Effects of Continuous Potato Cropping on Soil Chemical and Biological Properties in the Yellow River Irrigation Area of Central Gansu (Postprint)

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Abstract

The Yellow River irrigation area in central Gansu is a nationally important production base for processing potatoes and seed potatoes; however, continuous cropping obstacles arising from intensive cultivation have seriously affected the healthy development of the industry. Field experiments with different potato continuous cropping durations (0-5 years) were established to evaluate the effects of continuous cropping on soil chemical and biological properties and to explore the soil factors limiting potato continuous cropping. The results showed that soil organic carbon content gradually decreased with increasing continuous cropping duration, whereas available nitrogen, available potassium, and electrical conductivity exhibited the opposite trend; continuous cropping significantly increased soil available phosphorus content but had no significant effect on total nitrogen content, carbon-to-nitrogen ratio, or pH. Long-term continuous cropping (3-5 years) significantly reduced average soil enzyme activity by 33.07%-61.78% compared with non-continuous cropping (0 year), and the activities of urease, sucrase, and dehydrogenase also gradually decreased with increasing continuous cropping duration. Long-term continuous cropping reduced soil microbial biomass carbon content, and both soil basal respiration and FDA hydrolysis activity showed extremely significant negative correlations with continuous cropping duration. Biolog ECO analysis revealed that long-term continuous cropping significantly decreased total soil microbial activity and functional diversity, with the Shannon diversity index declining by 11.75%-13.65% compared with non-continuous cropping. Carbon source utilization pattern analysis indicated that continuous cropping significantly altered soil microbial community structure, with carbohydrates being the most sensitive carbon source type for distinguishing differences in soil microbial community structure under different continuous cropping durations; long-term continuous cropping significantly reduced the relative utilization rates of carbohydrate, amino acid, carboxylic acid, and amine carbon sources by soil microorganisms, and the utilization of single carbon sources by soil microorganisms showed a trend toward centralization. Linear stepwise regression and path analyses indicated that soil microbial community structure, microbial biomass carbon, total nitrogen, and dehydrogenase had significant effects on tuber yield, with microbial community structure contributing the most, followed by microbial biomass carbon. Changes in soil microbial factors may be an important cause of potato continuous cropping obstacles in the Yellow River irrigation area in central Gansu.

Full Text

Abstract

The irrigation area along the Yellow River in central Gansu Province is an important growing region for processing potatoes and seed potatoes in China. Continuous potato monoculture (CPM) stemming from intensive cultivation has severely affected the healthy development of the local potato industry. To better understand the barriers associated with CPM, a long-term field experiment was conducted with five potato cropping treatments corresponding to continuous potato cropping for 1-5 years, using maize-potato rotation as the control. This study focused on how soil chemical and biological properties changed under CPM and which soil variables contributed principally to CPM barriers. The results showed that soil organic carbon content gradually decreased with increasing years of CPM, contrary to the trends observed for alkaline hydrolyzable nitrogen, NH OAc-extractable potassium, and electrical conductivity. Compared with the control, CPM significantly increased soil NaHCO -extractable phosphorus content, but caused no significant changes in total nitrogen, C/N ratio, or pH. Long-term CPM (over 3-5 years) decreased mean soil enzyme activity by 33.07%-61.78% compared with the control. The activities of urease, sucrose, and dehydrogenase also decreased with increasing years of CPM. Long-term CPM decreased soil microbial biomass carbon content, while both soil basal respiration and FDA hydrolysis activity exhibited highly significant linear negative correlations with CPM duration. Biolog ECO assessment indicated that long-term CPM significantly decreased total activity and functional diversity of soil microbes, with the Shannon diversity index decreasing by 11.75%-13.65% compared with the control. Principal component analysis of carbon utilization profiles showed that long-term CPM clearly altered soil microbial community structure compared with the control. Among the six groups of carbon source substrates, carbohydrates were the most sensitive to changes in soil microbial communities under CPM. Long-term CPM significantly decreased the relative utilization ratios of selected carbon source substrates for soil microbes, including carbohydrates, amino acids, carboxylic acids, and amines. For 31 sole-carbon source substrates, the utilization pattern of soil microbes under long-term CPM was more centralized than under the control or short-term CPM. Linear stepwise regression and path analysis confirmed that four soil variables (soil microbial community structure, soil microbial biomass carbon, total nitrogen, and dehydrogenase) significantly affected tuber yield under CPM, with soil microbial community structure contributing most, followed by soil microbial biomass carbon. These results suggest that soil microbial variables are the main causes of CPM barriers in the Yellow River Irrigation Area of central Gansu Province.

Keywords: Potato; Continuous monoculture; Soil chemical property; Biological property

Introduction

The Yellow River Irrigation Area in central Gansu Province is a major production base for processing potatoes (*Solanum tuberosum*) and seed potato propagation in China. However, continuous cropping obstacles resulting from intensive production and contract farming models have seriously impacted the healthy development of the local potato industry. Elucidating the mechanisms underlying these obstacles and developing effective prevention and control measures have become urgent priorities for potato production in this region.

Previous studies have approached potato continuous cropping obstacles from plant growth and physiological perspectives, identifying reduced source production capacity and imbalanced source-sink relationships as important physiological mechanisms causing yield decline in continuous potato cropping systems [1-2]. A healthy soil environment is fundamental for high crop productivity, and although the mechanisms of continuous cropping obstacles may differ among crops, they primarily originate from soil [3]. Long-term continuous cropping leads to soil degradation, which negatively affects plant growth and economic yield [4-5]. However, which specific soil barrier factors trigger this negative feedback remains controversial.

Some researchers have investigated soil physicochemical properties [6-10], suggesting that potato continuous cropping causes nutrient depletion, soil acidification, or secondary salinization. Others have examined soil enzymes [11], noting that continuous cropping affects relevant enzyme activities, thereby influencing soil ecological functions. A healthy and efficient microbial community is essential for soil quality, and some scholars attribute potato continuous cropping obstacles to reduced soil microbial diversity, altered community structure, increased soil-borne diseases, and consequent yield reduction [12-20]. Others have explored allelopathy/autotoxicity as a mechanism [21-25]. Despite differences in climate, fertilization regimes, cultivars, and soil texture across these studies, potato continuous cropping obstacles likely result from multiple soil factors. Therefore, assessing changes in the soil environment under continuous cropping is a prerequisite for understanding these obstacles.

Most research on continuous cropping soil barriers has focused on greenhouse vegetables, field cash crops, medicinal herbs, and ornamental plants, with relatively few studies on potatoes, particularly in the Yellow River Irrigation Area of central Gansu, a major potato-producing region. Based on a long-term field experiment, this study examined soil chemical and biological property responses to potato continuous cropping across a temporal gradient, evaluated potential soil barrier factors, and aimed to clarify the mechanisms of potato continuous cropping obstacles and explore mitigation technologies.

Materials and Methods

1.1 Study Area

The field experiment was conducted at Tiaoshan Farm in Jingtai County, Baiyin City, located in the Yellow River Irrigation Area of central Gansu (37°12 25 N, 104°1 16 E). The site is at approximately 1,500 m elevation with a temperate continental arid climate. The average annual temperature is , the frost-free period is about 141 days, average annual precipitation is 185.6 mm, and average annual evaporation is 1,722.8 mm. The area receives 2,713 hours of annual sunshine with abundant light and heat resources (62% sunshine percentage, 618.1 kJ · m ^{2} annual solar radiation). The accumulated temperature 0°C is 3,614.8°C, and 10°C is 3,038°C, making it one of the most light- and heat-rich regions in China outside the Qinghai-Tibet Plateau. The test soil is a sierozem with sandy loam texture.

1.2 Experimental Design

A flat, uniform field previously planted with seed maize was selected. In 2005, random plots were designated for potato planting while the remaining area continued with seed maize. New potato plots were added annually, creating treatments with different continuous potato cropping durations that allowed simultaneous sampling of plants and soils across a continuous temporal gradient [2]. Plots planted with potato in the current year represented the 0-year continuous cropping treatment (rotation control), those with two consecutive potato crops represented the 1-year treatment, and so forth. Before the experiment began, the baseline topsoil (0–20 cm) properties were: organic matter 10.2 g · kg ^{1}, total nitrogen 0.55 g · kg ^{1}, alkaline hydrolyzable nitrogen 76.5 mg · kg ^{1}, available phosphorus 9.6 mg · kg ^{1}, available potassium 192.2 mg · kg ^{1}, and pH 8.43 (5:1 water:soil ratio).

In 2014, the 0-year treatment (non-continuous cropping, previous crop seed maize, designated RP) and 1-5 year continuous potato treatments (designated CP1–CP5) were selected for the experiment, with four replicates per treatment and plot sizes of 5.4 m × 10 m. A uniform potato cultivation model and fertilization rate were applied: wide-ridge double-row plastic film mulching, seed tubers cut one day before planting and disinfected with 1.5% KMnO solution, ridge width 1.35 m, row spacing 0.70 m, plant spacing 0.20 m, and planting density approximately 7.5×10 plants · hm ^{2}. Annual fertilizer application was 210 kg(N) · hm ^{2}, 150 kg(P O) · hm ^{2}, and 300 kg(K O) · hm ^{2}, using 15-15-15 compound fertilizer, 46% urea, and 51% K SO . No organic manure was applied.

Planting and fertilization were performed mechanically in one operation, followed by manual film mulching. All fertilizers were applied as basal dressing with no topdressing. Other cultivation, irrigation, and field management practices followed farm protocols and were consistent across treatments. Planting occurred on April 30 and harvest on September 8. The test cultivar was 'Atlantic' , a local main processing potato variety provided by Tiaoshan Farm.

1.3 Sample Collection and Analysis

Soil samples were collected at potato harvest in 2014 using a five-point sampling method from the ridges between potato rows near plant root systems at 0–20 cm depth. Fresh soil samples were mixed and divided into two portions: one air-dried, ground to pass 0.25 mm and 1 mm sieves for chemical property analysis; the other quickly ground to pass 1 mm sieve, stored at 4°C for biochemical analysis.

Plant samples were collected at harvest for agronomic evaluation, then separated into roots, stems, leaves, and tubers, killed at 105°C for 30 minutes, dried at 80°C to constant weight for biomass measurement, and tuber yield was recorded for each plot.

Soil chemical properties (organic carbon, total nitrogen, alkaline hydrolyzable nitrogen, available phosphorus, available potassium) were determined according to reference [26]. Electrical conductivity and pH were measured at a 5:1 water:soil ratio. Soil sucrase, urease, alkaline phosphatase, and polyphenol oxidase activities were measured using air-dried soil, while dehydrogenase and fluorescein diacetate (FDA) hydrolysis activities used fresh soil. All results were calculated on a dry weight basis. Enzyme activity measurements followed Li et al. [27], with average enzyme activity calculated as: (sucrase × urease × alkaline phosphatase × polyphenol oxidase × dehydrogenase)^(1/5) [28].

FDA hydrolysis activity followed Adam and Duncan [29]. Soil basal respiration followed Giovannini et al. [30] using dark incubation. Microbial biomass carbon was determined by chloroform fumigation extraction with 0.5 mol · L^{1} K SO , dichromate digestion, and FeSO titration [31]. Microbial quotient (%) = microbial biomass carbon / soil organic carbon [32]; microbial metabolic quotient (%) = soil basal respiration / microbial biomass carbon [33].

Soil microbial functional diversity was assessed using Biolog ECO plates containing 31 sole carbon sources: 6 amino acids, 10 carbohydrates, 7 carboxylic acids, 2 amines, 2 phenolic compounds, and 4 polymers, plus one blank control, all with three replicates. Soil pretreatment and measurement procedures followed previous reports [34]. Average well color development (AWCD) = (C - R)/n, where C is absorbance of the i-th non-control well, R is control well absorbance, and n is the number of carbon source types; negative (C - R) values were treated as 0. Functional diversity indices and relative carbon source utilization rates were calculated following Zou et al. [35], with the maximum AWCD value among treatments set as 100% and other values expressed as relative percentages. Relative utilization rate of each carbon source was also calculated as the ratio of its utilization to total utilization of all 31 carbon sources, using absorbance values at 168 h.

1.4 Data Processing

Data calculations and graphing were performed in Microsoft Excel 2007. SPSS 21.0 was used for one-way ANOVA ($P < 0.05$) to test for significant differences among treatments. Principal component analysis (PCA) was used for microbial community structure. Linear stepwise regression and path analysis evaluated the effects of different soil factors on tuber yield and their relative contributions.

Results

2.1 Changes in Soil Chemical Properties Under Different Continuous Cropping Durations

Soil chemical properties under different continuous cropping durations are shown in Table 1 . Organic carbon content in CP1-CP3 showed no significant difference from RP, while CP4 and CP5 decreased significantly by 15.68% and 11.47%, respectively. Total nitrogen content showed no significant differences among continuous cropping treatments and the rotation control. Compared with RP, the C/N ratio increased significantly in CP1, decreased significantly by 22.69% in CP2, and showed no significant changes in CP3-CP5. Alkaline hydrolyzable nitrogen content in CP1, CP2, and CP4 showed no significant difference from RP, while CP3 and CP5 increased significantly by 55.52% and 84.04%, respectively. Available phosphorus increased significantly by 49.00%-93.12% under continuous cropping compared with RP. Available potassium in CP1 and CP3 showed no significant difference from RP, while other treatments increased significantly by 30.52%-60.06%. Electrical conductivity increased to varying degrees under continuous cropping, with significant increases of 55.74%, 57.28%, and 51.22% in CP2, CP3, and CP5, respectively. Soil pH decreased significantly in CP1-CP4 compared with RP, while CP5 showed no significant change. Linear correlation analysis indicated that soil organic carbon content was highly significantly negatively correlated with continuous cropping years, while available nitrogen, available potassium, and electrical conductivity were significantly or highly significantly positively correlated.

2.2 Changes in Soil Enzyme Activities Under Different Continuous Cropping Durations

Soil enzyme activities under different continuous cropping durations are shown in Table 2 . Urease activity under continuous cropping decreased to varying degrees compared with RP, with only CP4 showing a significant decrease. Sucrase activity decreased significantly by 31.72%-75.19% under continuous cropping, while alkaline phosphatase and polyphenol oxidase activities showed no significant differences. Dehydrogenase activity decreased to varying degrees under continuous cropping, with CP4 showing a significant decrease of 83.53%. Overall calculations showed that average enzyme activity in CP1 and CP2 showed no significant difference from RP, while CP3-CP5 decreased significantly by 33.07%-61.78%. Urease, sucrase, dehydrogenase, and average enzyme activities all showed significant or highly significant linear negative correlations with continuous cropping years.

2.3 Changes in Soil Microbial Activity Under Different Continuous Cropping Durations

Soil microbial activity under different continuous cropping durations is shown in Table 3 . Microbial biomass carbon content in CP1, CP2, and CP5 showed no significant change compared with RP, while CP3 and CP4 decreased significantly by 28.63% and 24.85%, respectively. Compared with CP1, CP2-CP5 showed significant decreases of 23.55%-38.29%. Similar trends were observed for soil basal respiration and FDA hydrolysis activity, which showed no significant differences between continuous cropping treatments and the rotation control, but decreased substantially in CP2-CP5 compared with CP1, with significant differences in all treatments except CP3. No significant differences were observed in microbial quotient or metabolic quotient between continuous cropping and rotation treatments. Soil microbial biomass carbon, basal respiration, and FDA hydrolysis activity were all highly significantly negatively correlated with continuous cropping years.

2.4 Soil Microbial Functional Diversity Under Different Continuous Cropping Durations

As shown in Figure 1 [Figure 1: see original paper], CP1 and CP2 showed no significant difference from RP in average well color development (AWCD) throughout the incubation period, while CP3-CP5 decreased significantly, with AWCD at 168 h decreasing by 50.23%-56.80% compared with RP. Functional diversity indices are presented in Table 4 . Except for Pielou evenness and richness indices, CP3-CP5 showed significantly lower Shannon diversity index, Simpson dominance index, and McIntosh index compared with RP. Long-term potato continuous cropping significantly reduced both total soil microbial activity and functional diversity.

Based on carbon substrate utilization patterns from Biolog ECO plates, PCA was used to evaluate the effects of continuous potato cropping on soil microbial community structure (Figure 2 [Figure 2: see original paper]). Seven principal components were extracted from 31 factors, with PC1 and PC2 explaining 48.26% and 9.58% of total variance, respectively. Along the PC1 axis, RP and CP1, CP2, and CP3-CP5 formed three distinct groups, indicating substantial differences in carbon source utilization capacity and demonstrating that long-term continuous cropping altered soil microbial community structure. Correlation analysis between utilization of 31 sole carbon sources and PC1 showed that eight carbon sources were highly positively correlated with PC1 ($r > 0.8$, $P <$

0.01), including seven carbohydrates and one amino acid (Table 5), suggesting that changes in microbial community structure may be related to differences in carbohydrate-utilizing microbial communities under different continuous cropping durations.

The relative utilization rates of six major carbon source groups are shown in Figure 3 [Figure 3: see original paper]. Long-term continuous potato cropping significantly reduced the relative utilization rates of carbohydrates, amino acids, carboxylic acids, and amines, with carbohydrates showing the largest decrease (54.39%–67.36% reduction in CP3–CP5 compared with RP). As shown in Table 6 , carbon sources with low relative utilization (<2.5%) numbered 10 in RP, and 10, 11, 15, 16, and 16 in CP1–CP5, respectively. Those with medium utilization (2.5%–5.0%) numbered 17 in RP, and 15, 12, 9, 8, and 8 in CP1–CP5, respectively. Those with high utilization (>5.0%) numbered 4 in RP, and 6, 8, 7, 7, and 7 in CP1–CP5, respectively. Low utilization indicates declining microbial capacity, while high utilization indicates strong demand. For the 31 sole carbon sources, soil microbial utilization shifted from dispersed to centralized with increasing continuous cropping years. Under CP3–CP5, soil microbes primarily utilized L-asparagine, pyruvic acid methyl ester, D-malic acid, 4-hydroxybenzoic acid, Tween 40, and Tween 80. Statistical analysis showed that relative utilization rates of -methyl-D-glucoside, D-cellobiose, L-threonine, and D-glucosaminic acid were significantly or highly significantly negatively correlated with continuous cropping years, while pyruvic acid methyl ester and Tween 80 were significantly or highly significantly positively correlated.

2.5 Regression and Path Analysis

Using tuber yield as the dependent variable and soil factors as independent variables, linear stepwise regression analysis revealed that principal component factor 1 (PC1), microbial biomass carbon, total nitrogen, and dehydrogenase had significant positive effects on tuber yield, while other soil factors were not statistically significant ($P > 0.05$). The regression equation was: $y = 13.1882 + 3.0611x + 0.0938x + 6.5865x + 22.4721x$ ($r = 0.9611$, $P = 0.0226$, $n = 24$), where y represents tuber yield, x represents PC1, x represents microbial biomass carbon, x represents total nitrogen, and x represents dehydrogenase. Path coefficients for these four factors were calculated (Table 7). PC1 had the highest direct path coefficient (0.5536), indicating the greatest direct effect on tuber yield. Microbial biomass carbon ranked second (0.3821) and also indirectly affected yield through PC1 (indirect path coefficient = 0.3364). Total nitrogen and dehydrogenase had smaller direct effects (0.1975 and 0.1875, respectively), though dehydrogenase' s indirect effect through PC1 exceeded its direct effect (indirect path coefficient = 0.2163).

Discussion

3.1 Effects of Potato Continuous Cropping on Soil Chemical Properties

Organic carbon is a key factor maintaining sustainable soil productivity and is closely related to soil quality and crop productivity. This study demonstrated that long-term potato continuous cropping reduced soil organic carbon content, which gradually declined with increasing cropping years—consistent with previous reports [36-37]. Long-term continuous cropping can reduce stable organic matter structures while increasing easily decomposable fractions, simplifying organic matter structure and making it more susceptible to decomposition, thereby decreasing carbon content [38]. Cotton continuous cropping significantly increased the activity index of soil organic carbon but decreased the recalcitrant index within 0–40 cm depth [39]. Physical protection by aggregates is an important stabilization mechanism for soil organic carbon, and long-term continuous cropping may reduce organic carbon stability by altering aggregate size distribution and their carbon contents [40]. Long-term cultivation without organic inputs results in less carbon input and more output, also contributing to reduced organic carbon [41]. Some studies have reported higher organic carbon under long-term continuous cropping [42-43], yet crop yield still declined. Shen et al. [44] showed that even with large applications of ordinary or bio-organic fertilizer, continuous potato cropping still caused substantial yield reduction. Although this study found a significant positive correlation between soil organic carbon content and tuber yield, stepwise regression showed no significant effect of the former on the latter. Some researchers hypothesize that soil organic carbon quality, rather than quantity, may be more closely related to continuous cropping obstacles [43], though direct evidence remains lacking.

Field results showed that long-term potato continuous cropping increased soil alkaline hydrolyzable nitrogen, available phosphorus, available potassium, and electrical conductivity, with all except available phosphorus showing significant or highly significant positive linear correlations with cropping years. Under continuous cropping, poor plant growth reduced nutrient consumption, and with annual chemical fertilizer application, nutrient inputs exceeded outputs, leading to accumulation [45] and increased electrical conductivity. Unlike earlier reports [46], this study found no regular changes in soil pH with continuous cropping, possibly due to differences in test soil properties. Because crops do not absorb nutrients uniformly, some scholars attribute continuous cropping obstacles to nutrient depletion, imbalance, or disproportion [47-49], but our results do not support this hypothesis.

3.2 Effects of Potato Continuous Cropping on Soil Enzyme Activities

Potato continuous cropping reduced urease, sucrase, and dehydrogenase activities, with the latter two showing significant or highly significant negative linear correlations with cropping years. Overall, average enzyme activity under continuous cropping was significantly lower than under rotation. Soil enzymes originate from decomposition of plant and animal residues, microbial production, and root exudates; thus, soil organic matter, microbial metabolic intensity, and crop growth are the main factors affecting enzyme activity [50]. Generally, soils high in organic matter also have high enzyme activity [51], and increased organic matter promotes formation of complexes between organic/mineral colloids and enzyme molecules [52]. This study confirmed significant or highly significant positive correlations between soil organic matter content and urease, alkaline phosphatase, sucrase, and dehydrogenase activities. Reduced soil organic carbon under potato continuous cropping should be an important reason for decreased enzyme activity. Additionally, reduced microbial biomass carbon, basal respiration, and AWCD under long-term continuous cropping inhibited microbial metabolism, decreasing enzyme production [53].

Dehydrogenase activity characterizes soil redox status and is associated with microbial oxidation capacity. This study demonstrated that dehydrogenase activity was significantly or highly significantly positively correlated with soil basal respiration, FDA hydrolysis activity, and AWCD. Both dehydrogenase activity and tuber yield decreased with continuous cropping, and the former' s effect on the latter was statistically significant. Path analysis indicated this effect was largely indirect, mediated through soil microbial community structure. Polyphenol oxidase catalyzes oxidation of mono-, di-, and tri-phenols to quinones, playing an important role in converting aromatic organic compounds to humus components. Phenolic acids are common allelopathic/autotoxic substances, and some researchers suggest that reduced polyphenol oxidase activity can lead to phenolic acid accumulation, causing potential autotoxic effects and altering microbial community structure [54-56]. However, this study found no significant changes in soil polyphenol oxidase activity under potato continuous cropping.

3.3 Effects of Potato Continuous Cropping on Soil Microbial Functional Diversity and Carbon Source Utilization

This study demonstrated that long-term potato continuous cropping significantly reduced soil microbial activity and functional diversity, with clear changes in microbial community structure. Zhang et al. [57] reported that greenhouse cucumber continuous cropping significantly reduced soil microbial utilization intensity of carbohydrates, carboxylic acids, polymers, amino acids, and amines. Yue et al. [58] found that compared with continuous cropping, tobacco rotation significantly improved soil microbial utilization intensity of all carbon source types except amines. Li et al. [59] also showed that utilization of carbohydrates and amino acids by greenhouse vegetable soil microbes diverged greatly with continuous cropping years.

Under long-term potato continuous cropping, relative utilization rates of carbohydrates, amino acids, carboxylic acids, and amines all decreased significantly, with carbohydrates showing the largest decline. Changes in microbial community structure, particularly carbohydrate-utilizing communities, were the direct cause, as carbohydrates were the most sensitive carbon source for distinguishing microbial community differences among continuous cropping treatments. Carbohydrates are the most abundant organic compounds in nature with broad chemical structures and biological functions, serving as the most widely used carbon source by microorganisms and playing important roles in microbial catabolism. High-throughput sequencing revealed that long-term potato continuous cropping significantly reduced soil bacterial community structural diversity and richness [19], directly causing rapid decline in relative utilization of carbohydrate carbon sources. Ma et al. [60] found that soil microbial relative utilization of carbohydrates decreased significantly with potato continuous cropping years, while other carbon sources showed little change, suggesting metabolic function may be related to dominant microbial group composition, with functional changes determined by specific taxa. Correlation analysis between utilization of sole carbon sources and PC1 showed that seven of the ten carbohydrate carbon sources on the microplate were highly positively correlated with PC1 ($r > 0.8$, $P < 0.01$), indirectly confirming this report.

Root exudates are the main carbon source for rhizosphere microbes. Studies have reported [21-22] that potato continuous cropping markedly changed root exudate composition compared with rotation, decreasing sugar proportions while increasing organic acids. However, this study found that long-term continuous cropping reduced relative utilization rates of amino acids, carboxylic acids, and phenolic acids compared with rotation, possibly due to both carbon source selection on the microplate and reduced microbial numbers under continuous cropping. Classification of relative utilization rates for 31 sole carbon sources showed that long-term continuous cropping changed the carbon source utilization pattern, making it more concentrated on a few substrates—consistent with previous reports on continuous cucumber cropping [35]. Under CP3–CP5, soil microbes primarily utilized L-asparagine, pyruvic acid methyl ester, D-malic acid, 4-hydroxybenzoic acid, Tween 40, and Tween 80, with the first four being organic acids.

3.4 Relationship Between Soil Microbial Factors and Potato Continuous Cropping Obstacles

Linear stepwise regression showed that PC1 and microbial biomass carbon significantly affected tuber yield, while path analysis revealed that the former’ s direct contribution far exceeded the latter’ s. PC1 and microbial biomass carbon essentially represent soil microbial community structure and microbial quantity, respectively. Under our experimental conditions, microbial community structure was the most important soil factor affecting continuous potato productivity. Potato continuous cropping significantly affected soil microbial community structure, as also demonstrated in other crops [36,45,61-66]. Long-term continuous cropping has caused soil-borne diseases such as dry rot, damping-off, and verticillium wilt to become rampant in the Yellow River Irrigation Area of central Gansu, reducing tuber yield. Studies using PCR-DGGE, real-time PCR, and high-throughput sequencing have found that soil-borne pathogens such as *Rhizoctonia solani*, *Verticillium dahliae*, and *Fusarium* spp. accumulate massively with potato continuous cropping [14-20]. Long-term potato continuous cropping transforms soil from disease-suppressive to disease-conducive, with changes in microbial community structure being the primary cause [14,67]. Suppression of soil-borne diseases is largely a function of the soil microbial community; richer, more diverse microbial communities confer stronger comprehensive resistance to pathogens. Long-term continuous cropping destroys microbial community structure, weakening interspecies interactions [14,65], reducing beneficial or potentially biocontrol microorganisms [68], and decreasing competitive ability against soil-borne pathogens. Some scholars directly state that accumulation of soil-borne pathogens under continuous cropping occurs at the expense of beneficial microorganisms [68-69]. However, the deep mechanisms causing this directional change in microbial community structure remain unclear, though root exudates are hypothesized to play a role.

Root exudates are important regulators of the soil-microbe-plant system, influencing soil microbial community structure while microbes can directly act on root exudates or alter their composition by affecting plant growth. Contrary to traditional understanding, reports indicate [5,56] that continuous cropping obstacles relate more to root exudate-induced changes in soil microbial communities than to direct autotoxic effects on plants. Studies on continuous peanut showed [5] that root exudates selectively affect soil microbes, increasing relative abundance of pathogens like *Fusarium oxysporum* while suppressing beneficial organisms like PGPRs and mycorrhizal fungi. Zhang et al. [21] found that both rotation and continuous potato root exudates promoted growth of the damping-off pathogen *Rhizoctonia solani*, but the promoting effect was more pronounced under continuous cropping. Therefore, clarifying the relationship between continuous potato root exudates and soil microbial community structure will be key to understanding continuous cropping obstacle mechanisms and developing effective mitigation technologies in the Yellow River Irrigation Area of central Gansu.

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Note: Figure translations are in progress. See original paper for figures.