conducted during that particular season.

2.2. Calculation of Plant Species Diversity Indices

The importance values (*IV*) of each species in each plot were determined using the following methodology:

$$IV = \frac{(RD + RC + RH)}{3} \times 100\%$$
(1)

where *RD* is the relative density of a species, calculated as the number of plants of the species in the plot divided by the total number of plants in the plot; *RC* is the relative coverage of a species, calculated as the coverage of the species divided by the sum of the coverage of all plants in the plot; and *RH* is the relative height of a species, calculated as the average height of the species divided by the sum of the average height of all plants in the plot.

This study utilized four commonly used species diversity indices, namely the Shannon Diversity Index, the Simpson Dominance Index, the Pielou Evenness Index, and the Margalef Richness Index, to comprehensively evaluate different aspects of species diversity within the study area. The calculation formulas for each index are as follows:

Shannon Diversity Index [42]:

$$H = -\sum_{i=1}^{s} P_i ln P_i \tag{2}$$

Simpson Dominance Index [43]:

$$D = \sum_{i=1}^{S} Pi^2 \tag{3}$$

Pielou Evenness Index [44]:

$$J = \frac{H}{\ln S} \tag{4}$$

Margalef Richness Index [45]:

$$R = \frac{S - 1}{lnN} \tag{5}$$

where *Pi* is the proportion of the importance value (*IV*) of a species to the overall importance value of all species. *S* denotes the total number of species in the community, while *N* represents the total number of plants in the community.

2.3. Construction of Phylogenetic Tree and Calculation of Phylogenetic Indices

The Latin names and family information of all the herbaceous plants surveyed in the study region were verified using the Angiosperm Phylogeny Group IV (APG IV) classification system [46] and the Plant Science Data Center website (https://www.plantplus.cn/cn (accessed on 5 November 2022)).

To construct the phylogenetic tree, we utilized the "V.PhyloMaker2" package in the R software [47] and visualized the tree using the "ggtree" package [48] (Figure 1).



Figure 1. Phylogenetic tree showing the evolutionary relationships among the plant species surveyed in the study area. The classification of plant species was based on the Angiosperm Phylogeny Group IV (APG IV) system. The phylogenetic tree was generated and displayed using the "V.PhyloMaker2" and "ggtree" packages in R. The tree provides a framework for understanding the evolutionary history and relationships between the different plant species in the study area.

To characterize the phylogenetic diversity, we chose the Phylogenetic Diversity Index (PD), which represents the sum of the length of evolutionary branches of all species in the community [49]. The phylogenetic structure was evaluated using the Net Relatedness Index (*NRI*) and the Net Nearest Taxa Index (*NTI*) [50,51].

The NRI and NTI were calculated using the following formulae:

$$NRI = -1 \times \frac{MPD_s - MPD_{mds}}{SD(MPD_{mds})}$$
(6)

$$NTI = -1 \times \frac{MNTD_s - MNTD_{mds}}{SD(MNTD_{mds})}$$
(7)

Here, *MPD* represents the average phylogenetic distance between all species pairs in a community, while MPD_s and $MNTD_s$ denote the average observed paired phylogenetic distance and the average observed nearest neighbor phylogenetic distance, respectively. MPD_{mds} and $MNTD_{mds}$ represent the average paired phylogenetic distance and the average nearest neighbor phylogenetic distance, respectively, under 999 null model simulations. *SD* is the standard deviation.

2.4. Determination of Soil Physical and Chemical Properties

We conducted measurements of various soil environmental factors, including soil available phosphorus (AP), available potassium (AK), ammonium nitrogen (AN), soil organic matter (SOM), soil pH, and soil moisture content (SMC). In May and October of 2022, we randomly collected three soil samples at a depth of 20 cm in each plot using a soil auger and divided them into two layers of 0–10 cm and 10–20 cm. The mean values of the two sets of soil data were used to represent the soil properties of the study area.

Soil moisture content was measured using thermogravimetric analysis. The potentiometric approach was employed to determine the pH value of the soil. Soil organic matter was quantified using a high-temperature external heating potassium dichromate oxidation spectrophotometric technique, and ammonium nitrogen content was measured using the indophenol blue colorimetric method. The available phosphorus in the soil was assessed using the sodium hydrogen carbonate solution–Mo–Sb anti-spectrophotometric method, and soil available potassium was determined using the ammonium acetate extraction–flame spectrophotometry method [52–54].

2.5. Data Analysis

In this study, all plant classifications were based on the APG IV classification system [46]. The data were organized using Excel 2021. The diversity indices of species were calculated using R's "vegan" package [55]. The Phylogenetic Diversity Index (PD) and Phylogenetic Structure Index (*NTI* and *NRI*) were computed using the "picante" package [56]. The Kruskal–Wallis test was used to analyze the significance of variations in each diversity index between seasons [57]. The species diversity indices and phylogenetic diversity indices were subjected to Spearman correlation analysis using the "corrplot" package [58,59], with a significance level set at 0.05.

To assess the link between soil environmental factors and plant species composition, data on plant abundance were analyzed using detrended correspondence analysis (DCA analysis), revealing that all of the first axes' lengths were under 3. Therefore, redundancy analysis (RDA) was used, and z-score standardization was applied to the soil environmental factor data to eliminate the influence of different units among the factors. A Monte Carlo permutation test with 999 permutations was performed for all ordination axes in RDA to evaluate the significance of the relationship between soil environmental factors and changes in plant community [60]. Both RDA and DCA analyses were performed using the "vegan" package. Additionally, linear regression analysis was conducted on soil environmental factors and plant species diversity (Shannon Index) and phylogenetic diversity (PD) indices using the "Im" function in the R software.

All statistical analyses were performed using R 4.2.1 [61].

3. Results

3.1. Seasonal Variations in Plant Community Structure

In the research region, a total of 17 families and 34 plant species were identified in the spring, summer, and autumn. Annual herbs predominated in the study area, with *Chenopodium serotinum, Abutilon theophrasti, Humulus scandens*, and *Echinochloa crusgalli* being the most common species (Table 1).

Table 1. Seasonal variation in dominant plant species importance values. Species listed in this table are dominant plant species with average importance values greater than 1%, classified using the Angiosperm Phylogeny Group IV (APG IV) classification system.

Constant	E		Importance Values				
Species	Family	Spring	Summer	Autumn			
Chenopodium seroti	inum Amaranthaceae	42.52%	19.51%	0.32%			
Alopecurus japoni	cus Poaceae	9.85%	0.00%	0.00%			
Cyperus rotundi	<i>is</i> Cyperaceae	4.29%	1.95%	0.00%			
Descurainia soph	uia Brassicaceae	6.09%	0.00%	0.00%			
Abutilon theophra	asti Malvaceae	6.31%	16.35%	6.17%			
Rumex dentatu	s Polygonaceae	2.54%	0.61%	0.00%			
Humulus scande	ns Moraceae	5.99%	12.87%	20.24%			
Sonchus arvensi	is Asteraceae	2.62%	2.43%	2.39%			
Echinochloa crusg	alli Poaceae	4.38%	18.27%	23.12%			
Setaria viridis	Poaceae	1.72%	9.48%	10.44%			
Chenopodium alb	um Amaranthaceae	2.88%	4.49%	2.69%			
Cucumis acidus	S Cucurbitaceae	1.30%	5.76%	3.32%			
Digitaria sanguin	alis Poaceae	2.40%	3.98%	26.03%			

In the spring, 1442 individual plants were investigated, comprising 17 families, 28 genera, and 30 species. In the summer, 1093 individual plants from 11 families, 18 genera, and 19 species were investigated. In the autumn, 1098 individual plants were surveyed, belonging to 7 families, 14 genera, and 15 species.

Our results reveal a clear seasonal trend in the richness of families, genera, and species, with the highest number observed during spring, followed by summer and autumn, in descending order (Figure 2).



Figure 2. Seasonal changes in plant community characteristics in the study area: (**a**) seasonal shift in the number of families, genera, and species in plant communities; (**b**) seasonal shift in the importance value (IV) of dominating families in plant communities.

3.2. Seasonal Variations in Plant Species Diversity and Phylogenetic Diversity

In this study, we calculated plant diversity indicators during spring, summer, and autumn (Table 2) and observed a gradual decline in the seasonal variations in the Shannon

Diversity Index, Margalef Richness Index, and PD Index of the plants. Conversely, the phylogenetic structure indices, *NTI* and *NRI*, showed a progressive increase with changing seasons from spring to autumn.

Table 2. Seasonal variation in plant diversity indices, presented as the means \pm standard deviations of 12 samples.

Season	Shannon	Simpson	Pielou	Margalef	PD	NTI	NRI
Spring	1.79 ± 0.24	0.74 ± 0.08	0.78 ± 0.07	1.87 ± 0.32	936 ± 121	-0.2 ± 1.34	-0.5 ± 0.89
Summer	1.72 ± 0.12	0.79 ± 0.03	0.91 ± 0.02	1.3 ± 0.19	682 ± 66.7	0.08 ± 0.77	-0.2 ± 0.66
Autumn	1.62 ± 0.18	0.77 ± 0.03	0.91 ± 0.03	1.16 ± 0.27	566 ± 124	1.12 ± 0.59	1.55 ± 1.4

3.2.1. Seasonal Variation in Plant Species Diversity

According to the findings (Figure 3), the Shannon Diversity Index had a trend toward constant decline, but there was no discernible seasonal variation. Summer and autumn had a higher Pielou Evenness Index than spring (p < 0.01). The Margalef Richness Index exhibited a significant decrease with seasonal variations, with spring displaying considerably higher richness than summer (p < 0.01) and autumn (p < 0.01).



Figure 3. Seasonal variation in plant species diversity indices: (**a**) seasonal variation characteristics of the Shannon Diversity Index; (**b**) seasonal variation characteristics of the Pielou Evenness Index; (**c**) seasonal variation characteristics of the Simpson Dominance Index; (**d**) seasonal variation characteristics of the Margalef Richness Index. The *p*-value of the Kruskal–Wallis test between seasons is shown above each plot, with *p* < 0.05 represented by a "*" to indicate a significant difference.

3.2.2. Seasonal Variations in Plant Phylogenetic Diversity and Phylogenetic Structure

When analyzing the phylogenetic diversity (PD) from spring to autumn (Figure 4), significant seasonal variances were observed, along with a significant decline in the PD (p < 0.05).



Figure 4. Seasonal variation in plant Phylogenetic Diversity Index (PD). The "*" indicates a significant difference.

The seasonal changes in phylogenetic structural indices, *NTI* and *NRI*, were evident, with both indices increasing from spring to autumn (Figure 5). Notably, significant differences (p < 0.01) were observed between spring and autumn, as well as between summer and autumn.



Figure 5. Seasonal variation in plant phylogenetic structure indices: (**a**) seasonal variation characteristics of the Net Nearest Taxa Index (*NTI*) from spring to autumn; (**b**) seasonal variation characteristics of the Net Relatedness Index (*NRI*) from spring to autumn. The *NTI* and *NRI* show seasonal variations in plant phylogenetic structure from spring to autumn. The "*" indicates a significant difference.

In spring, the *NRI* and *NTI* were both less than 0, indicating that the phylogenetic structure of the plant community diverged and there were more distantly related species in the community. The *NRI* and *NTI* were close to 0 in summer, indicating that the phylogenetic structure of the plant community tended to be random in summer. The *NTI* and *NRI* were greater than 0 in autumn, indicating that the phylogenetic structure of the plant community was clustered, and there were more closely related species in the community.

3.3. Correlations among Various Plant Diversity Indices

The Shannon Diversity Index, the Pielou Evenness Index, and the Margalef Richness Index were all highly significantly correlated with the Phylogenetic Diversity Index (PD) (p < 0.001). Among the phylogenetic diversity and phylogenetic structure indices, PD, *NTI*, and *NRI* were all highly significantly correlated (p < 0.001) (Table 3, Figure 6).

	Shannon	Simpson	Pielou	Margalef	PD	NTI	NRI
Shannon		0 ***	0.023 *	0 ***	0 ***	0.157	0.167
Simpson	0 ***		0 ***	0.033*	0.105	0.714	0.776
Pielou	0.023 *	0 ***		0 ***	0 ***	0.129	0.017 *
Margalef	0 ***	0.033 *	0 ***		0 ***	0.025 *	0.001 **
PD	0 ***	0.105	0 ***	0 ***		0 ***	0 ***
NTI	0.157	0.714	0.129	0.025 *	0 ***		0 ***
NRI	0.167	0.776	0.017 *	0.001 **	0 ***	0 ***	

Table 3. The significance of the Spearman correlation analysis of each diversity index. Significance results are indicated by asterisks: "*", p < 0.05; "**", p < 0.01; "***", p < 0.001.



Figure 6. Spearman correlation among plant diversity indices. The number represents the correlation coefficient between two diversity indices. A correlation coefficient greater than zero indicates a positive correlation, while a correlation coefficient less than zero indicates a negative correlation.

3.4. Relationship between Plant Species Composition, Plant Diversity, and Soil Environmental Factors

The RDA ordination diagram (Figure 7) showed the relationship between plant species composition and soil environmental factors. Overall, RDA axes I and II explained 59.22% of the variation in the plant community in the 0–20 cm soil layer. Soil ammonium nitrogen (AN) and soil organic matter (SOM) content showed a significant positive correlation (Figure 7c).



Figure 7. Redundancy analysis (RDA) of soil environmental factors and plant communities. The soil environmental factors shown include soil organic matter (SOM), soil moisture content (SMC), available potassium (AK), ammonium nitrogen (AN), available phosphorus (AP), and soil pH. The soil environmental factors and plant species composition RDA plots for soil layers of 0–10 cm, 10–20 cm, and 0–20 cm are presented in panels (**a–c**), respectively. RDA axes I and II explain 56.24%, 62.27%, and 59.22% of the variation in the soil layers of 0–10 cm, 10–20 cm, and 0–20 cm, respectively.

Two soil factors, AK and SOM, significantly affected the variation in the plant community in the 0–20 cm soil layer (p < 0.05). Among them, AK had a significant impact on the plant community variation in both the 0–10 cm and 10–20 cm soil layers (Table 4).

Table 4. Values of soil environmental factors and their explanatory power for changes in plant communities. Monte Carlo permutation test analysis was conducted to determine the significance of soil environmental factors on plant community changes across 0–10 cm, 10–20 cm, and 0–20 cm soil layers. M \pm SD represents the mean \pm standard deviation of soil environmental factors in 12 plots. R2 represents the proportion of variation in plant community changes explained by the soil environmental factors. Significance levels are indicated as follows: "*", *p* < 0.05; "**", *p* < 0.01.

0 11 F /	.	0–10 cm			10–20 cm			0–20 cm		
Soil Factors	Unit	$\mathbf{M}\pm\mathbf{S}\mathbf{D}$	R ²	р	$\mathbf{M}\pm\mathbf{S}\mathbf{D}$	R ²	р	$\mathbf{M}\pm\mathbf{S}\mathbf{D}$	R ²	p
рН	-	8.13 ± 0.06	0.501	0.036 *	8.17 ± 0.10	0.246	0.301	8.15 ± 0.08	0.352	0.132
AK	mg/kg	246.60 ± 16.86	0.648	0.009 **	234.70 ± 11.95	0.562	0.036 *	240.65 ± 13.46	0.758	0.002 **
AP	mg/kg	54.34 ± 13.06	0.139	0.528	42.54 ± 6.42	0.307	0.207	48.44 ± 6.54	0.052	0.806
AN	mg/kg	28.33 ± 2.31	0.214	0.334	26.47 ± 3.05	0.577	0.023 *	2740 ± 2.47	0.429	0.102
SOM	g/kg	10.92 ± 2.36	0.47	0.056	10.95 ± 2.44	0.549	0.026 *	10.94 ± 2.35	0.493	0.038 *
SMC	%	16.76 ± 1.39	0.288	0.222	18.07 ± 1.46	0.365	0.123	17.41 ± 1.33	0.368	0.127

Linear regression analysis (Figure 8) showed that the soil AN and SOM content were significantly positively correlated with the plant Shannon Diversity Index and Phylogenetic Diversity Index (PD). However, no significant correlation was found between the other four soil environmental factors and species or phylogenetic diversity.



Figure 8. Linear regression analysis of soil environmental factors and diversity indices. Panels (**a**,**b**) show the relationship between ammonium nitrogen (AN), soil organic matter (SOM), and the Shannon Diversity Index. Panels (**c**,**d**) show the relationship between the same soil factors and the Phylogenetic Diversity Index (PD). The level of statistical significance is denoted by asterisks: "*", "**", and "***" indicate *p*-values of <0.05, 0.01, and 0.001, respectively.

4. Discussion

4.1. Seasonal Variation in Plant Species Diversity and Phylogenetic Diversity in Abandoned Farmland

This study revealed that abandoned farmland plant communities in the Huang–Huai Plain exhibit significant changes in species richness, evenness, and phylogenetic diversity throughout the year. Spring had the highest plant species diversity, richness, and phylogenetic diversity, which gradually decreased with seasonal changes, reaching its lowest point in autumn. This may be because, with the rapid growth of plants in summer, some more adaptable dominant species take over the ecological niche of other species, leading to a significant decrease in species [62,63]. In addition, some plants have fully undergone their growth cycle before autumn, which can also lead to fewer species.

In spring, the plant diversity was the highest, the phylogenetic structure tended to diverge, and competitive exclusion was the primary mechanism of plant construction. Spring is the initiation stage of herbaceous plant growth, with lower vegetation coverage and underutilized resources. Many new species take advantage of this environment to swiftly establish, germinate, grow, and flower, potentially increasing plant diversity [64,65]. Niche differentiation plays a significant role in shaping the plant community, while the competition among plant species occupying similar ecological niches intensifies, resulting in a greater genetic dissimilarity and divergence in the phylogenetic structure [66].

In summer, plant species diversity, species richness, and phylogenetic diversity were at levels between those of spring and autumn. The phylogenetic structure of plant communities in summer tended to be random, and the combined effects of habitat filtering and competitive exclusion may influence community construction. The study area has a temperate monsoon climate with four distinct seasons. Summer temperatures and precipitation are significantly higher, leading to rapid plant growth and intense competition for resources. This results in higher herbaceous plant coverage and denser vegetation, strengthening plant interactions. Some species with competitive advantages occupy the ecological niches of others, reducing diversity [62,63]. Additionally, the higher temperatures and precipitation during summer can also significantly influence plant diversity. Numerous studies have demonstrated that increasing temperatures tend to decrease plant diversity [67,68], while increased precipitation often promotes plant diversity [69,70]. The plant diversity in summer was between those of spring and autumn, possibly due to the combined effects of higher temperatures, increased precipitation, and intensified plant interactions.

Autumn was found to have the lowest plant species diversity, richness, and phylogenetic diversity due to unfavorable conditions with reduced essential resources like temperature and precipitation. Plant growth, flowering, and leafing decline, with some species completing their growth cycle [63,71], potentially leading to decreased species richness. Habitat filtering becomes the dominant factor influencing community development [72]. Moreover, under habitat filtration, species with similar functions or traits tend to occupy similar ecological niches, leading to the convergence of species' functional characteristics and genetic relationships. Consequently, the phylogenetic diversity during autumn is notably low, with a tendency for the phylogenetic structure to cluster [73,74].

In general, environmental filtering leads to the emergence of closely related species with similar adaptive abilities in the same habitat, resulting in a phylogenetically aggregated community structure. Conversely, competitive exclusion prevents closely related species with similar ecological niches from coexisting in the same environment, causing species within a community to diverge in phylogenetic structure [50]. In this study, interspecific competition primarily influenced community assembly in spring, while environmental filtration was the dominant factor in autumn. As the seasons progressed from spring to autumn, environmental conditions became increasingly important in shaping plant communities, replacing interspecific competition.

We found significant correlations between the Phylogenetic Diversity Index and the Shannon Diversity Index, the Pielou Evenness Index, and the Margalef Richness Index (Table 3). This indicates that phylogenetic diversity is affected by species richness, evenness, and diversity. The higher the species diversity, the higher the phylogenetic diversity, similar to most studies' results [75,76]. It has been suggested that the alpha diversity of a community is significantly correlated at the species and phylogenetic levels, and to a certain extent, its diversity index can represent each other [77].

4.2. Relationship between Plant Community, Plant Diversity, and Soil Environmental Factors

The results of this study indicate that soil environmental factors, particularly soil available potassium (AK) and soil organic matter (SOM), play an important role in determining plant species composition. Among these factors, AK has a more significant impact on the changes in plant community structure. Potassium (K^+) is an essential macronutrient for plant growth, as it is the most abundant cation in plants and participates in various physiological functions and processes. Potassium is indispensable for regulating plant metabolism, growth, development, and responses to abiotic stress [78,79]. However, only 2% of K⁺ exists in water-soluble and exchangeable forms that are directly available for plants, and this low availability of potassium results in its deficiency in both soil and plants [78]. After agricultural fields are abandoned, the absence of human-induced fertilization can result in a potassium (K⁺) deficiency in the soil, making soil available potassium a crucial limiting factor for plant growth in abandoned lands.

This study revealed that soil ammonium nitrogen (AN) and soil organic matter (SOM) content were significantly positively correlated with plant species diversity and phylogenetic diversity (Figure 8). Soil nitrogen and organic matter are important nutrients for plant growth, which can affect plant biomass, competitiveness, and functional traits [80,81]. Many studies have shown that soil nitrogen content, organic matter content, and plant diversity have significant correlations [82–84], but this relationship is not always positive [85]. For instance, a study conducted in Haikou Malin Volcano Park showed that different vegetation types (plantations, secondary forests, and abandoned lands) had significantly different correlations with soil total nitrogen (TN), soil organic matter (SOM), and plant diversity [83]. Generally speaking, excessively high or low contents of soil total nitrogen and soil organic carbon have negative effects on plant diversity, while moderate contents have positive effects on plant diversity [82]. In this study, AN and SOM contents showed significant positive correlations with plant diversity, which might be due to the fact that abandoned land, without human disturbance and fertilization, is more conducive to the accumulation and stabilization of soil organic matter and ammonium nitrogen [86]. In addition, plant diversity in abandoned land could increase the input of organic carbon into the soil, enhance soil microbial activity and diversity, and thus improve the mineralization and transformation of soil organic nitrogen [81,87]. Therefore, soil AN and SOM content have positive correlations with plant diversity.

5. Conclusions

This study revealed significant seasonal dynamics in the community structure, species diversity, and phylogenetic diversity of plants in abandoned farmland in the Huang–Huai Plain. The number of plant families, genera, and species was highest in spring, followed by summer, and lowest in autumn. Similarly, species diversity, richness, and phylogenetic diversity showed a decreasing trend with the change in seasons, with the highest values observed in spring, followed by summer, and the lowest in autumn. The phylogenetic structure of plant communities tended to be divergent in spring, random in summer, and aggregated in autumn. Species diversity was found to be positively correlated with the phylogenetic diversity of plant communities. Soil available potassium (AK) and soil organic matter (SOM) emerged as important factors influencing plant species composition. Specifically, the content of soil organic matter (SOM) and ammonium nitrogen (AN) level were significantly positively correlated with the species diversity and phylogenetic diversity of plants.

We discovered that, even within the same year, changes in plant diversity were significant; in addition, the plant phylogenetic structure exhibited contrary traits between spring and autumn. It is therefore recommended that future research on plant diversity consider seasonal and temporal dynamics to provide a more comprehensive understanding of the ecological processes driving plant community diversity. **Supplementary Materials:** The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/d15080922/s1, Table S1: Original plant data used in this study; Table S2: Original soil data used in this study.

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