

Soil microbes are linked to the allelopathic potential of different wheat genotypes

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Received: 26 September 2013 / Accepted: 22 December 2013 / Published online: 7 January 2014
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Abstract

Background and Aims Soil micro-circumstance and biological stress resistance were studied to validate our hypothesis that the allelopathic potential that was enhanced by breeding resulted partially from rhizosphere microbes associated with the different varieties.

Methods The rhizosphere soils from four wheat genotypes with different allelopathic potential were collected so as to compare their soil micro-environments and bio-pressure tolerances.

Results The levels of these three categories such as bacteria, fungi, and actinomycetes ranged among $1.54\text{--}26.59 \times 10^6$, $0.43\text{--}4.12 \times 10^4$, and $1.36\text{--}18.25 \times 10^5$ CFU/g soil, respectively. Wheat 22 Xiaoyan with greater allelopathic potential had higher levels of micro-organisms than the other three genotypes having weak allelopathy. The soil microbial carbon and nitrogen analyses suggested that wheat could create an active

microhabitat with high activities of key soil enzymes such as urease, catalase, sucrase, and dehydrogenase. Using the approximate concentrations detected in wheat rhizosphere soils, the leachates of all four wheat materials significantly inhibited the growth of the weed *Descurainia sophia* and take-all pathogen *Gaeumannomyces graminis* var *Tritici*. **Conclusions** Wheat exudates provided carbon and nitrogen resources for the relevant microorganism. Meanwhile, the rhizosphere soil microbes contributed to allelopathic potential of wheat by positive feedback.

Keywords Allelopathic potential · Facilitated effect · Microhabitat · Soil microorganism · Wheat

Abbreviations

MBC	Soil biomass carbon
MBN	Soil biomass nitrogen
CFU	Colony forming units
TPF	Tri-phenyl formazan
PDA	Potato dextrose agar
IR	Inhibition rate
DIMBOA	2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one
C	Carbon
N	Nitrogen

Responsible Editor: Inderjit.

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Introduction

Allelopathy is a process where secondary metabolites produced by plants, micro-organisms, and fungi control

the growth and development of other biological systems. Some plants may affect other plants beneficially or antagonistically via allelochemical compounds, which may be released directly or indirectly from live or dead parts to cause allelopathic and phytotoxic effects (Rice 1984). Crop allelopathy may be useful for minimizing serious problems that affect agricultural production, such as environmental pollution, unsafe products, human health concerns, depletion of crop diversity, and reduced crop productivity. Especially, Soil sickness was more often associated with allelopathy than with herbicides (Khanh et al. 2005). Several crops, such as alfalfa, barley, black mustard, buckwheat, rice, sorghum, sunflower, and wheat (*Triticum aestivum*) exhibit weed suppression effects, either by exuding allelochemicals from their living plant parts or from decomposing residues (Ferrero and Tesio 2010). The exploitation of the allelopathic traits of crops or cultivars with strong weed inhibition qualities, as well as standard weed control strategies, could facilitate the establishment of sustainable agriculture.

Wheat allelopathy can be inhibitory or stimulatory. Li et al. (2011) reported that increasing the density of allelopathic wheat improved its competitiveness and significantly inhibited the growth of annual ryegrass (*Lolium rigidum*) in a laboratory bioassay. In addition, it was shown that cultivating corn after winter wheat in Kerman, Southeast of Iran, usually reduced the growth and yield of corn. Straw extracts had negative and significant effects on the growth of corn varieties, and significant allelopathic effects remained up to 90 days after wheat harvest, although they decreased gradually up to 180 days after the harvest (Saffari and Torabi-Sirchi 2011). The negative impacts of wheat autotoxicity on agricultural production systems have also been identified, where wheat straw is retained on the soil surface for conservation farming purposes (Wu et al. 2001b). Of course, we also need to consider the stimulatory effects of wheat. Dong et al. (2013) concluded that wheat exudates collected hydroponically induced *Orobancha minor* germination. Wheat varieties with different ploidy levels differed in their allelopathic stimulation of *O. minor* germination, where hexaploid wheat was the most stimulatory. Therefore, the allelopathic activity of wheat could be used as a non-chemical option for *O. minor* control. At present, numerous allelochemicals have been identified in wheat, which are mainly phenolic acids, hydroxamic acids, and

short-chain fatty acids (Ma 2005). Our research group demonstrated that the variation in the allelopathic properties of dryland winter wheat differed significantly among genotypes. Allelopathic effects had high heritability (55–95 %) throughout the life cycle of wheat. The heritability was highest in the tillering stage and weakest in the seed filling stage. Thus the allelopathic potential variation was discontinuous throughout the wheat life cycle. Putative genes related to the weed control ability of wheat due to its allelopathic potential have been detected on chromosomes 1A, 2B, and 5D (Zuo et al. 2012 and 2007).

The rhizosphere is the narrow region of soil that is affected directly by root secretions and associated soil microorganisms. The rhizosphere soil is a complex region of the soil because it is in contact with plant roots. It contains many microorganisms and its composition is affected by root activities. Singh et al. (2008) determined the allelopathic effects of rhizosphere soils from different altitudes and under agroforestry trees in Garhwal Himalaya, India. The rhizosphere soil collected under *Ficus roxburghii* was most toxic to the germination of the test crops, whereas the rhizosphere soil collected under *Boehmeria rugulosa* was less harmful to germination but inhibited plumule growth in the test crops. Kato-Noguchi et al. (2007) concluded that UV-irradiation increased the production of momilactone B in rice seedlings and its secretion into the rice rhizosphere. Momilactone B is an antimicrobial and allelopathic agent, so its secretion into the rhizosphere may provide a competitive advantage during root establishment via the local suppression of soil microorganisms and inhibition of the growth of competing plant species. The chemical, genetic, and physiological bases of wheat and rice allelopathy have been explored widely (Wu et al. 2000; Xu et al. 2011; Zuo et al. 2011 and 2012). However, there have been few reports of the microbiological dimension of the allelopathic potential of wheat. Thus, the present study aimed to identify and quantify the typical microorganisms found in the rhizosphere soils of four wheat cultivars. We also evaluated their effects on the soil biomass carbon (MBC) and nitrogen (MBN) levels, and on the activities of soil enzymes. Furthermore, we assessed the allelopathic potential of these rhizosphere soils using selected weeds and pathogens to understand the enhanced allelopathy of wheat genotypes.

Materials and methods

Wheat genotypes

Based on previous assessments of their allelopathic potential (Zuo et al. 2005 & 2007), four wheat genotypes were selected, i.e., 22 Xiaoyan, 1 Ningdong, 3 Fengchan, and 1 Bima, which exhibited strong, medium, weak, and no allelopathy, respectively. A field plot trial was conducted from 2005 and 2007 at the Institute of Soil and Water Conservation, Yangling, Shaanxi Province, China. The soil conditions, water, and fertilizer management regimes were the same as those used in a previous trial (Zuo et al. 2008). In the fall of each year, four wheat genotypes (National Engineering Research Centre for Wheat, Zhenzhou, China) were sown individually (monoculture) in the plots, where the control of no wheat made a total of five treatments. Each treatment was replicated six times. The plots measured 4.25 m² and were arranged in a completely randomized block design with a total of 30 plots. Each year, crude root samples of the four wheat types were collected from six plots at four different growth stages (seedling, heading, filling, and mature stages). In the control plots, samples of the surface 5 cm of soil were collected. These samples were collected in aseptic bags and dried at room temperature for 1 day. For the root samples, the soil sticking to the roots was shaken off lightly and collected after sieving through a 0.01- μ m sieve, and this was considered to be the rhizosphere soil. All of the soil materials were stored at 0–5°C in a refrigerator until use.

Determination of the typical amounts of microorganisms in the wheat rhizosphere soils

Solutions were prepared from soil suspensions using the gradient dilution method. In a 500 mL conical flask, 90 mL of sterile distilled water, 10 g of soil sample, and some glass beads were mixed together to produce the soil suspension, which was then shaken for 10 min. The solution obtained was diluted in a stepwise manner using sterile distilled water up to 1 million-fold. Next, 1 mL of resulting solution was poured into 50 mL of culture medium after melting at 55°C (Table 1). The solution and the medium were mixed, cooled, solidified, and cultured in a biochemical incubator at specific temperatures/periods (i.e., 4 days at 30°C for bacteria, 4 days at 28°C for fungi, and 7 days at 28°C for actinomycetes). Counts were made after the microbe

communities were established. Table 1 shows the culture conditions used for quantitative determination of selected microorganisms in rhizosphere soils. The amounts were measured three times using the plate counting method. The final value was the mean of 54 counts (three years \times six plots \times three counts) minus the soil background value (the control without wheat). The results were expressed as colony-forming units (CFU) per gram of dry soil. The soil was dried to a constant weight at 105°C for 6–8 h.

Determination of MBC and MBN, and the enzyme activities in the wheat rhizosphere soils

The MBC and MBN were determined using the chloroform fumigation-extraction method, with minor modifications (Zhou et al. 2013). Each dried soil sample was divided into two portions, each of which comprised 10 g of dry soil. One portion was fumigated with ethanol-free chloroform for 24 h in the dark at 25 °C, whereas the other portion was not fumigated (control). The fumigated and unfumigated soils were extracted with 0.5 M K₂SO₄ solution for 30 min. The supernatant was filtered and the filtrate was frozen. The amounts of extractable carbon and nitrogen were determined using the K₂CrO₄ oxidation method and the Kjeldahl nitrogen determination method, respectively. MBC was calculated as: $MBC = E_c / K_c$, where $E_c = (C \text{ extracted from fumigated soil}) - (C \text{ extracted from unfumigated soil})$ and K_c was a constant used for calibration (0.38). Similarly, MBN was calculated using the same formula, where K_N was 0.54. The activities of urease, catalase, sucrase, and dehydrogenase were measured using the indophenol colorimetric method, KMnO₄ titration method, dinitrosalicylic acid colorimetric method, and the triphenyl formazan (TPF) colorimetric method, respectively. The actual procedures used to determine the enzymes activities were reported by Guan (1986). The MBC and MBN, and soil enzyme activities were corrected to eliminate any soil background effects.

Effects of wheat rhizosphere soil leachates on weed and pathogen growth

To test the allelopathic potential of un-autoclaved rhizosphere soils on weed seed germination, seeds of the weed *Descurainia sophia*, which were collected in wheat fields at the Institute of Water and Soil Conservation, were surfaced-sterilized with 1.2 % NaClO

Table 1 Culture methods used for the quantitative determination of selected microorganisms in rhizosphere soil

Culture conditions	Bacterium	Fungus	Actinomycete	Cellulose decomposing bacteria	Nitrogen-fixing bacteria	Nitrifying bacteria	<i>Thiobacillus</i>
Culture medium	Beef extract peptone	Martin substratum	Gause's No.1	Cellulose Congo red	Ashby's without nitrogen	Improved Stephenson's	Sodium thiosulfate
Temperature (°C)	30	28	28	30	28	30	28
Time (days)	4	4	7	6	5	7	7

solution, rinsed three times with sterile distilled water, and conditioned for pre-germination in moist gauze for 15 h. Twenty preconditioned weed seeds were distributed evenly on 10 g of rhizosphere soil (for each wheat genotype) at the bottom of a Petri dish (9 cm diameter). Each treatment was replicated three times. In the control, the test soil came from the plots without any wheat. The seeds were cultured for 7 days and the dry weights of plants in the Petri dishes were measured. The bioassay method was reported previously (Zuo et al. 2005). The suspension solution (soil leachate) prepared from rhizosphere soil was filtered with qualitative filter paper. The filtrate obtained was then used to test its inhibitory potential on a wheat pathogen. We diluted 1 mL of the filtrate one million times and added it to sterilized potato dextrose agar medium (PDA). The two components were mixed completely and cooled. Strain 9812 of wheat root take-all (*Gaeumannomyces graminis var. Tritici*) was inoculated onto the surface of the medium according to the method of Penrose (1985). The control was based on soil collected from no-wheat plots. The plates were then cultured in the biochemical incubator at a constant temperature of 24°C. After 7 days culture, the number of take-all pathogen colonies and their diameters were recorded. Take-all pathogen (Strain 9812, *G. graminis var. Tritici*) was provided by the Institute of Plant Pathology, College of Plant Protection, Northwest A & F University.

Data analyses

The weed inhibition rate (IR) was calculated as: $IR = (CK - TR) / CK$, where, TR is the dry weight of the treatment and CK is the dry weight of the control. $IR > 0$ indicated inhibition, whereas $IR < 0$ indicated stimulation. Analysis of variance (ANOVA) was performed based on the LSD, or a *t*-test. The IR of the pathogen was also determined, where TR was the average

diameter of the take-all pathogen colonies with the treatment and CK was the mean diameter of the colonies in the control. A multiple comparisons analysis was then performed using SPSS15.0. Significant differences ($P < 0.05$) between the four wheat genotypes at the same growth stage (represented by small letters in the figures) were detected using the Student's *t*-test.

Results

Population dynamics of rhizosphere soil microbes with different allelopathic wheat genotypes

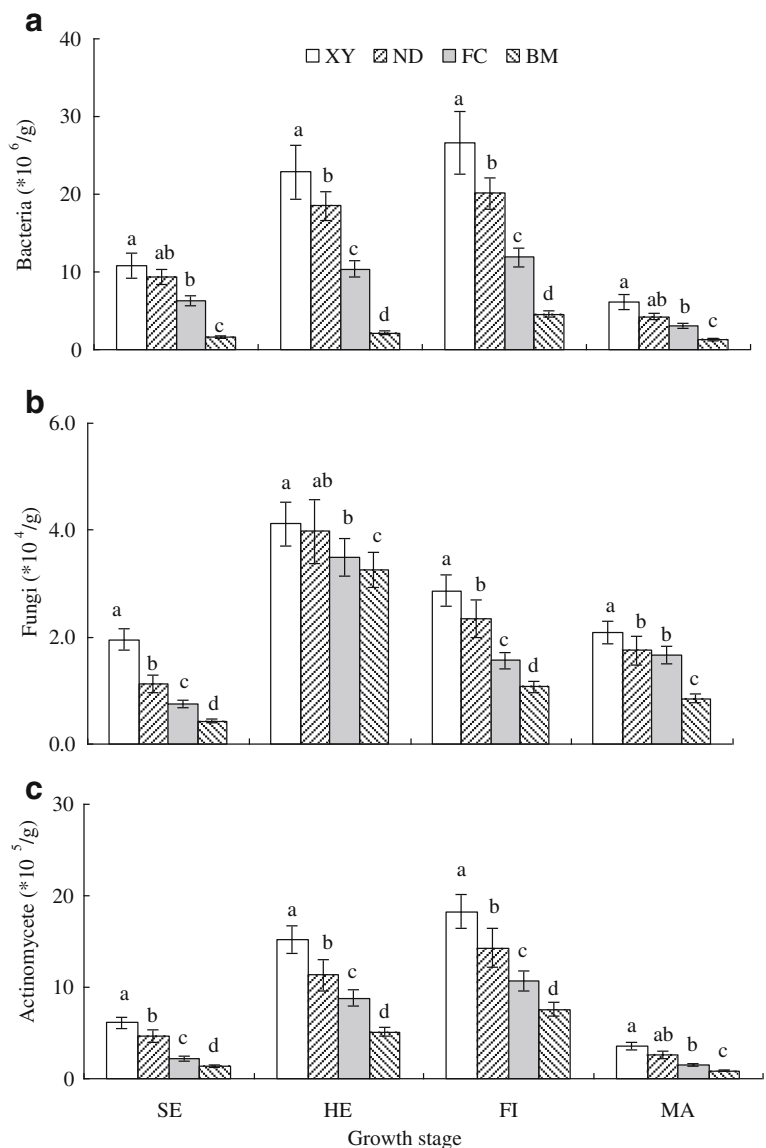
Three types of microorganisms were identified in the rhizosphere soils of the four allelopathic wheat genotypes, which declined in the following order: bacteria, actinomycetes, and fungi. The levels of bacteria were highest in the filling stage of wheat and lowest in the maturity stage. All four allelopathic wheat genotypes exhibited the same distribution of bacterial quantities during different stages: filling > heading > seedling > maturity. In the same growth stage, the rhizosphere soil of 22 Xiaoyan contained the highest amount of bacteria, followed by 1 Ningdong, 3 Fengchan, and 1 Bima in descending order of abundance, which agreed with the order of the allelopathic potentials of the four wheat genotypes. In particular, there were significant differences in the amounts of bacteria in the heading and filling stages among the four wheat genotypes (Fig. 1a). For fungi, the maximum amounts occurred during the heading stage of wheat with the minimum in the seedling stage. Each allelopathic wheat genotype exhibited the same order of fungal quantities in the different stages: heading > filling > maturity > seedling. In the same growth stage, the amount of fungi in the rhizosphere soil increased as follows: 1 Bima, 3 Fengchan, 1 Ningdong, and 22 Xiaoyan. This also

matched allelopathic potentials of the four wheat genotypes. During the filling stage, there were significant differences in the amount of fungi among the four wheat genotypes (Fig. 1b). For actinomycetes, the variation in the amounts between the four growth stages and the four wheat genotypes resembled the results obtained for bacteria (Fig. 1c).

Four typical bacterial types were identified and quantified (Fig. 2). For each wheat genotype, the quantity of cellulose-decomposing bacteria peaked in the maturity stage and the minimum values occurred in the other three stages. However, there were no significant differences between the seedling, heading, and filling stages.

The wheat genotype 22 Xiaoyan with the highest allelopathic potential possessed more cellulose-decomposing bacteria in its rhizosphere soil. The same trend occurred in all four growth stages (Fig. 2a). From the seedling to the filling stages, the amount of nitrogen-fixing bacteria increased gradually. Subsequently, the bacterial quantity declined until the maturity stage. Nitrogen-fixing bacteria had their highest and lowest abundance during the filling and maturity stages, respectively. We also found that the wheat genotypes with the highest allelopathic potential hosted the most nitrogen-fixing bacteria, and vice versa (Fig. 2b).

Fig. 1 Soil microbial quantitative dynamics in the wheat rhizosphere during different growth stages. XY, ND, FC, and BM represent the four wheat genotypes Xiaoyan, 1 Ningdong, 3 Fengchan, and 1 Bima, respectively, which had strong, medium, weak, and no allelopathy. SE, HE, FI, and MA are the four growth stages of seedling, heading, filling, and maturity respectively. Small letters indicate significant difference at $P < 0.05$ between the four allelopathic genotypes at the same growth stage



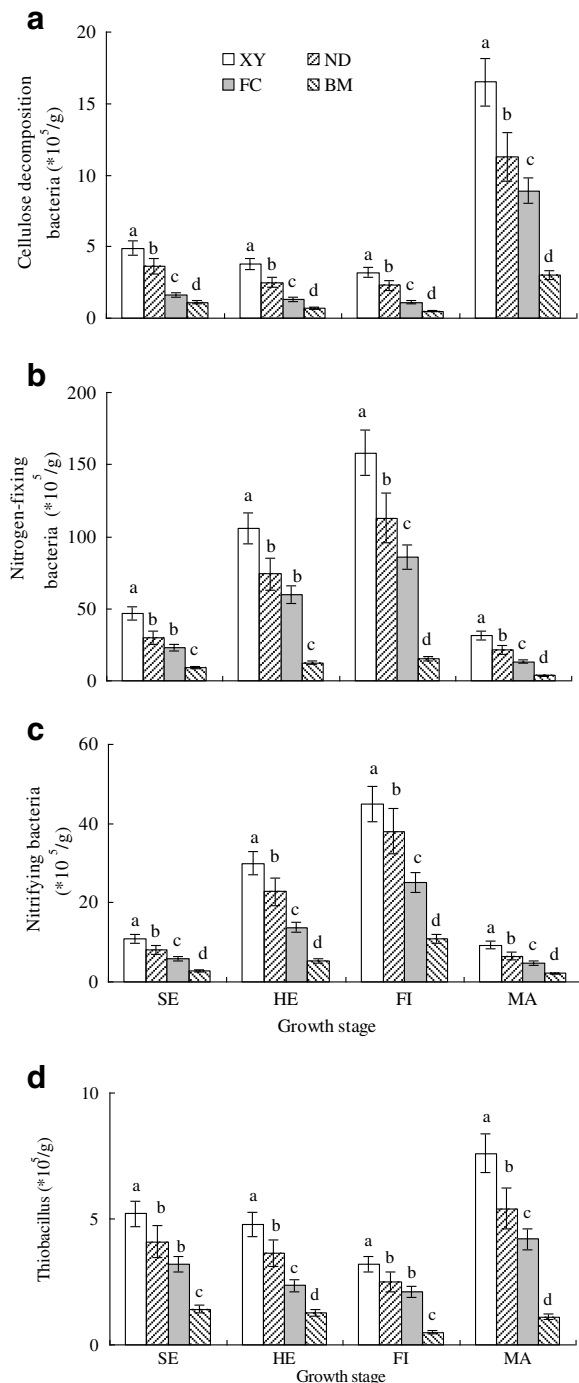


Fig. 2 Amounts of selected bacteria in wheat rhizosphere soil during different growth stages. XY, ND, FC, and BM are the four wheat genotypes 22 Xiaoyan, 1 Ningdong, 3 Fengchan, and 1 Bima, respectively, which had strong, medium, weak, and no allelopathy. SE, HE, FI, and MA are the four growth stages of seedling, heading, filling, and maturity, respectively. Small letters indicate significant difference at $P < 0.05$ between the four allelopathic genotypes at the same growth stage

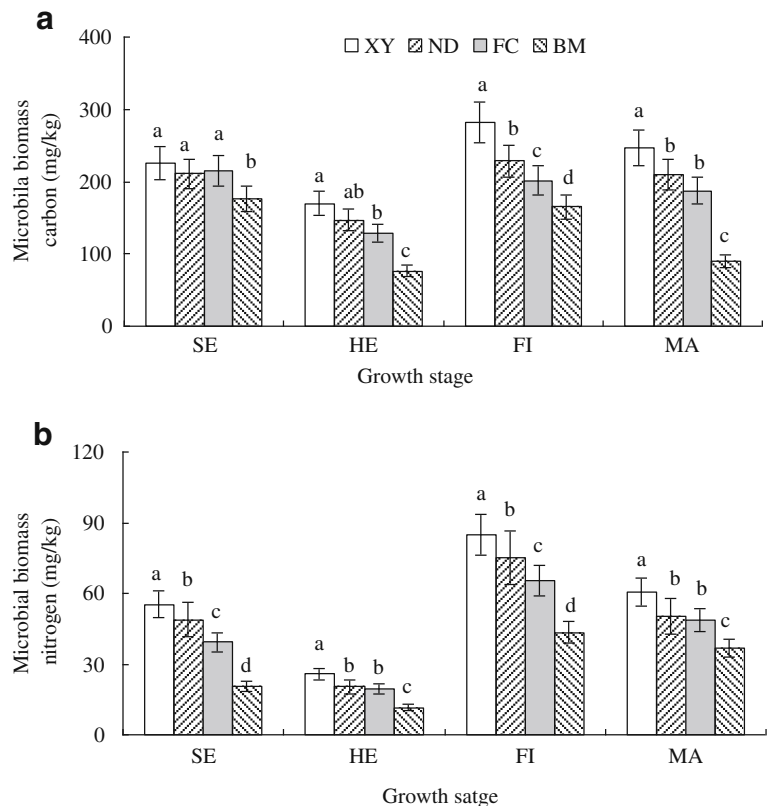
The quantities of nitrifying bacteria had a similar trend to nitrogen-fixing bacteria. The amounts of nitrifying bacteria followed the order: maturity < seedling < heading < filling stages for each wheat genotype. At the same growth stage, the bacterial quantity increased in the order: 1 Bima, 3 Fengchan, 1 Ningdong, and 22 Xiaoyan, i.e., a positive correlation with the allelopathic potential (Fig. 2c). The abundance of *Thiobacillus* decreased gradually from the seedling to the filling stages, before increasing in the maturity stage. Interestingly, the bacterial quantity also increased in the order: 1 Bima, 3 Fengchan, 1 Ningdong, and 22 Xiaoyan, which agreed with the allelopathic variation among these wheat genotypes (Fig. 2d).

MBC and MBN, and the enzymes activities in the wheat rhizosphere soil

The content of MBC was greater than that of MBN in the rhizosphere soils of four wheat genotypes (Fig. 3). Before the reproductive growth phase, the MBC increased gradually in the rhizosphere soil. By contrast, MBC reached its maximum value during the filling stage. Among the four wheat genotypes, the rhizosphere microbes of 22 Xiaoyan had the strongest carbon utilization activity whereas those of 1 Bima had the lowest (Fig. 3a). The nitrogen utilization potential variation was similar to the carbon status. For each wheat genotype, the highest and lowest soil MBN values occurred during the filling and heading stages, respectively. At the same growth stage, the soil MBN content declined in the order: 22 Xiaoyan > 1 Nongdong > 3 Fengchan > 1 Bima (Fig. 3b). The C/N ratio of the soil microbial biomass increased from the seedling stage (5.62) to the heading stage (6.75), before decreasing until the filling stage (3.31), and increasing slightly up to the maturity stage (3.63). In contrast to the allelopathic variation among the four wheat genotypes, the C/N ratio followed the order: 22 Xiaoyan (4.52) < 1 Ningdong (4.69) < 3 Fengchan (4.75) < 1 Bima (5.34).

The soil enzymes activities increased from the seedling stage to the filling stage, before declining up to the maturity stage. 22 Xiaoyan had the highest allelopathic potential and the greatest soil enzyme activity. By contrast, the allelopathic potential of genotypes such as 3 Fengchan was weak and the soil enzyme activity in its rhizosphere was also low. The enzymes activities followed the order: sucrase > catalase > urease > dehydrogenase (Fig. 4).

Fig. 3 Microbial biomass carbon and nitrogen in the wheat rhizosphere soil during different growth stages. XY, ND, FC, and BM are the four wheat genotypes 22 Xiaoyan, 1 Ningdong, 3 Fengchan, and 1 Bima, respectively, which had strong, medium, weak, and no allelopathy. SE, HE, FI, and MA are the four growth stages of seedling, heading, filling, and maturity, respectively. Small letters indicate significant difference at $P < 0.05$ between the four allelopathic genotypes at the same growth stage



Effects of rhizosphere soil leachates from different wheat genotypes on weeds and pathogens

The rhizosphere soil leachates significantly inhibited the weed *D. sophia* and the pathogen *G. graminis* (Fig. 5). For all of the wheat soil leachates, the weed inhibition rate increased from the seedling stage to the filling stages, before decreasing up to the maturity stage. For the different wheat genotypes, the order of weed inhibition was: 1 Bima < 3 Fengchan < 1 Ningdong < 22 Xiaoyan. There were significant differences in the weed inhibition rates among the four wheat genotypes (Fig. 5a). Interestingly, the inhibition rate of the pathogen was similar to that of the weed in the different growth stages for each wheat genotype. However, the weed *D. sophia* was more susceptible to the rhizosphere soil leachates than the pathogen *G. graminis* (Fig. 5b).

Discussion

Wheat has allelopathic potential and it inhibits harmful weeds and pathogens, mainly by releasing functional

chemicals. Wu et al. (2000) identified various allelochemicals in wheat seedlings, i.e., p-hydroxybenzoic, trans-p-coumaric, cis-p-coumaric, syringic, vanillic, trans-ferulic, and cis-ferulic acids, and 2,4-dihydroxy-7-methoxy-1,4-benzoxazin-3-one (DIMBOA), which were detected in both the shoots and roots of 17-day-old wheat seedlings and their associated agar growth media. The quantities of exuded allelochemicals varied depending on the specific compound and the ranges were 2.3–18.6, 0.6–17.5, 0.1–4.9, 0.0–52.7, 0.33–12.7, 1.5–20.5, and 1.6–23.4 $\mu\text{g/L}$ of water/agar for p-hydroxybenzoic, vanillic, cis-p-coumaric, syringic, cis-ferulic, trans-p-coumaric, and trans-ferulic acids, respectively (Wu et al. 2001a). Wheat accessions with well-characterized allelopathic activities tended to contain higher levels of these compounds than weakly allelopathic types. In addition, our research group reported some indirect results. The breeding histories of 1 Bima, 3 Fengchan, 1 Ningdong, and 22 Xiaoyan show that the agronomic properties of winter wheat, such as the thousand-grain weight and the yield, have increased gradually. Thus, their superior agronomic performance may compensate for the

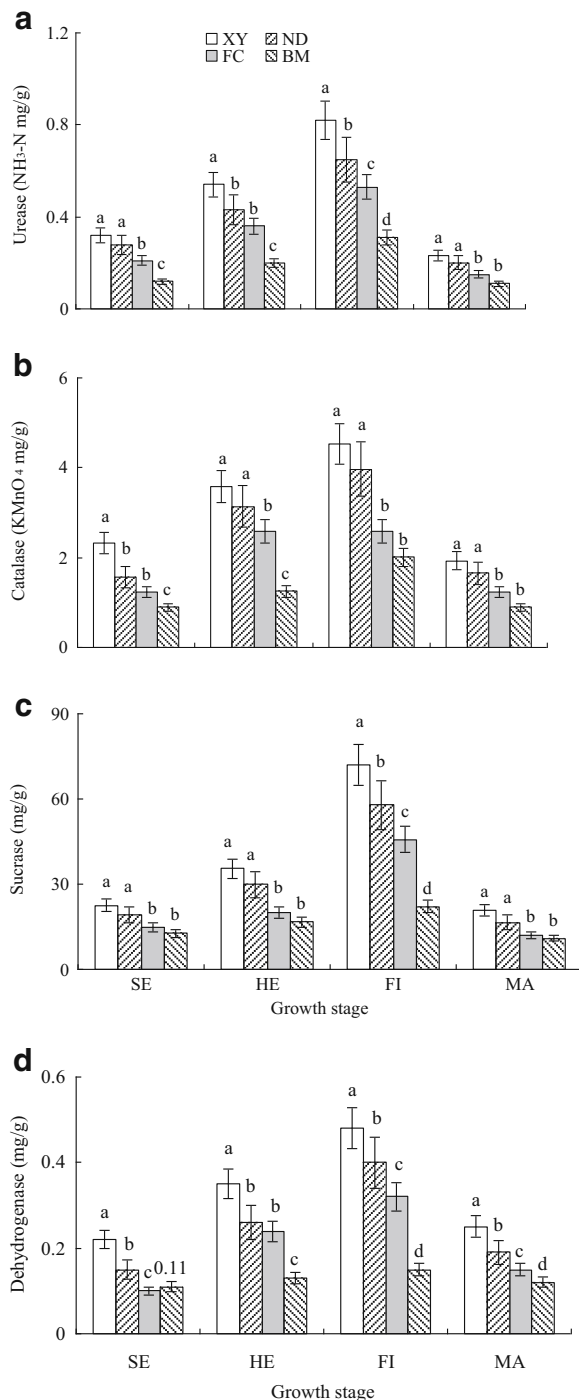
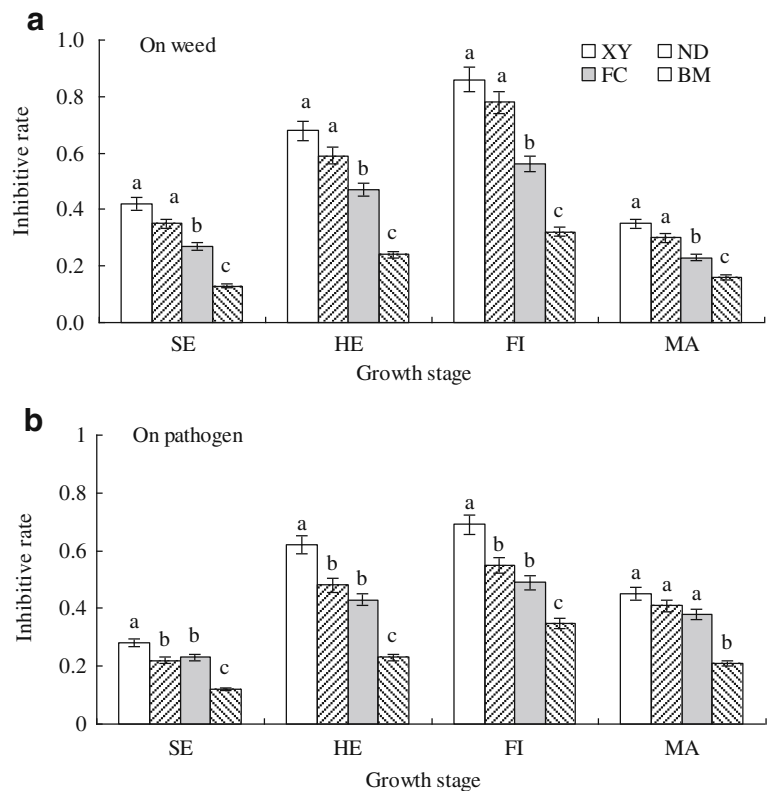


Fig. 4 Enzyme activities of the rhizosphere soils of the four wheat genotypes during different growth stages. XY, ND, FC, and BM are the four wheat genotypes 22 Xiaoyan, 1 Ningdong, 3 Fengchan, and 1 Bima, respectively, which had strong, medium, weak, and no allelopathy. SE, HE, FI, and MA are the four growth stages of seedling, heading, filling, and maturity, respectively. Small letters indicate significant difference at $P < 0.05$ between the four allelopathic genotypes at the same growth stage

physiological cost of weaker allelopathy (Zuo et al. 2011). Other evidence has a genetic basis, e.g., the average genetic similarity between all possible pairs of selected accessions of *Triticum speltoides* L. was 55 % with a range of 44 % to 88 %. This may explain why the allelopathic accessions contain higher amounts of DIMBOA than the nonallelopathic accessions (Motiul et al. 2001).

In the present study, we identified a potential link between wheat allelopathy and the levels of soil microbes. The soil levels of bacteria, fungi, and actinomycetes with 1 Xiaoyan, which has high allelopathy, were 4.86–7.00, 1.27–4.53, and 2.42–4.51 -fold higher, respectively, than those in the soils of other types. When the bacterial types were divided further, 22 Xiaoyan accumulated more beneficial microbes, such as nitrogen-fixing bacteria, nitrifying bacteria, and *Thiobacillus*. Based on the results of Zuo et al. (2005 & 2007) on the separate allelopathic potential of four wheat genotypes, a significantly positive relationship between wheat allelopathy and soil microbial amount was discovered ($r=0.9985$, 0.9991 , and 0.9989 for bacteria, fungi, and actinomycetes). Although there was a random correlation with no real causal relationship between allelopathy and rhizosphere microbes, it implied that soil microbes played an important role in allelopathic expression of different wheat genotypes. The allelopathic wheat genotype(s) supported a much higher range of soil microbes than did the non- or less-allelochemical ones. Obviously in view of soil MBC and MBN this could be related to C source, N source availability for microbes, or perhaps more importantly the exudation ability of different cultivars (Li et al. 2002). Meanwhile, soil microbes would show a positive feedback on wheat allelopathy. Firstly, the microbes might produce phytotoxins that contributed to or enhanced plant allelopathy. Yu et al. (2005) reported that changing soil microbial community might be an important part of *Eupatorium adenophorum* invasion process by chemical interference. Secondly, the microbes might induce the plant to produce allelochemicals from existing biochemical pathways via an elicitation process. In the present study, some harmful microorganisms in the rhizosphere of allelopathic wheat cultivar would form a possible pressure or produce certain stimulating force so as to release allelochemicals under such selective pressure from environmental stress (Kong et al. 2000). Thirdly, the microbes might enhance the health of the plant in such a way that it had the capacity to

Fig. 5 Effects of wheat rhizosphere soil leachates at different growth stages on weed and pathogen growth. XY, ND, FC, and BM are the four wheat genotypes 22 Xiaoyan, 1 Ningdong, 3 Fengchan, and 1 Bima, respectively, which had strong, medium, weak, and no allelopathy. SE, HE, FI, and MA are the four growth stages of seedling, heading, filling, and maturity, respectively. Small letters indicate significant difference at $P < 0.05$ between the four allelopathic genotypes at the same growth stage



make more allelochemicals. More nitrogen-fixing bacteria were found in the rhizosphere of strong allelopathic wheat cultivar comparing to weak allelopathic wheat accession. Moreover, soil enzymes showed a high activity in the roots of the former. However, the interaction between wheat allelopathy and soil microbes needs further exploration.

Similarly, Klironomos (2002) discovered that some invasive plants accumulate more mycorrhizal fungi than native plants, which improves their colonization success in alien habitats via beneficial interactions with these fungi. In general, soil microorganisms have important roles in soil interaction networks (Prin et al. 2009). The abundance of soil microbes varies with the effects of the allelopathic potential of weeds and crops in most studies (Wurst and van Beersum 2009). Weeds may also affect crop growth via their allelopathic potential and their interactions with soil microbes, as well as other organisms (Zhou et al. 2013). In the present study, rhizosphere soil microorganisms were related to beneficial effects on crops and harmful effects on weed. The wheat genotype 22 Xiaoyan promoted the production of an active microbial microhabitat,

which had high soil MBC and MBN levels, high soil enzymes activities, and the potential to inhibit noxious weeds. In the present study, there were more soil microbes supported in the rhizosphere of the allelopathic cultivar, it was much more likely that the allelochemicals produced might be more quickly degraded in this rhizosphere versus one in which the microbes are lacking. Therefore, it should be evaluated by collecting exudates and testing their activity in sterile and non-sterile soils from each rhizosphere. The emergence of this situation demands further investigation.

Soil leachates are known to have complex compositions. In the present study, the rhizosphere soils from various wheat genotypes inhibited the noxious weed *D. sophia* and the plant pathogen *G. graminis*. These effects were probably attributable to a mixture of secretions from the crop roots and rhizosphere soil microbes. Thus, crop allelopathy may be a suitable alternative for the efficient control of harmful biota such as weeds and pathogens. There have been few reports of the allelopathic potential of soil microbes (Veiga et al. 2012). Thus, it would be useful to explore the effects of

allelochemicals related to different wheat genotypes on the soil biota in the future.

Acknowledgments We thank Dr Duncan Jackson for his useful comments and language editing, which have greatly improved the manuscript. This study was supported by State Key Laboratory of Crop Stress Biology in Arid Areas, Northwest A&F University (CSBAKF1301), National Natural Science Fund of China (30900186), Natural Science Research Project of Anhui Province of China For Universities (KJ2012A140), and State Key Laboratory of Soil Erosion and Dryland Farming on the Loess Plateau, Institute of Soil and Water Conservation, Chinese Academy of Sciences and Ministry of Water Resources, Northwest A&F University (10501-1203). The authors thank the anonymous reviewers of this paper for their useful suggestions.

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