

RESEARCH PAPER

Ecological adaptation of weed biodiversity to the allelopathic rank of the stubble of different wheat genotypes in a maize field

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The objective of this study was to integrate allelopathic bioassay and point sampling methods to investigate the allelopathic rank of the stubble of different wheat genotypes and its effect on weed biodiversity in a maize field. The study consisted of 17 wheat stubble treatments derived from ten wheat genotypes planted individually (monoculture) or in pairs (mixed culture). The maize was planted in the plots immediately following the wheat harvest and the number of weed species, total weed number, weed density, weed height, and weed cover were determined 50 days later. The results indicate a significant rank effect of allelopathic potential in the stubble of the different wheat genotypes. There was a stronger allelopathic effect from the straw in the mixed-culture treatments compared to the monoculture treatments. *Acalypha australis* and *Setaria viridis* were the dominant weed species in the maize fields. The regression analysis shows that the weed biodiversity indices were significantly related to the allelopathic rank. The allelopathic potential exhibited spatial heterogeneity in all the scales, which would trigger resource heterogeneity and change the microhabitat conditions. Therefore, weed biodiversity would respond spatially and biologically to the heterogeneous distribution of allelochemicals from the wheat stubble. The allelopathic rank of the wheat stubble would lead to changes in weed biodiversity by regulating the ecological niche of the weed population. The weeds showed resistance or an adaptive response to exterior pressure, including allelopathic pressure. This study on the effect of allelopathic potential on weed biodiversity provides a solid theoretical basis for sustainable weed management of agro-ecosystems.

Keywords: allelopathic rank, ecological adaptation, species correlation, stubble mulch cropping system, weed biodiversity.

INTRODUCTION

Crops compete with weeds for resources, such as sunlight, nutrients, and water (Petersen 2005). Crops and weeds also can influence each other through allelopathic potential (Qasem & Foy 2001; Weston & Duke 2003).

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Weeds must be properly controlled in order to maintain good crop development. However, weeds are important components of agricultural ecosystems (Marshall *et al.* 2003). A biodiverse weed population maintains the proper balance and function of the agro-ecosystem by protecting against natural enemies, controlling pests, preventing soil erosion, enhancing nutrient cycling, and reducing environmental pollution (Chen *et al.* 2000). Therefore, it is important to preserve the weed biodiversity in crop fields.

The ideal crop management system would control weed populations and, at the same time, maintain the

biodiversity of the weed population. Currently, tillage systems, such as stubble or straw mulching, fallowing, and straw incorporation, are commonly used as a means of increasing the soil moisture, either by increasing rainfall interception or by reducing water loss due to run-off or evaporation (Ronald & Phillips 1984; Luo 1991). Stubble mulching changes the conditions at the air and soil interface and influences the physical, chemical, and biological properties of the soil. In addition, stubble mulching efficiently controls weed propagation and enhances the capacity of crops to compete with weeds for growth resources (Blum *et al.* 2002). These changes have a large effect on the growth and development of crops. Thus, stubble mulching has ecological, social, and economic benefits (Shen *et al.* 1998) and is important for the sustainable development of agriculture.

China is one of the main maize-growing countries in the world, with a total annual production area of 2×10^7 ha. In northern China, a winter wheat–maize rotation is common. In this system, maize is planted amid standing stubble immediately after the wheat harvest in June. This system has led to a serious weed problem in the maize fields. Weeds such as *Digitaria sanguinalis*, *Eleusine indica*, *Echinochloa crus-galli*, *Portulaca oleracea*, *Amaranthus retroflexus*, *Convolvulus arvensis*, *Chenopodium glaucum*, *Eragrostis pilosa*, *Setaria viridis*, *Cyperus rotundus*, *Acalypha australis*, and *Herba solani* are widespread. These weed populations generally result in a 10–20% decrease in maize productivity, though occasionally the reduction can be as high as 30–50% (Li 2003).

Weeds in maize fields have a strong adaptive capacity to adverse environmental conditions. For example, seed production in weed species, such as *C. rotundus*, *C. glaucum*, *Polygonum lapathifolium*, *P. oleracea*, and *C. arvensis*, ranges from 600–10 000-fold higher than most crops. These seeds can germinate even after being buried in the subsoil for 20 years. Field investigations have shown that individual *D. sanguinalis* plants produce as many as 2.2×10^5 seeds (Li 2003). Furthermore, most weeds are more efficient than crop plants at using limited resources. For example, weeds can grow and reproduce rapidly after rainfall. They also have a relatively short growing period and reproduce before the crop is harvested. Some weeds are able to survive against almost every type of control measure. Perennial weeds, like *P. oleracea*, have been shown to have the ability to resume growth after being removed from the soil and exposed to 3 days of sunlight (Grime 1979). All of these factors can make it difficult to eliminate weeds.

Quantitative studies have indicated that standing stubble in fallow systems not only affect crop development, but

also impact weed growth and biodiversity (Crutchfield *et al.* 1985; Ma & Han 1995; Chou 1999). However, there are no concrete reports comparing weed biodiversity in fields containing the stubble of wheat genotypes that differ in allelopathic rank (Barberi 2002).

In this study, we combined the dot sample survey method for measuring weed biodiversity in maize field plots with bioassays for the determination of the allelopathic rank of monoculture and mixed-culture wheat stubble. The objectives were to investigate the allelopathic effect of wheat stubble on the weed biodiversity in the subsequent maize crop. We tried to determine the effect of the allelopathic rank of wheat stubble on the weed species composition, density, biodiversity, and species correlation. Our study provides a preliminary analysis of the effect of the allelopathic microhabitat on weed biodiversity and explains the ecological adaptation of weeds facing allelopathic stress. The results can be used for the sustainable management of the stubble mulch cropping system.

MATERIALS AND METHODS

Field trial

The field plot trial was conducted from 2002 to 2005 at the Institute of Soil and Water Conservation, Yangling, Shaanxi Province, China. The field had been in agricultural production for many years and had received balanced fertilization. At the beginning of the experiment, the amount of soil organic C was 5.83 g kg^{-1} , the total P was 0.50 g kg^{-1} , the labile P was 1.93 mg kg^{-1} , the total K was 18.6 g kg^{-1} , the available K was 78.8 mg kg^{-1} , and the available N was 9.51 mg kg^{-1} .

In the fall of each year, ten wheat genotypes (National Engineering Research Centre for Wheat, Zhenzhou, China) were sown individually (monoculture) in the plots or in pairs (mixed culture) to make a total of 17 treatments (Table 1). The 4.25 m^2 plots were arranged in a completely randomized block design and replicated three times for a total of 51 plots. The row spacing within the plots was 20 cm and the distance between the wheat plants within each row was 5 cm.

At harvest, the grain was removed and the stubble was cut evenly to a height of 15 cm above the ground. After that, maize (*Zea mays* var. no. 10 Shendan; Shaanxi Provincial Academy of Agriculture Sciences, Yangling, China) was planted directly amid the standing stubble. A fertilizer was applied to the wheat in the form of 150 kg N ha^{-1} (urea), 60 kg P ha^{-1} (CaPO_4), and 150 kg K ha^{-1} (K_2SO_4). Additional N fertilizer was

Table 1. Stubble left from the different wheat genotypes in the monoculture and mixed-culture systems

| Treatment | Monoculture system | Mixed-culture system |
|-----------|---|-----------------------------------|
| 1 | <i>Triticum boeoticum</i> Boiss | – |
| 2 | <i>Triticum monococcum</i> L. | – |
| 3 | <i>Triticum dicoccides</i> Koern. | – |
| 4 | <i>Triticum dicoccon</i> (Schrank) Schuebl. | – |
| 5 | No. 1 Bima | – |
| 6 | No. 1 Ningdong | – |
| 7 | No. 6 Xinxiaoyan | – |
| 8 | No. 9525 Lankao | – |
| 9 | No. 22 Xiaoyan | – |
| 10 | No. 66 Yumai | – |
| 11 | – | No. 1 Bima + No. 9525 Lankao |
| 12 | – | No. 66 Yuma + No. 22 Xiaoyan |
| 13 | – | No. 9525 Lanka + No. 66 Yumai |
| 14 | – | No. 9525 Lankao + No. 1 Ningdong |
| 15 | – | No. 22 Xiaoyan + No. 6 Xinxiaoyan |
| 16 | – | No. 1 Ningdong + No. 6 Xinxiaoyan |
| 17 | – | No. 1 Bima + No. 1 Ningdong |

Wheat genotypes without Latin names are varieties of *Triticum aestivum*.

applied to the maize in the form of 60 kg N ha⁻¹ at planting and 90 kg N ha⁻¹ later in the growing season according to the needs of the maize. The maize was irrigated as necessary. The management practises described above were the same during all 3 years of the study.

Field investigation of the weed biodiversity

After the wheat stubble had decomposed for 50 days, we established three random sample dots (1 m²) in each plot for weed sampling. By this time, the maize had reached the grain-filling stage, which is a critical period for determining the final yield. The number of weed species, total weed number, weed density, weed height, and weed cover were determined at each sample dot as indices of the weed biodiversity. A single maize plant was harvested at each dot and the maize plant height, mean stem diameter, mean distance between two nodes, and biomass (constant weight after drying at 60°C for 48 h) were measured (data not shown).

The dominance status of each weed species in the experimental field was determined by averaging the relative density of the weeds, the temporal density of some weeds, and the total density of all the weeds. The weed biodiversity was estimated by the following common indices of biodiversity (Pielou 1969, 1975; Grime 1979):

- 1 Gleason's species richness index (G): $G = S/\ln A$, where S is the species number in the sample dot and A is the area of the sample dot.
- 2 Gini index (D): $D = 1 - SP = 1 - N(N-1) / \sum_{i=1}^S n_i(n_i-1)$, where SP is Simpson's species diversity index.
- 3 Shannon-Wiener (H) species diversity index: $H = 3.3219(\lg N - 1) / \sum_{i=1}^S n_i \lg n_i$.
- 4 Encounter ratio of both species (PIE): $PIE = \sum_{i=1}^S n_i(N-n_i) / N(N-1)$, where N is the total number of individuals of all species, n_i is the coverage rate of species i, and s is the total number of species.
- 5 The species correlation (PC) was calculated by modifying the formula of Smith (1983), in which $PC = a / (a + b + c) \times 100$, where a is the number of dots at which the same two weed species appeared, b is the number of dots in which species x, but not species y, appeared, and c is the number of dots in which species y, but not species x, appeared.
- 6 The Pielou index (also Pielou's evenness index, abbreviated to J or JSW index): $J = -\sum(P_i/\ln P_i) / \ln S$, where S has the same meaning to that of the Gini index and $P_i = N_i/N$, where N is the total species abundance of all the species in the sample dot and N_i is the specific species abundance of species i.

Allelopathic bioassay

The allelopathic potential is determined through the interaction of biological factors (i.e. wheat accession) and ecological conditions (i.e. climate and soil conditions). This is reflected very well by the mathematical formulae of comprehensive environmental rank based on the compensation principle (Whittaker 1967).

Above-ground wheat stubble and below-ground wheat roots were collected from each test plot. For each plot, the stubble and roots were combined and then used to determine the allelopathic rank of the whole straw, with annual ryegrass as an acceptor, according to the methods of Zuo *et al.* (2005). The allelopathic potential index (A) was determined by modifying the formula of Williamson and Richardson (1988) to obtain the following formula:

$$A = 1/3(A_T + A_W + A_S),$$

in which A_T is the allelopathic potential index for the ryegrass radicle, A_W is the allelopathic potential index for the ryegrass coleoptile, and A_S is the allelopathic potential index for the germination rate.

Statistical analyses

The allelopathic index and biodiversity parameters (species richness, Gini index, PIE, Shannon–Wiener index, and the Pielou index) were calculated with SPSS software (version 10.0; SPSS, Chicago, IL, USA). The regression analysis was performed between each of the biodiversity indices and the allelopathic rank. If necessary, the significant differences were tested afterwards at the level of $P < 0.05$.

RESULTS

Allelopathic rank of the stubble of the different wheat genotypes

Significant differences in the allelopathic rank of the straw (stubble + roots) were observed in both the monoculture and mixed-culture treatments. In the monoculture treatment, the allelopathic rank increased from 0.365 for the 2n genotypes to 0.485 for the 4n genotypes and 0.693 for the modern, 6n wheat genotypes (Fig. 1). Three wheat genotypes, var. no. 6 Xinxiaoyan, var. no. 66 Yumai, and var. no. 22 Xiaoyan, showed a strong allelopathic rank, with a mean value of 0.79. In the mixed-culture treatments, the allelopathic rank ranged from 0.63–0.85 (Fig. 2). Among all the treatments, the highest rank of allelopathic potential appeared

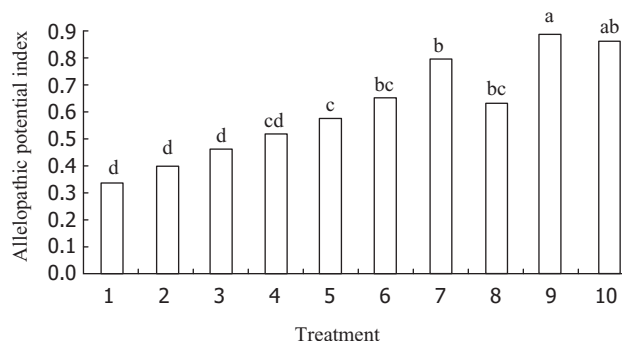


Fig. 1. Allelopathic rank of the wheat stubble in the monoculture system due to allelopathic differences among the wheat genotypes. Treatment (T) numbers 1–10 represent the following types of wheat stubble: T1, *Triticum boeoticum*; T2, *Triticum monococcum*; T3, *Triticum dicoccides*; T4, *Triticum dicoccon*; T5, no. 1 Bima; T6, no. 1 Ningdong; T7, no. 6 Xinxiaoyan; T8, no. 9525 Lanka; T9, no. 22 Xiaoyan; T10, no. 66 Yumai. The wheat genotypes without Latin names are varieties of *Triticum aestivum*. The values followed by the same lowercase letter are not significantly different at the 0.05 probability level.

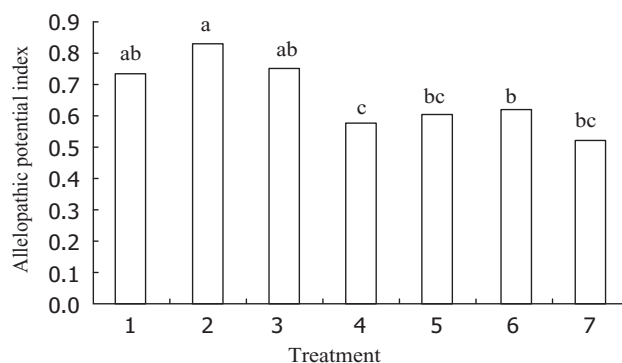


Fig. 2. Allelopathic rank of the wheat stubble in the mixed-culture treatments of common wheat accessions. Treatment (T) numbers 1–7 represent the following wheat stubble treatments: T1, no. 1 Bima × no. 9525 Lanka; T2, no. 66 Yumai × no. 22 Xiaoyan; T3, no. 9525 Lanka × no. 66 Yumai; T4, no. 9525 Lanka × no. 1 Ningdong; T5, no. 22 Xiaoyan × no. 6 Xinxiaoyan; T6, no. 1 Ningdong × no. 6 Xinxiaoyan; T7, no. 1 Bima × no. 1 Ningdong. The wheat genotypes without Latin names are varieties of *Triticum aestivum*. The values followed by the same lowercase letter are not significantly different at the 0.05 probability level.

in the var. no. 66 Yumai × var. no. 22 Xiaoyan treatment, which indicates that, theoretically, this mixed culture would be more effective in suppressing weeds than the monoculture treatments.

Effect of the allelopathic microhabitat on total density and the dominant weeds

Thirteen weed species were identified in the field experiment: *A. australis*, *C. glaucum*, *S. viridis*, *P. oleracea*, *Equisetum ramosissimum*, *Veronica persica*, *Cyperus microiria*, *Bidens pilosa*, *Euphorbia humifusa*, *Pharbitis nil*, *C. rotundus*, *Cephalanoplos segetum*, and *Artemisia argyi* (Table 2). The weed density in the maize field varied significantly depending on the type of wheat stubble. In the monoculture treatments, the weed density was highest in the plots containing stubble from the 2n genotypes, intermediate in the plots with stubble from the 6n genotypes, and lowest in the plots with stubble derived from the 4n genotypes. The weed density was lower in the mixed-culture treatments compared with the monoculture treatments. These results show that the type of stubble (i.e. wheat genotype) and the planting system (i.e. mixed *vs* monoculture) not only affected the total weed density in the maize, but also influenced the dominance status of some weed species in the community (Table 1).

Acalypha australis and *S. viridis* were the dominant weeds (relative density >10%) in most treatments (Table 2). In addition to these two weed species, *P. nil* was a dominant weed in treatments 3, 13, and 14, *E. ramosissimum* was a dominant weed in treatment 7, and *C. segetum* was a dominant weed in treatment 16. The relative density of *S. viridis* was low in treatments 4, 12, and 17 and it did not qualify as a dominant weed. In treatments 4 and 12, only *A. australis* had a density >10%, while in treatment 17, *A. australis* and *E. ramosissimum* were dominant weeds.

Overall, *A. australis* and *S. viridis* were the dominant weeds in the maize. *Acalypha australis* was more dominant than *S. viridis*, regardless of the wheat genotype or planting method. The distribution of both species was affected by the allelopathic rank of the stubble; however, these results show that *A. australis* and *S. viridis* were more adapted to the allelopathic microhabitat created by the different types of wheat stubble compared to the other weed species.

Effect of the allelopathic microhabitat on the weed biodiversity

The allelopathic rank of the stubble from the different wheat genotypes had a significant effect on the weed species and frequency. The weed biodiversity varied among the plots, reflecting differences in the species number, as well as the weed type, frequency, and coverage (Table 3). The species number was the same in treatments 1, 5, and 13; however, there were significant differences

among the Gini, PIE, Shannon–Wiener, and Pielou indices. Possibly, microhabitat variation related to the allelopathic stubble caused a significant difference in the species richness and other biodiversity parameters under various treatments, which led to heterogeneity in the distribution of the weeds.

The number of weed species varied from three in treatment 12 to 10 in treatment 2 (Table 3). The greater-than-two-fold difference between the maximum and minimum number of weed species can be explained by differences in the allelopathic rank, particularly in the mixed-culture treatment. In contrast, the indicators of weed biodiversity used in this study showed quite different results. For example, the maximum values occurred in treatment 10 for the Gini and PIE indices, treatment 7 for the Shannon–Wiener index, and treatment 14 for the Pielou index. The minimum values occurred in treatment 16 for the Gini index, treatment 6 for the PIE index, treatment 14 for the Shannon–Wiener index, and treatment 15 for the Pielou index. Additional data in Table 2 implied that the treatments with maximum species richness had a relatively low index of species biodiversity. For example, treatments 2 and 10 had the maximum values for species number, but not for the biodiversity indices. Perhaps, species biodiversity is not only related to species richness, but also to species frequency and/or coverage (Peet 1978). In this study, allelopathic variation would be one of the primary factors affecting biodiversity.

Effect of the allelopathic microhabitat on the species correlation of the dominant weeds and related weeds

Species correlation refers to the mutual relationship of two weed species among all the species within a space. Negative correlation indicates that one species displaced another species because the two species have the same habitat requirement. In contrast, positive correlation indicates a synergistic relationship between the two weed species due to differences in their environmental requirements or similar responses to environmental induction (Jari 1997). A species correlation analysis was conducted to investigate the correlation between the dominant weed in these pots, *A. australis*, and the other weeds listed in Table 3. The results show that species correlation was affected by the wheat stubble treatment and the correlation index varied from 0–93.3%.

In general, the plots contained two-to-six non-dominant weed species in addition to *A. australis*. Specifically, a relatively large number of non-dominant weed species

Table 2. Weed species and density under different types of wheat stubble (plants m⁻²)

| Treatment† | <i>Acalypha australis</i> | <i>Chenopodium glaucum</i> | <i>Setaria viridis</i> | <i>Portulaca oleracea</i> | <i>Equisetum ramosissimum</i> | <i>Veronica persica</i> | <i>Cyperus microiria</i> | <i>Bidens pilosa</i> | <i>Euphorbia humifusa</i> | <i>Pharbitis nil</i> | <i>Cyperus rotundus</i> | <i>Cephalanoplos segetum</i> | <i>Artemisia argyi</i> | Total density |
|------------|---------------------------|----------------------------|------------------------|---------------------------|-------------------------------|-------------------------|--------------------------|----------------------|---------------------------|----------------------|-------------------------|------------------------------|------------------------|---------------|
| 1 | 25.7 | 7.0 | 19.5 | 6.0 | 0.0 | 0.0 | 1.2 | 0.0 | 0.8 | 0.0 | 4.3 | 0.0 | 0.0 | 64.5 |
| 2 | 41.3 | 1.2 | 8.8 | 0.8 | 0.9 | 0.0 | 0.6 | 0.0 | 0.0 | 0.0 | 3.4 | 0.0 | 0.2 | 57.2 |
| 3 | 31.5 | 0.0 | 31.0 | 0.0 | 0.0 | 0.3 | 3.8 | 0.3 | 1.1 | 8.9 | 0.0 | 0.0 | 0.0 | 76.9 |
| 4 | 49.1 | 0.3 | 0.0 | 0.0 | 0.6 | 0.1 | 1.2 | 0.0 | 0.3 | 0.0 | 0.0 | 0.0 | 0.0 | 51.6 |
| 5 | 29.2 | 0.4 | 12.1 | 0.0 | 2.5 | 0.0 | 0.1 | 0.0 | 0.3 | 15.0 | 0.0 | 0.0 | 0.0 | 59.6 |
| 6 | 9.5 | 3.4 | 53.7 | 0.0 | 1.0 | 0.0 | 0.1 | 0.4 | 0.2 | 0.0 | 0.0 | 1.8 | 2.3 | 72.4 |
| 7 | 26.7 | 0.0 | 18.9 | 0.0 | 25.2 | 0.0 | 0.2 | 0.0 | 0.2 | 0.0 | 0.0 | 1.2 | 0.0 | 72.4 |
| 8 | 37.8 | 0.0 | 34.8 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.5 | 0.0 | 0.0 | 1.6 | 1.8 | 76.5 |
| 9 | 84.3 | 0.0 | 23.1 | 0.0 | 0.6 | 0.0 | 0.8 | 0.0 | 0.4 | 0.0 | 2.1 | 0.0 | 0.0 | 111.3 |
| 10 | 104.2 | 0.0 | 51.5 | 0.0 | 7.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 162.9 |
| 11 | 24.0 | 0.0 | 35.2 | 0.0 | 0.0 | 0.0 | 0.1 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 59.3 |
| 12 | 17.2 | 0.0 | 0.0 | 3.0 | 1.5 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 21.7 |
| 13 | 10.1 | 1.8 | 6.1 | 2.5 | 0.0 | 0.0 | 0.4 | 0.3 | 0.0 | 5.0 | 0.0 | 2.5 | 0.0 | 28.7 |
| 14 | 10.4 | 0.0 | 1.8 | 0.0 | 0.0 | 0.0 | 0.1 | 0.8 | 0.0 | 2.6 | 0.0 | 0.0 | 0.0 | 15.7 |
| 15 | 16.8 | 0.0 | 5.6 | 0.0 | 1.8 | 0.0 | 0.0 | 0.2 | 0.0 | 0.0 | 0.0 | 1.2 | 0.0 | 25.6 |
| 16 | 16.5 | 0.0 | 3.2 | 0.0 | 3.0 | 0.0 | 0.0 | 1.7 | 0.0 | 0.0 | 0.0 | 6.1 | 0.0 | 30.5 |
| 17 | 1.6 | 0.0 | 0.6 | 0.0 | 2.2 | 0.0 | 0.0 | 0.0 | 0.0 | 2.3 | 0.0 | 0.0 | 0.0 | 6.7 |

† Treatment numbers 1–17 denote the monoculture and mixed-culture wheat stubble treatments in the maize field: 1, *Triticum boeoticum*; 2, *Triticum monococcum*; 3, *Triticum dicoccoides*; 4, *Triticum dicocou*; 5, no. 1 Bima; 6, no. 1 Ningdong; 7, no. 6 Xinxiaoyan; 8, no. 9525 Lankao; 9, no. 22 Xiaoyan; 10, no. 66 Yumai; 11, no. 1 Bima × no. 9525 Lankao; 12, no. 66 Yumai × no. 22 Xiaoyan; 13, no. 9525 Lankao × no. 66 Yumai; 14, no. 9525 Lankao × no. 1 Ningdong; 15, no. 22 Xiaoyan × no. 6 Xinxiaoyan; 16, no. 1 Ningdong × no. 6 Xinxiaoyan; 17, no. 1 Bima × no. 1 Ningdong. The wheat genotypes without Latin names are varieties of *Triticum aestivum*.

Table 3. Richness and diversity indices of the surrounding weeds

| Treatment† | Weed species number | Species richness | Gini index | PIE‡ | H index§ | J index¶ |
|------------|---------------------|------------------|------------|-------|----------|----------|
| 1 | 7 | 10.1 | 0.640 | 0.693 | 1.750 | 0.699 |
| 2 | 10 | 14.4 | 0.725 | 0.746 | 2.079 | 0.804 |
| 3 | 7 | 10.1 | 0.628 | 0.713 | 1.654 | 0.753 |
| 4 | 6 | 8.7 | 0.659 | 0.788 | 2.065 | 0.676 |
| 5 | 7 | 10.1 | 0.688 | 0.741 | 1.206 | 0.741 |
| 6 | 9 | 13.0 | 0.502 | 0.602 | 1.631 | 0.651 |
| 7 | 6 | 8.7 | 0.742 | 0.796 | 2.500 | 0.685 |
| 8 | 6 | 8.7 | 0.668 | 0.737 | 2.013 | 0.650 |
| 9 | 6 | 8.7 | 0.655 | 0.708 | 1.787 | 0.874 |
| 10 | 6 | 8.7 | 0.751 | 0.808 | 1.652 | 0.815 |
| 11 | 4 | 5.8 | 0.647 | 0.695 | 1.236 | 0.658 |
| 12 | 3 | 4.3 | 0.670 | 0.721 | 1.287 | 0.714 |
| 13 | 7 | 10.1 | 0.712 | 0.658 | 1.576 | 0.781 |
| 14 | 5 | 7.2 | 0.665 | 0.676 | 1.006 | 0.896 |
| 15 | 6 | 8.7 | 0.702 | 0.732 | 1.564 | 0.564 |
| 16 | 5 | 7.2 | 0.498 | 0.654 | 1.328 | 0.589 |
| 17 | 4 | 5.8 | 0.562 | 0.798 | 1.467 | 0.776 |

† Treatment numbers 1–17 denote the monoculture and mixed-culture wheat stubble treatments in the maize field: 1, *Triticum boeoticum*; 2, *Triticum monococcum*; 3, *Triticum dicoccides*; 4, *Triticum dicoccon*; 5, no. 1 Bima; 6, no. 1 Ningdong; 7, no. 6 Xinxiaoyan; 8, no. 9525 Lankao; 9, no. 22 Xiaoyan; 10, no. 66 Yumai; 11, no. 1 Bima × no. 9525 Lankao; 12, no. 66 Yumai × no. 22 Xiaoyan; 13, no. 9525 Lankao × no. 66 Yumai; 14, no. 9525 Lankao × no. 1 Ningdong; 15, no. 22 Xiaoyan × no. 6 Xinxiaoyan; 16, no. 1 Ningdong × no. 6 Xinxiaoyan; 17, no. 1 Bima × no. 1 Ningdong. The wheat genotypes without Latin names are varieties of *Triticum aestivum*; ‡ PIE, encounter ratio of both species; § H index, Shannon-Wiener species diversity index; ¶ J index, Pielou index.

(*S. viridis*, *C. glaucum*, *E. ramosissimum*, *C. microiria*, *B. pilosa*, and *E. humifusa*) had a significant relationship with *A. australis* in treatment 6. However, in treatments 11, 12, and 17, the number of weed species with a significant relationship with *A. australis* was much smaller. The non-dominant weed species in these treatments included *S. viridis* and *C. microiria*, *P. oleracea* and *E. ramosissimum*, and *S. viridis* and *E. ramosissimum*, respectively. The community might have consisted of related weeds growing in a similar habitat, but significant differences in the composition of the weed community were still observed among the wheat stubble treatments. An analysis of the heterogeneous distribution of the non-dominant weeds showed a significant difference in the spatial frequency, which ranged from 8.33–91.67%.

These results imply an inner species correlation, which impacted the weed population. The weed communities in Table 4 could be divided into two categories. One weed community category included at least one adaptive weed species that had a positive species correlation with *A. australis* of >50. This weed community was in treatments 1–7, 12, and 15. In the second weed community category, there was a negative (<50) species correlation

between the non-dominant weed species and *A. australis*. This indicates that these weeds were sensitive to allelopathic stress. This weed community was in treatments 8–11, 13, 14, 16, and 17. Positive correlation indicated a wider ecological niche under the allelopathic microhabitat, while a negative correlation indicated a narrower ecological niche. Overall, the results suggest that the allelopathic background of the wheat stubble in the maize field was the primary reason for differences among the weed communities.

DISCUSSION

Rank effect of the allelopathic potential of the wheat stubble in the maize fields

The allelopathic rank of the different types of wheat stubble was determined by combining the results from the allelopathic bioassay of aqueous extracts from the stubble of annual ryegrass (Wu *et al.* 2003) with integrated environment theory by Whittaker (1967). The wheat stubble in the mixed-culture treatments showed stronger allelopathy compared to the stubble in the monoculture treatments. Among the wheat genotypes,

Table 4. Species correlations of *Acalypha australis* and community weeds under the wheat stubble treatments

| Treatment† | <i>Setaria viridis</i> | <i>Chenopodium glaucum</i> | <i>Portulaca oleracea</i> | <i>Equisetum ramosissimum</i> | <i>Veronica persica</i> | <i>Cyperus microiria</i> | <i>Bidens pilosa</i> | <i>Euphorbia humifusa</i> | Mean correlation | Surrounding species |
|------------|------------------------|----------------------------|---------------------------|-------------------------------|-------------------------|--------------------------|----------------------|---------------------------|------------------|---------------------|
| 1 | 73.3* | 93.3* | 16.3 | 0.0 | 0.0 | 65.2* | 0.0 | 45.3 | 36.67 | 5.0 |
| 2 | 60.0* | 53.3* | 13.4 | 23.3 | 0.0 | 55.1* | 0.0 | 0.0 | 25.64 | 5.0 |
| 3 | 53.3* | 0.0 | 0.0 | 0.0 | 34.8 | 21.7 | 4.3 | 26.7 | 17.60 | 5.0 |
| 4 | 0.0 | 46.7 | 0.0 | 50.0* | 4.3 | 24.3 | 0.0 | 43.3 | 21.08 | 5.0 |
| 5 | 43.3 | 20.0 | 0.0 | 56.7* | 0.0 | 30.4 | 0.0 | 30.0 | 22.55 | 5.0 |
| 6 | 40.0 | 16.7 | 0.0 | 36.7 | 0.0 | 13.0 | 55.6* | 56.6* | 27.33 | 6.0 |
| 7 | 33.3 | 0.0 | 0.0 | 13.3 | 0.0 | 60.9* | 0.0 | 50.8* | 19.79 | 4.0 |
| 8 | 20.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 31.5 | 6.44 | 2.0 |
| 9 | 20.0 | 0.0 | 0.0 | 10.0 | 0.0 | 47.8 | 0.0 | 26.4 | 13.03 | 4.0 |
| 10 | 16.7 | 0.0 | 0.0 | 3.3 | 0.0 | 26.1 | 0.0 | 0.0 | 5.76 | 3.0 |
| 11 | 6.7 | 0.0 | 0.0 | 0.0 | 0.0 | 22.7 | 0.0 | 0.0 | 3.68 | 2.0 |
| 12 | 0.0 | 0.0 | 6.7 | 66.7* | 0.0 | 0.0 | 0.0 | 0.0 | 9.18 | 2.0 |
| 13 | 7.6 | 15.6 | 3.3 | 0.0 | 0.0 | 13.0 | 12.3 | 0.0 | 6.48 | 5.0 |
| 14 | 3.3 | 0.0 | 0.0 | 0.0 | 0.0 | 8.7 | 28.9 | 0.0 | 5.11 | 3.0 |
| 15 | 5.3 | 0.0 | 0.0 | 20.0 | 0.0 | 0.0 | 56.5* | 0.0 | 10.23 | 3.0 |
| 16 | 6.3 | 0.0 | 0.0 | 16.7 | 0.0 | 0.0 | 44.7 | 0.0 | 8.46 | 3.0 |
| 17 | 3.5 | 0.0 | 0.0 | 3.3 | 0.0 | 0.0 | 0.0 | 0.0 | 0.85 | 2.0 |
| Weed plots | 22.0 | 6.0 | 4.0 | 11.0 | 2.0 | 12.0 | 7.0 | 8.0 | — | — |

† Treatment numbers 1–17 denote the monoculture and mixed-culture wheat stubble treatments in the maize field: 1, *Triticum boeoticum*; 2, *Triticum monococcum*; 3, *Triticum dicocoides*; 4, *Triticum dicoccum*; 5, no. 1 Bima; 6, no. 1 Ningdong; 7, no. 6 Xinxiayuan; 8, no. 9525 Lankao; 9, no. 22 Xiaoyan; 10, no. 66 Yumai; 11, no. 1 Bima × no. 9525 Lankao; 12, no. 66 Yumai × no. 22 Xiaoyan; 13, no. 9525 Lankao × no. 66 Yumai; 14, no. 9525 Lankao × no. 1 Ningdong; 15, no. 22 Xiaoyan × no. 6 Xinxiayuan; 16, no. 1 Ningdong × no. 6 Xinxiayuan; 17, no. 1 Bima × no. 1 Ningdong. The wheat genotypes without Latin names are varieties of *Triticum aestivum*. * Significant difference at $P < 0.05$.

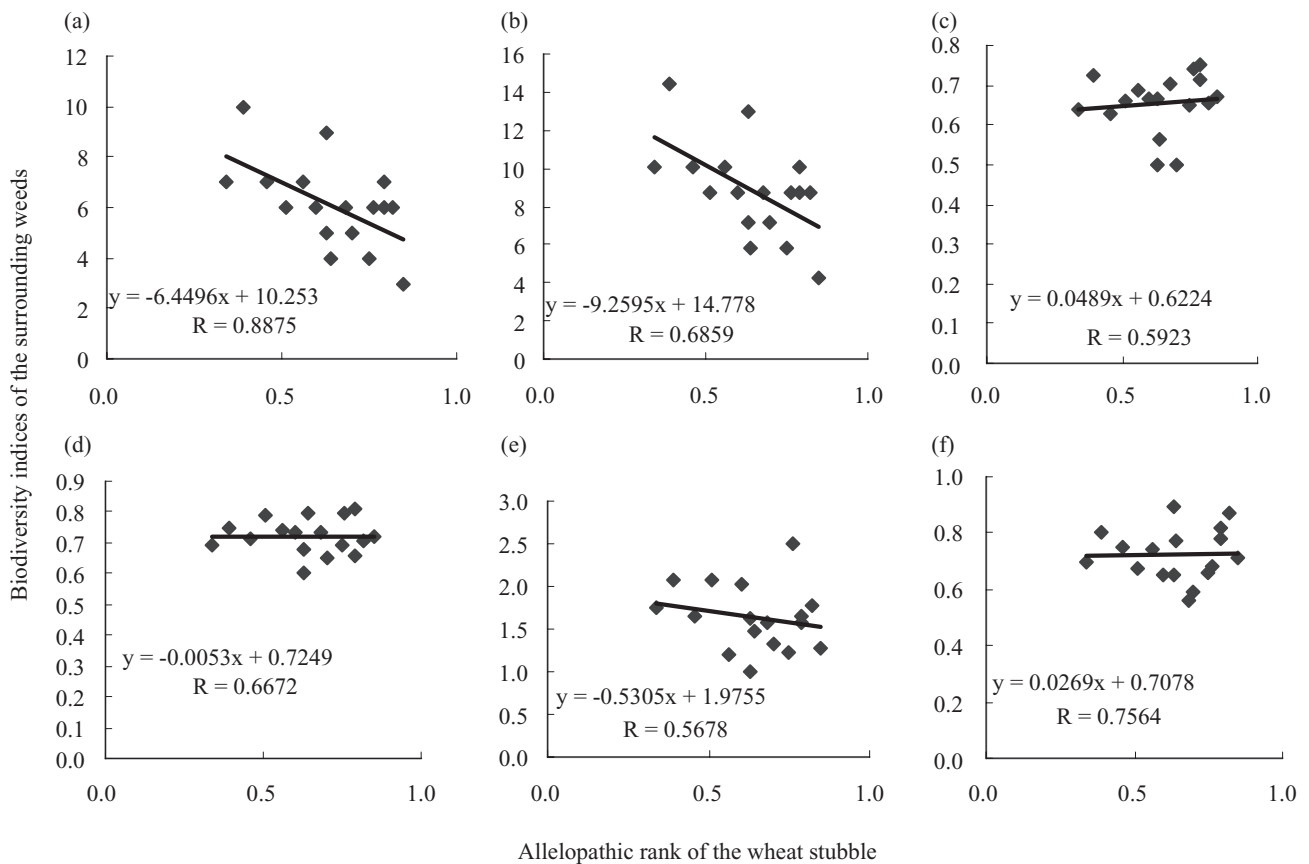


Fig. 3. Relationship between the allelopathic rank of the wheat stubble and the biodiversity indices of the surrounding weeds. (a) Species number, (b) Gleason's species richness index, (c) Gini index, (d) encounter ratio of both species index, (e) Shannon-Wiener species diversity index, and (f) Pielou index.

the allelopathic rank increased in the order, $2n < 4n < 6n$, and from the monoculture treatments to the mixed-culture treatments of the common wheat accessions. Among the monoculture treatments, the common wheat varieties, no. 6 Xinxiaoyan, no. 66 Yumai, and no. 22 Xiaoyan, had the highest allelopathic potential, while var. no. 66 Yumai and var. no. 22 Xiaoyan had the highest allelopathic potential in the mixed-culture treatments. These results indicate that the use of two common wheat accessions in a mixed-culture planting system would provide a novel approach for weed control in the maize crop that follows. We suggest that the allelopathic rank was induced by the allelochemicals exuded by the microbial decomposition of the wheat stubble and/or their catabolic products (Huang *et al.* 2003; Macias *et al.* 2005). In addition, the selection of wheat varieties for mixed cultivation, the rank dynamics of allelochemicals, and the interaction of rhizospheres' metabolic secondary products and their movement need further investigation and discussion.

Effect of the allelopathic microhabitat on the spatial heterogeneity of weed distribution in the maize fields

In certain areas, weed species are affected by environmental resources, such as water, nutrients, and light, as well as by other factors, such as competition, succession, and scattering (Alpert & Mooney 1996). In this study, the weed species diversity in the maize plots was significantly ($P < 0.05$) related to the allelopathic rank (Fig. 3). The results indicate that the allelopathic rank of the stubble derived from the different wheat genotypes influenced the weed species number and richness. However, the Gini index, PIE, Shannon-Wiener index, and Pielou index showed a lack of overlap of weed biodiversity among the majority of the treatments. The differences among the indices could be explained by chemical stress related to stubble allelopathy. The weed biodiversity reflects the different response of species type, coverage, and frequency to the wheat stubble treatments. In similar

allelopathic microhabitats, the species type, richness, and community composition would differ among the treatments because of variation in the other factors. The allelopathic microhabitat is never the same, but always heterogeneous. Therefore, the population of weed species would be diverse in the allelopathic treatments. Moreover, the indices of species diversity, like the Gini index, PIE, Shannon-Wiener index, and Pielou index, would respond to heterogeneous allelopathy. Generally, the physical factors, biological factors, and allelopathic background are heterogeneous on all scales. This causes resource heterogeneity (Palmer & White 1994) and determines the heterogeneous distribution of the surrounding weeds.

Relationship of the weed species correlation with the allelopathic microhabitat of the wheat stubble

Species correlation refers to the mutual, spatial relationship of two weed species, as affected by habitat variation on a community scale (Berasategui *et al.* 2005). In this study, an analysis of weed biodiversity, and especially the analysis of the relationship between the dominant weed (*A. australis*) and the surrounding weeds, was conducted using the dot sampling methods proposed by Jari (1997) and the species correlation or vicinity method of Roxburgh and Chesson (1998). The allelopathic rank of the wheat stubble had a significant effect on the non-dominant weed species and the weed number. The correlation value of *A. australis* with the non-dominant weeds ranged from 0–93.3%, depending on the allelopathic rank. The heterogeneous coupling of the surrounding weeds resulted from similar resource requirements and allelopathic rank, which implies that the allelopathic rank is the driving force for dynamic succession in the weed community (Van *et al.* 2000). A community consists of many species linked by food chains, food nets, and a tight or loose connection of resource-borne relationships (Albertsson 2004). However, the components of agricultural systems and their connections with other ecosystems are influenced by human management. For example, incorporating the stubble into the soil would lead to a change in the microhabitat and cause the fragmentation of the habitat for the weeds. This would affect the stability and normal growth of the weeds. In summary, the allelopathic microhabitat has a significant effect on species correlation which, in turn, affects weed biodiversity. Additional studies need to be done to explain the interaction of signals between the wheat stubble and the weed roots.

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