Literature Cited

1. Introduction

The primary objective of ecology is determining how communities change alongside environmental circumstances, and it is a necessity for estimating ecological reactions to
global changes [1,2]. Agriculture itself has been considered one of the leading causes of biodiversity loss because of the huge quantity of land dedicated to just this activity [3,4]. Agricultural intensification has impacted soil organisms at several taxonomic levels [5,6]. Agricultural practices like grazing, tillage, crop rotation, drainage, and exhaustive use of fertilizers and pesticides have major impacts on the soil flora and fauna [3,7]. However, the effect on soil organisms, especially Collembola, is extremely variable and highly dependent on the character and frequency of agricultural techniques applied, such as crop rotation, soil tillage, pesticide use, etc. [8,9]. Decreased or no-tillage techniques, on the other hand, can be beneficial for preserving populations of native species [3]. Global demands for food manufacturing are rising, as is the requirement for sustainable agricultural intensification [10]. Knowing ways to maximize yields while minimizing the loss of structure and function of soil is vital for agriculture’s long-term viability [11]. It is essential and helpful to understand the impacts of agricultural management intensity on communities of soil fauna in order to sustain, re-establish, and enhance the roles of biodiversity in the soil function of agricultural areas [5]. Goals of conservation agriculture are to build a sustainable agricultural system that maximizes crop productivity while significantly decreasing adverse environmental effects [12,13]. To do this, agronomical techniques should incorporate ecological processes to depend on more efficiency in the self-regulation of agroecosystems [14,15]. Usually, sustainable systems are centered on minimizing the disturbance of soil through the reduced intensity of tillage, reduced nitrogen fertilization, and increased crop residue retention to replenish organic matter content in soil [16,17].

The soil biota performs a variety of services that are critical in defining the physical, chemical, and biological characteristics of soils, particularly agricultural soils [18–20]. Soil communities of mesofauna are made up of populations of various species (for example, Collembola) that interact with one another and are possibly impacted by environmental factors and the management of soil [21]. Collembola performs a critical role in ecological processes and soil performances. For instance, they have a substantial impact on nutrient cycling and microbial community control by consuming soil microbes and dead organic debris, therefore influencing plant production [22–27]. Many writers have suggested the study of springtails as an indicator of ecological conditions in this situation [28–30]. Significant changes have been observed in the quantity and diversity of soil fauna, including both pests and useful organisms, by variations in tillage, rotation, and residue methods. Tillage alters the soil’s chemical and physical qualities, especially affecting the matrices that enable the growth of microbial populations [31–33]. The composition and structure of a community are widely acknowledged as indicators of ecological status [34–36], as well as the utilization of biological data to measure ecological health is a hot topic of research nowadays [37]. Despite the fact that diversity can be utilized to distinguish the structure of ecosystems, another significant element of the system is the variation within the abundance of its constituents [38].

Generally, beneficial impacts of modern conservation agriculture strategies on communities of springtails have been noticed [39–43], but these effects might vary depending on the soil depth investigated [42]. Wardle [44] concluded as a result of 106 pieces of research that while switching from conventional to no-tillage treatment, Collembola is often mildly stimulated, most likely as a result of relieving stress. Additionally, it has been demonstrated that returning crop remains (organic material) has a significant effect on microclimatic conditions as well as increases trophic resources for decomposers [45,46], as well as springtails, also see [47]. Nevertheless, various research indicated contradicting results, with conservation approaches having no or a negative influence on springtails when contrasted to conventional treatment [5,17,48–52]. Thus, we remain unclear about the agricultural strategies that are beneficial to Collembola populations. The impacts of crop rotation and monoculture on soil mesofauna are unclear in a sum of studies. Akkerhuis, et al. [53] discovered a considerably higher number of Mites in crops grown on a rotation of six-year than in crops grown on a rotation of three-year, but no significant differences in Collembola between treatments were found. According to Rebek, et al. [54], lower input
cropping systems (grasslands) are more favorable to epiphytic Collembola than higher management cropping systems (monoculture). Gruss and Twardowski [55] discovered that the collembolan assemblage’s diversity was not significantly differed between crop rotation and monoculture, and the structure of species was typically similar for each treatment. Additionally, numerous studies compared only one agricultural technique, such as residue management, tillage type, or nitrogen fertilization rate. The impacts of merging these different techniques have attracted little attention. In the aboveground systems, both physical disruption and resource availability are assumed to be major attributes of biological variety [48,56].

In this study, we did an experiment to investigate the responses of Collembola communities of two groups of Collembola differed based on the strength of furca (strong furca and weak furca) under different treatments varying according to tillage (mould plow, ridge tillage, no-tillage) and crop rotation (continuous corn, corn–soybean) to compare their different reactions. The main objective of this study is to estimate the differences between the responses of two groups of Collembola (strong furca and weak furca) to agricultural practices, so we can choose the group that responds well for further research and explore the co-occurrences of these Collembola assemblages by using Network analysis for the first time. In order to mitigate the objectives of this study, we hypothesized that: (1) Collembola communities with strong furca will give good response to the agricultural practices than Collembola communities with weak furca because of their fast movement. (2) There will be strong co-occurrence between species of Collembola communities belonging to the treatments with less intensity of soil disturbance and more variation in crop rotation. This study will be able to enrich our understanding of the different reactions of these two groups of Collembola and select one of them in future analysis for a better understanding of the responses of Collembola communities to agricultural techniques.

2. Materials and Methods

2.1. Study Site

The Northeast Institute of Geography and Agroecology, Chinese Academy of Sciences, Experimental Station (44°12′ N, 125°33′ E) was used for this study since it is located in a continental temperate monsoon zone. The mean yearly temperature is 4.4 degrees Celsius, and the mean yearly precipitation is 520.3 mm, with most of the precipitation (70%) between June and August. Prior to the experiment, the experimental location had already been homogenized using maize (corn) as monoculture and conventional tillage treatment for more than 30 years. The experiment was started in the fall of 2012 on a clay loam soil classed as Black soil (average soil texture was 360 g kg\(^{-1}\) clay, 245 g kg\(^{-1}\) silt, and 395 g kg\(^{-1}\) sand) [57].

2.2. Experimental Design

A randomized block design was used to conduct the experiment. Diverse tillage methods such as mould plow (MP), ridge tillage (RT), and no-tillage (NT), as well as two crop rotation systems, monoculture (corn) and corn–soybean rotation, were used in different combinations to differentiate the 6 treatments being used in this experiment. The MP system included residue return after harvest, drop mouldboard plow (20 cm), and secondary seedbed preparations in the spring, which included disking (7.5–10 cm), ridge-building, and harrowing. In RT, ridges were generated using a scrubber and a moderated lister and kept maintained with a cultivator, and the residue was restored in June of every year. For the NT, without disturbing the soil unless when planting with a no-till planter. Soybean remains were restored straight to the surface of the soil, while corn residue was chopped into roughly 30 cm parts and placed on the surface soil with 30–35 cm of standing stubble after harvesting. For corn, starter fertilizer was sprayed using a planter at the rate of 89-kg N ha\(^{-1}\), 51-kg P ha\(^{-1}\), and 51-kg K ha\(^{-1}\), while for soybean, the rate was 40-kg N ha\(^{-1}\), 49-kg Pha\(^{-1}\), and 53-kg K ha\(^{-1}\). The rates of application of N, P, and K stayed similar across all treatments of tillage. Four replicates of all six treatments were
prepared in this design (24 plots in total). Each four-replication treatment area measured 5.2 m × 30 m, with 5 m buffers rows across treatments. The six treatments observed in this experiment are:
1. MP-MC: Mould plowing among monoculture (corn)
2. MP-CS: Mould plowing among corn–soybean rotation
3. RT-MC: Ridge tillage among monoculture (corn)
4. RT-CS: Ridge tillage among corn–soybean rotation
5. NT-MC: No-tillage among monoculture (corn)
6. NT-CS: No-tillage among corn–soybean rotation

2.3. Sampling Design
The current study sampled the corn phase of all six treatments. At the study site, we collected surface living Collembola using pitfall traps [58,59]. Pitfall traps expose the captured species’ movement activities and thus can be used to estimate their activity density [60]. A total of three samples were chosen from each of the 24 plots (northeast, central and southwest) (in total, 72 sampling points). In September 2020, we set a pitfall trap (10 cm depth, 5.6 cm diameter) at each sampling point [59]. The kind of trap used for sampling was with alcohol (100%) in a cup for each of 3 replicates of samples. They were spaced approximately 2 m apart along a transect running through the interrow in autumn, when the majority of Collembola species are active, allowing for the capture of most surface-active species. After a seven-day exposure period (15–22 September 2020), the traps were removed. All captured invertebrate specimens were preserved in pure alcohol (100%) for subsequent analysis [61]. The springtails were placed on slides one by one with 100 percent alcohol. They were recognized and then counted to the species level using an optical microscope [62–65]. Individuals (springtails) captured in alcohol were numbered and recognized utilizing classification keys [65], and we compared the sequences in GenBank and also identified traits of Collembola because our identification mainly relied on the traits of Collembola and our gene sequences were mainly auxiliary functions, so we did not get all the data. We have provided the names of all the species (Supplementary Data S2). After that, we collected three specimens of each specie and performed DNA extraction using a DNA extraction Kit. The extracted DNA can be immediately carried out for the next experiment or stored at −20 °C. We use two types of primers (LCO1490 and HC02198) to prepare extracted DNA for further PCR analysis. After PCR, we send it to the company to get COI gene sequence data to differentiate between species (For the identification of all the species, please see Supplementary Data S1). Analyses were carried out at the system level of soil management. The total of individuals (abundance) and a total of species (specie richness) was then computed [66]. Later we divided the data into two parts (1) Species with strong furca and (2) Species with weak furca. Furca is an important functional trait, and strong/weak furca represents the development degree of different furca. Significant differences in their living habits and range of activities; therefore, they play different functions in the farmland ecosystem. Collembola with strong furca must have a retinaculum to manage the furca when they do not jump or move, which are tucked under the abdomen. Collembola with weak furca seldom use their retinaculum; this is our criteria. We did not upload the gene sequence to GenBank, and our identification work mainly relied on morphological identification. Thus, the data were collected as; Strong furca abundance (SA), Strong furca species richness (SSR), Weak furca abundance (WA), and Weak furca species richness (WSR).

2.4. Statistical Analysis
The numbers of Collembola have been utilized to determine density prior to statistical data analysis (ind m⁻²). The data set of abundance and species richness have been subjected to a normality and homogeneity test. Using the R software, the main effects of analysis of variance (ANOVA) were operated to identify the considerable variances between the Collembola abundances and community compositions of different experi-
mental treatment. In order to figure out what the impacts of the agricultural activities on soil Collembola assemblages are, operating R software, version 4.0.4, network analysis was used to visualize a correlation matrix of Spearman rank based on springtail biomass data [67,68]. The co-occurrence pattern of collembolan taxa was investigated for each treatment using network analysis. Species showing relative abundances higher than 0.05 percent were chosen. If Spearman’s correlation coefficient \( r \) is >0.6 and the p-value is <0.01, Spearman’s correlation among the two species was declared statistically robust [69]. Every robust correlation detected through pairwise comparisons of abundances of genera creates a correlation network, with every single node representing a single genus and every single edge representing a significant and strong association among the nodes. To characterize the produced networks topology, a set of parameters (numbers of nodes and edges, clustering coefficient, average path length, graph density, average degree, modularity, and network diameter) were measured in the R environment utilizing the igraph package [70], and an interactive platform called Gephi was used to visualize the networks [71–73]. However, 10,000 Erdős-Rényi randomized networks were produced to correlate the original network’s topology, with every edge holding the equal possibility of giving to any node [74]. Unless otherwise stated, all the statistical analyses were contained using the R environment (http://www.r-project.org, accessed on 25 September 2021).

3. Results

3.1. Community Structure Indices

In total, 9098 surface-active Collembola were recorded from 9 taxonomic families and 35 species. Out of 35 species, specie 1, 2, 3, and 8 were the dominant species because they appeared in all the treatments with high abundances almost (>10%), and species 17, 28, 30, and 35 were the rare species that appeared only once in one treatment out of 6 treatments. Collembola having strong furca were counted 3562 individuals, and Collembola having weak furca were counted 5666 individuals out of a total number of Collembola. Out of 35 species, 16 species have strong furca, and 19 have weak furca. From our six treatments, the lowest total number of Collembola was found in NT-MC (793 individuals), and the highest number of total Collembola was found in NT-CS (2854 individuals). The species richness of all the treatments varied between 9 to 28, although the overall species richness did not change significantly among treatments at the 5% error level (\( p < 0.05 \)). The Hypogastruridae family was the most abundant, accounting for 54.55% of total individuals. The Entomobryidae family was the second most abundant, accounting for 36.97% of total individuals. In this experiment, four dominant species that show the highest abundances (>10%) in almost all the six treatments belong to Entomobryidae and Hypogastruridae families. (Supplementary Data S2) Therefore, these two families are the most dominant families found in our research experiment.

3.2. Different Responses of Species Richness and Abundances of Two Collembola Groups (Strong Furca and Weak Furca) to Different Tillage Types and Rotation Types

The ANOVA-based analysis of both data sets of two Collembola groups displayed those abundances of Collembola belonging to strong furca species differed significantly among tillage types (MP > RT > NT) but did not show any variations based on rotation type. The capitalized letters (A, B, AB) indicate the significant differences between tillage types (mold plowing, ridge tillage, and no-tillage). Different letters mean they have significantly different abundances, A is significantly higher than B, and AB means it does not have significant differences with both A and B, and the lowercase letter (a) indicates no significant differences between the two rotation types (Table 1; Figure 1A). However, the specie richness of strong furca species remains unchanged by both factors (Table 1; Figure 1B). Two-way ANOVA revealed that no agricultural management element (soil tillage type, plant rotation type) had a significant influence on specie richness and abundances of Collembola having weak furca (Table 1; Figure 1C,D). There were no significant changes discovered
between the diversity (Shannon index), relative abundance (Simpson index), and evenness (pielou) of the six types of treatments observed in this research (Table 2; Figure 2A–C).

Table 1. Results of analysis of variance (ANOVA) of the effects of tillage type and crop rotation on the abundance and species richness of Collembola with strong furca and Collembola with weak furca.

| Factors | Abundance | Richness |
|---------|-----------|----------|
|         | Weak Furca| Strong Furca| Weak Furca| Strong Furca|
|         | F | p | F | p | F | p | F | p |
| Til     | 0.024 | 0.976 | 3.891 | 0.039 | 0.324 | 0.727 | 0.656 | 0.531 |
| Mag     | 4.198 | 0.055 | 0.164 | 0.69 | 1.362 | 0.258 | 0.057 | 0.813 |
| Til × Mag | 1.062 | 0.366 | 2.565 | 0.105 | 0.676 | 0.521 | 0.248 | 0.783 |

![Figure 1](image-url)
Table 2. Results of analysis of variance (ANOVA) of the effects of tillage type and crop rotation on the Shanon index, Simpson index, and Pielou index of Collembola communities.

| Factors  | Shanon |          |       | Simpson |          |       | Pielou |          |
|----------|--------|----------|-------|---------|----------|-------|--------|----------|
|          | F      | p        | F     | p       | F        | P     | F      | P        |
| Til      | 0.262  | 0.773    | 0.364 | 0.7     | 0.09     | 0.914 |
| Mag      | 0.355  | 0.558    | 0.385 | 0.543   | 0.887    | 0.359 |
| Til × Mag| 0.402  | 0.675    | 0.679 | 0.52    | 1.968    | 0.169 |

Figure 1. Analysis of variance (ANOVA) barplot of the treatments data showing (A) abundance of strong furca, (B) species richness of strong furca, (C) abundance of weak furca, (D) species richness of weak furca across three tillage types are differentiated by capitalized letters (A, B, AB) and across corn, and corn–soybean rotation is differentiated by lower case letters (a, b). Superscripts indicate significant differences between factors at the 0.05 level.

Figure 2. Cont.
3.3. Co-Occurrence Pattern of Collembola Communities under Six Different Treatments

Collembola networks for each community consist of different numbers of nodes (genera) and edges (Table 3). The nodes in the networks were assigned to nine Collembola families (Figure 3). Significant topological characteristics were evaluated to explain the intricate structure of inter-relationships between nodes (taxa) of each treatment under the experiment and to compare these networks with each other (Table 3). This network analysis shows clear differences between the network graphs of different types of soil tillage, but there are no clear differences between networks belonging to different crop rotation types (Figure 3). Here is the pattern for the types of soil tillage showing the strong networks among all the treatments (RT > NT > MP). For the RT-MC network with 25 nodes and 72 edges (with 2.88 edges/node mean), the average path length (APL) was 2.091 edges with a diameter of 4 edges. Graph density was 0.240 as well as the average degree was 2.880. In terms of clustering and modularity, our results came in at 0.629 (CC) and 0.341 (MD), respectively; values > 0.4 indicate that this network comprises a modular structure (Table 3). The structural characteristics of this network indicated that this network graph of Collembola was constructed of highly associated genera and presented a “small world” topology (it is, the RT-MC network graph is more significantly clustered than the other five graphs) (Table 3, Figure 3a).

Table 3. Network data for the communities of six treatments (RT-MC, RT-CS, MP-MC, MP-CS, NT-MC, NT-CS) were included in this experiment to identify the correlation between species.

| Treatments | Nodes Number | Edges Number | Modularity (MD) | Clustering Coefficient (cc) | Average Path Length (APL) | Network Diameter (NA) | Graph Density (GD) | Average Degree (AD) |
|------------|--------------|--------------|-----------------|-----------------------------|--------------------------|----------------------|-------------------|-------------------|
| MT-MC-SR   | 17           | 22           | 0.459           | 0.556                       | 1.5                      | 3                    | 0.162             | 1.294             |
| MT-CS-SR   | 19           | 20           | 0.609           | 0.551                       | 2.418                    | 6                    | 0.117             | 1.053             |
| RT-MC-SR   | 25           | 72           | 0.341           | 0.629                       | 2.091                    | 4                    | 0.24              | 2.88              |
| RT-CS-SR   | 22           | 49           | 0.397           | 0.54                        | 2.519                    | 6                    | 0.212             | 2.227             |
| NT-MC-SR   | 19           | 32           | 0.482           | 0.549                       | 2.62                     | 5                    | 0.187             | 1.684             |
| NT-CS-SR   | 25           | 46           | 0.424           | 0.622                       | 2.802                    | 6                    | 0.153             | 1.84              |
Figure 3. Cont.
would be alleviated by the establishment of plant roots throughout the growth period. Certain species are known to achieve their highest abundance in the spring, whereas others are highest in the autumn [81]. Loring, et al. [82] recommended that certain collembolan morphological types could be targeted by distinct tillage practices [83]. In a study population of *Pratylenchus thornei* with other plant-parasitic and non-plant parasitic nematodes have been assessed in another research. It shows that continuous maize had a greater *P. thornei* population than corn–wheat rotation, while conventional tillage had a higher *P. thornei* population than No-tillage [84]. Few significant impacts on total Collembola abundance were found by Sabatini, et al. [85], which can be attributed to differences in long-term conventional plowing and reduced tillage. However, some species, such as *Protaphorura armata* and *Isotoma notabilis*, were favored by reduced tillage, whereas the others were favored by conventional plowing. MooRE, et al. [86] found that no-tillage had a detrimental effect on Collembola (springtails) in comparison to conventional plowing. On the other side, the differences in agricultural practices between plots did not result in a growth in collembolan species diversity of both Collembola groups, corroborating with certain prior research that failed to demonstrate an influence of agricultural practices on soil animal communities.
This might be because (1) the tillage and rotation types highly appropriate for Collembola were underreported, (2) apparently little Collembola diversity in all experimental plots excludes a growth in overall species richness under different treatments, and (3) Collembola communities learn to adjust and normally work under harsh condition after long-term continuous application of harmful agricultural practices as well as (4) soil characteristics, particularly texture (particle size distribution), influenced Collembola distribution despite our best efforts (randomized seeding) to account for this natural result in our experimental design. In addition, a possible reason can be the effects of these agricultural activities on soil; the Collembola community structure may be weakened after a 12-year time period. For example, in an experiment, although treatment shows differences in abundances, the plots under conventional tillage were very similar to the plots with ECO tillage treatments in terms of species diversity and trends [83]. Another study found no significant difference in the average species richness between management systems [87]. Moreover, several factors, e.g., environmental circumstances, soil characteristics (soil pH, soil type, organic matter content, soil structure, etc.), species community (soil fauna, plants, and microbes), and period of sampling can affect the density, composition and species activity [8,88–91]. This change could be explained by regional or local differences in Collembola abundance [92], but there were no differences found in the Shannonindex, Simpsonindex, and pielou of the total number of Collembola between six different treatments studied in our experiment. According to a study, there was very little difference between NT and CLI systems in terms of species richness, biodiversity (Margalef), evenness (Pielou), and diversity (Shannon-Wiener) [87]. In another study, it was discovered that the soil management technique tested had no effect on the total number of individuals or their richness [87].

Coulibaly et al. [6] result demonstrated an overall rise in springtails species richness and density through decreasing tillage intensity, which is consistent with several past pieces of research [42,44,83]. However, Capelle et al. [51] found contradictory results that showed no change in Collembola abundance between reduced and conventional tillage and observed a greater number of collembo in conventional tillage in comparison to the systems with no-tillage, in a German data-based meta-analysis. Capelle et al. [51] showed that tillage systems with reduced-tillage intensity enhanced the total earthworm population, species diversity, and biomass considerably. At the same time, Nakamoto, et al. [93] discovered a similar effect on nematode counts. House and Parmelee, on the other hand, discovered that under no-tillage, all main microarthropod taxa, including Collembola, had higher abundances than under conventional tillage. However, according to another study, Collembola species richness was positively correlated with higher tillage intensities. Under grapevines, the inter-row Collembola activity density was positively linked with inter-row plowing and herbicide applications [61]. However, in our research, there were no noticeable impacts of soil tillage or rotation type on specie richness, with each treatment having a similar average number of species. Widespread, Common and eurytopic species dominated the assemblages. Out of the thirty-five species obtained, four (species 1, 2, 3, 8) were more abundant in almost all the treatments. Entomobryidae and Hypogastruridae families were the most abundant families accounting for 91.5% of the total number of Collembola collected during this experiment. The latter was apparently attributable to these families’ ability to reproduce quickly and invade new areas. In a study, it was also discovered that species similar to both systems (conventional and conservation) had greater densities and a higher difference in their densities than those unique species [87]. It is essential to notice that only one -time sampling was done during this research (in September), and it is well known that the communities of Collembola alter greatly during the year. The management techniques had a restricted influence on the average abundance and species richness of Collembola. Nevertheless, springtail community co-occurrence differed according to soil management systems, corroborating Hypothesis 2 that agricultural practices will alter species co-occurrence and community structure. There are clear differences between the network graphs of different communities of Collembola belonging to different tillage types that can be seen visually. However, we must acknowledge that crop rotation type had no influence on Collembola.
populations. Although it has been repeatedly demonstrated that plant species richness and diversity encourage the growth, densities, and diversification of soil fauna [94,95], possibly by increasing the quality or diversity of underground resources, numerous studies have found no significant, or even contradictory, effects of plant variety on soil organisms [95], emphasizing the lack of confidence in the obtained results. Differences in the influence of plant diversity on Collembola species richness seen in several research suggest that these influences are minor or disguised by interaction processes, all of which confirm our findings. Crop diversity’s effect may be influenced by additional factors, for example, farming systems (e.g., organic vs. conventional farming), the surrounding landscape [96,97], and soil characteristics [98]. Besides that, site conditions might well influence how soil organisms respond to changes in land use. Soil organisms living in the topsoil (0–10 cm) more accurately reflect present management practices than soil biota living deeper in the soil, which may more accurately reflect management history as well as properties of soil [99]. Only monoculture planting in experimental plots can also be the reason for not significant effects of rotation type on Collembola assemblages.

According to our research, the ANOVA and network analysis results show that tillage type is the primary factor responsible for the fate abundances of strong furca and assemblages of springtails regarding co-occurrence and species composition. Certainly, Collembola seemed to react more to the tillage intensities than to some other management intensities [6]. Other studies, however, suggest that springtails are not always harmed by the mechanical disturbance caused by repeated tillage, at least in comparison to alternate tillage on rather compacted soils [59,100]. However, to understand the underlying processes, more comprehensive studies with additional sampling for every season are required. It’s also worth noting that we just examined epigeic Collembola species, and other life forms of Collembola could respond differently or more accurately because techniques for calculating the ecomorphological index show that euedaphic Collembola species are more responsive to many mechanical disturbances than epigeic Collembola species [101]. Still, there is a gap in the knowledge about the response of springtails present in the agricultural ecosystem. Therefore, further studies are needed to have a deeper understanding of this kind of production system, apart from improving our ability to better understand the relationships among springtails, environmental factors, and certain soil properties, as well as to identify the cause and effects of springtails and different responses of different groups of Collembola species to understand which group can give a better understanding of this relationship of Collembola and their agricultural environment. Secondly, some of the mysterious differences could be ascribed to unmeasured crop as well as soil characteristics, for instance, pore spaces factors (tortuosity, size distribution) and roots of the crop, so further research must be done in this field to understand the impacts of tillage and crop rotation on soil collembolan assemblages including other important factors more deeply.

5. Conclusions

This study, along with the abundance and richness of Collembola, allowed us to investigate the co-occurrence pattern of collembolans under six distinct experimental treatments on one site. Our study established that the abundances of Collembola with strong furca varied considerably across the tillage types, but the abundances of Collembola with weak furca did not respond to tillage or rotation type. Although, tillage had a greater impact on the co-occurrence pattern of Collembola assemblages than crop rotation. This reveals that collembolan assemblages respond to mechanical disturbances. Network graphs of treatments with ridge tillage were more significantly clustered than other graphs. These results indicate that Collembola with strong furca responds better to these disturbances than Collembola with weak furca, but it will affect the community structure of total Collembola by affecting co-occurrence between species. In further studies, seasonal sampling is required to predict the dynamic pattern of Collembola assemblage. Secondly, investigating all Collembola life forms could react more clearly to these agricultural activities, and their co-occurrence patterns will give a better understanding of this relationship.
Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/d14110994/s1, Supplementary Data S1: Collembola species information that was identified during the research; Supplementary Data S2: Table S1. The dominance of each species except species 20 and 31 (because of 0% in all treatments) in 6 types of treatments used in our experiment is shown in this table by (***) for more than 10% of the total number of Collembola collected from the treatment type mentioned in the column, (**) for 1–10% of the total number of Collembola collected from the treatment type mentioned in the column and (*) for 0–1% of the total number of Collembola collected from the treatment type mentioned in the column.

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