

Differentiation of Allelopathic Potential of Sorghum (*Sorghum bicolor*) Cultivars Using Chemical and Molecular Techniques

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ABSTRACT

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Laboratory tests were conducted to detect the differential allelopathic potential of two sorghum (*Sorghum bicolor*) cultivars (Enqath and Rabeh) residues. Chemical analysis of residues indicated that total phenolics were found to be higher in Enqath than in Rabeh plants suggesting the superiority of the allelopathic potential of the first cultivar over the second one against weeds. Results indicated that total phenolics were two folds in shoot than in root of both cultivars. These compounds appeared to be higher in Enqath shoot and root (1.60 and 0.80 mg/g, respectively) than in Rabeh shoot and root (1.2 and 0.50 mg/g, respectively). The increments in total phenolics in root and shoot of Enqath were clearly reflected on the increase of total phenolics in the whole plant reaching about 2.40 mg/g compared to Rabeh (1.70 mg/g). Chemical analysis by high performance liquid chromatography (HPLC) revealed the presence of seven allelochemicals namely ferulic, *p*-coumaric, gallic, vanillic, syringic, *p*-hydroxybenzoic, and sinapic acid in the residues of both cultivars. Total phenolic acids were found to be higher in Enqath than in Rabeh. Results of RAPD-PCR technique performed for sorghum genomic DNA revealed that all the 10 primers used in this study scored different amplification monomorphic and polymorphic bands in the tested genotypes with the exception of 3 RAPD primers which generated a unique amplification bands, one of them (125 bp) scored by OPN 16 primer, present in high allelopathic sorghum genotypes and absent in the low allelopathic ones (Rabeh). Further work is recommended to analyze the sequence of this band to find out whether it is related to allelopathic trait or not. These results recommend screening more sorghum cultivars in order to offer a potential source of allelopathic germplasm that could be manipulated to enhance weed suppression in an effective and environmentally sustainable approach.

Keywords: Allelopathy, RAPD-PCR, residues, sorghum cultivars, total phenolics

The allelopathy has existed for thousands of years but the intensive scientific research into the recognition and understanding of allelopathy has only

occurred over the past few decades (Narwal et al. 2005). Allelopathy is an ecological term which was first introduced by Hans Molisch in 1937 and derived from two Greek words "Allelon" means mutual and "Pathos" means harm. Rice was the pioneer in the growing of this field. Allelochemicals are present in sizeable amounts in all parts of

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allelopathic plant including roots, stems, leaves, fruits, seeds, and flowers. They may be released from plants into the environment by volatilization, root exudation, leaching, and decomposition of plant residues (Kim et al. 1993; Narwal et al. 2005; Rice 1984). The crop allelopathic effects on weeds revolutionized the scientists to put much effort on this aspect with the aims of using this to reduce the dependence on chemical herbicides for weed control (Alsaadawi and Dayan 2009; Weston and Duke 2003). Several crops including *Sorghum bicolor* have been reported to have allelopathic potential against weeds and considerable variations have been reported among cultivars of the same crop species (Weston et al. 2013). Sorghum is a summer crop cultivated for grain and forage production in many countries such as Iraq (Al-Hashimi et al. 2010). The crop is included in a rotation system with several leguminous crops. The early work on weed suppression using sorghum residues was cited by many authors (Kim et al. 1993; Kohli et al. 2001; Netzly and Butler 1986; Weston 1996; Weston et al. 1989). These scientists found that phytotoxicity of residues varies with genotype, plant part, plant age, environmental factors, and the target weed species. Sorghum was explored as residues or as a water extract for weed control.

Field observations indicated that growth and population of companion weeds are variable within the stands of two locally cultivated sorghum cultivars (Enqath and Rabeh). This suggested that allelopathy might be the mechanism responsible for the variation in weed growth and population, and that the recorded differences among stands could be attributed to genetic diversity for allelopathic traits among the test cultivars. With this in mind, several

experiments were conducted to i) isolate, identify and quantify the allelochemicals in residues of the tested sorghum cultivars, and ii) find out if there is marker(s) linked to allelopathic trait by using DNA fingerprinting techniques.

MATERIALS AND METHODS

Preparation of sorghum residues.

To prepare sorghum residues, at the end of the season, mature sorghum plants of both cultivars (Enqath and Rabeh) grown in field were harvested in July 2013. They were air-dried for several days under plastic shed during summer and chopped into pieces of about 2-3 cm pieces using electrical grinder (Abar Company, Syria) and kept in dry and dark place until use.

Determination of total phenolics in sorghum residues.

Total phenolics in tested sorghum cultivars residues were extracted and quantified according to the Folin-Denis method (Helrich 1990). Sorghum plants, cvs. Enqath and Rabeh, were washed gently with distilled water and separated into two parts, shoots and roots, then chopped into 1-cm long pieces. All sorghum plant parts were dried at 70°C for 24 h. A quantity of 1.5 g of each plant part was placed in 25 ml distilled water in 100 ml flask and agitated on a rotary shaker for 24 h at 200 rpm. Extracts were filtered by Whatman No.2 filter paper under vacuum and centrifuged at 12000 rpm for 20 min at 8°C, prior to total phenolics analysis. A volume of 1 ml of sorghum extracts + 0.5 ml Folin-Denis reagent + 1 ml Na₂CO₃ reagents were mixed and the total volume was completed to 10 ml with distilled water.

Absorbance was determined at 750 nm and the content of total phenolics was obtained using the standard curve. Units of total phenolics were expressed in

milligrams of ferulic acid equivalents per milliliter extract. Ferulic acid equivalents were multiplied by 10 based on an extraction ratio 1:10 (w/w) as described by Ben-Hammouda et al. (1995).

Identification of allelochemicals in sorghum cultivars residues by HPLC method.

Phenolic acids in the residues of both cultivars (Rabeh and Enqath) was quantified by HPLC system (Shimadzu HPLC system Model LC-2010A HT) components, which includes a column of Hyper Clone 5u CN 120A (250 × 4.6 mm) phenomenon. Mobile phase is phosphoric acid 0.1% and acetonitrile (50:50 v/v), flow rate 0.5 ml/min. The injection volume for each sample was 1 µl lasted for 20 min. The amount of phenolic acids in each extract was quantified at 280 nm based on a calibration curve obtained with pure phenolic acids as standards.

Determination of genetic diversity between tested sorghum cultivars by PCR technique.

The present experiments were conducted to determine the genetic diversity between the tested cultivars and to find out if this technique may help to determine the allelopathic potential of the tested sorghum genotypes.

Plant material. Four sorghum cultivars were used in the present PCR experiments i.e. Rabeh, Enqath, Giza 15, and Giza 113. Sorghum seeds were provided by State Board for Agriculture Researches (SBAR), Ministry of Agriculture, Iraq. Previous work reported that cultivars Enqath, Giza 15 and Giza 113 were of high allelopathic potential compared to Rabeh (Alsaadawi et al. 2007). RAPD-DNA marker was used in this study to find out if there is any

marker(s) link to gene(s) that control allelopathic traits.

Sorghum genomic DNA extraction. For DNA extraction, two grams of fresh leaf tissue (2-week-old) was taken from a single seedling plant of the four cultivars. Genomic DNA was extracted according to the cetyltrimethyl ammonium bromide (CTAB) method (Doyle and Doyle 1990). Genomic DNA was dissolved in 250 µl 1X TE buffer using labeled Eppendorf tube (1.5 ml) and stored at 2-8°C until use.

Determination of DNA concentration and purity. Ten microliters (10 µl) of each DNA sample were added to a tube containing 990 µl of sterile distilled water and mixed well. The optical density (OD) of the samples was measured according to Sambrook et al. (1989) by spectrophotometer at wave length of 260 nm and 280 nm. The OD of 1 corresponded to approximately 50 µg/ml for double stranded DNA (Maniatis et al. 1982; Sambrook et al. 1989). The concentration of DNA was calculated according to the formula $\text{DNA concentration } (\mu\text{g/ml}) = \text{OD } 260 \text{ nm} \times 50 \times \text{Dilution factor}$, $\text{DNA purity ratio} = \text{OD } 260 / \text{OD } 280$. DNA fragments were separated using the following concentrations of agarose gel as follows i) 1% (w/v) used for detection of total genomic DNA, ii) 1.5% (w/v) used for separation of RAPD-PCR products.

Agarose gels were stained with ethidium bromide stain (Sigma-Aldrich C). The final concentration of stain solution was 1 µg/ml. DNA bands were visualized by UV transilluminator at 366 nm wave length in a UV cabinet. A gel documentation system was used to document the observed bands.

RAPD-PCR technique. PCR reactions were performed using the following components:

1- Primers: Ten of random oligodecamers primers (10-mer) commercially available from Bioneer Company, Korea, were used for detection of polymorphism

in this study. The lyophilized primers were dissolved in sterile distilled water to get a final concentration of 5 p mole/ μ l as recommended by provider. The sequences of the primers used in this study are listed in Table 1.

Table 1. The sequence of RAPD primers used in determining the genetic diversity of the tested sorghum cultivars

No.	Primer's name	Sequence 5' - 3'
1	OPA-10	G T G A T C G C A G
2	OPA - 11	C A A T C G C C G T
3	OPA - 12	T C G G C G A T A G
4	OPC - 16	C A C A C T C C A G
5	OPN - 16	A A G C G A C C T G
6	OPM - 14	A G G G T C G T T C
7	OPD - 6	A C C T G A A C G G
8	OPR - 17	C C G T A C G T A G
9	OPT - 19	G T C C G T A T G G
10	OPV - 14	A G A T C C C G C C

2 - PCR pre master mix: An AccuPower PCR pre-mix kit (Bioneer) was used for PCR amplification. The PCR pre master

mix which contained the components of PCR reagent optimized for more accurate PCR amplifications is listed in Table 2.

Table 2. Bioneer pre-mix components of PCR reagent used in determining the genetic diversity of the tested sorghum cultivars

Component	Concentration per reaction (in 25 μ l)
<i>Taq</i> DNA polymerase	1 U
Each: dNTP (dATP, dCTP, dGTP, dTTP)	250 μ M
Tris-HCl (pH 9.0)	10 mM
KCl	30 mM
MgCl ₂	1.5 mM
Stabilizer and tracking blue dye	-

For RAPD assay, PCR amplification was carried out on ice in a laminar air flow using 0.5, 0.2 μ l tight cap Eppendorf tubes, by adding about 50 ng of genomic DNAs and 10 pmole of primer to PCR

pre-mixture (Bioneer) containing buffer, dNTP and *Taq* DNA polymerase (Table 3). Final reaction volume was equal to 25 μ l.

Table 3. Components of RAPD- PCR reaction

Material	Final concentration	Volume for 1 tube
Bioneer pre- master mix	1 X	5 µl
Primer 5 p mol	10 p mol	2 µl
DNA samples	50 ng/ µl	2 µl
Sterile distilled water	-	16 µl

In each PCR experiment set up a negative control containing all components of the reaction except template DNA was prepared.

3 - *RAPD-PCR program*. The following steps were used for DNA amplification (Iqbal et al. 2010) as shown in Table 4.

Table 4. RAPD- PCR program used

Step		Temperature (°C)	Time (min)
Initial denaturation	1 cycle	94	4
Denaturation	36 cycles	94	1
Annealing		36	1
Extension		72	2
Final extension	1 cycle	72	10

4 - *Gel electrophoresis*. Approximately 24 µl of PCR amplified products were loaded and separated by electrophoresis in 1.5% agarose gels (2 h, 5V/cm, 1X TBE buffer). After that, the gel was immersed for 20 min in 30 µl/100 ml ethidium bromide stain (stock concentration of 10 mg/ml, Sigma-Aldrich, USA). The gel was visualized under the ultraviolet light (UV) transillumination (366 nm) and then was imaged by gel documentation system using a Photo Gel System.

Data analyses.

Molecular weight estimation.

Molecular weights for DNA bands were calculated by comparing the PCR products with the known size of standard DNA molecular weight marker (100 bp DNA Ladder: ranged from 100-2000 base pairs, or 1 Kb DNA Ladder: ranged from 0.5-10.2 kilo base pairs) provided by Bioneer Company was specially designed

for determining the size of double strand DNA samples (Sambrook et al. 1989).

Polymorphism estimation. Data generated from the detection of polymorphic fragments were analyzed. The amplification profiles of all tested genotypes for any given primer were compared with each other and the absence of each band was scored as '0' while the presence of each band was scored as '1'. The intensity of bands was not taken into consideration. Only major bands consistently amplified were scored and faint bands were not considered. Monomorphic, unique, and polymorphic bands were scored for each primer. The polymorphism percentage of each primer was calculated according to Blair et al. (1999) and Ali (2003) methods and based on the formula: Polymorphism (%) = $(N_p/N_t) \times 100$, where N_p = Number of polymorphic bands of the primer, N_t = Total number of bands of the same primer.

RESULTS

Quantification of total phenolics in sorghum residues.

Results indicated that total phenolics were two folds more in shoot than in root of both cultivars (Fig. 1). Total phenolics content was variable with the tested sorghum genotypes. These compounds appeared to be higher in

Enqath shoot and root (1.60 and 0.80 mg/g, respectively) than in Rabeh shoot and root (1.20 and 0.50 mg/g, respectively). The increments in total phenolics in root and shoot of Enqath were clearly reflected on the increase of total phenolics in the whole plant reaching 2.40 mg/g compared to Rabeh (1.70 mg/g).

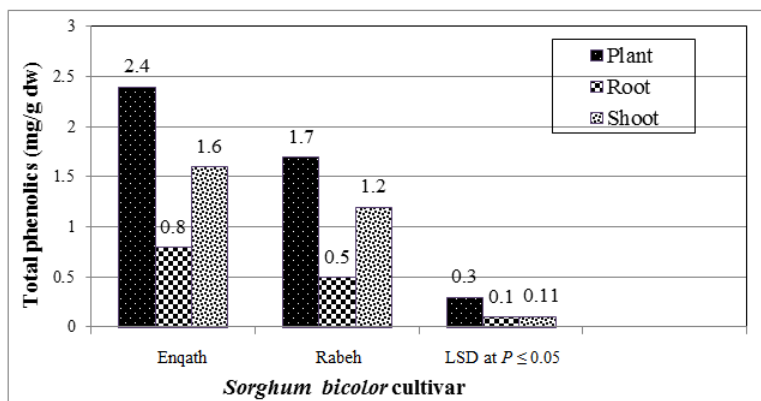


Fig. 1. Total phenolics in residues of *Sorghum bicolor* cultivars.

Identification of allelochemicals in sorghum residues by HPLC method.

Chemical analysis by high performance liquid chromatography (HPLC) revealed the presence of several allelochemicals namely ferulic, *p*-

coumaric, gallic, vanillic, syringic, *p*-hydroxybenzoic acid, and sinapic acid in the residues of Enqath and Rabeh cultivars. Total phenolic acids were found to be higher in Enqath cultivar than in Rabeh (Table 5).

Table 5. Isolation and quantification of phenolic acids in residues of two *Sorghum bicolor* cultivars

Compound	Concentration $\mu\text{g/g dry weight}$	
	cv. Enqath	cv. Rabeh
Ferulic acid	280.35	195.30
<i>p</i> -coumaric acid	195.00	100.70
<i>p</i> -hydroxybenzoic acid	270.20	190.48
Protocatecheuic acid	050.00	028.10
Sinapic acid	050.75	040.72
Syringic acid	250.64	200.81
Vanillic acid	078.00	044.81
Total	1175.00	800.92

Molecular analysis of test *Sorghum bicolor* cultivars.

Genomic DNA isolation. The genomic DNA isolated from the fresh leaf tissue of four test sorghum cultivars is

presented in Fig. 2. Total DNA yield was approximately 60 µg/ml from 2 g of fresh leaf tissue with purity ranging between 1.6 and 1.8.

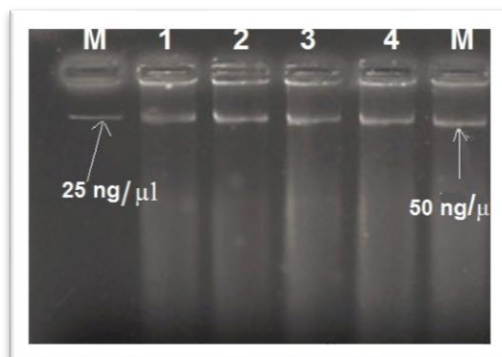


Fig. 2. Genomic DNA of sorghum cultivars visualized on 1% agarose gel. Lanes: 1. Rabeh; 2. Enqath; 3. Giza1; 4. Giza113. M: Standard size marker (λ DNA).

RAPD- PCR analysis. The tested sorghum genotypes were genetically differentiated by using the 10 RAPD primers. There were differences in the number of bands generated by each primer. The number of amplified bands produced per primer varied from 4 to 7, with a mean of 5.5 bands. These RAPD primers produced amplified fragments which varied from 125 to 1650 bp in size. The ten RAPD primers generated a total of 171 bands which appeared on agarose gels. Of these bands, only 10 were polymorphic across the 4 sorghum genotypes tested. Several primers produced only monomorphic bands (share) with no polymorphism detected in the template DNA of the tested genotypes, such as bands scored using OPA 10, OPA 11, and OPR 17 primers. Other RAPD primers scored some polymorphic bands between the tested genotypes such as OPA 12, OPC 16, OPD 6, OPM 14, OPN 16, OPT 19, and OPV 14. Also, some primers generated unique

bands (5 unique bands) that could be used as DNA marker to distinguish sorghum genotypes. A band was considered as polymorphic if the band differentiates at least any 2 of the 4 genotypes.

Out of ten RAPD primers used in this study, only 3 primers generated a unique amplified band which was present in only one sorghum genotype and absent in the others. The OPN 16 primer (Fig. 3; Table 6) produced 16 amplified bands, only one of them with molecular size 1250 bp present in 3 sorghum genotypes (with high allelopathic potential) namely Enqath, Giza 15, and Giza 113 and absent in Rabeh (with low allelopathic), and that may represent a first step towards the initial differentiation of genetic variation among four sorghum cultivars using RAPD markers. In addition, two unique bands of 1650 and 1400 bp produced by the same primer were present in Rabeh and absent in all the other studied genotypes.

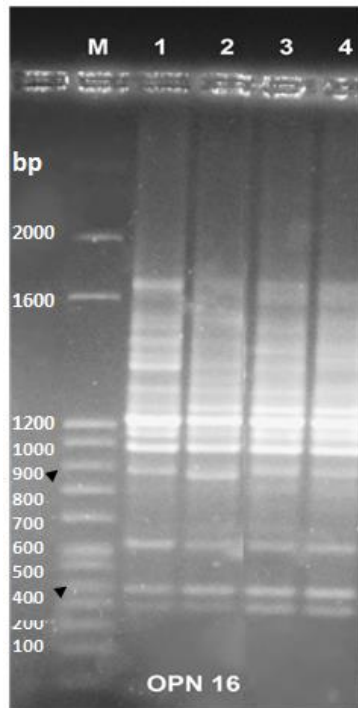


Fig. 3. RAPD banding profile of four sorghum cultivars visualized on 1.5% agarose gel using primer OPN 16. Lanes: 1. Rabeh; 2. Enqath; 3. Giza15; 4. Giza 113. M: DNA Molecular weight marker (100 bp DNA Ladder).

Table 6. Bands scored and molecular weight of amplification products with OPN 16 primer

Band number	DNA samples				Molecular weight (bp)
	1	2	3	4	
1	1	0	0	0	1650
2	1	0	0	0	1400
3	0	1	1	1	1250
4	1	1	1	1	1200
5	1	0	1	1	1150
6	1	1	1	1	1000

Total number of bands = 16

Polymorphism of each primer was calculated as the percentage of number of polymorphic bands to the number of total bands scored by the primer. Polymorphism ranged from 17 to 50%. Primer OPT 19 produced the highest

percent of polymorphism 50% compared with the primer OPC 16. Table 7 shows the number of total bands, polymorphic, unique and the percentage of genetic polymorphism among tested genotypes.

Table 7. Band characteristics detected by the RAPD primers

Primer name	Total number of bands	Monomorphic bands	Polymorphic bands	Unique bands	Polymorphism rate (%)
OPA 10	7	7	0	0	0
OPA 11	4	4	0	0	0
OPA 12	5	3	1	1	20
OPC 16	6	3	1	2	17
OPD 6	4	3	1	0	25
OPM 14	6	4	2	0	33.3
OPN 16	6	2	2	2	33.3
OPR 17	4	4	0	0	0
OPT 19	4	2	2	0	50
OPV 14	5	4	1	0	20
Total number of bands	51	36	10	5	-

DISCUSSION

The results of the present study indicated that the variation in allelopathic potential between the stands of Enqath and Rabeh sorghum cultivars observed in the fields depended not only on the differences in their root exudates as shown in the previous study (Alsaadawi et al. 2015) but also on their residues. Incorporation of residues of both cultivars into the field soil had significantly suppressed density and biomass of weeds grown in bean fields such as mung bean and broad bean with superiority of Enqath cultivar over Rabeh (Alkhateeb et al. 2013; Alsaadawi et al. 2013). The weed density and biomass reduction seems to be an outcome of inhibitory effects

exerted by sorghum residues. Such a reduction is believed to be originated by the release of phytotoxic allelochemicals from sorghum residues in the immediate vicinity during their decomposition by soil microorganisms. Chou and Lin (1976) first reported that several microorganisms contribute in decomposition of rice residues in soil and liberate several allelopathic compounds including phenolics and short fatty acids.

Rice (1984) indicated that several species of soil microorganisms are involved in the decomposition of plant residues and in the release of the allelopathic compounds which were found to be toxic to several weed species. Chemical analysis revealed the presence

of sizeable amount of phenolic compounds in roots and shoot residues of Enqath cultivar compared to Rabeh. Chemical analysis by HPLC revealed the presence of seven allelochemicals as phenolic acids. Many attempts were made to identify the phenolic acids in the total phenolic content of residues. However, several investigators indicated that sorghum contains several putative allelochemicals of phenolic nature such as vanillic acid, syringic acid, ferulic acid, *p*-hydroxybenzoic acid, and coumaric acid (Al-Bedairy et al. 2013; Alsaadawi and Dayan 2009; Cheema et al. 2009; Weston et al. 1989).

The isolated phenolic acids are known to inhibit ion uptake (Olmsted and Rice 1970), chlorophyll biosynthesis (Weir et al. 2004), cell membrane stability (Bogatek et al. 2005; Keck and Hodges 1973), protein and hormone biosynthesis (Holappa and Blum 1991; Rice 1984), cell division and change of the ultra-structural components of cells (Sanchez-Moreiras et al. 2004). Inhibitory allelopathic activity of sorghum allelochemicals against grassy and broad-leaved weeds has been reported in previous studies (Alsaadawi et al. 2007; Cheema and Khaliq 2000). In most cases, greater weed inhibition was observed at higher residue incorporation rates. Khanh et al. (2005) and Khaliq et al. (2010, 2011) pointed out that suppression magnitude in allelopathic interactions is directly proportional to the applied dose of an allelopathic product. The positive effects of residues on growth and yield of some crops was not only due to the reduction of weed population and biomass but also due to improvement of physical, chemical and nutritional status of field soil, and thus enhance growth and yield of crops (Sangakkara et al. 2004, 2006).

The results obtained using DNA molecular markers especially RAPD technique revealed that all the 10 primers scored different amplification products, monomorphic, polymorphic and unique bands in the tested genotypes with the exception of one RAPD primer which generated a unique amplification band (1250 bp) present in highly allelopathic sorghum genotype and absent in the low allelopathic one (Rabeh). Further work is recommended to analyze this band to find out if it is related to allelopathic trait or not. If the responsible gene(s) for allelopathic effects are identified, allelopathic traits can be incorporated into improved cultivars through plant breeding programs. To achieve the goal of this allelopathic breeding program, a multidisciplinary team of a wide range of scientists, including weed scientists, ecologists, natural-product chemists, plant breeders and molecular biologists is required. Further studies on the identification of specific allelochemicals and genes responsible for their biosynthesis using other novel selection methods of allelochemicals fingerprinting will undoubtedly shed more light on breeding allelopathic crop cultivars (Weston et al. 2013).

The differential allelopathic potential between the tested cultivars was apparently due to different phenolic acids content of their residues. Chemical analysis revealed the presence of sizeable amount of phenolic compounds in roots and shoot residues of Enqath cultivar compared to Rabeh. Chemical analysis by HPLC revealed the presence of seven allelochemicals as phenolic acids. Incorporation of sorghum residues in field soil can be used as a tool for weed suppression in other field crops and thereby increasing crop yield. The molecular technique revealed the presence of one sharp band with high

intensity in highly allelopathic cultivars compared to low allelopathic cultivar (Rabeh). Screening of allelopathic potential in allelopathic crops needs to be recommended as an essential step for utilizing allelopathy in weed

management. Finally, allelopathy can be considered as a useful agricultural practice for weed management in organic farming in order to reduce dependence on herbicides and to achieve an agroecosystem sustainability.

RESUME

Al-Khateeb T.A., Alsaadawi I.S. et Hadwan, H.A. 2017. Différenciation du potentiel allélopathique de cultivars de sorgho (*Sorghum bicolor*) moyennant des techniques chimiques et moléculaires. Tunisian Journal of Plant Protection 12: 1-13.

Des tests au laboratoire ont été conduits pour détecter le potentiel allélopathique différentiel des résidus de deux cultivars de sorgho (*Sorghum bicolor*), Enqath et Rabeh. L'analyse chimique des résidus a indiqué que les teneurs en composés phénoliques totaux sont plus élevés chez les plants d'Enqath que chez ceux de Rabeh suggérant la supériorité du potentiel allélopathique contre les adventices du premier cultivar par rapport à celui du second. Les résultats ont indiqué que les composés phénoliques totaux sont deux fois plus importants dans les tiges que dans les racines des deux cultivars. Ces composés semblent être plus élevés dans les tiges et les racines d'Enqath (1,60 et 0,80 mg/g, respectivement) que celles de Rabeh (1,2 et 0,50 mg/g, respectivement). Les augmentations des teneurs en composés phénoliques totaux dans les racines et les tiges d'Enqath ont été traduites par une augmentation des composés phénoliques totaux dans toute la plante en atteignant 2,40 mg/g comparé à Rabeh (1,70 mg/g). L'analyse chimique par HPLC a révélé la présence de sept composés allélochimiques à savoir les acides férulique, *p*-coumarique, gallique, vanillique, syringique, *p*-hydroxybenzoïque et sinapique dans les résidus des deux cultivars. Les acides phénoliques totaux sont plus élevés chez Enqath que chez Rabeh. Les résultats de la technique RAPD-PCR menée sur l'ADN génomique du sorgho a révélé que les 10 amorces utilisées dans cette étude ont généré différentes bandes d'amplification monomorphique et polymorphique chez les génotypes testés excepté trois amorces RAPD qui ont généré des bandes uniques d'amplification, une parmi elles (125 bp) est générée par l'amorce OPN 16 et est présente dans les génotypes de sorgho hautement allélopathiques et absente chez les faiblement allélopathiques (Rabeh). Plus de travail est recommandé pour l'analyse de la séquence de cette bande pour voir si elle est liée au caractère allélopathique ou non. Ces résultats recommandent aussi le criblage de plus de cultivars de sorgho dans le but de trouver des sources potentielles de germoplasmes allélopathiques qui peuvent être utilisés pour la suppression des adventices moyennant une approche efficace et environnementalement durable.

Mots clés: Allélopathie, composés phénoliques totaux, cultivars de sorgho, RAPD-PCR, résidus

ملخص

الخطيب، تمارا عدنان و إبراهيم شعبان السعداوي وحديد علي هذوان. 2017. تمييز قدرة المجاهضة لأصناف من الذرة البيضاء (*Sorghum bicolor*) باستخدام تقنيات كيميائية وجزيئية.

Tunisian Journal of Plant Protection 12: 1-13.

نفذت تجارب مخبرية لتحديد الاختلافات في قدرة المجاهضة لمخلفات صنفين من الذرة البيضاء (*Sorghum bicolor*) إنقاذ وراج. بينت نتائج التحاليل الكيميائية لمخلفات الذرة البيضاء تفوق صنف إنقاذ في المحتوى الكلي للفينولات على الصنف راج مما يشير إلى قدرة مجاهضة عالية لمخلفات هذا الصنف. أشارت النتائج إلى أن المحتوى الكلي للفينولات كان أعلى مرتين في المجموع الخضري من المجموع الجذري في كلا الصنفين. وتفوق تركيزها في المجموع الخضري والجذري لصنف راج (1,6 و 0,8 ملغ/غ، على التوالي) على تركيزها في المجموع الخضري والجذري لصنف إنقاذ (1,2 و 0,5 ملغ/غ: على التوالي) وهذا يقود إلى تفوق المحتوى الكلي للفينولات في نبات الذرة البيضاء صنف إنقاذ حوالي 2,4 ملغ/غ مقارنة بصنف راج حوالي 1,7 ملغ/غ. أعطت نتائج التحليل الكيميائي بعمود الفصل السائل العالي

الأداء بوجود سبعة أنواع من الأحماض الفينولية في المخلفات النباتية لصنفي رابح وإنقاذ مع تفوق المحتوى الكلي لهذه الأحماض في الصنف إنقاذ مقارنة بالصنف رابح. وهذه الأحماض هي الفيروليك والـب-كوماريك والغاليك والفانيليك والسيرانجيك والـب-هيدروبانزويك والسيناويك. كشفت نتائج استخدام تقنية التضخيم العشوائي متعدد الأشكال للحمض النووي (RAPD) عن طريق التفاعل المتسلسل للبوليميراز (PCR) للحمض النووي الجينومي للذرة البيضاء باستعمال عشرة بادئات عن وجود حزم متماثلة وأخرى متباينة من حيث العدد والوزن الجزيئي في الأصناف المدروسة، باستثناء 3 بادئات أعطت نتائج تضاعف أظهرت فيها حزم مميزة منفردة في صنف معين وفقدت في الأصناف المدروسة الأخرى. ظهرت الحزمة ذات الوزن الجزيئي 1250 زوج قاعدي عند التضاعف بوجود البادئ OPN 16، إذ تميزت هذه الحزمة بظهورها في الأصناف عالية القدرة على المجاهضة في حين فقدت في الصنف الأقل قدرة (رابح). يوصى بالعمل في تحليل هذه الحزمة المميزة ومعرفة تسلسلها من النيوكليوتيدات وذلك لمعرفة فيما إذا كان لها صلة بقدرة المجاهضة، وإذا ما تم تحديد الجينات المسؤولة عن صفات المجاهضة قد يمكن نقل هذه الصفات إلى أصناف الذرة المحسنة من خلال برامج التربية. كما يوصى بإجراء مسوحات على أصناف أخرى من الذرة البيضاء واستغلال الأصناف ذات قدرة مجاهضة عالية في برامج مكافحة الأعشاب الضارة.

كلمات مفتاحية: أصناف الذرة البيضاء، فينولات كلية، مجاهضة، مخلفات، RAPD-PCR

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