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Preface

Now commencing its seventh year, Jordan Journal of Biological Sciences (JJBS) will continue to provide biologists with first class research articles, review articles and short communications in various disciplines and frontiers of Biological Sciences. Here, I ask active researchers from all over the world to consider JJBS as one of their first choices for submission to publish their data. JJBS is now indexed with and included in DOAJ, EBSCO, CABI, HINARI, Google Scholar, Chemical Abstract Service, Zoological Abstract, Ulrich's, Index Copernicus International, ISC, Directory of Research Journal Indexing (DRJI) and others. Moreover, the journal is under the indexing process with ISI and Scopus. As always submitted research articles will get published. One of the great benefits we can provide to our prospective authors, regardless of acceptance of their manuscript or not, is the mentoring nature of our review process. JJBS provides authors with high quality, helpful notes and comments to assist authors in improving their manuscripts.

Moreover, the Editorial Board of JJBS are very much interested in publishing significant review articles that outline and discuss current hot topics in the frontiers of Biological Sciences. Putting such topics in perspective and fitting pertinent data together is of utmost importance in guiding future research and helping new scholars in the field to address important and pertinent issues. I encourage experts in various fields of Biological Sciences who wish to review certain front line topics in their specialties to contact me if they wish to contribute one or more review articles. In this way, the Editorial Board hopes to include at least one major or mini review in each journal issue as of March 2014.

As in prior two years, this seventh volume of JJBS will include four issues with at least twelve articles in each issue. In the coming year, it is my vision to have JJBS publishes more outstanding articles from distinguished scholars in various areas of Biological Sciences. In addition, I will be working on the inclusion of JJBS in Scopus, ISI and other international information retrieval services, which will lead to a good impact number.

Again, I must congratulate and thank all the researchers who contributed to research and review articles published in previous issues of JJBS during the past six years. Also, I thank my esteemed reviewers of previous articles submitted to the journal. They are assurance of high quality of published research work. To all our former contributors and potential new ones, I welcome further manuscripts for submission. Your manuscripts will receive careful consideration to maintain a high quality publication in JJBS.

I would like to thank the JJBS International Advisory board members for their continuous support. Furthermore, I would like to thank the JJBS Editorial board members for their exceptional work and continuous support to JJBS. Finally, I very much appreciate the support of The Hashemite University and Jordanian Scientific Research Support Fund for their continuous support to JJBS.

Professor Khaled H. Abu-Elteen Editor-in-Chief, JJBS Hashemite University Zarqa, Jordan <u>jjbs@hu.edu.jo</u>

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Pathogenicity of Syrian Isolates of *Bacillus thuringiensis* (Berliner) Against the Cereal Leafminer *Syringopais temperatella* Led. (Lep., Scythrididae) Under Laboratory Conditions

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Abstract

This study investigates the efficacy of 22 Syrian isolates of *Bacillus thuringiensis* (Berliner) (*Bt*) against *Syringopais temperatella* under laboratory conditions by feeding larvae on bacteria-contaminated barley leaves. The results indicated that all *Bt* isolates caused concentration and time related mortality, in which the highest mortalities were recorded at the highest concentration (original concentration), and at the latest time after *Bt* application(72 h). Mortality caused by all *Bt* isolates was significantly higher than mortality in the control. Isolate no. 1 gave significantly (*P*<0.05) the highest mortality percentage (73.3%) against the early larval instars. For the late larval instars, the isolates no. 21 and 22 were at bar with each other and gave significantly (*P*<0.05) the highest percentage of mortality (53.3%). Early larval instars were significantly (*P*<0.05) more susceptible to all concentrations of *Bt* isolates used than the late larval ones. In conclusion, the study showed that some of *B. thuringiensis* isolates tested in this study were pathogenic to *S. temperatella*.

Keywords: Bacillus thuringiensis, Cereal leafminer, Bio-insecticide, Biological control, Syrian Bt isolates, Syringopais temperatella.

1. Introduction

Wheat and barley are the main cereal crops grown in Jordan (Jordan Statistical Yearbook, 2011). One of the major constraints to the production of these crops in Jordan is the cereal leafminer, *Syringopais temperatella* Led. (Al-Zyoud *et al.*, 2009). The pest causes serious annual forage and yield reduction. Outbreaks of this pest have mostly occurred in southern Jordan for the last 12 years (Al-Zyoud, 2013) with a crop infestation estimated at 25% to 75% (Al-Zyoud, 2012).

The use of synthetic insecticides is currently the predominant method of controlling *S. temperatella* in Jordan (Al-Zyoud, 2007; Al-Zyoud, 2008). In spite of the intensive use of insecticides to suppress the pest, the infested areas are continuously increasing(Al-Zyoud *et al.*, 2011). In addition, the massive use of pesticides in modern agriculture caused their widespread diffusion to all environmental compartments including humans (Samiee *et al.*, 2009). Increased public concerns about adverse effects of pesticides prompted search of alternative methods (i.e.,biopesticides) for pest control.

The most widely used biopesticide worldwide is the bacterium, Bacillus thuringiensis (Berliner) (Bt) (Lacey et al., 2001). Bt occurs naturally in soil, dead insects, water and grain dust (Bernhard et al., 1997; Schnepf et al., 1998). During the sporulation process, the bacteria produce large crystal proteins that are toxic to many insect pests (Daly and Buntin, 2005). When orally ingested by insects, the crystal δ -endotoxins proteins of Bt formed, which are highly toxic to insects (Candas et al., 2003; Balaraman, 2005; Roh et al., 2007). The Bt preparations are the most successful bio-control products worldwide (Kaur, 2002). Bt has been used to control lepidopteran, coleopteran and dipteran pests on food crops, ornamentals, forest trees and stored grains (Iriarte et al., 1998; Theunis and Aloali'i, 1999; Balaraman, 2005). Ammouneh et al. (2011) reported that Bt isolates are very toxic to Ephestia kuhniella, Phthorimaea operculella and Cydia pomonella larvae (Lepidoptera). In addition, Giustolin et al. (2001) and Gonzalez-Cabrera et al. (2011) found that Bt is highly efficient in controlling the tomato borer, Tuta absoluta (Meyrick). In spite of Bt was used in spray formulations for more than 40 years against nearly 3,000 species (Huang et al., 2004), only

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one study has evaluated its efficacy on S. temperatella using the israelensis strain (Al-Zyoud et al., 2011). However, since some Bt isolates produce diverse insecticidal proteins that show differential insecticidal activities (Meihiar et al., 2012), there is a high possibility to find some isolates which may be used to effectively control S. temperatella. Nevertheless, the continued damage to cereal crops by the pest is a daunting challenge and requires the use of new control methods. Therefore, this study aimed at evaluating the toxicity of 22 Syrian Bt isolates against S. temperatella. It is hoped that the application of Bt will play a central role in protecting cereal crops; thereby, it will drastically replace, at least in part, some of the most dangerous insecticides currently used against S. temperatella.

2. Materials and Methods

2.1. Rearing of Syringopais temperatella

The rearing of S. temperatella was initiated from hundreds of first larval instarscollected from a barley field in Al-Rabbeh/ Karak-Jordan (Latitude of 31°11" N and Longitude of 35°42" E, altitude of 980 m). The larvae were maintained on potted (12x12 cm) barley plants in a rearing room. The infested plants were kept in meshed cages of 50x50x50 cm under laboratory conditions of 20±5°C temperature, 60±10% relative humidity and 12: 12 (L: D) h photoperiod. Barley of Mu'tah cultivar was used for rearing the pest and conducting the experiments. The plants were frequently replaced whenever needed to maintain adequate host-plant supply. Two groups of larvae were used in the experiments, which were randomly selected from the culture. The first group consisted of early larval instars (L1 and L2), while the second group consisted of late larval instars (L₄ and L₅).

2.2. Culturing, Preparation and Characterization of Bacillus thuringiensis Isolates

The Bt isolates were obtained from Dr. Maysa Meihiar as 22 biochemical types. Bt was isolated from Syrian soils of different plant communities (Meihiar et al., 2012) following the method described by Ohba and Aizawa (1986). Bt subsp. Kurstaki HD1 (Abbott Laboratories, Chicago, USA) was used as a reference for comparison with the previous results of the nearest insect species (Ephestia kuehniella Zeller) and also as a positive control for results of the present study. One ml of each Bt isolatesuspension was added into 10 ml of T₃ medium (g per liter: 3 tryptone, 2 tryptose, 1.5 yeast extract, 0.05 M sodium phosphate at pH 6.8 and 0.005 of MnCl₂). The suspension was incubated at 30°C for 7 days until the bacterial cells have sporulated for crystal production (Travers et al., 1987; Martin and Travers, 1989). In order to know the number of viable cells at the time of bioassay and after 7 days of incubation,1 ml of each of the 22 cultures was separately poured in 9 ml of sterile distilled water, and hereafter 9-fold serial dilutions were made. Aliquots of 1 ml of 7-9 fold dilutions were plated in duplicate by pour-plate technique using nutrient agar, and incubated at 30°C for 2 days. The colony forming units (CFU) were visually counted for the 22 different bioassayed isolates (Kango, 2010) (Table 1).

Table 1.Colony forming units (CFU) and shape of crystals of the twenty two bio-assayed Bacillus thuringiensis soil isolates.

| Isolate | Isolate | CFU/ml | Crystal morphology | | |
|---|-----------|-------------|------------------------|--|--|
| no. | subsp. | (mean) | | | |
| <i>Bt</i> 1 | Untypable | 9.00 E + 08 | Bipyramidal + Cuboidal | | |
| <i>Bt</i> 2 | Untypable | 3.50 E + 09 | Bipyramidal + Cuboidal | | |
| *Bt3 | Kurstaki | 6.00 E + 09 | Bipyramidal + Cuboidal | | |
| | HD1 | | | | |
| Bt 4 | kurstaki | 5.20 E + 09 | Bipyramidal + Cuboidal | | |
| Bt 5 | Untypable | 8.25 E + 09 | Spherical + | | |
| | | | Bipyramidal + Cuboidal | | |
| <i>Bt</i> 6 | Sotto | 1.50 E + 11 | Bipyramidal | | |
| Bt 7 | Untypable | 1.44 E + 11 | Rectangular + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 8 | Untypable | 1.05 E + 11 | Irregular + | | |
| | | | Bipyramidal + Cuboidal | | |
| <i>Bt</i> 9 | Untypable | 1.57 E + 11 | Bipyramidal + Cuboidal | | |
| Bt 10 | Untypable | 1.95 E + 09 | Bipyramidal + Cuboidal | | |
| Bt 11 | Untypable | 9.50 E + 08 | Rectangular + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 12 | kurstaki | 2.50 E + 08 | Bipyramidal + Cuboidal | | |
| Bt 13 | kurstaki | 8.50 E + 08 | Bipyramidal + Cuboidal | | |
| Bt 14 | Untypable | 1.65 E + 10 | Rectangular + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 15 | Untypable | 8.50 E + 09 | Spherical + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 16 | Untypable | 9.00 E + 08 | Rectangular + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 17 | Untypable | 2.15 E + 09 | Spherical + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 18 | Untypable | 9.50 E + 08 | Rectangular + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 19 | Untypable | 1.45 E + 09 | Rectangular + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 20 | Untypable | 1.60 E + 10 | Rectangular + | | |
| | | | Bipyramidal + Cuboidal | | |
| Bt 21 | Untypable | 1.00 E + 09 | LikeBtsubsp. Finitimus | | |
| | | | (rhomboid in shape) | | |
| Bt 22 | Untypable | 1.00 E + 09 | Bipyramidal + Cuboidal | | |
| *Bt subsp. Kurstaki HD1 (Dipel®- Abbott Laboratories, | | | | | |

Chicago, USA) used as a reference strain

2.3. Bioassay

The bioassay was set up in Petri-dishes of 5.5 cm in diameter that were partially filled with 0.5 cm thick layer of wetted cotton pad. The lid of each Petri-dish had a hole closed with organdie fabric for ventilation. Barley leaf strips of 10 cm² area, which were cut from un-infested barley plants, were placed in the Petri-dishes. Either S. temperatella early or late larval instars were gently transferred using a Camel hairbrush into the Petri-dishes in groups of ten larvae/Petri-dish. Larvae in the control treatments (n=10) were provided with leaf strips dipped in sterilized distilled water for 30 sec, while larvae in the Bt treatments (n=10) were provided with leaf strips dipped in an aqueous solution of the required Bt isolate and concentration (original and twofold serial dilutions) for 30 sec. The Petri-dishes were kept under the abovementioned laboratory conditions. Larval mortality was recorded 1, 2 and 3 days post-treatment with Bt. Larvae were considered dead if they do not move when gently prodded with fine brush. Data obtained for mortality percentages of early and late larval instars of S.

temperatella were plotted as a linear correlation function versus the CFU.

2.4. Statistical Analysis

The statistical analysis was performed using the proc GLM of the statistical package Sigma Stat version 16.0 (SPSS, 1997). The experimental design was a complete randomized design (CRD) with three replications for each isolate and concentration. The data were analyzed using one way ANOVA to detect any differences in the pest mortality (Zar, 1999). When significant differences were detected, means were compared using LSD at 0.05 probability level (Abacus Concepts, 1991). The *t-test* was used for comparison between only two means (Anonymous, 1996). In addition, the correlation between mortality and progress of time after spraying as well as mortality and concentration of Bt was calculated by Spearman's correlation method (Zar, 1999).

3. Results

The results presented herein are for Bt isolates as an original concentration (named conc. 1), first-fold dilution (named conc. 2) and second-fold dilution (named conc. 3). However, the results revealed that the original concentration of *Bt* (ranged between CFU = 2.5×10^8 for isolate Bt 12 (Bt kurstaki) to 1.57×10^{11} for isolate Bt 9) gave the highest percentage of mortality for both S. temperatella early (F=4.250; 2, 195 df; P=0.016) and late (F=6.655; 2, 195 df; P=0.002) larval instars tested, but it was at bar with the first-fold dilution, while it differed significantly from the second-fold dilution (Figure 1). The mortality percentages resulted from the original and the second dilutions were 20.8% and 12.5% (early instars), and 16.5% and 8.6% (late instars), respectively. Furthermore, early larval instars were significantly more susceptible to all Bt isolates and concentrations used than the late larval instars (Figure 1).

The highest larval mortality was recoded after 72 hr of *Bt* application, and it was significantly different from those at24 and 48 hr post application for both early (*F*=6.990; 2, 63 df; *P*=0.002) and late larval instars (*F*=22.987; 2, 63 df; *P*=0.000) (Figure 2). Mortalities of 26.8% and 21.0% for early and late larval instars' were reported 72 hr post *Bt* application, respectively, while the mortalities were only 9.6% and 3.6% after 24 hr of *Bt* application, respectively. Early larval instars were more susceptible to *Bt* than the late instars at all times after application (24, 48 and 72 hr) (Figure 2).

Overall mortality percentage of *S. temperatella* as a result of leaf-dipping in the three different concentrations of *Bt* isolates for both early and late larval instars are presented in Figure 3. Mortality caused by all *Bt* isolates was significantly higher than that of the control. Moreover, the isolates; *Bt*1, *Bt* 21 and *Bt*13 (*Bt kurstaki*) caused significantly the highest mortality percentages with 28.2%, 26.5% and 25.7%, respectively (*F*=4.884; 22, 391 df; *P*=0.000). In contrast, the isolates; *Bt*8, *Bt*17 and *Bt*4 (*Bt kurstaki*) caused significantly the lowest mortality with 4.3%, 5.8% and 5.9%, respectively.

Since the results in Figure 1 and 2 showed that the highest efficacy of Bt was obtained 72 hr post Bt application at the original concentration, further statistical

analysis was made at these time and concentration to check the efficacy of all Bt isolates tested as shown in Figure 4. The results indicated, for early larval instars, that the isolate Bt 1 gave significantly the highest mortality percentage (73.3%), followed by the isolates; Bt 13 (Bt kurstaki) (66.7%), 19 (63.3%) and 16 (63.3%), while the isolates; Bt 8, Bt9, Bt 17, Bt14 and Bt 12 (Bt *kurstaki*) were at bar with the control treatment (mortality: 0.0-6.7%) (F=23.040; 22, 46 df; P=0.000). For late larval instars, the isolates; Bt 21 and Bt22 were at bar with each other and gave significantly the highest percentage of mortality (53.3%). Moreover, all isolates gave significantly higher mortalities to the late larval instars than control (F=20.996; 22, 46 df; P=0.000). Out of 22 isolates, three isolates (Bt20, Bt21 and Bt22) caused higher mortality for both early and late larval instars.

There was a positive significant correlation between time after Bt application and mortality percentage as well as between Bt isolate's concentration and mortality percentage (Table 2). This means that with increasing time after Bt application and Bt concentration there was an increase in the mortality of S. temperatella. No clear relationship was noticed between the efficacy of Bt isolates and shape of crystal proteins they have; however, it is to be mentioned that most of the effective and ineffective isolates have bipyramidal and cuboidal parasporal crystal protein shapes. The correlation between CFU and larval mortality was plotted for the promising isolates (that gave mortality higher than 40%) against early (Figure 5A) and late (Figure 5B) larval instars. The results indicated that the relationship isof increasing function; higher mortalities were obtained from effective isolates of higher CFU.

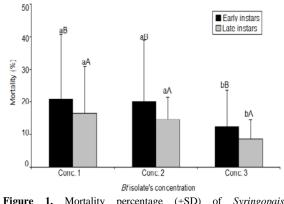


Figure 1. Mortality percentage (\pm SD) of *Syringopais temperatella* in relation to larval instars resulted from application of different *Bacillus thuringiensis* isolates in a feeding larval test on bacterial contaminated barley leaves under laboratory conditions. [Different small letters above bars indicate significant differences among the different *Bt* concentrations within the same instar, while capital letters above bars indicate significant differences between the different instars within the same concentration at *p*<0.05 (one-factor analysis of variance)].

Table 2. Correlation analysis of mortality percentage of *Syringopais temperatella* versus time and concentration of *Bt* isolates in a feeding larval test on bacteria-contaminated barley leaves under laboratory conditions.

| Correlated | Instar | R value | Significance |
|--------------------|--------------|--------------|--------------|
| variables | | | |
| Time vs. Mortality | Early | 0.411** | 0.001 |
| percentage | instars | | |
| | Late instars | 0.707^{**} | 0.000 |
| | Both (early | 0.682^{**} | 0.000 |
| | and late) | | |
| Bt isolate's | Early | 0.233^{*} | 0.050 |
| concentration vs. | instars | | |
| Mortality | Late instars | 0.385^{**} | 0.001 |
| Percentage | Both (early | 0.365** | 0.003 |
| | and late) | | |

*Correlation is significant at the 0.05 probability level.

**Correlation is significant at the 0.01 probability level

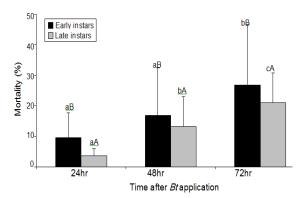


Figure 2. Mortality percentage (\pm SD) of *Syringopais temperatella* in relation to time after *Bt* application resulted from different isolates in a feeding larval test on bacterial contaminated barley leaves under laboratory conditions. [Different small letters above bars indicate significant differences among the different times within the same instar, while capital letters above bars indicate significant differences between the different instars within the same time at *p*<0.05 (one-factor analysis of variance)].

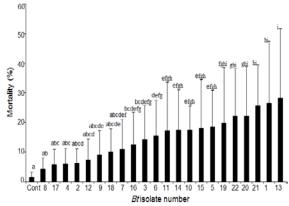


Figure 3. Overall effect of *Bacillus thuringiensis* different isolates (all concentrations) on *Syringopais temperatella* mortality percentage (\pm SD) in a feeding larval test on bacterial contaminated barley leaves under laboratory conditions. Isolate no. 3 (*Bt* subsp. *kurstaki* HD1) is the reference strain.[Different small letters above bars indicate significant differences among the different *Bt* isolates at *p*<0.05 (one-factor analysis of variance)].

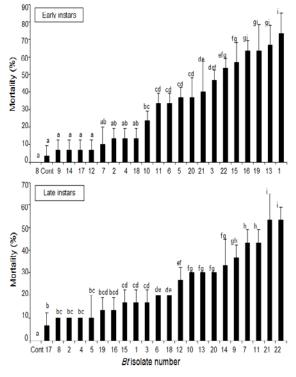


Figure 4.Mortality percentage (\pm SD) of *Syringopais temperatella* early and late larval instars as a result of application by the higher concentration of *Bacillus thuringiensis* different isolates after 72 hrin a feeding larval test on bacterial contaminated barley leaves under laboratory conditions.Isolate no. 3 (*Bt* subsp. *kurstaki* HD1) is the reference strain.[Different small letters above bars indicate significant differences among the different *Bt* isolates at *p*<0.05 (one-factor analysis of variance)].

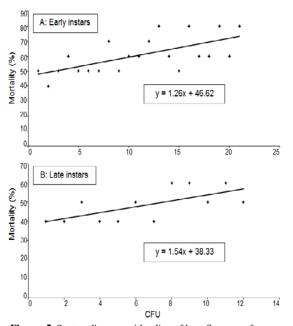


Figure 5. Scatter diagram with a line of best fit curve of obtained mortality percentages of the early (A) and late (B) larval instars of *Syringopais temperatella* after 72 hr as a function of colony forming units (CFU) of the effective *Bacillus thuringiensis* isolates.

4. Discussion

In this study four variables were considered; the Bt isolates (22 different isolates), the target larval instar (early and late), the Bt concentration (original, first-fold and second-fold dilutions) and the effect of time after exposure to Bt (24, 48 and 72 hr). The reference strain we used (Bt subsp. kurstaki HD1) is the same used by Meihiar et al. (2012). We reported 48% mortality for the reference strain against S. temperatella while 53% mortality was reported by Meihiar et al. (2012) against E. kuehniella from the same insect order. For the 72 hrmortality at the higher Bt concentration used, 6 and 2 isolates out of the 22 isolates were effective against early and late larval instars of S. temperatella, respectively. They reported mortality percentages more than that reported for the reference strain. We think that these promising isolates produce cry gene toxic against the pest larvae as reported by many researchers (Tabashnik et al., 1994; Porcar et al., 2000; Song et al., 2003). In addition, the level of gene expression plays a role in the toxicity as proposed by Porcar et al. (2000). However, the Bt toxicity did not depend on cry gene content only, because factors other than cry proteins may contribute to the toxicity as well as spore interaction with crystal protein and the other soluble toxins such as β -exotoxin (Porcar *et al.*, 2000). Moreover, Martinez et al. (2004) suggested that the biological activity of a strain cannot be fully predicted on the basis of its cry gene content alone. The relative proportion of the cry proteins produced, their interaction, and the possible presence of undetected crystal proteins are all important. The present results revealed that the isolate number 13 (Bt kurstaki) caused 68% mortality after 3 days of exposure to early instar larvae of S. temperatella which is coincide with the previously reported results for this bacteria subspecies using the same pest with 71.4%% mortality (Al-Zyoud et al., 2011). Furthermore, we suggest that isolates are mostly produced the toxic proteins after two days of infection. What Al-Zyoud et al. (2011) found is supporting our suggestion, where they found that a gradual increase in mortality with time post Bt spraying against S. temperatella larvae. Moreover, the current results indicated that all Bt isolates caused concentration related mortality, in which the highest mortality was recorded at the highest concentration. Therefore, the results showed that both time and concentration play an important role in the bacteria efficacy. On the contrary of Obeidat et al. (2004) and Meihiar et al. (2012) findings, the shape of the isolates' crystal proteins did not correlate with the isolate efficacy; where bipyramids and cuboids crystal proteins were found in our both effective and ineffective isolates. Obeidat et al. (2004) found that out of the twenty-six strains of Bt, serotypes kenyae, kurstaki and kurstaki HD1 produced bipyramid crystal proteins which were toxic to E. kuehniella. Moreover, Meihiar et al. (2012) confirmed Obeidat et al.(2004) finding, in which Bt strains producing bipyramid and cuboid crystal shapes are the most toxic to the same insect. In the current study, the remaining 11 isolates were found less effective against the S. temperatella larvae. The reason behind this is that such isolates might not produce Cry proteins or their genes were of low level of expression. In addition, the same isolates investigated in this study were previously bioassayed against *E. kuehniella* by Meihiar *et al.*(2012), and PCR was used to examine their *cry* genes content. Their findings demonstrated that the most toxic isolates harbor different specific *cry* genes including *cryI* and *cryIV* which have an insecticidal activity to lepidopteran insects. This finding is also proposed previously by Ammouneh *et al.* (2011), in which the type of the *cry* genes was found to correlate with its insecticidal activity.

The present results revealed that the isolate Bt 1 was effective in controlling the early instars larvae but it showed low efficacy against late instars. This might be due to the low number of bacterium cells in the original concentration due to the low sporulation rate, and as a result low number of crystal proteins (as shown in Table 1) as compared with the isolates; Bt 21 and Bt 22, which were efficient against the late instars. Therefore, this little number of crystal proteins in the isolate could not produce enough amounts of toxins to affect the late larval instars which are much larger in size than the early ones. This justification is supported in our findings (as shown in Figure 5) as indicated by the relationship between the number of bacterial cells and the mortality obtained. This relationship is of a positive trend; the more number of bacterial cells the higher the mortality obtained. It is to be mentioned that the number of bacterial cells is positively correlated with the amount of crystals and subsequently the amount of toxins they produced to cause death to the pest larvae.

In conclusion, some of Bt isolates used in this study exhibit a toxic potential against the pest and, therefore, they could be adopted for future control program to suppress the pest as a part of IPM program, and thus will reduce and/or replace the most dangerous chemical insecticides currently used against the pest in Jordan and surrounding countries. Better pest control strategy can increase farm incomes and reduce the hazards in rural areas associated with insecticides' use as well as will contribute to improve food security where wheat and barley are major sources of food for human and their animals in the region.

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Inhibitory Effect of Mediterranean Sage and Rosemary on Clinical and Community Isolates of Methicillin-Resistant Staphylococcus aureus

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Abstract

Plant extracts are traditionally used for treating many infectious and non- infectious diseases. This study aimed at assessing the inhibitory effect of the ethanol extracts of two medicinal plants; Mediterranean Sage (*Salvia libanotica*) and Rosemary (*Rosmarinus officinalis*) on clinical and community strains of methicillin-resistant *Staphylococcus aureus* (MRSA). Ethanol extracts of the two plants were tested for their antibacterial effect against 25 clinical (n=15, 60%) and community (n=10, 40%) strains of MRSA. Rosemary and Mediterranean Sage extracts demonstrated activity against all isolates, 50µl of 100 mg/ml of each plant extract yielded inhibition zone reaching as high as 27 and 30 mm by agar well diffusion method. Effective MICs and MBCs of ethanol extracts of Rosemary and Mediterranean Sage against MRSA were 0.125 to 0.5mg/ml and0.25 to 1 mg/ml respectively. Mixed ethanol extract of Rosemary and Mediterranean Sage showed antagonistic effect on MRSA strains. These results suggest the potential therapeutic implications of the ethanol extract from Rosemary and Mediterranean sage in the treatment of MRSA infections.

Key words: Mediterranean Sage; Rosemary; MRSA; Jordan.

1. Introduction

Traditionally, the dependence on alternative medicine in developing countries and other parts of the world is clearly obvious, they use preparations of any part of the plants for the purpose of pain relief, infection prevention or even as cosmetics (Ahmad *et al.*, 1998). Studies evaluating medicinal plants as a source of antimicrobials proved that plants' active components might be used as bacterial inhibition agents (Emori and Gaynes, 1993; Cos *et al.*, 2006). Medicinal plants may play a role as a natural source of antimicrobial drugs (Habeeb *et al.*, 2007).

Methicillin-resistant *Staphylococcus aureus* (MRSA) infections of both hospital and community acquired have increased remarkably during the last decade (Chambers, 1997). Hospital acquired MRSA (HA-MRSA) strains are mainly distinguished from community acquired MRSA (CA-MRSA) using molecular techniques. The *SCC mec* in HA-MRSA belongs to type I, II or III and is bigger than that of CA-MRSA, which belongs to *SCC mec* type IV or V. In addition, CA-MRSA strains frequently carry the gene for PVL (Panton Valentine Leukociden) toxin which is not commonly found in HA-MRSA (Naimi *et*

al., 2003). Antibiotic options for patients with MRSA infection are usually restricted due to the wide range of MRSA antibiotic resistance. This has enhanced researchers to use other natural agents to fight MRSA, especially from medicinal plants (Schito, 2006). In Jordan, data revealed that MRSA infections both hospital and community acquired have been increased in the last few years, with percentage of 62% and 8% respectively (Borg *et al.*, 2007; Aqel *et al.*, 2012).

In a previous study carried out by some authors of this study (Ibrahim *et al.*,2013), the effect of crud extract of *S. libanotica* and *R. officinalis* against two test strains of *Staphylococcus aureus* ATCC (25923) and an MRSA isolate was clearly identified. The present study aims to further assess the antimicrobial effect of *S. libanotica* and *R. officinalis* against clinical and community isolates of MRSA. Both Mediterranean Sage and Rosemary tested in this study are used traditionally in Jordan for purposes such as the treatment or relief of respiratory and gastrointestinal infections (Obeidat, 2011; Abu-Shanab *et al.*, 2004).

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2. Materials and Methods

2.1. Plant Samples and Manipulation

Two medicinal plants, *Salvia libanotica* (Mediterranean Sage) and *Rosmarinus officinalis* (Rosemary) were tested in this study (Table 1).The experimental part of the study was done in the department of microbiology and immunology, faculty of medicine, Mu'tah University, from 1 May 2013 to 15 September 2013. Plants were purchased locally from the markets. Leaves were collected to be air dried for 14 days and then powdered using mortar and pestle.

Table 1. Profile of the two medicinal plants used

| Botanical Name | Family | Local Name | Plant part used |
|------------------------|-----------|------------|--------------------|
| Rosmarinus officinalis | Lamiaceae | Hasa-alban | leaves |
| Salvia libanotica | Lamiaceae | Miramiyah | leaves |

2.2. Ethanol Extracts Preparation

One hundred grams of each powder were extracted by cold maceration with 80% ethanol for 48 hrs at room temperature. Filtration by Whatman filters paper no. 2; evaporation and concentration of the extract under low pressure were applied consequently for each plant extract (Ahmad *et al.*, 1998).Powder samples were stored at 4°C. Primary active components and essential oils extraction were performed according to Böszörményi (2009). Briefly, oil extraction was done under water steam distillation for 3 hrs of 30 gm of the plants powder.

2.3. Test Organisms

A total of 25 non-repeat MRSA strains, 15 (60%) strains from different patients admitted to Al-Karak hospital, Jordan, and other 10 (40%) MRSA nasal swabs strains obtained from healthy individuals in the year 2013 were studied. The clinical strains were isolated from respiratory samples (n = 3; 20%), wound swabs (n = 3; 20%), urine (n =4; 26.6%), pus (n = 1; 6.7%), catheter tip (n = 1; 6.7%), blood (n = 3; 20%). Isolates were identified morphologically and biochemically by standard microbiological procedures using Gram stain, catalase test, coagulase test and an API system (bioMérieux, France). Cefoxitin (30 µg) discs (Oxoid, Basingstoke, UK) were used for methicillin resistance determination. Susceptibility tests were applied according to guidelines of Clinical Standards Laboratory Institute (CLSI, 2012). Detection of MecA gene (encoding high-level resistance to methicillin) and 16S rRNA gene (internal control) were performed with DNA extraction, primers and amplification conditions according to Petinaki (2001). Staphylococcus aureus ATCC 29213 and 2 methicillinsusceptible Staphylococcus aureus (MSSA) strains were used as control strains during susceptibility testing and PCR procedures. Bacterial samples were preserved in transport media at 4°C and subcultured overnight before use. Consent was obtained from all participants after explaining the purpose of the study. The ethics and

scientific committee of the faculty of medicine at Mu'tah University approved the study (approval no. 22/2/12).

2.4. Agar Well Diffusion Method

Extracts inhibition effects were assessed by agar well diffusion method according to the National Committee for Clinical laboratory Standards (NCCLS, 2000a). About 20 ml of Mueller Hinton agar (Oxoid, Hampshire, England) was poured into Petri dishes. After solidification, inoculum of 0.5 McFarland of each test strain was seeded on the media. Allowing inoculum to dry; 5 mm size wells was made with sterile borer. About 50 µl of 100 mg/ml of each extract was introduced into the well and plates were incubated at 37°C for 24 hrs. All samples were tested in duplicates. Other 2-32 mg/ml dilutions were prepared to determine the concentration effect (CE) on bacterial inhibition. Water, vancomycin (30 µg) and oxacillin (1 µg) disks were used as negative and positive controls (Abu-Shanab et al., 2004). Antimicrobial effect was determined by measuring the diameter of zone of inhibition around the holes and disks.

2.5. Minimal Inhibitory Concentration (MIC) and Minimal Bactericidal Concentration (MBC) by Broth Dilution

MIC and MBC were detected by using different extract concentrations from 0.0625 mg/ml to 32 mg/ml. In a test tube equal volume (0.5 ml)of both plant extracts and nutrient broth were mixed together. Standard microbial inoculums were added to each tube (0.1 ml of $1-2 \times 10^8$ cfu/ml). Tubes were aerobically incubated at 37°C for 24 hrs according to NCCLS (2000b). Vancomycin and oxacillin dilution tubes were prepared and used as positive and negative controls in all tests.

Test tube with no visible growth (no turbidity) was considered as the lowest extract concentration that inhibits bacterial growth (MIC), whereas, tube with no visible growth that yielding no colonies when subcultured on extract or drug free nutrient agar was considered as MBC tube (Weckesser *et al.*, 2007).

3. Results

3.1. Primary Assessment of Antimicrobial Activity

Qualitatively and quantitatively antibacterial activities of *S. libanotica* and *R. officinalis* against MRSA were in vitro assessed (Table 2). Fifty micro-liters of 100 mg/ml of *R. officinalis* and *S. libanotica* showed the greater effect with MIC and MBC values range of 0.125-0.25 mg/ml and 0.25-0.5 mg/ml and 0.25-0.5 mg/ml and 0.5-1 mg/ml of each plant extract respectively (Table3).

Our results indicate that ethanol extract mixture of both *S. libanotica* and *R. officinalis* will diminish their potent antibacterial effect against MRSA with MIC and MBC increasing up to 4 to 8 mg/ml and 8 to 16 mg/ml, respectively (Table 3).16S rRNA gene was positive for all staphylococcal strains. PCR product of *MecA* gene was detected in all MRSA strains but not MSSA strains.

Table 2. Antibacterial activity of the ethanol crude plant extract on *S. aureus* strains

| Plant used | MRSA ^a (n=10) | MRSA ^b (n=15) | * <i>S. aureus</i> and MSSA |
|-----------------------------|-----------------------------|-----------------------------|--------------------------------|
| Rosmarinus officinalis | 28# | 26 | 28 |
| Salvia libanotica | 23 | 22 | 26 |
| Vancomycin 30µg | 21 | 21 | 22 |
| Oxacillin 1µg | NA | NA | 16 |
| Negative control (Water) | NA | NA | NA |

#Inhibition zone average in mm;*S. aureus = standard strain used ATCC 29213.

a Community MRSA isolates; b Clinical MRSA isolates; n = number

Vancomycin, Oxacillin = standard antibacterial drug used as positive control of MRSA tested. NA=No activity

 Table 3. MIC and MBC (mg/ml) of ethanol extracts of

 Rosemary and Mediterranean Sage and their combination on

 MRSA.

| Plant used | MRSA ^a (n=10) | | MRSA ^b (n= | MRSA ^b (n=15) | |
|----------------------------------|--------------------------|----------|-----------------------|--------------------------|--|
| | MIC | MBC | MIC | MBC | |
| Rosmarinus officinalis | 0.125-0.25 | 0.25-0.5 | 0.25-0.5 | 0.5-1 | |
| Salvia libanotica | 0.25-0.5 | 0.5-1 | 0.25-0.5 | 0.5-1 | |
| R. officinalis/ S. libanotica | 4-8 | 8-16 | 4 – 8 | 8 – 16 | |
| Vancomycin | 0.25-0.5 | 0.5-1 | 0.5-1 | 1-2 | |
| Oxacillin | NA | NA | NA | NA | |

Vancomycin, Oxacillin = standard antibacterial drug used as positive and negative controls. ^aCommunity MRSA isolates; ^b Clinical MRSA isolates; n = number

of MRSA tested. NA=No activity

 Table 4. The concentration effect of the ethanol extracts of

 Rosemary and Mediterranean Sage on S. aureus and MRSA

 strains

| Plant | Conc. | Diameter (mean ± SD) of inhibition zone (mm) including well diameter of 6 mm | | | |
|----------|-------|---|--------------------------|----------------------------|--|
| extract | | Staphylococcus aureus ATCC 29213 | Community MRSA (n=10) | Clinical MRSA (n=15) | |
| | 2 | 10.66 ± 1.15 | 8.75 ± 1.06 | 8.0 ± 1.04 | |
| | 4 | 11.83 ± 0.28 | 10.5 ± 0.7 | 9.5 ± 0.1 | |
| Rosemary | 8 | 15.33 ± 1.52 | 14.75 ± 1.76 | 13.05 ± 1.5 | |
| | 16 | 16.66 ± 0.57 | 17.00 ± 2.82 | 16.00 ± 2.5 | |
| | 32 | 20.00 ± 0 | 19.00 ± 1.41 | 18.00 ± 1.4 | |
| | 2 | 8.16 ± 1.04 | 8.00 ± 0 | 7.8 ± 0.2 | |
| | 4 | 10.16 ± 0.28 | 9.25 ± 1.06 | 9.1 ± 1.0 | |
| Sage | 8 | 16.33 ± 1.52 | 13.00 ± 1.41 | 12.00 ± 1.3 | |
| | 16 | 17.66 ± 2.02 | 16.25 ± 0.35 | 15.5 ± 0.75 | |
| | 32 | 19.00 ± 1.73 | 17.5 ± 0.7 | 16.2 ± 0.5 | |

3.2. Determination of Concentration Effect (CE)

Results of CE for the bacterial samples are listed in Table 4. Ethanol extracts of both *S. libanotica* and *R.*

officinalis revealed inhibitory action on *Staphylococcus aureus* ATCC 29213 and MRSA in all added doses. No significant difference in bacterial inhibition zone for both extracts was noticed for all isolates sources at any specified concentration. Nevertheless, increasing concentrations resulted in greater inhibition zone for *S. libanotica* and *R. officinalis* against all isolates.

4. Discussion

World Health Organization encouraged health systems in different countries since 1980s to interact with herbal medicine for identifying and assessing means that build up bases for new and safe herbal agents which can be used for treatment of infectious and noninfectious diseases (WHO, 1978). The development of new antibacterial drugs for the treatment of MRSA infections is of increasing interest (Schito, 2006). Herbal medicine has long been used in Jordan for the treatment of various ailments (Obeidat, 2011; Ibrahim et al., 2010). The incidence of MRSA infections in Jordan was obvious over the last few years (Aqel et al., 2012). MRSA detection rate has been increasing especially in the hospitals. The resistance has been emerging not only to methicillin but also to other many antibiotics, including vancomycin leading to further restriction on available antibiotic options (Bakri et al., 2007; Mohammad, 2010).

Experiments of microbial growth inhibition by agar well diffusion and broth dilution methods revealed that two plants (*S. libanotica* and *R. officinalis*) were active against MRSA strains. Similar antimicrobial results were obtained by other researchers (Abu-Shanab *et al.*, 2006; Obeidat, 2011).

In this study, volatile oils and other triterpenoids, the active components determined primarily from S. libanotica and R. officinalis showed antibacterial activity against MRSA, S. aureus and other tested isolates, this is in agreement with previous Jordanian study by Al-Bakri et al. (2010). A study by Nascimento et al. (2000) showed that the active chemical constituents obtained from S. libanotica and R. officinalis were mainly flavonoids, phenolic acids, rosmarinic, caffeic, chlorogenic acids, carnosol, diterpenes, camphor, thuyone and cineole; all these compounds and oils have remarkable antimicrobial activity. In the current study, the MIC and MBC results revealed that low extract concentration had a bacteriostatic action, whereas bactericidal action was detected at higher concentrations, this might be due to increased intracellular uptake of the extract and more cellular damage. The antagonistic effect of the combination of ethanol extracts of S. libanotica and R. officinalis was the major finding of our study; this finding is in agreement with other previous study by Abu-Shanab et al. (2006). Therefore, the combination of both previous extracts which are traditionally used in Jordan against number of diseases obviously has no efficient antibacterial effect.

5. Conclusion

Our previous study by Ibrahim *et al.* (2013) showed the inhibitory action of crud extract of *S. libanotica* and *R. officinalis* against two test strains of *S. aureus;* therefore, and depending on the previous results, we tested the antibacterial effect of *S. libanotica* and *R. officinalis* against clinical and community strains of MRSA as a second phase. The results presented here indicate that *R. officinalis* and *S. libanotica* extract preparations can be used as antistaphylococcal agent, for both MSSA and MRSA infections. *In vivo* assessment of the dose, toxicity, tolerance and clearance of the active elements of the herbal plants need more investigations.

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Molecular Identification of *Trametes* Species Collected from Ondo and Oyo States, Nigeria

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Abstract

Internal Transcribed Spacer (ITS) region of the rDNA was used in the identification of *Trametes* species collected from Nigeria. Ribosomal DNA of *Trametes* species were extracted using CTAB lysis method. The extracted DNAs were amplified using ITS region and the amplicons sequenced. BLAST search on NCBI GenBank revealed that *Trametes* species from Nigeria are more related to *T. lactinea*, *T. elegans*, *T. polyzona*, *T. cingulata* and *T. ijubarskii* with percentage relationship of 96 to 99%. Phylogenetic tree generated from *Trametes* sequences from Nigeria and sequences obtained from NCBI GenBank revealed 7 clades, out of which *Trametes* from Nigeria were placed in 3 separate clades. This study showed that most of the gene sequences of *Trametes* species indigenous to Nigeria are not 100% homologous with existing gene sequence found in NCBI GenBank. The closest *Trametes* species to the *Trametes* species indigenous to Nigeria are *T. lactinea* and *T. polyzona* with 99% level of similarity.

Keywords: Trametes species, Nigeria, rDNA, ITS.

1. Introduction

For centuries, mushrooms have been appreciated as sources of food nutrients and pharmacologically important compounds useful in medicine. Mushrooms are known to be medically active in several therapies, such as antioxidant. antitumor, antibacterial, antiviral. hematological and immunomodulation (Wasser and Weis, 1999; Lindequist et al., 2005). The above health promoting properties of mushrooms have been attributed to the presence of some bioactive compounds such as glycolipids, compounds derived from shikimic acid, aromatic phenols, fatty acid derivatives, polyacetylamine, polyketides, nucleosides, sesterterpenes, polysaccharides and many other substances of different origins (Lorenzen and Anke, 1998; Wasser and Weis, 1999; Mizuno, 1999; Liu, 2007).

Mushroom belonging to the following genera; Ganoderma, Tremella, Fuciformis, Lentinus, Grifola, Schizophyllum, Trametes, Cordyceps, and some others had been used in treating various ailments (Oyetayo, 2011). Both cellular components and secondary metabolites of a large number of mushrooms have been shown to boost the immune system of the host and, therefore, could be used to treat a variety of diseases (Wasser and Weis, 1999).

Trametes Fr. consist of polyporoid white rot fungi (Tomsosky et al., 2006). This genus is distinguished by a pileate basidiocarp, di- to trimitic hypha systems and a smooth non-dextroid spores (Ryvarden, 1991). It is widespread in distribution and consists of about fifty species (Kirk et al., 2008). Some species of Trametes has been used in medicine in China (Cui et al., 2011). A β glucans, krestin from cultured mycelia biomass of T. versicolor (Turkey Tail) had been reported to possess (Ikekawa 2001; Wasser, antitumor activity 2002). Antioxidant property of extracts from T. versicolor collected from Nigeria had also been reported (Oyetayoet al., 2013). In the preparation of medicinal mushrooms as functional health-aid and a nutritional supplement as well, correct identification and quality control is essential (Lee

In the last three decades, attention had been paid to the myconutraceutical potentials of macrofungi. It has been estimated that about 140,000 mushrooms are on earth, but only 14,000 (10%) are known. A large number of the unknown species exists in major parts of Africa because there are no records available on mushrooms that are indigenous to this part of the globe. Identification of mushrooms is mainly done by morphological description of the fruiting bodies, host specificity, and geographical distribution (Seo and Kirk, 2000). In most cases, morphological characteristics have their limitations in allowing a reliable distinction of intraspecific characteristics.

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et al., 2006).Species constituting the genus *Trametes* are similar in morphology, hence it is difficult to identify and separate these species based on traditional taxonomy (Zhang *et al.*, 2006).

Molecular techniques could be used to adequately characterize and identify intra and inter specific characteristics (Zakaria*et al.*, 2009). The present study is, therefore, on the molecular characterization of wild *Trametes* species collected from Ibadan and Akure, Nigeria using ITS region of rDNA. Moreover, the phylogenetic relationship of the wild *Trametes* species was compared with existing *Trametes* sequences obtained from NCBI GenBank was also ascertained.

2. Materials and Methods

2.1. Fungal Material

Fruit bodies of Trametes species were collected from Oyo and Ondo States, Nigeria, between September 2012 and July 2013. The fruit bodies were kept dry in tissue papers that were placed in a polythene paper containing silica gel. The polythene bags containing the samples were well labeled for easy identification and taken to the laboratory for further examination. Herbarium samples of Trametes species fruit bodies were kept at the herbarium of Institute of Microbiology, Chinese Academy of Sciences, Beijing.

2.2. Extraction of DNA

Standard DNA isolation methods employing Cetyltrimethyl ammonium(CTAB) lysis buffer (Zolan and Pukkila 1986) were used. Briefly, dried portions of Trametes fruit bodies (2g) were ground with a mortar and pestle. The grounded materials were transferred into well labeled microtubes. Pre-warmed (600C) extraction buffer (CTAB) was added and the tubes were incubated at 650 C for 30 to 60 min. Equal volume of chloroform and alcohol (24:1) was added and mixed by inverting tubes for 15 min. The tubes were centrifuged for 10 min at 10,000 g (13000 rpm). The process was repeated, but the time of mixing was 3 min and the time of centrifugation was 5 min at the same speed referred to above. Upper aqueous layers were removed into clean tubes and 40µl Sodium acetate (NaAc) was added followed by 260µl of cold isopropanol. This was gently mixed by inverting tubes. The tubes were incubated at -200 C overnight. On the second day, the mixture was centrifuged at 10,000 g (13000 rpm) for 10 min. The supernatant was discarded and pellets rinsed with 70% alcohol and mixed for sometimes. This procedure was repeated three times. After discarding the supernatant, the sample was dried in a dryer for 20 min at room temperature. Pellets were resuspended in 30µl of Tris EDTA (TE) buffer. DNA concentration and quality were checked by observing the band on an ethidium-stained agarose gel (0.7%) using 0.2µl of each sample.

2.3. PCR Amplification of the ITS Region

The entire region of rDNA of *Trametes* species was amplified by PCR using the primers, ITS4 and ITS5. The

reaction mix was made up to a total volume of 25 μ l, composed of 23 μ l of Taq polymerase "Ready to Go" mixture (Pharmacia, Sweden) with 0.2 μ l of each primer (100 pM) and 2 μ l of DNA solution. The tubes were placed in a thermal cycler (GenAmp PCR System 2400, Perkin–Elmer, USA) for amplification under the following conditions: 30 cycles of (1) denaturation at 95°C for 30 s, (2) annealing at 50°C for 1 min, (3) extension at 72°C for 1 min. The amplification products were purified using a PCR Purification Kit (USA) and electrophoresed on ethidium-stained agarose gel (0.7%) to check the purity. DNA sequencing was performed using the same primer pair used in the PCR reactions (ITS 4 and ITS 5) in an Applied Biosystem DNA Analyser (USA).

2.4. Alignment of Sequence

Alignments were performed with the Clustal W package (Thompson et al., 1997). The aligned sequences were corrected manually and through focusing on gap positions. DNA sequence data were analyzed to provide pairwise percentage sequence divergence. The data obtained from the sequence alignment were used to plot a tree diagram (MEGA 4 Software).

3. Results

Internal transcribed spacer (ITS) region of the nuclear rDNA sequences of the 19 *Trametes* specimens was used for molecular identification. The ITS discriminated between all the *Trametes* species collected from Ondo and Oyo States, Nigeria and *Trametes* species sequences obtained from NCBI GenBank (Table 1). The level of relatedness of *Trametes* species collected in Nigeria and the already existing gene sequences of *Trametes* species in NCBI GenBank ranges between 96 to 99% (Table 1).

The closest relatives of *Trametes* species designated specimens 1 to 19 collected from Nigeria were *Tramete* slactinea, *T. elegans*, *T. polyzona*, *T. cingulata* and *T. ijubarskii* (Table 1).

Phylogenetic tree generated from the gene sequence of Trametes species collected from Nigeria and the sequences from NCBI GenBank showed a marked difference. A total of 8 clades were generated in the final phylogenetic tree (Figure 1). A clade is made up of organisms from the same ancestral stock (Dupuis, 1984). Clade 1 has Trametes species collected from Nigeria and designated specimens 5, 12, 18, 24, 25 and 26 placed alongside macrofungi such as Trametes lactinea, Trametes elegans, Trametes cubensis, Lenzites elegans and Pycnoporus sanguineus. Clade 2 is made up of made up of Trametes cubensis (JN164923.1); Trametes sp. (HQ916734.1); Lenzitese legans (HQ248217.1) is placed in clade 3 while clades 4 and 5 are made up of Trametes menziesii (JN645071.1) and four Trametes sanguine(with numbers JN164981.1, JN164982.1, ascension KC243780.1, JX082366.1) respectively. Three separate clades (6, 7 and 8) were observed for Trametes species collected in Nigeria.

Table 1. Genomic identification of Trametes species collected from Nigeria based on ITS Region of rDNA

| | - | - | - | |
|----------|--------------------|---------------------|------------------|----------------------|
| Specimen | Tentative Identity | Closest Relative | Accession Number | % Level of Closeness |
| 1 | Trametes sp | Trametes polyzona | JN164978.1 | 99 |
| 2 | Trametes sp | Trametes ijubarskii | AY684174.2 | 96 |
| 3 | Trametes sp | Trametes lactinea | JN048769.1 | 99 |
| 4 | Trametes sp | Trametes polyzona | JN164980.1 | 99 |
| 5 | Trametes sp | Trametes lactinea | JN048769.1 | 99 |
| 6 | Trametes sp | Trametes polyzona | JN164980.1 | 99 |
| 7 | Trametes sp | Trametes lactinea | JN048769.1 | 99 |
| 8 | Trametes sp | Trametes elegans | JN164921.1 | 98 |
| 9 | Trametes sp | Trametes elegans | JN164921.1 | 98 |
| 10 | Trametes sp | Trametes elegans | JN048766.1 | 98 |
| 11 | Trametes sp | Trametes lactinea | JN048769.1 | 99 |
| 12 | Trametes sp | Trametes lactinea | JN048769.1 | 99 |
| 13 | Trametes sp | Trametes lactinea | JN048769.1 | 99 |
| 14 | Trametes sp | Trametes polyzona | JN164978.1 | 99 |
| 15 | Trametes sp | Trametes elegans | JN048766.1 | 98 |
| 16 | Trametes sp | Trametes elegans | JN164978.1 | 99 |
| 17 | Trametes sp | Trametes polyzona | JN164978.1 | 99 |
| 18 | Trametes sp | Trametes elegans | JN048766.1 | 98 |
| 19 | Trametes sp | Trametes cingulata | JN645075.1 | 98 |
| | - | 0 | | |

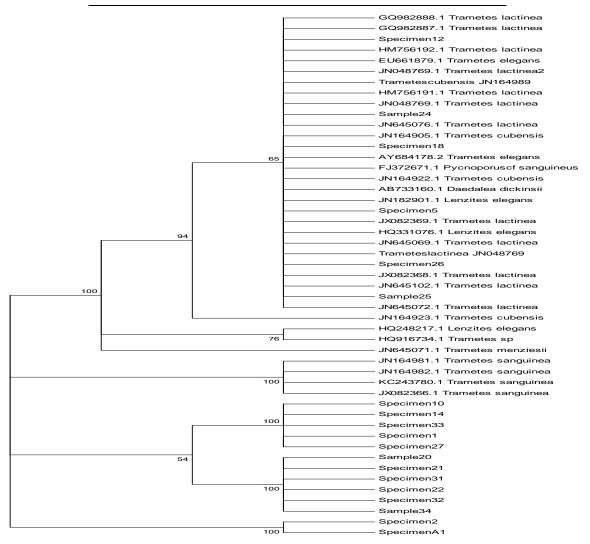


Figure 1. Phylogenetic tree of the genus Trametes species collected from Nigeria based on sequences of the ITS Region

4. Discussion

Trametes is regarded as one of the most confused group of genera in Polyporaceae (Cui et al., 2011). Zhang et al. (2006) had earlier questioned the current taxonomy of Trametes. Hence, mycologists have attempted to use sequence data to resolve the taxonomic problems in Trametes and in the related genera (Ko and Jung, 1999; Tomšovský et al., 2006; Zhang et al., 2006; Miettinen and Larsson, 2010). Analysis of the ITS region of the nuclear rDNA of Trametes species collected from Nigeria revealed the genetic difference in the 19 Trametes species and the Trametes species sequences obtained from NCBI GenBank (Table 1). The ITS region of rDNA has been reported to be the most used genomic region for molecular characterization of fungi (Gardes and Bruns, 1993). The ITS region of Nuclear rDNA has several characteristics making it a pertinent tool to identify and analyse phylogenetic molecules of fungi at species level (Anderson and Stasovski, 1992; Gardes and Bruns, 1993).ITS sequences are useful in distinguishing the genera with similar morphological characteristics (Cui et al., 2011). Moreover, the core structure of ITS is conserved in the mature rRNA molecules, and it is much diverse in both sequence and size (Lalev and Nazar, 1998).

Trametes species designated specimens 1, 2, 4, 6, 8, 9, 10, 14, 15, 16, 17, 18 and 19 were placed in three different clades. This shows that the macrofungi are not from the same ancestral stock with Trametes species whose sequences are already in NCBI GenBank. In an earlier study on the phylogeny of European and one American species of the genus Trametes, all Trametes species except T. cervina were reported to form a clade (Tomsovsky et al., 2006). Similarly, in a phylogenetic tree generated by Zhang et al. (2006) Trametes species was separated from other groups and most strains of T. versicolor formed a single clade with a high percentage support. However, Trametes species designated specimens 3, 5, 7, 11, 12 and 13 were placed in the same clade with T. lactinea and T. cubensis. This shows that they are more related to these two species.

This study revealed that most of the gene sequences of *Trametes* species indigenous to Nigeria are not 100% homologous with existing gene sequence found in NCBI GenBank. The difference in the gene sequences of *Trametes* species from Nigeria and its counterpart from other parts of the world maybe due to the different ecological zones where they exist. In a recent report, Wu *et al.* (2013) stated that geographic distance is the dominant factor driving variation in fungal diversity at a regional scale (1000–4000 km), where as environmental factors (total potassium and total nitrogen) explain variation in fungal diversity at a local scale (<1000 km). The closest *Trametes* species to the *Trametes* species indigenous to Nigeria are *T. lactinea* and *T. polyzona* with 99% level of similarity.

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Coronary Atherosclerosis: Adiponectin and Leptin as Predictors of Disease Severity

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Abstract

Adipose tissue is known to produce and release numerous bioactive substances, known as adipokines (such as leptin and adiponectin), which have been found to be involved in various physiological processes, including the regulation of arterial tone and they are related to cardiovascular risk factors. The objective of the present study was to determine the relationship between the levels of serum leptin and adiponectin and the degree of coronary heart disease, also, to compare the sensitivity and specificity of serum circulating levels of the these two biomarkers in CAD diagnosis. Forty nine patients with established coronary artery disease (CAD) defined as old myocardial infarction and angina pectoris classified as CAD group. The control group included twenty normal healthy subjects. All patients and controls were subjected to complete clinical history taking, clinical examination including 12 lead electrocardiograms (ECG), diagnostic coronary angiography (CA) and the colorimetric measurement of serum levels of triacylglycerols (TGs), total cholesterol (total-C), low density lipoprotein-cholesterol (LDL-C), high density lipoprotein-cholesterol (HDL-C), also, ELISA for measurement of leptin and adiponectin. The predictors of coronary atherosclerosis severity include higher LDL-C, low serum adiponectin level, higher leptin level and previous myocardial infarction. Serum levels of leptin, LDL-C and total-C showed highly significant (p < 0.0001) increase, while, adiponectin levels showed highly significant (p < 0.0001) decrease in the group of patients when compared to the levels of the control group. The levels of HDL-C in the group of patients were significantly (p < 0.05) lower than in the control group. There was no significant difference between the levels of TGs in the patients versus the controls. The levels of leptin showed negatively significant correlation with the levels of adiponectin (r=0.76, p < 0.001), it was positively significant with the levels of LDL-C (r=0.302, p = 0.035), while, there was no significant correlation between the levels of leptin and HDL-C and the levels of adiponectin and HDL-C, there was a weak but significant correlation between the levels of serum adiponectin and LDL-C (r=0.2, p=0.001). The overall positive rates obtained from Receiver Operating Characteristic (ROC) curve for evolution of sensitivity and specificity of the different biomarkers is obtained. The sensitivity was 100% for both leptin and adiponectin. ROC curve results revealed that the specificity for leptin and adiponectin were 100% and 90%, respectively. The results obtained in the present study indicate that serum leptin and adiponectin might play an important pathogenic role not only in the occurrence but also in the severity of CAD. The circulating level of leptin provides highly specific biomarker for CAD more than adiponectin.

Keywords: Adiponectin, Leptin, Coronary Artery Disease

1. Introduction

White adipose tissue stores excess energy in the form of triglycerides, while brown adipose tissue is actively involved in the regulation of body temperature (Mariman and Wang, 2010). Recent studies have shown that adipose tissue is an active endocrine and paracrine organ secreting several mediators called adipokines. Adipokines include hormones, inflammatory cytokines and other proteins (Nele and Johan, 2011). These adipokines include hormones as leptin and adiponectin, inflammatory cytokines as tumor necrosis factor α , interleukin-6 and other proteins as plasminogen activator inhibitor-1, angiotensinogen and resistin (Wozniak *et al.*, 2009).

Furthermore, adipose tissue is known to release an unidentified adipocyte-derived relaxing factor (Löhn *et al.*, 2002), which relaxes several arteries. Leptin is an ob

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gene-expressed protein mainly secreted by adipose tissues, with a primary role of inhibiting food intake, modulating weight balance and promoting energy metabolism (Brubeck, 2006).

Previous research has revealed that leptin is a stress mediator after injuries, and it proceeds to maintain homeostasis by accelerating oxidation of glucose and fatty acids, alleviating reactive oxygen species-induced apoptosis, and ameliorating post-septic multiple organ dysfunction (Eguchi *et al.*, 2008, Lin *et al.*, 2007).

Several experimental studies have shown that increased leptin level may directly or indirectly exert multiple actions at the cardiovascular level (Beltowski, 2006), where leptin receptors have been identified in various peripheral tissues, including the cardiovascular system and in human coronaries; it seems to have both vasodilatory and vasoconstrictory actions on vascular smooth muscle (Quehenberger *et al.*, 2002).

Furthermore, leptin is involved in a number of diverse physiological processes, such as regulation of endocrine functions, inflammation, immune response, reproduction and angiogenesis (Otero *et al.*, 2005). Several studies have found a significant association between circulating plasma leptin with insulin resistance and inflammatory markers, suggesting leptin as a risk factor for cardiovascular disease (Van Dielen *et al.*, 2001).

Adiponectin is a protein hormone secreted by adipocytes; it binds to two different seven transmembrane domain receptors called AdipoR1 and AdipoR2. AdipoR1 is predominantly expressed in skeletal muscles, whereas AdipoR2 is predominantly expressed in liver and throughout the brain (Bjursell *et al.*, 2007). Many other cells have adiponectin receptors as macrophages, osteoblasts, adipocytes, endothelial and muscular cells of the vascular wall, pancreatic cells and central nervous system (Zhou *et al.*, 2005).

Adiponectin has been considered an antiinflammatory and antioxidative adipokine that protects against cardiovascular disease (Antoniades et al., 2009). Plasma adiponectin has been correlated with endotheliumdependent vasorelaxation in humans (Tan et al., 2004). These results were confirmed by other studies that have shown an increase in NO production as well as NOmediated and potassium channel-mediated (voltagedependent) vasorelaxation in rats by adiponectin (Greenstein et al., 2009, Xi et al., 2005, Fésüs et al., 2007). Increased NO production inhibits platelet aggregation, leucocyte adhesion to endothelial cells and vascular smooth muscle cell proliferation. Furthermore, it reduces oxidative stress by decreasing ROS production in endothelial cells. All of these effects protect the vascular system against endothelial dysfunction (Antoniades et al., 2009).

The aim of the present study is to determine the relationship between the levels of serum leptin & adiponectin and the degree of coronary heart disease; also, to compare the sensitivity and specificity of serum

circulating levels of these two biomarkers in CAD diagnosis.

2. Materials and Methods

2.1. Patients And Study Protocol

The criteria for the diagnosis of CAD include myocardial infarction and angina pectoris based on the clinical history, ECG and diagnostic coronary angiography (CA) was carried out on forty nine consecutive patients with age ranging between 50-65 years with mean ±SD of 59.175±3.112 years (31 males and 18 females) who were selected from the Interventional Cardiology Department, Istishari Hospital to participate in the current study, the duration between the onset of disease and the time of performing the assay of the biomarkers was ranging between 90-270 days with mean ±SD of 136.48±4.96 day. The control group included 10 normal healthy subjects with age ranging between 54-61 years with mean ±SD of 57.200±2.573 years (17 males and 3 females) who were non-diabetic, non-hypertensive, with no history of previous CAD; having normal ECG and normal (CA). A written informed consent was obtained from each participant. All patients and the control groups were subjected to diagnostic coronary angiography (CA) in Cath-Lab of Interventional Cardiology Department, Istishari Hospital and the biochemical analyses were carried out in the Biochemistry and Molecular Biology Department, Faculty of Medicine, Mu'tah University.

2.2. Diagnostic Coronary Angiography (CA)

It was done for all participants using a flat-panel imaging system. All subjects were fasting and sedated. It was performed from the femoral artery approach. After local groin infiltration of 10-20 ml xylocaine 2% using modified seldinger's technique and injection of 5000 IU of Heparin, 6F JL then JR coronary catheters were used to engage the corresponding arteries. The study was conducted with a General Electric Innova 2000 angiographic unit (GE medical system Milwaukee, WI, USA). The selection criteria of the patients were presence of more than 50% of coronary lesions in their angiographic projections and normal (CA) to be used as a control group.

2.3. Laboratory Measurements

Blood samples were drawn after an overnight fast from each patient of the test group and each healthy subject of the control group. Each blood sample was centrifuged to collect serum, which was stored at -200C till the time of analysis. Total-C, HDL-C and TGs were measured by enzymatic colorimetric methods as described by Richmond (1973), Gordon et al. (1977) and Jacobs and Vandemark (1960), respectively, using reagents from (Human Gesellschaft fur Biochemica Diagnostica mbH, Germany). LDL-C was calculated by Friedewald's formula (Friedewald *et al.*, 1972). Leptin was measured using Human Leptin ELISA kit (SRL, Tokyo) and adiponectin was estimated using Human Adiponectin ELISA kit (Otsuka Pharmaceutical Inc., Tokyo), as described by Engvall *et al.* (1971).

2.4. Statistical Analysis

All data were analyzed using analysis of variance (ANOVA) test for the comparison between the different means of variables and the data summarized as mean and standard deviation (mean \pm SD). Correlation between different numerical variables was done using Spearman correlation test (r). Differences were accepted as significant at p<0.05. ROC curve analysis was done using MedCalc software for evolution of sensitivity and specificity of the different biomarkers.

3. Results

The biochemical parameters of the patients' group versus the control group are presented in Table 1, in the form of mean \pm SD. The results showed highly significant (*p*< 0.0001) increase in the levels of leptin, LDL-C and total-C of the CAD group versus the control group, also, there was highly significant (*p*< 0.0001) decrease in the levels of adiponectin of patients when compared to the controls. HDL-C values revealed a significant (*p*< 0.05) decrease for CAD group in respect to the control group, while, the values of TGs showed insignificant difference (*p*=0.0871).

 Table 1.Baseline biochemical parameters of CHD and control groups

| Parameter | CAD group (n=49) | Control group (n=20) |
|-------------------------------------|------------------|-------------------------|
| Leptin (ng/mL) ^a | 27.72±4.28* | 12.75±1.72 |
| Adiponectin (µg/dL) ^a | 7.23±1.01* | 12.12±1.14 |
| TGs (mg/dL) ^a | 298.562±30.34** | 237.95±8.73 |
| LDL-C (mg/dL) ^a | 148.24±6.16* | 105.09 ± 5.32 |
| HDL-C (mg/dL) ^a | 32.10±2.07*** | 37.18±3.24 |
| Total-C (mg/dL) ^a | 289.37±23.68* | 187.31±2.38 |
| | | |

^a Values were expressed as mean \pm standard deviation (SD), *=P < 0.0001 is highly significant, **=P > 0.05 is insignificant and ***=P < 0.05 is significant when compared with the values of the control group.

In CAD group, the obtained results revealed a negatively significant correlation between the levels of serum leptin and adiponectin (r=0.76, p<0.001), positively significant correlation between the levels of serum leptin and LDL-C (r=0.302, p=0.035), while, there was no significant correlation between levels of leptin and HDL-C (r=0.011, p=0.94) & the levels of adiponectin and HDL-C (r=0.007, p=0.96), there was a weak significant correlation between the levels of serum adiponectin and LDL-C (r=0.2, p=0.001) (Figure 1).

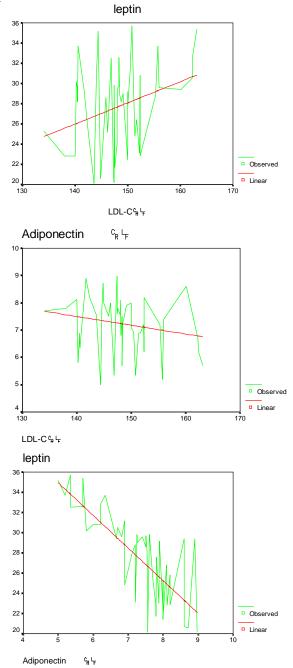


Figure 1.Correlations between some of the biochemical parameters of the study (CAD) group

Table 2 shows the area under the ROC curves for leptin and adiponectin in (1.00 and 0.00 for the two parameters, respectively). Also, the optimal cutoff value of leptin (27.7 ng/mL) (sensitivity 100% and specificity 100%) (Figure 2), of adiponectin ($7.6\mu g/dL$) (sensitivity 100% and specificity 90%) (Figure 3)

Table 2. Area under the (ROC) curves for the two parameters

| | Asymptotic 95% Confider Interval | | | |
|-------|-------------------------------------|---------------------------------|--|--|
| Area | Lower Bound | Upper Bound | | |
| 1.000 | 1.000 | 1.000 | | |
| 0.000 | 0.000 | 0.000 | | |
| | 1.000 | In Area Lower Bound 1.000 1.000 | | |

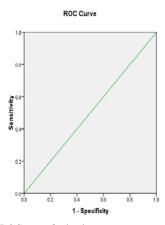


Figure 2.ROC curve for leptin.

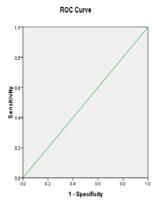


Figure 3. ROC curve for adiponectin

4. Discussion

Leptin and adiponectin differ from almost all other adipocytokines in being secreted exclusively by adipocytes, the details of all the factors regulating their synthesis, secretion and clearance remain incomplete (Finucane *et al.*, 2009).

Adiponectin is a 244 amino acid protein (Sattar *et al.*, 2009). It has been shown to have several beneficial effects in the cardiovascular system including an essential role in the maintenance of heart architecture, as the cytokine may attenuate angiotensin II-induced cardiac hypertrophy (Shibata *et al.*, 2004). Also, it represses atherosclerotic lesions in a mouse model of atherosclerosis and adiponectin-deficient mice exhibit an accelerated vascular remodeling response to injury (Ouchi *et al.*, 2003).

In addition, adiponectin stimulates nitric oxide production in endothelial cells through AMPK-dependent and AMPK-independent phosphorylation of endothelial nitric oxide synthase (eNOS) (Cheng *et al.*, 2007) and hypoadiponectinemia is associated with the progression of left ventricular hypertrophy (LVH), which is accompanied by diastolic dysfunction (Hong *et al.*, 2004).

Through the induction of cAMP-activated protein kinase, adiponectin can stimulate glucose uptake by muscles, fatty acids oxidation in muscles and liver, also, decrease hepatic glucose production, cholesterol and triacylglycerols synthesis and lipogenesis (Ouchi *et al.*, 2000). Therefore, increased blood lipid concentrations in this study may be explained by our results which showed decreased adiponectin concentrations in the CAD group of patients.

Although whether low levels of adiponectin predict hypertension remains controversial (Asferg *et al.*, 2010) and whether adiponectin levels in hypertension are decreased (Adamczak *et al.*, 2003), low adiponectin levels might contribute to the pathogenesis of obesity-related hypertension.

This study confirms the previous reports (Hara et al., 2007, Selcuk et al., 2008) that plasma adiponectin levels are lower in patients with CAD and correlated significantly to the severity of disease. However, Lim et al. (2005) found no significant relation between serum adiponectin and the severity of coronary atherosclerosis. Studies in experimental animals have shown that adiponectin has the potential to inhibit neointimal formation (Jaleel et al., 2006), which is supported by the report of (Kubota et al., 2002) who stated that adiponectin-deficient mice have severe neointimal thickening and increased proliferation of vascular smooth muscle cells in mechanically injured arteries that can be attenuated by adenovirus-mediated adiponectin administration (Matsuda et al., 2002). Our findings show that the levels of adiponectin are correlated positively and negatively with the values of HDL-C and LDL-C values, respectively, in CAD group which is in agreement with the results obtained by Yutaka et al. (2011).

Adiponectin suppresses lipid accumulation in macrophages, resulting in markedly decreased uptake of oxidized LDL and inhibition of foam cell formation which provides vasculoprotection through improvement of lipid metabolism (Ouchi et al., 2001), which is supporting the results obtained in the present study. The group of patients showed increase in the levels of total cholesterol, LDL-C and triacylglycerols, while, the levels of HDL-C is decreased with the decrease in the levels of adiponectin. The mechanism by which adiponectin influences lipid metabolism suggests that the positive effects of adiponectin on HDL levels which might result from its significant positive relationship with lipoprotein lipase activity. Furthermore, the discussion about the mechanism of adiponectin in atherosclerosis is inappropriate because of a lack of direct data regarding this issue. Nevertheless, these reported findings, with the present results, indicate that lower levels of adiponectin may provide certain information for predicting CAD (Yutaka et al., 2011).

Leptin is a 26 kDa (Von *et al.*, 2004), almost exclusively secreted by white and brown adipocytes (Buyse *et al.*, 2001). Its expression and secretion are also regulated by a variety of other factors; for example, leptin is increased by insulin, glucocorticoids, TNF- α , and estrogen (Ouchi *et al.*, 2001). Under normal conditions; leptin contributes to blood pressure homeostasis by its vasorelaxing and vasocontractile effects (Lembo *et al.*, 2000). While the contractile effect of leptin is attributed to sympathetic nervous system activation (Frühbeck, 1999). Various mechanisms seem to be responsible for leptininduced vasorelaxation. This latter effect can be endothelium-dependent, either through the release of NO (Vecchione *et al.*, 2002) or by other mechanisms (Matsuda *et al.*, 2003). The vascular effects in an isolated preparation are independent of any neutrally mediated actions of leptin. They are consistent with several previous researches demonstrating leptin-induced vasodilatation of coronary artery in humans and activation of endothelial nitric oxide production in human aortic endothelial cells (Matsuda *et al.*, 2003).

The administration of leptin may increase oxidative stress *in vitro* cultured human endothelial cells (Bouloumie *et al.*, 2002). The increase in oxidative stress may interact with nitric oxide to form peroxy nitrite and thereby, decrease the bioavailability of nitric oxide, which is associated with an impairment of endotheliumdependent vasodilatation (Cooke and Oka, 2002).

Leptin stimulates synthesis of endothelin-1, a potent vasoconstrictor and mitogen (Quehenberger *et al.*, 2002). Also, under effect of leptin, there is increase in the secretion of lipoprotein lipase enzyme in macrophages (Maingrette and Renier, 2003), and accumulation of cholesterol esters in the foam cells especially at high plasma glucose concentration (O' Rourke *et al.*, 2001). There is a positive correlation between leptin and plasma concentration of fibrinogen and von Willebrand factor (Thogersen *et al.*, 2004) and leptin promotes ADP-platelet aggregation (Corsonello *et al.*, 2003).

Leptin may also activate adult human progenitor cells and promote angiogenesis (Wolk *et al.*, 2005), protect macrophages from cholesterol overload (O Rourke *et al.*, 2002). The apparent discrepancy between the protective actions of leptin and its association with impaired cardiovascular outcome in the epidemiological studies can be explained by: first, the broad spectrum actions of leptin on the cardiovascular system; second, dose dependent effects of leptin; and third, the concept of selective leptin resistance (Wolk and Somers, 2006).

In the present study, the mean value of serum leptin levels of CAD group were higher when compared to the control group and inversely correlated to the levels of serum adiponectin and correlated positively with the severity of CAD. Our findings are in agreement with the reported results of Yutaka *et al.* (2011) and Wolk *et al.* (2004), also, leptin levels show positive insignificant correlations with values of HDL-C and LDL-C. However, other investigators emphasized a potential protective role in CAD (Matsuda *et al.*, 2003, Couillard *et al.*, 1998, Piemonti *et al.*, 2003).

From the results of Receiver Operating Characteristic (ROC) curve for the studied parameters, it is shown that leptin and adiponectin have the same sensitivity (100%) as biomarkers for CAD, also, leptin is more specific than adiponectin. A previous report showed that leptin levels were the most sensitive marker for predicting the accumulation cardiovascular risk factors in the general population of elementary school children (Yoshinaga *et al.*, 2008). Nakatani *et al.* (2008), reported that serum leptin was a useful biomarker of metabolic abnormalities than high molecular weight adiponectin in general male adolescents.

5. Conclusion

Serum leptin and adiponectin are biomarkers for and correlated to CAD not only in the role they might play in the pathogenesis of the disease but also in their severity and leptin is a more specific biomarker than adiponectin.

The limitation to the present study is the relatively small patients' number included in the study.

The future plan will be directed towards leptin receptor gene polymorphisms and their effects on the circulating levels of leptin and the signaling capacity of leptin.

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Fish Species Assemblages in Two Riverine Systems of Mujib Basin in Jordan and the Effects of Impoundment

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Abstract

Mujib and Haidan rivers were sampled in July 2011 to identify fish populations in the riverine system, and to investigate the impact caused by the existence of two dams. Fishes were sampled by electofishing gear through 14 sampling points distributed along the two rivers. The Mujib Dam lake was sampled by gillnets. A total of 2,854 fish specimen were caught during the study of which most consisted of native species but included small numbers of invasive species.

The native *Capoeta damascina* and *Oxynoemacheilus insignis* were found in both rivers but *Garra rufa* was only recorded below their confluence to the west. Four invasive species were recorded. The cichlids *Oreochromis aureus* and *Tilapia zillii* were sampled along Mujib River, and the African Catfish *Clarias gariepinus* and the Common Carp *Cyprinus carpio* were observed only in the lake of Mujib Dam but were not sampled. The construction of the two dams has led to significant changes in the habitats, water flow, and hydrology of the two rivers both upstream and downstream, and enhanced the colonisation of invasive species. There is, therefore, an urgent need to review the management of the system across all stakeholders and to continue monitoring on a regular basis.

Key words: Fish diversity, Conservation, Oxynoemacheilus insignis, Invasive, Impact.

1. Introduction

In arid regions, the escalating demands for water have resulted in the substantial modification of many river systems (Propst *et al.*, 2008). In conjunction with the widespread invasion of many rivers by non-native fishes, this has increased the threat of local native fish populations being extirpated and endemic fishes becoming extinct (Kingsford, 2000; Olden and Poff, 2005; Propst *et al.*, 2008).

This situation exists in most of the Jordanian water bodies because Jordan is considered the fourth world poorest country in water (Denny et al., 2008). Damming became a growing activity in the past decades, and major rivers in the country were impounded to allocate water for domestic use. Two of these major rivers are the Mujib and Haidan, both located within the Mujib Basin [Centre coordinates: E 36° 1' 35" N 31° 9' 52"] flowing from east to west before entering the Dead Sea. In 2002 and 2003, two dams were constructed on the Haidan (Waleh Dam) and Mujib (Mujib Dam) rivers, respectively, which caused a concern for the wellbeing and long term survival of their native fish populations. The two dams were constructed to provide a regular and more sustained supply of water year round to charge the aquifer, for drinking and agricultural purposes.

Although there are few recent studies on the fresh water fish of Jordan (e.g. Hamidan and Mir, 2003; Hamidan, 2004), none of them addressed the Mujib Basin in particular except for the tentative work jointly performed by RSCN and the Limnology Department in the University of Vienna in 2001, and the Length-weight relationships assessment of the three native species in the basin (Hamidan and Britton, 2012). Details of the fish fauna of Jordan are largely confined to taxonomic revisions provided by Krupp and Schneider (1989) all of which were completed before the above rivers were impounded. The aim of the current study is to establish a baseline data on fish diversity in the two river systems, and to identify the existing and potential threats to their survival posed by changes in water flow and impoundment.

In 2003 when the reservoir was filled for the first time, fish sampling by the author revealed large numbers of introduced cichlids. Seven years later, analyses of water samples showed evidence of contamination by heavy metals (Manasreh *et al.*, 2010), after which fish monitoring was carried out by the Royal Society for the Conservation of Nature (RSCN), to assess the impact caused by the dams using the native fish populations as an indicator of impact level.

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2. Materials and Methods

2.1. Study Area

The Mujib basin (Figure 1) covers an area of 6,600 $\rm km^2$ and consists of two major sub-catchments, the Wadi Mujib catchment (4,500 $\rm km^2$), and the Wadi Wala (or Haidan) catchment (2,100 $\rm km^2$). The rivers' beds are covered in soft sediments derived from windblown, while, in the downstream area, the slopes are steep due to flush flood erosion and the comparatively more rainfall occurrence (Al-assa'd and Abdulla, 2010). Perennial flow only occurs in downstream reaches where elevations are (- 400 m) lower than the mean sea level. The elevation in Mujib basin ranges from about 950 m a.m.s.l. southern of Karak city to an approximate of 400 m below sea level at the outlet of Wadi Mujib. The two rivers were divided into three sections for the purpose of sampling:

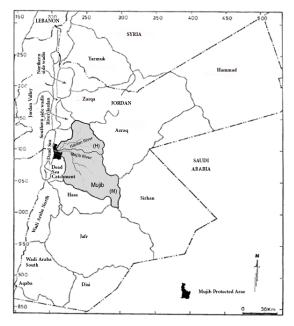


Figure 1. Location of Mujib basin in Jordan according to JICA/WAJ (Japan International Cooperation Agency/Water Authority of Jordan) (1987) Hydrologeological and water use study of the Mujib watershed, appendix (I) Final report. Amman, Jordan. Mujib Protected Area's location was added to the original map. Adapted by the author: Mujib Basin is showing the two sub-catchments: Haidan sub-catchment (H) and Mujib sub-catchment (M).

Section 1: Mujib River: This section starts from the riverhead 20 km east of the dam at Um Al-Rasas (E 35°53'46" N 31°23'59"), down to the confluence point locally known as *Malagi* with Haidan River passing through the Mujib dam. Two main wadies drain into the Mujib Dam locally known as Wadi Al-Sawalqah and Wadi Nkhailah where the southern wadi Nkhailah is completely dry, unlike the running northern wadi Al-

Sawalqah. The water within the Mujib River is shallow and there are no deep water bodies. The water current ranges between 0.6-0.8 m/s and varied according to the area of water spreading. Most of the river is heavily vegetated with reeds. The river substrate consists of small to medium sized rocks.

In 2010, after the establishment of the dam, Manasrah *et al.* investigated the contamination of water and sediment in Mujib Dam by heavy metals. Manasrah revealed that the sediments are polluted with Cadmium (Cd), relatively contaminated with Nickel (Ni), and Zink (Zn), and uncontaminated with respect to Magnesium (Mn), Led (Pb), and Cupper (Cu).

Section 2: Haidan River: The area is located in upper Haidan River west to the Walah Dam down to the confluence point. Most of the upper wadi is dry, especially the area east to the dam; water appeared west of Walah Dam (due to the recharging process the dame is applying on the aquifer). The water is being utilised for agriculture where local farms exist along this section. Continuing west toward the Dead Sea, water disappeared and the whole wadi became dry through the Mujib Protected Area deep in a basalt canyon until reaching a 45 meter height waterfall, water starts to flow with the aid of side springs supplying the river.

Water depth varies from few centimeters of flowing water to 4 metre deep ponds within the canyon areas. Current speed varies from 0 m/s up to 0.5 m/s. For agricultural purposes, water is being pumped from the river or from the dam pond to irrigate the high water consuming corps. The substrate consists of small sized rock beds to larger sized rocks within the canyon. A few areas downstream are heavily vegetated with reeds that cover the whole river area.

Section 3: Mujib and Haidan: This is the last section where both Mujib and Haidan Rivers meet then drain to the Dead Sea along 3.4 km distance through Mujib canyon, where 12 metres height water fall occurs after 1.2 km to the west of the Mujib canyon entrance. Water is shallow, and the current speed is the highest where it reaches 1 m/s in the canyon. Vegetation is minimal except for the downstream where the canyon is becoming wide (maximum of 8 metres) and vegetation of reeds, Oleander and *Typha* are the most dominant plant species. Before reaching the Dead Sea, water is converted to water treatment station, treated, and pumped for human consumption leaving behind a minimum amount of water drained to the Dead Sea.

2.2. Fish Sampling

Fish were sampled in 14 sites along the basin during July 2011. The sampling location was distributed to six sites in Mujib River section, three sites in Haidan River system, and five sites in Mujib-Haidan system downstream of the confluence point (Figure 2).

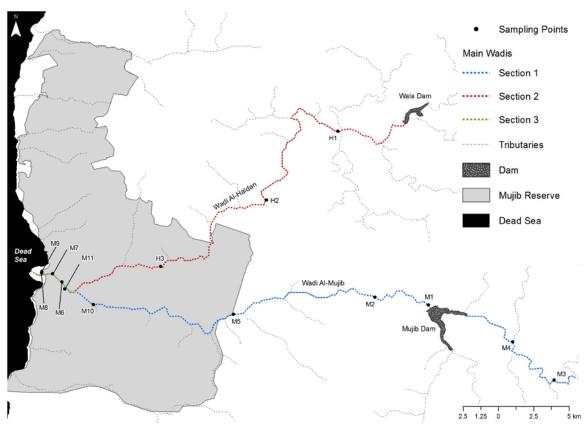


Figure 2. The study area where water was available along the two rivers, including the sampling points.

The sampling sites were designed to reflect a representative sample of habitats along each section. Sampling is comprised by battery-powered, back-mounted electric fishing gear, while gill nets of mesh sizes up to 22 mm was only used in the lake of the Mujib Dam. Once captured, fish were identified to species level, measured (standard length, SL, nearest 1 mm), weighed (to 0.01 g), and immediately released alive at the sampling site. Data on length-weight relationship were reported by Hamidan and Britton (2012). Fish standard length were categorised into 1 cm groups, and plotted against number of fish individuals in the same size group.

3. Results

A total of 2,854 specimens representing seven species were caught during the study. These species include *Capoeta damascina* (92% of total catch), *Oxynoemacheilus insignis* (6.1 %), *Garra rufa* (1.15 %), and the alien *Oreochromis aureus* (3.5%) and *Tilapia zillii* (7.02%). The African Sharptooth Catfish *Clarias gariepinus* and the Common Carp *Cyprinus carpio* were both observed in the Mujib dam lake.

Mujib River section: Four species were identified in this section including two native species *C. damascina* and *O. insignis* coexisting with two introduced cichlids *O. aureus* and *T. zillii*. The population structure of *C. damascina* was dominated by Young of the Year (YOY) fish from 10-40 mm length class, while few large specimens of length 230 mm were presented (Figure 3-A). As for *O. insignis* the population structure was dominated by medium sized fish class of 50-70 mm length (Figure 3-B).

Haidan River: large numbers of fishes were found trapped in isolated ponds as a result of flow discontinuity, while others were found dead in other ponds that were dried up completely (Figure 4). Two native species were found to inhabit this river, *C. damascina* and *O. insignis*. No introduced fish were sampled, although local fishermen assured the existence of cichlids in the river. Population structure for the *C. damascina* showed dominance of (YOY) fish of 30-40 mm length class. (Figure 3-C), while for *O. insignis* the population structure showed the dominance of YOY from the 3-4 mm length class (Figure 3-D).

Mujib-Haidan: the native *Garra rufa* appeared after the high waterfall in addition to the two native species *C. damascina* and *O. insignis.* One specimen of *T. zillii* was found close to the river mouth at point M7. *Capoeta damascina* showed a population structure dominated by YOY from 30-50 mm, few individuals from the length class 210-220 were frequently sampled (Figure 3-E). *Oxynoemacheilus insignis* population structure was found to be dominated by larger seized individuals, with few YOY presented, while *G. rufa* population structure showed a population dominated by YOY from the size class of 20-30 mm (Figure 3-F), and (Figure 3-G), respectively.

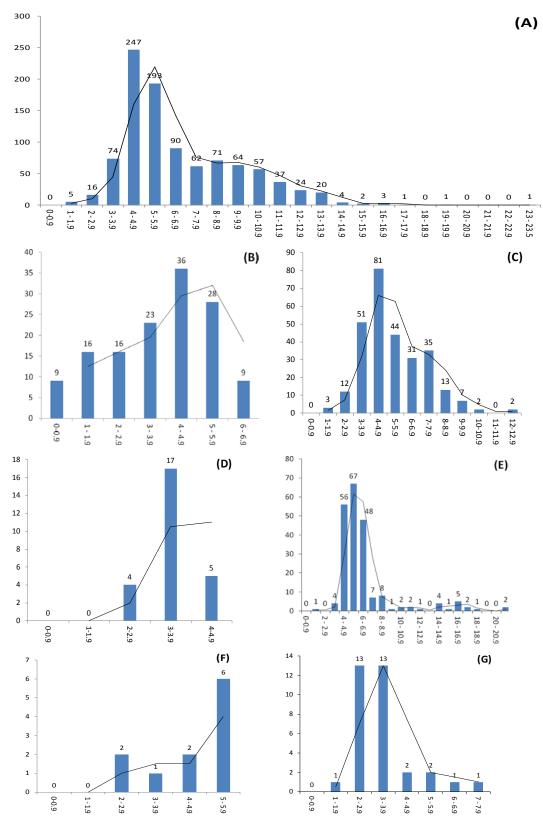


Figure 3. Population structures of native fishes in each section of the study area. Standard length is plotted on the X-axis in centimetre, and the number of individuals in each category at Y-axis. (A) Population structure of *C. damacina* in Mujib River (n=972), (B) Population structure of *O. insignis* in Mujib River (n=137), (C) Population structure of *C. damacina* in Haidan River (n=281), (D) Population structure of *O. insignis* in Haidan River (n=26), (E) Population structure of *C. damacina* in Mujib-Haidan River section (212), (F) Population structure of *O. insignis* in Mujib-Haidan River section (n= 11), and (G) Population structure of *G. rufa* in Mujib-Haidan River section (n=33).

4. Discussion

This study assures the importance of Mujib basin in hosting three populations of native species of the Jordanian ichthyofauna, including G. rufa at its southern most edge of distribution in Jordan, represented by an isolated population down to the Mujib River close to the Dead Sea. Mujib Dam is known for its high catch of fish in general among fishermen (Hamidan, Per. Comm., 2010). The low number of fish in the dam is probably due the recent introduction of the Catfish Clarias gariepinus, and the accumulative impact caused by the Common Carp, Cyprinus carpio, while Clarias gariepinus is well known for its predation of fish fry and even juveniles (Tawwab, 2005); Cyprinus carpio is the third most frequently introduced species in the world "known to be the keystone ecosystem engineer that altering habitats for native fish and other native aquatic species" as stored on the Global Invasive Species Database.

In Walah Dam, the system is different than Mujib, since the dam receives water from the rain water runoff; the water then recharges the aquifer, and no permanent rivers feed into the dam. As a result the dam lake is not a favourable habitat for native or introduced species. In addition, the dam lake dries regularly, and is mechanically cleaned. In addition to the limited accessibility to the dam, these factors reduce the chance of introducing invasive fish species. The extensive water pumping from the Haidan River over a long distance from Walah Dam west to the entrance of the river into the protected area clearly resulted with discontinuity of the water flow. A large number of fish was found dead in groups due to the gradual drying of their isolated water bodies where they were trapped (Figure 4). This, happening prior to the spawning season, resulted in the removal of breeding adults which will consequently cause the population declining at long run. This was not the case in Mujib River where the fish content and structure were healthier.



Figure 4. Number of native fish found dead along Haidan River because of drought.

In terms of the fish compositions in the river, the introduced cichlids start to appear in low numbers, where the numbers became lower when moving west. This is due to the nature of those cichlids since they are not well adapted to the fast running water, although they are well known for their great breeding potential and the explosive increases in population (Buntz and Manooch, 1968). The number of juveniles was very limited and restricted to the stagnant water on river banks, where this kind of water is regularly washed off in the seasonal floods and cause drifting of those cichlids down to the Dead Sea.

In Mujib-Haidan section, the water velocity starts to increase since the elevation is decreasing, and the well adapted bottom dweller *G. rufa* starts to appear after the natural barrier, represented by the Mujib Waterfall. The relative abundance of *O. insignis* was found to be lower than those of *G. rufa* and this could be linked to the fact that *G. rufa* is well adapted to fast running water due to its specialised mental desk. *Capoeta damascina* is still dominating the whole system since it is widely distributed in the basin and is being well adapted to both stagnant and running water.

The population structure of *C. damascina* showed healthy population dominated by YOY, which confirms the breeding success in the past season. *Oxynoemacheilus insignis* did not present such type of structure except in Haidan, however, for this species, in particular, there is almost nothing known about its biology (Krupp and Schneider, 1989); this is challenging the judgment on the species' population structure.

Several threats were identified during the present survey and earlier when the Mujib dam in particular was in operation. The first and most important impact causing factor is the controlling of the natural flow regime resulting in unexpected flooding.

Flow regime is an important determinant of the reproductive success of native and non-native fish species in regulated rivers (Brown and Ford, 2002). Controlling the flow enhances the growth of reed along the river, where it used to be washed out annually. Reed, in some location, is in high density covering the river and minimising the fish utilised habitats and forming a natural barrier along the river. The unexpected floods in summer due to cleaning processes in the dam causes significant removal of fish fry and YOY by washing them down to the Dead Sea, knowing that the period of May to June is the breeding season of the dominant *C. damascina* (Asadollah, 2011).

The dam lakes also promotes "invasive friendly receiving environment" since the introduced species, including one of the globally worst invaders, the Common Carp, which cannot adapt to the fast running water in Mujib, and/or the regular flooding cycle. The Lake of the dam makes such environment suitable for introduced species, and induces a 30-40 meters deep pool that is not known along the river system. Having no native species in the dam is only an indicator that those species (native) could be overstepped by the new invading species mainly the Common Carp and the Catfish. On the other hand, cichlids leaked to the river system out of the dam, but they did not succeed to establish a viable population because they are not adapted to such an environment.

The risk of the river has been invaded by more invasive species that can adapt to the running water and the flood cycle is not excluded. The potential expansion of catfish down the river is possible since this species is found in other running water bodies, like Zarqa River (Hamidan, personal observation, 2011). On the other hand, pollution will be - if not already is - transferred to the native and introduced fish in the dam, and consequentially to the river system down to the Dead Sea. Notes from the protected area staff show a high number of dead fish downstream from time to time.

Fishing is being practiced in and around the Mujib dam, where it is strictly illegal in the dam lake due to safety considerations. This fishing practice encouraged fishermen to introduce more high fish meat contents like Carp and Catfish, although the native C. damascina is well known to fishermen for its local name Haffaf and its taste, and is still targeted. As a result, productive individuals from the populations have been removed annually. Both dams and the surroundings are located in the "allow-hunting" area, where hunters used to target wildfowl species using the lead shots. In Mujib Dam, hunting is not allowed by the dam authority, and the lake of the dam is designed not to have any shoreline, where hunters cannot bring their hunts. A number of ducks was found dead in the dam after being shot, where they deteriorated, enriching the organic matter concentration in the impounded water. Furthermore, the type of shots that were used in hunting also enhanced the lead content in the lake of the dam, and this will eventually be transferred to fish and birds.

In conclusion, this survey confirmed the importance of Mujib-Haidan basin for three native species of Jordanian ichthyofauna. However, establishing the dams of Mujib and Walah has modified the natural water system, and blocked large amount of water behind. This water used to flow down to the Dead Sea without being controlled. In addition, the dam controls the annual flooding cycle that forms one of the major determinant features in this kind of river system. The dam indirectly facilitates the introduction of alien species including the globally third introduced species C. carpio. Currently, none of the invasive species has managed to establish viable population out of the dam lake. But potential coming threats are still possible if "fast running water" adaptive species are introduced, or if the catfish manages to escape into the river.

The major impact on the river system and the consequences of the impoundment are classified as anthropogenic factors mainly for agricultural practice, fishing, and hunting. Management of Mujib Protected Area needs to consider the integrated approach in watershed management including multi-sectorial involvement of stakeholders, while promoting both the upstream management concept, and environmental friendly and agriculturally sustainable practices.

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In Vitro Activity of Novel Metronidazole Derivatives on Larval Stages of Echinococcus granulosus

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Abstract

The effects of metronidazole (MTZ) and novel synthesized MTZ derivatives on *in vitro* cultured *Echinococcus granulosus* protoscoleces (PSCs), 30 day old segmentation stage and hydatid cysts (HC) developing secondarily in BALB/c mice were compared to those caused upon treatment with comparable doses of albandazole (ABZ) and mebendazole (MBZ) drugs. The highest protoscolicidal action resulted from the use of a non-schiff based MTZ derivative (MTZ-w: 4-[2-(2-methyl-5-nitro-1H-imidazol-1-yl) ethyoxy] benzeyldehyde). Incubation of PSCs with MTZ-w concentrations of 25, 12.5 and 6.25 µg/ml resulted in significantly higher mortality rates than those caused by ABZ or MBZ at all periods post incubation. Total mortality of PSCs always occurred one day earlier using MTZ-w. Moreover, incubation of PSCs with MTZ-w at 6.25 µg/ml concentration resulted in greater mortality of PSCs to those caused by ABZ or MTZ. Light microscopy revealed that changes in PSCs exposed to MTZ derivatives and ABZ reflected their relative actions in targeting scolex hooks, suckers and tegument. MTZ-w and ABZ caused rupture of hooks, deformation in suckers and disintegration in tegument of both PSCs and *in vitro* cultured segmentation stage. Less detrimental changes occurred upon the exposure to other MTZ derivatives. Exposure of HC to MTZ-w and ABZ caused regression in their size, damage in germinal membrane, fragmentation of underlining tissue, and scaling of laminated membrane. MTZ-w warrants further assessment as a potential chemotherapeutic drug against cystic echinococcosis in both animals and humans.

Keywords: Echinococcus granulosus, Protoscolex, Hydatid cysts, Albendazole, Metronidazole, Metronidazole derivatives.

1. Introduction

Cystic echinococcosis (CE) or unilocular hydatidosis is a cosmopolitan cyclozoonotic helminthic disease of livestock and humans with great public health and economic effects in various continents. While it is currently spreading into new developing countries and increasing in prevalence, CE is still classified with the emerging or re-emerging neglected diseases (Moro and Schantz, 2009; McManus, 2010; Da Silva, 2010).

The disease is caused by the ingestion of embryonated eggs of the tiny dog tapeworm *Echinococcus granulosus* (Eucestoda, Platyhelminthes) whose adult stage inhabits the small intestine of dogs, or any of the canid family as the main definitive host. In livestock and humans, unilocular hydatid cysts (HC) develop in various visceral organs – mainly liver and lungs. Each HC contains an outer a cellular laminated layer (LL) and inner cellular germinal layer (GL) that undergoes asexual reproduction resulting in huge number of protoscoleces (PSC) in a fluid filled environment. Symptoms are often caused when cysts make mechanical pressure on the surrounding tissues and by cyst rupture and aggregated secondary infection. Moreover, spillage of cyst fluid containing PSC leads to secondary hydatidosis (Eckert and Deplazes, 2004; McManus, 2010).

Current treatment of CE depends on one or a combination of the following strategies: surgery, puncture of cyst- aspiration-injection of protoscolicidal chemicals

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and re-aspiration (PAIR), and chemotherapy (Eckert and Deplazes, 2004; Kern, 2006). However, none of these strategies is a conclusive treatment of human CE. Chemotherapeutic treatment of CE depends mainly on the use of benzimidazole compounds particularly albendazole (ABZ) and alternatively mebendazole, praziquantel and nitazoxanide (Hemphill and Muller, 2009). However, the non-optimal efficacy of these drugs, long periods of treatment needed, and the suffering caused to patients from serious side effects warrant careful search for alternative therapeutic approaches(Moro and Schantz, 2009; Hemphill and Muller, 2009; Vuitton, 2009). Chemotherapeutic applications based on the discovery of novel drugs for treatment of CE are thus needed (Vuitton, 2009; Ceballos et al., 2009; Gavidia et al., 2009). Such drugs should have selective and rapid scolicidal effects for both PSCs and HC stages with minimal local and systemic adverse effects on the host. It has been postulated that drugs which have been found to be effective against other eukaryotic protozoal and helminthic parasites and/or cancer cell lines are primary candidate choices for testing against CE (Hemphill and Muller, 2009). Metronidazole (MTZ) and many of its newly synthesized derivatives match these properties, and also have been found to inhibit certain cancer cell lines and the growth of cultured Giardia intestinalis and Entamoeba histolytica (Abu Shaireh et al., 2009; Saadeh et al., 2010; 2011).

This study was designed to investigate the effects of MTZ and many of its newly synthesized Schiff-based and non-Schiff based derivatives against freshly prepared PSC and *in vitro* cultured stages of *E. granulosus*. Moreover, the ultrastructural effects of the most effective protoscolicidal compounds on secondary HC developing in mice were explored.

2. Materials and Methods

2.1. Parasites

PSCs were isolated from the livers of infected indigenous sheep slaughtered at abattoirs in Jordan as described previously (Hijjawi et al., 1992). All steps were done under sterile conditions using a vertical laminar flow hood (Flow lab, Irvine, Scotland, UK). Infected sheep offal was washed using soap, and well defined cysts were painted three times with a solution of 1% iodine in 95% ethanol. The hydatid fluid (HF) containing PSCs was aspirated using 20 ml sterile syringe fitted with a 19g needle. PSCs were collected aseptically from the HF of fertile cyst or by scrapping the GL of fertile cysts. The viability of fertile cysts was measured as a relative number of live PSC to total number of them. At least three samples were counted to determine PSC viability with a minimum of 100 PSC/ sample. Discrimination between live and dead PSC was made using methylene blue dye as a vital stain (Gold, 1997, Liu et al., 2013). Only HC with at least 80% viability and free from bacterial contamination were used. Live PSC were separated from dead ones that were digested out using trypsin suspension solution prepared in phosphate buffer saline (PBS) in a 1:10 ratio. Trypsin treatment was made in water bath at 37°C with gentle shaking (60 cycles per minutes) for 30 min. *In vitro* culturing of freshly prepared PSCs and subsequent developing stages was carried out as described by Hijjawi *et al.* (1997). All experiments were carried out in 24 well culture plates. RPMI 1640 containing 20% (v/v) fetal calf serum (Invitrogen, Grand Island, New York, USA), 0.45% (w/v) yeast extract, 0.4% (w/v) glucose, penicillin/streptomycin suspension containing 400 IU penicillin and 400 μ g/ml streptomycin (Flow Lab, Irvine, Scotland) and amphotericin B suspension containing 400 μ g (Hyclone Labs, Thermo Scientific, Logan, Utah, USA) was used as the standard culture medium (SCM).

To prepare the first segmentation stage of *E. granulosus*, PSCs were cultured in RPMI-1640 SCM for 30 days in 160 ml culture flasks. The culture medium was changed weekly. These 30 day old cultured stages reached the first segmentation stage (S5 stage using Smyth's designation) (Smyth, 1967).

Secondary hydatidosis was developed in five BALB/c female mice which were injected subcutaneously with 1000 freshly isolated PSCs prepared in 1ml PBS (pH 7.2) when mice were two weeks old (Kakru *et al.*, 2008). After four months, mice were killed by cervical dislocation and developing HCs were dissected out from subcutaneous tissue and maintained in RPMI-1640 medium. Clumped cysts were separated individually and washed three times in PBS (pH 7.2) containing 400 IU/ml penicillin and 400 μ g/ml streptomycin before being exposed to standard drugs and chemical compounds (see below).

2.2. Drugs and Chemical Compounds

Drugs and chemical compounds (Figure 1) that were tested for their efficacy against cultured PSCs and metacestode stages include Albendazole (ABZ) [Methyl 5-propylthio-2-benzimidazolecarbamate] (Satish Joshi, Kikma Pharmaceuticals, Mumbai, India) which was used as a positive control drug of choice for the treatment of CE, Mebendazole (MBZ) [5-benzoyl-1H-benzimidazol-2yl] (Satish Joshi, Kikma Pharmaceuticals, Mumbai, India) which was used as another positive control commercial drug, Metronidazole (MTZ) [1-(2-Hydroxy-1-ethyl)-2methyl-5-nitroimidazole] (Acros Organics, New Jersey, USA) and the following novel MTZ derivatives that were prepared, purified, and characterized previously (Abu Shaireh *et al.*, 2009; Saadeh *et al.*, 2010; 2011).

(MTZ-a):(4-Fluoro-benzylidene)-[2-(2-methyl-5-nitroimidazol-1-yl)-ethyl]-amine, (MTZ-b:((4-Methyl-benzylidene)-[2-(2-methyl-5-nitro-

imidazol-1-yl)-ethyl]-amine,

(MTZ-c): (4-Methoxy-benzylidene)-[2-(2-methyl-5-nitroimidazol-1-yl)-ethyl]-amine,

(MTZ-d):(4-Nitro-benzylidene)-[2-(2-methyl-5-nitroimidazol-1-yl)-ethyl]-amine

(MTZ-e):2-{[2-(2-Methyl-5-nitro-imidazol-1-yl)-

ethylimino]-methyl}-phenol,

(MTZ-f):4-Chloro-2-{[2-(2-methyl-5-nitro-imidazol-1-yl)-ethylimi-no]-methyl} phenol,

(MTZ-g):(2-Chloro-benzylidene)-[2-(2-methyl-5-nitroimidazol-1-yl)-ethyl]-amine,

(MTZ-h):[2-(2-Methyl-5-nitro-imidazol-1-yl)-ethyl]thiophen-2-yl methylene-amine,

(MTZ-w):4-[2-(2-methyl-5-nitro-1H-imidazol-1-yl) ethyoxy] benzeyldehyde.

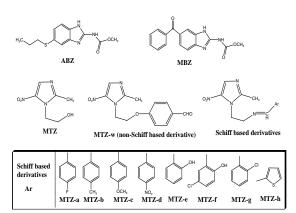


Figure 1. Schematic representation of the chemical structure of: ABZ: Albendazole; MBZ; Mebendazole; MTZ: Metronidazole MTZ derivative compounds (MTZ-w, a non-Schiff based derivative and MTZ-a - MTZ-h Schiff based derivatives).

2.3. Experimental Assays

2.3.1. Exposure of in vitro cultured PSCs and meta cestode stages to standard drugs and MTZ derivatives

For each drug or MTZ derivative, a stock of 200 µg/ml was dissolved in 50% DMSO solution that was initially prepared in sterile double distilled H2O. The stock compounds were sterilized using 0.20 µm filters (Whatman, NJ, USA). Each well received 2 ml of SCM containing 25, 12.5 or 6.25 µg/ml of each compound that was freshly prepared from the original standard drugs or chemical compound stocks. Some 2000 PSCs were added to each culture well and incubated for 13 days at 37 °C with 95% humidity and 5% CO2 in air. The pH of the cultures was adjusted to pH 7.4 at the beginning of the experiment. The PSC viability was tested daily by counting viable and dead PSC in a minimum of 50 PSC taken from each well and various drug and derivatives treatments were carried out in triplicate wells for each concentration used. Viability of PSCs was determined using methylene blue vital stain. The stain penetrates dead PSCs which appeared intensely stained with the dye. ABZ was used as positive control in addition to three negative controls: SCM, 50% DMSO solution and a combination of SCM and 50% DMSO solution in a 1:1 ratio.

2.3.2. Exposure of in Vitro Cultured First Segmentation Metacestode Stage to Standard Drugs and MTZ Derivatives

The first segmentation stages (S5 metacestodes) that were prepared upon *in vitro* culturing of PSCs for 30 days were exposed to the same drug concentrations following a similar protocol to that described above for freshly prepared PSCs. The morphological, anatomical and parasiticidal effects on the developing stages was followed for 14 days.

2.3.3. Exposure of secondarily developed HC to MTZ-w and ABZ

Five secondarily developing HCs that were isolated from BALB/c mice as described above were incubated with SCM containing 25 μ g/ml of MTZ-w for 21 days. Other HCs were incubated with a comparable concentration of ABZ that was used as a standard positive control drug, while others were incubated with a solution made of SCM and 50% DMSO in a 1:1 ratio and used as negative control.

2.4. Microscopic Examination

2.4.1. Light microscopy

Morphological and tegumentary changes in cultured PSCs subjected to various drug and MTZ derivatives were studied under light microscopy using aceto-carmine staining protocol (Meyer and Olsen, 1980). Briefly, PSCs or cultured larval stages were fixed in 10% formalin solution for at least 48 hs. The specimens were washed three times with distilled water before being dehydrated through an ascending ethanol series (35%, 50% and 70%) for 30 min each. Then, 70% ethanol was replaced by Semichon'saceto carmine stain for 30 min. Samples were washed with 70% ethanol for few seconds. Excessive staining was avoided by placing specimens in 70% ethanol containing 2-4 drops of HCL for few minutes until they differentiated well. Subsequently, specimens were washed quickly with 70% ethanol for few seconds before they were transferred to 70% ethanol with 2 drops of NaHCO3 solution and kept there for 30-60 min. Further dehydration was made through further ascending ethanol series (85%, 95% and 100%) for 15 min each. After further dehydration with 100% ethanol, samples were transported to glass vials containing xylene and kept there for at least 15 min before being mounted on a glass slide supported with one drop of Canada balsam, covered and dried.

A minimum of 25 stained specimens were examined to determine the microscopic effects of compounds on treated PSCs and *in vitro* cultured metacestode stages.

2.4.2. Scanning electron microscopy

Metacestodes that were exposed to standard positive control drugs or MTZ derivatives were picked from culture medium and washed three times with sodium cacodylate buffer (SCB) (pH 7.2) for 5 min each. Then, they were fixed in 2.5% glutaraldehyde in 0.1M SCB for four h. After washing three times with 0.1 M SCB for 5 min each, specimens were post fixed in 1% osmium tetroxide (OsO4) prepared in the same buffer for two hours. The cysts were washed further three times with SCB for 5 min each. Next, they were dehydrated through an ascending ethanol series (30, 50, 70, 90, and 100%) for 20 min each. Finally, the specimens were dried using Balzers critical point drier 0301 (Wanner et al., 2005) and sputter coated with gold on stubs. The specimens were studied and photographed using Zeiss scanning electron microscope at 20 KV on a rotator.

3. Results

3.1. In vitro effects of MTZ derivatives on fresh PSCs

Among all MTZ derivatives tested, the highest protoscolicidal action resulted from the use of MTZ-w compound in which the mortality rates were consistently higher than comparable ABZ or MBZ drug concentrations (25, 12.5 and 6.25 μ g/ml) throughout the periods of post-incubation with these compounds (Figures 2-4).

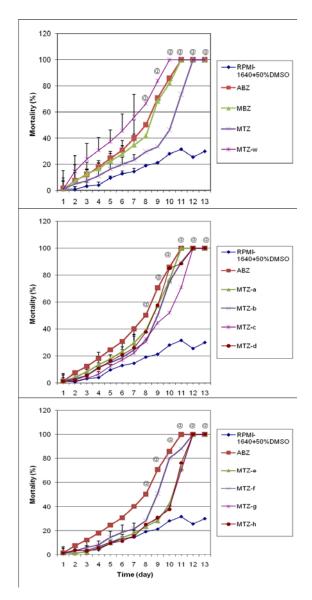


Figure 2. Mean percent mortality rates of freshly cultured *E. granulosus* PSCs with RPMI-1640 and treated with 25 μ g/ml ABZ, MBZ, MTZ or its derivatives." @: standard deviation was not placed because the values represent only one or two observations".

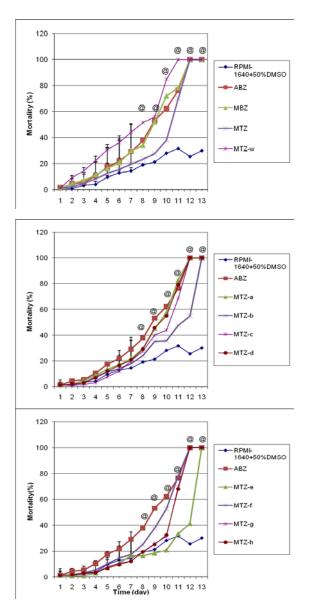


Figure 3. Mean percent mortality rates of freshly cultured *E.* granulosus PSCs with RPMI-1640 and treated with 12.5 μ g/ml ABZ, MBZ, MTZ or its derivatives." @: standard deviation was not placed because the values represent only one or two observations".

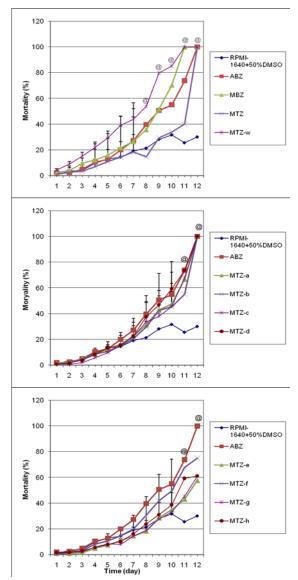


Figure 4. Mean percent mortality rates of freshly cultured *E.* granulosus PSCs with RPMI-1640 and treated with 6.25 μ g/ml ABZ, MBZ, MTZ or its derivatives." @: standard deviation was not placed because the values represent only one or two observations".

Moreover, total mortality always occurred one day earlier upon the use of MTZ-w compared to that when PSCs were exposed to ABZ. Mortality of cultured PSC in the presence of ABZ increased slowly during the first 8 days, while in the presence of MTZ-w it increased steadily in form of straight line during the same period. Thus, the death of 50% of cultured PSCs due to MTZ-w occurred at least one day prior to their exposures to comparable concentrations of ABZ or MBZ, respectively (Figures 2-4). During the early periods, incubation with 25 μ g/ ml MTZ-w resulted in 3-5 fold mortality rates that caused by the standard positive control drug ABZ as depicted in Figure 5.

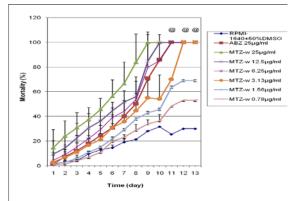


Figure 5. Mean percent mortality rates of freshly cultured *E. granulosus* PSCs with RPMI-1640 and treated with different concentration of MTZ-w compared with ABZ (+ control). "@: standard deviation was not placed because the values represent only one or two observations ".

For the three drug concentrations used, MTZ showed poor protoscolicidal effect that was significantly less than that caused by MTZ-w or ABZ. However, incubation of cultured PSCs with MTZ-a, MTZ-b and MTZ-d caused significantly less mortality values than those caused by MTZ-w but were closer to those caused by the standard positive control drug ABZ (Figures 2-4). In contrast, incubation with the three different concentrations of MTZ-c and MTZ-f was less effective in killing PSCs and MTZ-e, MTZ-g and MTZ-h were the least effective compared to other MTZ derivatives and standard drugs used.

Figure 5 shows that the protoscolicidal effect of MTZ-w followed a concentration gradient and the most effective was at concentration of 25 μ g/ml and the lowest at a concentration of 0.78 μ g/ml. Evidently, incubation with an MTZ-w concentration as low as 6.25 μ g/ml was more effective in killing PSCs than that caused by ABZ at a concentration of 25 μ g/ml.

Light microscopy of in vitro cultured stages incubated with various drugs and MTZ-derivatives for 14 days reflected the relative detrimental changes caused by these compounds. The greatest morphological changes which included disruption of scolex hooks, deformation of suckers, and disintegration of the tegument was seen in case of PSCs exposed to MTZ-w or ABZ (Figure 6). Less drastic changes in form of dentated suckers, disrupted hooks and tegument were observed when MTZ-a, MTZ-b and MTZ-d were used. The use of MTZ-c caused tegumental and scolex changes which were intermediate between those caused by the above mentioned compounds in one hand and those caused by MTZ-e, MTZ-g and MTZ-h which were the least effective (Figure 6). Incubation of cultured PSCs to MTZ-a, MTZ-f and ABZ, appeared to shift PSCs differentiation into a globose shape. The degree of degenerative changes that included disruption of hooks, rupture of tegument and peritegumental accumulation of disrupted tissue increased with time following incubation with various compounds.

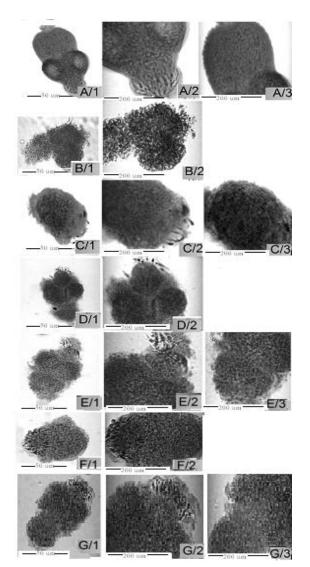


Figure 6. Light microscopy of 14 day old cultures of evaginated PSCs in RPMI-1640 incubated with 25μ g/ml ABZ,MTZ or its derivatives in 25μ g/ml: (A) RPMI-1640 represent negative control (A/1), (A/2) normal suckers and hooks, (A/3) body tegument; (B) ABZ: (B/1) ,(B/2) dentated suckers, disrupted hooks and disrupt body tegument; (C) MTZ (C/1) , (C/2) dentated suckers and disrupted hooks, (C/3) disrupted body tegument; (D) MTZ-w (D/1) , (D/2) dentated suckers, disrupted hooks and disrupted body tegument; (E) MTZ-a, MTZ-b or MTZ-d: (E/1) , (E/2) dentated suckers and disrupted hooks, (E/3) disrupted body tegument; (F) MTZ-c or MTZ-f: (F/1) , (F/2) dentated suckers and disrupted hooks, (F/3) disrupted body tegument; (G) MTZ-e, MTZ-g or MTZ-h: (G/1), (G/2) dentated suckers and normal hooks (G/3) disrupted body tegument.

3.2. Effect of MTZ and its derivatives on 30 day old cultured stages in vitro

The effects of ABZ and MTZ drugs as well as MTZ derivatives (all at 25 μ g/ml concentration) on 30 day old cultured stage(S5 developmental stage) were followed for an additional 14 days. The metacestode stages in cultures treated with ABZ, MTZ-w, MTZ-a, MTZ-b, MTZ-d and MTZ-f revealed dentated suckers and disruption of both hooks and tegument. Less detrimental effects were observed using MTZ and other derivatives.

3.3. In vitro effects of MTZ and its derivatives on secondary developing HC in mice

Figure 7 displays typical ultrastructural effects of ABZ drug and MTZ-w on metacestodes cysts that were incubated in RPMI-1640 containing 25 μ g/ml of each compound. During culturing and incubation with these compounds, HC regressed in size. Under SEM, the wall of HC incubated with RPMI-1640 appeared intact with smoothly lined LL and GL with intact tegument. In contrast, ABZ treated HC showed damaged GL, fragmentation of underlining tissue and scaling of LL with oval depressions that appear to lead to the involution and regression in HC size. HC incubated in MTZ-w revealed greater dentated damage in GL and more patchy LL with many deep depressions than those seen in cysts treated with ABZ.

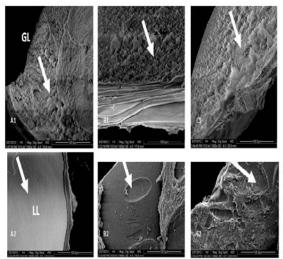


Figure 7. Scanning electron microscopy of laminated (LL) and germinal layer (GL) of secondary hydatid cysts developing in BALB /C mice 14 weeks post subcutaneous inoculation with PSCs: Cysts were incubated for 21 days in following media and compounds: RPMI-1640 as negative control showing intact GL (A1) and LL (A2) with remnants of host tissues towards the periphery of LL; RPMI- 1640 containing 25 μ g/ml ABZ as positive control showing scaling of LL (B1), oval depressions and damaged GL with fragmented cellular elements (B2); RPMI- 1640 containing 25 μ g/ml MTZ-w showing carpet like appearance of GL with dentated endings (C1), and fragmentation of LL with many deep depressions and patchy appearance (C2).

4. Discussion

The present study documented for the first time the effects of several Schiff based and non-Schiff based MTZ derivatives on cultured *E. granulosus* PSCs and subsequent *in vitro* cultured stages. Indeed, one of the non-Schiff based MTZ derivative, MTZ-w, revealed remarkable activity and showed more protoscolicidal activity than ABZ, the drug of choice in CE treatment, even at one fourth the concentration of the latter drug. The mortality of PSCs and metacestode stages exposed to MTZ-w was about twice than ABZ at the same concentration and exceeded three times that of ABZ during early periods of exposure. Moreover, the damaging effects on hydatid cyst LL and GL incubated with MTZ-w was more than that on those incubated with ABZ at the

same concentration. In terms of molarity, exposure of PSCs and other *in vitro* cultured metacestodes to 25μ g/ml concentration of MTZ-w or ABZ is equivalent to 110 and 94 μ M solutions, respectively. Taking molarity into consideration does not change the comparative parasiticidal effects of these two compounds *in vitro*. MTZ-w remains significantly more effective than ABZ. Even the exposure of cultured metacestodes to as low as 27.5 μ M solution of MTZ-w was significantly more lethal than that caused by exposure to 90 μ M solution of ABZ.

Some other Schiff based MTZ derivatives, particularly MTZ-a, MTZ-b and MTZ-d showed protoscolicidal effects and mortality values close to those caused by the standard positive control drug, ABZ. These, in addition to the most potent MTZ-w, are thus important candidates for assessment as alternatives for ABZ both in vitro and in vivo. In contrast, MTZ itself does not seem to be a suitable drug against CE as it showed a much less protoscolicidal than ABZ.ABZ and MTZ must have different modes of action from that of MTZ-w which showed significant activity against PSCs and other cultured stages. MTZ-w, is an imidazole benzeyldehyde analogue, having imidazole ring as in ABZ [Methyl 5propylthio-2-benzimidazole carbamate]. However, MTZw (4-[2-(2-methyl-5-nitro-1H-imidazol-1-yl) ethyoxy] benzeyldehyde) has 2-methyl-5-nitro with para-aldehyde benzene ring. Whether there is a synergistic effect of MTZ-w nucleus and the benzyldehyde group that renders it more effective on cultured PSCs than ABZ remains to be investigated. The activity of ABZ includes disruption of glucose uptake by inhibition of ß-tubulin of the endoplasmic reticulum and mitochondria of parasite GL (Polat et al., 2009). As with MTZ (Halloran et al., 2010; Lofmark, et al., 2010), the activities of Schiff bases is comparable to MTZ which suggests a similar mechanism of action. The differences in protoscolicidal activity between the several MTZ derivatives may reflect differences in stability and transport properties.

The in vivo dose of ABZ for chemotherapy against CE in human and livestock is 50 mg/kg body weight. Lower dosages of ABZ were given after the surgical treatment for maintenance purposes (Moreno et al., 2001; Adas et al., 2009; Creul et al., 2012). In the present study, the doses that were chosen to test the effects of ABZ and the various other drugs and MTZ derivatives in in vitro cultures of PSCs and subsequent stages were 25 µg/ml or lower. It should be pointed that lower dosages that prove effective against CE are more beneficial than higher dosages. In addition to decrease in cost, fewer side effects are expected with the use of lower dosages. Although the in vivo effect of MTZ derivatives, particularly MTZ-w requires further intensive assessment, comparisons of their effects on in vitro cultured metacestode stages with those caused by standard drugs are important initial steps towards searching for effective and safe drug alternatives. Thus, MTZ-w and other derivatives that showed sufficient in vitro parasiticidal activity at lower dosages should be followed further for potential use as chemotherapeutic drugs. Moreover, the fast action showed by MTZ-w and some other derivatives is of great importance. Fast action lowers the number and volume of drugs for treatment (Taylor et al., 1990; Todorov et al., 1992).

Cultures of PSCs reaching 30 days old stage are useful to assess the effect of the compounds on developing parasite stages. The effect of MTZ derivatives on this stage was studied after 14-days of incubation with single dose of $25\mu g/ml$ and MTZ-w showed the greatest detrimental effect. However, daily follow up is needed to compare the effect of these compounds and the timing needed to reach total (100%) parasiticidal effect. This should be carried out on various pre-segmentation and post- segmentation stages as well as adult worms. If proved effective, drug development against the developing and adult parasite stages in the dog definitive host are valuable. It should be pointed out that the experimental set up of in vitro culturing of PSCs and metacestode stages was done in a microenvironment where oxygen was in excess. MTZ and possibly its derivatives normally function under anaerobic or low oxygen tension conditions. As Echinococcus granulosus metacestode stages possess both aerobic and anaerobic respiratory systems (Cue et al., 2013), there is urgent need to explore further the effect of MTZ derivatives, particularly MTZ-w on in vitro cultured stages that are maintained under low oxygen microenvironment.

The target of MTZ-w and other effective derivatives on PSCs appear to be the tegument with subsequent effects on suckers and hooks. Tegument disruption, sucker collapse, and hook rupture were all noted using the most effective MTZ-w compound in addition to ABZ. The loss of rigidity and the size reduction of treated HCs with ABZ or MTZ-w may be due to changes in osmolarity inside and outside HC layers as a result of drug internalization through the cyst wall. Scanning electron microscopy results showed additional evidence about disruptive action of MTZ-w on HC. Here, we provide strong evidence of its potential as an antihelminthic compound using the E. granulosus model. These findings build on the uniquely wide spectrum of this compound as antiprotozoal and antimicrobial activity (Gavidia et al., 2009; Abu Shaireh et al., 2009; Saadeh et al., 2010). There is an urgent need to examine the chemotherapeutic potential of this compound in vivo using the mouse secondary hydatidosis model. This is a prerequisite for further studies on its toxicity, side effects, and bioavailability.

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Measurements of Homogentisic Acid levels in Alkaptonuria Patients Using an Optimized and Validated Gas Chromatography Method/Mass Spectrometry

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Abstract

Alkaptonuria is a very rare genetic disorder, characterized by a lack of homogentisate dioxygenase and causes accumulation of homogentisic acid. Clinical manifestations include dark urine, dark-black pigmentation of connective tissues (ochronosis), and arthritis of large joints and spine. The disease is usually diagnosed in adulthood by assessment of signs and symptoms of ochronosis. Confirmation of suspected diagnosis can be achieved by quantitative measurements of homogentisic acid levels. In this study, homogentisic acid was analyzed in 17 alkaptonuria patients. After liquid-liquid extraction, the analyte was determined by Gas Chromatography/ Mass Spectrometry (GC-MS) method. For quantitation purposes, external calibration was applied first, regression coefficient of ≥ 0.995 indicated the linearity in the concentration range of 1-100 ng/µl. The instrumental detection limit (IDL) and lower limit of quantitation were 3.82 and 12.7 µg/L, respectively. Recovery rate was $\geq 89\%$. Precision given as relative standard deviation (RSD) ranged from 3 – 10 %. The results showed that the concentration of homogentisic acid ranged from 0.46 to 1.5 g/24 hours.

Keywords: Homogentisic acid, Black urine, Ochronosis, GC-MS, Jordan.

1. Introduction

Alkaptonuria (AKU) was designated by Sir Garrod as the first inherited metabolic disease (Garrod, 1908). AKU is a rare autosomal recessive disease caused by a deficiency of a specific enzyme, homogentisate 1,2 dioxygenase (HGD), leading to accumulation of homogentisic acid (HGA) (La Du, 1958). Most of the HGA is excreted in urine, and some is deposited in connective tissues as a melanine-like polymer in a process known as ochronosis (Zannoni et al., 1969). The pathophysiological mechanism of AKU is still unclear. Oxidative stress and amyloid formation may play a fundamental role in AKU. Indeed, recent studies have shown the presence of serum amyloid A (SAA) and serum amyloid P (SAP) in vitro and ex vivo AKU models and highlighted AKU as a secondary amyloidosis (Millucci et al., 2012; Braconi et al., 2013). The clinical features of AKU are characterized by homogentisic aciduria, bluish-black discoloration of connective tissues and arthropathy of weight-bearing joints such as hips and knees and spondyloarthropathy (O'Brien *et al.*, 1963). Complications of the disease include stones formation in kidneys, prostate, gall bladder and salivary glands, rupture of tendons, ligaments, muscles and cardiovascular manifestations (cardiac arrhythmias, aortic valve disease) (Phornphutkul *et al.*, 2002). AKU severity score index (AKUSSI) have been developed for the first time as an assessment tool to quantitate disease severity, to compare the severity between AKU patients and to measure the progression of the disease (Ranganath, 2011; Cox, 2011).

AKU can be diagnosed at birth. The earliest clinical signs are dark urine and discoloration of nappies. However, some AKU patients are asymptomatic, and the majority of patients are diagnosed late in the third decade of life when they are affected by the ochronotic arthropathy (Ranganath *et al.*, 2013). The urine of the

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AKU patient turns dark-black when exposed to air. This reaction can be accelerated by alkalinizing urine (Castagna *et al.*, 2006). Other screening tests include darkening of urine after adding ferric chloride (FeCl3). Confirmation of diagnosis is established by the identification and quantification of urinary HGA using chromatographic techniques, such as gas chromatography mass spectrometry (GC-MS) and high-performance liquid chromatography (HPLC) (Abdulrazzaq *et al.*, 2009; Bory *et al.*, 1989).

The incidence of AKU around the world is as low as 1 in 250,000; however, high incidences have been reported in Slovakia and the Dominican Republic (1 in 19,000) (Srsen et al., 1978; Milch, 1960). The incidence of AKU in Jordan is unknown; however, recent studies have identified 60 cases with AKU. Most of these cases were identified in a small village in south Jordan, were nine AKU patients were diagnosed in the same family. The high rate of this rare genetic disease in Jordan is believed to be due to high rates of consanguineous marriages (Alsbou et al., 2012a; Al-sbou et al., 2012b). Several methods have been used to measure HGA in subjects with AKU include chromatographic techniques such as spectrophotometric methods, high-performance liquid chromatography (HPLC), and gas chromatography mass spectrometry (GC-MS) (Seegmiller et al., 1961; Borry et al., 1989 Markus et al., 2001). The aim of this study is to describe the determination of urinary HGA using a sensitive and specific GC-MS method.

2. Materials and Methods

2.1. Chemicals and Standard Solutions

m-Methoxy-acetophenone (internal standard-I.S.) and N, O-bis(trimethylsilyl) trifluoroacetamide (BSTFA) used for derivatization were purchased from Across Chemical (USA). Homogentisic acid was supplied from Sigma Aldrich/ Germany. The following solvents of GC-grade were purchased from Riedel-de Haën (Germany): n-Hexane, ethyl acetate, methanol and pyridine.

2.2. Sampling and Sample Preparation

Twenty four hours urine samples were collected from 17 AKU patients. Those patients were registered in the Jordanian Society of Alkaptonuria and were diagnosed having the disease based on results of laboratory investigations and clinical assessment. First, urine samples were left standing at room temperature for 48 h and were observed for changing the color. Urine samples of AKU patients turned dark-black upon standing as shown in Figure 1. Second, ferric chloride test was performed by adding one drop of ferric chloride solution and was positive if a transient blue color was observed. Clinical assessment and radiological examinations of patients were conducted to confirm the presence of signs and symptoms of ochronosis.

N,O-bis (trimethylsilyl) trifluoroacetamide (BSTFA) is mostly used as derivatizing agent and it has a high reactivity. The derivatization of homogentisic acid compound for GC-MS analysis was performed according

to (Zafra et al., 2006) with slight modification, in which a mixture of 20: 5:25 (v/v/v) BSTFA-pyridine-ethyl acetate (containing homogentisic acid) is allowed to stand for 2 min at room temperature. The procedure is enough to get adequate derivatization. 1.0 mL of liquid urine sample was transferred into polypropylene test tube and 1g NaCl, 200µL of 5M HCl and 6mL ethyl acetate were added to the sample. The last mixture was shaken well for 10 min and centrifuged at 4000 rpm for 3min, and then the upper layer (ethyl acetate) transferred into vacuum test tube. The extracts were evaporated to dryness using a gentle stream of nitrogen. The residues were reconstituted in750 µL of 6.65 mg/L internal standard dissolved in ethyl acetate using. 250µL of the previous solution were mixed with50µL pyridine and 200µL BSTFA. The mixture was shaken well for two minutes in order to derivatize the



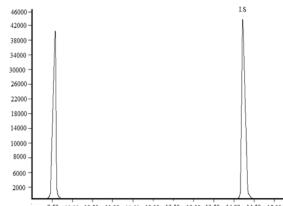
phenolic compounds. Finally, a volume of 1μ L of the prepared solution was injected into GC-MS instrument.

Figure 1. Urine samples from AKU patient, fresh (left) and after 48 hours (right).

2.3. GC-MS Analysis

The gas chromatographic analysis was performed using an Agilent 6890 Series II. A gas chromatograph fitted with an auto sampler injector. A capillary column HP-5 fused silica column ($30m \times 0.25mm$, film thickness $0.25\mu m$,(5%)-biphenyl-(95%)-dimethylsiloxane

copolymer) was used. A silanized injector liner split/splitless (2mm I.D.) was used. Detection was carried out with a 7683 mass-selective single quadrupole detector (Agilent Technologies). The injector temperature was 250°C. The oven temperature was held at 80°C for 3 min, and then increased to 240°C at a heating rate of 13°C \min^{-1} , and the temperature was held for 20 min. The detector temperature was 280°C. The carrier gas used was helium (purity 99.999%) at a flow rate of 1.0mL min⁻¹. The samples were injected in the splitless mode and the splitter was opened after 7 min (delay time). The sample volume in the direct injection mode was 1µL. The ion energy used for the electron impact ionization (EI) mode was 70eV. The mass range was scanned from 150-550m/z. Single ion monitoring (SIM) acquisition mode was used (Deeb et al., 2012). The mass spectrum showed the molecular ions at m/z 384, 341 at 14.2 min and 150, 135 at 9.5 min which corresponds to the correct molecular formula C17H32O4Si3 (homogenistic acid) and C9H9O2 (I.S.), respectively as shown in Figure 2.



950 10.00 10.50 11.00 11.50 12.00 12.50 13.00 13.50 14.00 14.50 15.00 **Figure 2.** GC-MS chromatogram of the 5.0 mg/L level homogenisctic acid (9.5 min) with 6.65mg/L IS (14.2min)

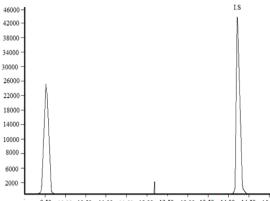
2.4. Analytical Quality Assurance

Standard mixture solutions of 1.0, 5.0, 20, 50, 100 mg/L of the derivatized homogentisic acid with 6.65mg/L IS were prepared in order to define the linear working range. Internal standard method was preferred in order to correct any loss of phenolic compound (homogentisic acid) during sample preparation. Regression coefficient (r2) was in all cases > 0.995, indicating the linearity of the calibration function in this concentration ranges.

Extraction recovery of homogentisic acid was determined for urine samples at 3 spiking levels, 1, 20, 100μ g/L, where the average recovery was found between 89 – 105%. Additionally, blanks were analyzed for background concentration. Precision of the method for homogentisic acid, calculated as relative standard deviation (RSD) was ranged between 2-9 %. The instrumental detection (IDL) was estimated form injections of standard solutions successively diluted until reaching a concentration level corresponding to a signal-to-noise ratio of 3. The method quantification limits (MQL) was determined form spiking urine sample, as the minimum detectable analyte concentration, which give signal-to-noise ratio of 10.

3. Results and Discussion

AKU patients in this study were 12 males and 5 females with a mean age of 29 years (age range 5-53 years). All patients had a history of dark urine since birth. Ferric Chloride test was positive for all patients. Quantitative measurements of urinary HGA showed that all patients excreted large quantities of HGA, the mean was (0.95 g/24 h). A GC/MS representative chromatogram for a real sample of AKU patient is shown in Figure 3.



9.50 10.00 10.50 11.00 11.50 12.00 12.50 13.00 13.50 14.00 14.50 15.00 Figure 3. Representative GC-MS chromatogram for a real sample of AKU patient

There was a marked variation in the concentration of HGA excreted between different AKU patients (a 3-fold variation) and the range was (0.46 - 1.5 g/24 h) (Table 1). This variation could be due to different dietary protein content between different individuals.

Table 1. Urinary HGA levels in 17 alkaptonuria patients

| Case Age | | Sex | Urinary HGA | | |
|----------|---------|-----|-------------|--|--|
| No | (Years) | | g/24 hrs | | |
| 1 | 5 | М | 0.46 | | |
| 2 | 5 | М | 0.53 | | |
| 3 | 6 | М | 1.17 | | |
| 4 | 8 | F | 0.8 | | |
| 5 | 13 | М | 1.2 | | |
| 6 | 24 | F | 1.37 | | |
| 7 | 26 | М | 0.51 | | |
| 8 | 33 | М | 0.9 | | |
| 9 | 34 | М | 0.8 | | |
| 10 | 37 | М | 1.47 | | |
| 11 | 37 | М | 0.79 | | |
| 12 | 39 | М | 1.1 | | |
| 13 | 44 | М | 0.7 | | |
| 14 | 44 | F | 0.77 | | |
| 15 | 44 | F | 1.5 | | |
| 16 | 44 | М | 0.88 | | |
| 17 | 53 | F | 1.1 | | |

M=male, F=female

AKU is a very rare genetic condition and in most cases it is misdiagnosed at childhood. Few signs and symptoms of this disease appear before the 3rd decade of life, apart from passage of dark urine.

The reason for the delay appearance of ochronotic manifestations is unknown. Therefore, the majority of cases with AKU are recognized in adulthood (Ranganath et al., 2013). Homogentisic acid is a normal intermediate in the metabolism of tyrosine and normal individuals do not excrete HGA because it is converted into maleylacetoacetic acid by the homogentisate 1,2 dioxygenase. AKU patients excrete high concentrations of HGA in urine (range 4-8 g/day) (Castagna et al., 2006). Therefore, testing urine samples for the presence of HGA is crucial for establishing the diagnosis of AKU. Some screening tests can provide help in diagnosis of AKU such as darkening of urine after addition of sodium hydroxide, and ferric chloride test. This test can be used to detect metabolites in urine samples of patients with inborn error of metabolism diseases such as AKU (Frohlich et al., 1973). The basis of this test is that phenols of HGA form a violet complex with Fe (III), which is intensely colored, therefore, the urine containing HGA yields a transient blue color after adding few drops of ferric chloride solution. In this study, this test was positive for all tested AKU patients, thus it can be used to help in screening for AKU. However, confirmation of diagnosis of AKU can be achieved by specific identification and quantification of HGA in urine and blood samples.

The present Gas Chromatography/ Mass Spectrometry method was developed for the determination of homogentisic acid in AKU patient's urine; in addition the derivatization of homogentisic acid compound was performed with a slight modification to Zafra's method (Zafra *et al.*, 2006). The main advantage of this method includes its high sensitivity, with MQL for HGA in urine as low as 12.7 μ g/ L, also this method showed a very good separation of analyte (homogentisic acid) in less than 15 min.

4. Conclusion

The described method represents a useful and suitable analytical tool that can be used for diagnosing AKU and for the monitoring treatment effect on HGA levels in AKU patients.

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Microscopic Analysis of *in vitro* Digested Milled Barley Grains: Influence of Particle Size Heterogeneity

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Abstract

In this study, Scanning Electron Microscopy (SEM) is used to characterize the structure of ground and whole barley grain before and after the exposure to *in vitro* enzymatic digestion at different incubation times (0, 0.5, 1, 2, 6 and 24 h). SEM analysis showed that digestion started to take place in barley grain fragments after 0.5 h of incubation time. SEM indicated that complete starch digestion is dependent on grain fragment size in barley. Starch digestion seems to be completed after 24 hours of digestion in small fragments of barley grains (<0.5 mm) which was not the case for larger fragment size (>1.0mm). In case of whole barley grain, SEM showed that alpha amylase was not capable of penetrating and diffusing through barley grain husk after 24 h of incubation. In conclusion, microscopic examination for *in vitro* digested milled and unprocessed barley fragments differ in particle size, indicating that the extent of starch digestion is dependent on fragment particle size.

Keywords: Scanning Electron Microscopy, Starch granules, in vitro digestion, Barley fragments

1. Introduction

Grains usually represent the main energy source in animal's diets where starch represents the main nutrient components (Svihus et al., 2004). From a processing prospective, grains, such as barley, should be ground in order to facilitate further processing steps such as mixing and enhancing nutritive value by increasing digestibility (Al-Rabadi et al., 2009). Hammer mill is widely used in the feed industry in order to mill grains as it is characterized by high production capacity and lower maintenance requirements (Amerah et al., 2007). However, grains milled using hammer mill have been reported to produce wide variation in grain particle size (Audet, 1995). Heterogeneity of particle size within milled grains has been reported to influence nutrient digestibility even when the average particle size was the same (Wondra et al., 1995). Within grain type, different grain fragment size, after being fractionated by sieving process, have been reported to posses different surface area per unit mass and different chemical composition (Al-Rabadi et al., 2013). These factors have been reported to extensively influence the magnitude of starch digestion (Al-Rabadi et al., 2012). Scanning electron microscopy (SEM) have been extensively used to track structural changes that occur into starch granules after being exposed to thermo mechanical treatments and amyloytic digestion (Srikaeo, 2008; Srikaeo et al., 2006). The first objective of this study is to examine the influence of adding enzymes mixture (amylase, glucosidase, pepsin and proteases) in a sequence that mimic the digestion process *in vivo* with taking into consideration the heterogeneity of different size fragments of barley. A previous study reported that starch digestion of milled grains by alpha amylase is controlled by a diffusion process (Al-Rabadi *et al.*, 2009). However, this study aims at confirming the capability of alpha amylase to diffuse through barley grain husk using SEM.

2. Materials and Methods

2.1. Barley Grain Milling

Barely grains were milled using 4 mm hammer mill screen size when constant motor load was recorded. Ground and whole barley grains were collected and were sealed into plastic bags and stored at 4 °C until visual examination by using scanning electron microscopy and further being digested using in vitro starch digestibility method.

2.2. In vitro Starch Digestibility

In vitro starch digestion method was used as previously described by Al-Rabadi *et al.* (2009). In vitro digestion method was performed in a three-step enzymatic digestion to mimic digestion in the mouth, in the stomach and the small intestine in a closed system. Different digestion times (0, 0.5, 1, 2, 6 and 24 h) were used to simulate digestion process in monogastric animals and

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young ruminates before weaning. The zero hour digestion was started at the start of the small intestinal simulation step (where most of starch digestion take place).

2.3. Scanning Electron Microscopy (SEM)

Milled barley grains fragments (before and after digestion at different incubation times) were placed onto aluminium stubs with carbon tabs. Fragments then were sputter coated (10-15 nm layer) of platinum using an Platinum Sputter Coater (model EIKO IB-5). Digested and undigested barley fragments were examined in either a JEOL 6300 or JEOL 6400 field emission scanning electron microscope. Micrographs were chosen by taking many pictures (i.e., 5 to 10 pictures) for the selected samples to obtain representative Scanning electron micrographs. The selected sample contains many barley grain fragments on the carbon tabs. Comparable appearance was selected as a representative picture. Many pictures (6-10 pictures) were taken at different magnifications to find any main structural difference at both grain fragment size level and starch granule size level.

3. Results and Discussion

Scanning electron micrographs for milled raw barley samples by using 4 mm hammer mill screen size is shown in Figure 1. Milling process resulted in breaking barley grains into different levels of fragment sizes that ranged from very fine particles to quarter and half broken grains (Figure 1). Previous studies showed that milling grains using hammer mill resulted in high heterogeneity in grain particle size distribution when compared with other milling equipments such as roller mill (Seerley et al., 1988; Douglas et al., 1990; Audet, 1995). It can be also seen from Figure 1 that barley grains milled by using hammer mill produce spherical shape fragments. In his report, Kim (2002) reported that the hammer mill produces spherical shape grain fragments while the roller mill produces more rectangle grain fragments after milling.

The effect of alpha amylase on starch granules digestion, at different incubation times (0, 0.5, 1, 2, 6 and 24 h), using three enzymatic step models were examined (Figures 2, 3, 4, 5, 6, 7 and 8). As expected, there was no enzymatic activity on starch granules at 0 hour incubation time (Figure 2) although starch granules were exposed to salivary alpha amylase. It is hardly for any enzymatic digestion to take place on starch granules after 30 minutes of the incubation time (Figure 3). It has been previously shown that the enzymatic digestion by amylase is controlled by diffusion process through channels present on granules surface (Helbert et al., 1996) and this may suggest that starch digestion may take place inside starch granules. Magnitude of diffusion coefficient for amylase has been previously quantified in barley starch granules (1.7 x 10-7 cm2 s-1) (Al-Rabadi et al., 2009). Extant of starch digestion for different grain fragment size, ranging from 0.045-2.8 mm, have been reported to range from 23-1%, respectively after a 30-minute incubation time (Al-Rabadi et al., 2012).

Enzymatic digestion by amylase started to take place on starch granules surface after one hour incubation time (Figure 4). However, enzymatic activity by alpha amylase does not seem to be associated with every starch granules. On the other hand, digestion by alpha amylase seems to be associated with every starch granules after 2 h of incubation time (Figure 5). A number of holes on starch granules resulted from enzymatic activity increased as the incubation time progresses (i.e., digestion 6 h) as shown in Figure 6. Integrity of oval shape structure of starch granules starts to disappear after 24 h of incubation time for large fragment size (>1mm) as shown in Figure 7. However, starch granules in smaller fragment size disappeared after a 24-h digestion time, as shown in Figure 8. Complete starch digestion was achieved for barley fragment.

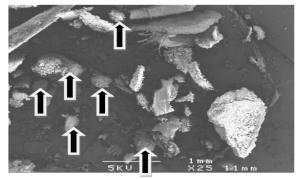


Figure 1. Raw milled barley grain fractions using 4 mm hammer mill screen size (heterogeneity of milled grain particle size range from very fine particles to half broken grains). Round oval shape particles indicated by black arrows.

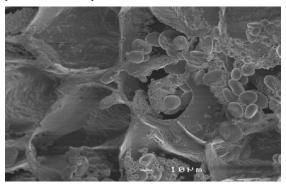


Figure 2. Undigested starch granules embedded in protein matrix.

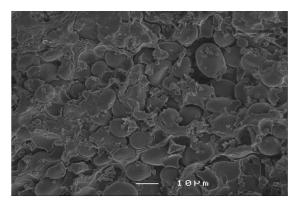


Figure 3. Digested starch granules after 0.5 h incubation time (no appearance for any enzymatic activity on starch granules). Image was taken from small fragment size (<0.5mm)).

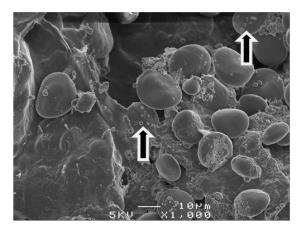


Figure 4. Digested starch granules after 1 h incubation time (initial enzymatic activity (holes) on certain starch granules as indicated by arrow). Image was taken from small fragment size (<0.5mm)).

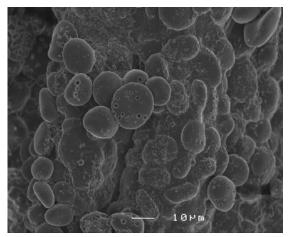


Figure 5. Digested starch granules after 2 h incubation time (initial enzymatic activity (holes) on most starch granules). Image was taken from small fragment size (<0.5mm))

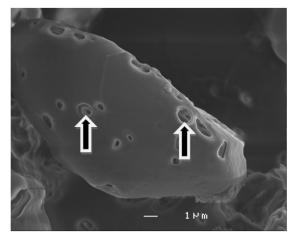


Figure 6. Digested starch granule after 6 h incubation time (increase the number and size of digestion holes compared to starch granules digested at 2 h incubation time as indicated by black arrows). Image was taken from small fragment size (< 0.5mm)).

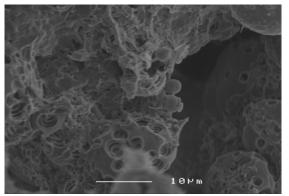


Figure 7. Digested starch granule after 24 h incubation time (increase the number and size of digestion holes). Image was taken from large fragment size (>1.0 mm)).

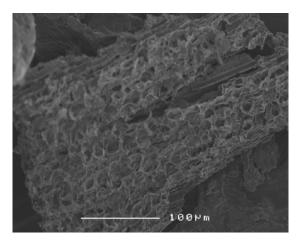


Figure 8. Absence of any starch granules after 24 h incubation time. Image was obtained from particles < 0.5mm.

It was found that the electron micrographic features of the granules after treatment with alpha amylase and glucosidase possesses synergistic influance (Matsubara et al., 2004). The synergetic influences by both enzymes were explained by Sun and Henson (1990) and Robertson et al. (2006). The ability of the alpha-glucosidases to breakdown glucosidic bonds other than alpha-1,4- and alpha-1,6- that are present at the granule surface can eliminate bonds which were barriers to digestion by alpha-amylases. In addition, the presence of protease in the current in vitro digestibility method may enhance indirectly the synergy influence of both alpha amylase and glucosidase by increasing the exposure of starch granules to enzymatic digestion. It has been reported that the interaction between protein and starch granules can decrease the exposure of raw starch granules to enzymatic digestion by alpha amylase (Rooney and Pflugfelder, 1986). The interactions between the protein granules (size range 5-60 kDa) and starch may affect starch digestibility; it is important to take into consideration that protein digestion usually precedes starch digestion (Svihus et al., 2005).

The size of the starch granules within grain type can influence the starch digestion process when examined using SEM. Large starches granules displayed massive degradation and were described by sever corrosion toward the radial axis of granule (Franco and Preto, 1992). On the other hand, small starch granules showed a surface attrition and, later on, followed by solubilization (Franco and Preto, 1992). The difference in the behavior of starch digestion between small and large particles could be attributed to many factors. A previous study showed that large and small starch granules possess different chemical compositions and endothermic properties and thus possess a different enzymatic response to digestion by alpha amylase (Szczodrak and Pomeranz, 1991). Chiotelli and Le Meste (2002) reported that large starch granules have a lower water affinity due to more compact structure (i.e., higher crystallinity) than small starch granules and this could increase their susceptibility to enzymatic hydrolysis by alpha amylase. In addition, small starch granules

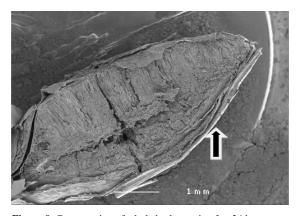


Figure 9. Cross section of whole barley grain after 24 h incubation time (barley grain husk is indicated by arrow).

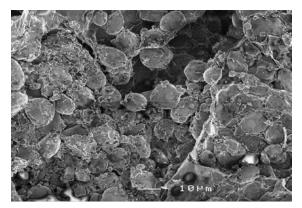


Figure 10. Absence of any enzymatic activity of whole barley grain .

have a higher surface area to weight ratio and this may suggest that alpha amylase binding to starch granules and the potential hydrolysis would be higher compared to large starch granules when all other factors being the same (Tester *et al.*, 2004).

In this study, the presence of large fragment size of barley fragments and the absence of fiber digesting enzymes may inhibit the synergetic influence of both alpha amylase and glycosidase. To confirm the capability of both alpha amylase and glycosidase to diffuse through barley grain husk which is mainly composed of cellulose, hemicelluloses and lignin (Adrados *et al.*, 2005). Whole barley grain was incubated into digestion solution for 24 h to investigate whether any enzymatic digestion can take place (Figure 9). As shown in Figure 10, no enzymatic digestion took place on starch granules after cutting the whole barley grains into two halves, which indicates that barley husks work as a strong barrier against enzymatic diffusion of both amylase and glycosidase. Large particles have been shown to survive ruminal attack and pass to small intestine for digestion (Owens *et al.*, 1986).

In conclusion, microscopic examinations for in vitro digested milled barley fragments differ in particle size and this indicates that the extent of starch digestion is dependent on fragment particle size (i.e., heterogeneity of particle size distribution). SEM for whole barley grain revealed that the presence of barley husk prevents any enzymatic diffusion and thus no starch digestion takes place.

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Evaluation of Antioxidant, Antimicrobial and Cytotoxicity of Alcea kurdica Alef

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Abstract

The purpose of this study is to evaluate the aqueous extract of *Alcea kurdica* Alef for antioxidant and antimicrobial activity as well as potential toxicity. Antioxidant activities were evaluated using 1,1-diphenyl-2- picrylhydrazyl (DPPH) free radical scavenging and Ferric Reducing Antioxidant Power (FRAP) reducing capacity assays as well as total phenolic compounds (TPC). Antimicrobial activity was assessed against some Gram-positive and Gram-negative bacteria, yeasts and filamentous fungi using the agar dilution method. The plant extract was also assessed for *in-vitro* toxicity using the Promega Cell Titer 96 AQueous Non-Radioactive Cell Proliferation (MTS) assay. The aqueous extract of *A. kurdica* demonstrated potent free radical scavenging activity of $64\% \pm 1.64\%$ and ferric reduction capacity of 2955.0 ± 0.04 mmol/g, as well as having 88.0 ± 0.002 mg gallic acid equivalents /gram plant extract. The aqueous extract of *A. kurdica* had modest antimicrobial activity against most tested microorganisms. Moreover, the plant extract did not have any toxic effects on human lung fibroblasts. Based on these findings, we conclude that *A. kurdica* may be utilized to prevent the growth of some microorganisms. The plant constituents behind these effects are the antioxidants and phenols. Further studies are needed to evaluate the therapeutic utility of *A. kurdica* extracts as antimicrobial agents.

Keywords: Alcea kurdica Alef, Antioxidant, Antimicrobial activity, Cytotoxicity.

1. Introduction

Recently, scientists have paid more attention to the role of natural antioxidants, mainly phenolic compounds, which may have more antioxidant activity than synthetic antioxidants (Velasco and Williams, 2011). Natural products, particularly those present in medicinal plants, have gained more interest as food ingredients because of their safety, accessibility, and positive impact on health (Ebrahimabadi et al., 2010). A variety of natural antioxidant compound purified and derived from plant resources have been demonstrated to scavenge free radicals (Loo et al., 2007). Epidemiological studies suggest that the consumption of plants can protect humans against oxidative damage by inhibiting or scavenging free radicals and reactive oxygen species (ROS) (Sun et al., 2002; Materska and Perucka, 2005). Natural antioxidants exhibit a wide range of pharmacological activities, and have shown anticancer, anti-inflammatory, anti-aging, anti-ulcer, and antimicrobial properties (Mayne, 2003; Pinnell, 2003). For the past several decades, a variety of vegetables, crops, spices, and medicinal herbs have been analyzed in an effort to identify new and potentially useful antioxidants (Zheng and Wang, 2001). It has become evident that natural products may reduce oxidative stress through antioxidant action. For example, various phenolics and flavonoids, which are found naturally in fruit, vegetables, and some beverages, have been demonstrated to exert antioxidant effects through a number of different mechanisms (Nijveldt *et al.*, 2001).

Alcea kurdica, which belongs to the family Malvaceae, is a very polymorphic and widespread species found in east Iraq and west Iran. Alcea is an important source of mucilage and are widely distributed with about 70 species (Pakravan and Ghahreman, 2003). Alcea are usually found in the Penjween, Sharbazher area, and in Haji Omran and Garaguin in Kurdistan of Iraq. The Alcea is a delicate plant having sharp, pale yellow, dark reddish stems, and greyish green foliage. Traditionally A. kurdica have been widely used among the Kurdish population to treat a variety of diseases including tonsillitis, gastric ulcers, duodenal ulcers, pneumonia, urinary tract infections, and alopecia (Mati and de Boer, 2011). Based on literature survey, there are no ethnopharmacological studies on A. kurdica that originate from Kurdistan of

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Iraq. Based on the importance of *A. kurdica* in medicinal folk, this study was conducted to evaluate the antioxidant and antimicrobial activities of *A. kurdica* as well as potential toxicity against the human normal lung fibroblast cell line (Hs888Lu).

2. Materials and Methods

2.1. Plant Extract

The dried leaves of the *A. kurdica* plant were purchased at the herbal market, Erbil, Iraq. The Voucher-ID and Vernacular name of *A. kurdica* were identified as Alef. EM2.1 Malvaceae Gule hero (Mati and de Boer, 2011). After identification, the plant leaves were ground into powder using an electrical blender then extracted using water solvent at a ratio of 1:20. The mixture was heated and stirred on a hotplate for 3 hrs at 65° C followed by cooling and filtration using Whatman No. 1 filter paper and a filter funnel. The mixture was evaporated under reduced pressure in EyelaTM rotary evaporator (Sigma-Aldrich, USA) and subjected to lyophilisation by freeze-drying (Labconco, Kansas, USA) to produce a powdered form of the extract. The extract was stored at -20° C for later use.

2.2. Antioxidant Experiments

The antioxidant activity of the aqueous extract was determined using the 1,1-diphenyl-2- picrylhydrazyl (DPPH) radical assay which is based on the transfer of electrons between the DPPH reagent and the plant extracts. The method described by (Loo et al., 2007; Erel, 2004; Gorinstein et al., 2003) was utilized with minor modifications. The DPPH value was expressed as percentage scavenging of the DPPH based on the following equation: DPPH (%) = (Absorbance of blank -Absorbance of sample) x 100 / Absorbance of sample. Each test was performed three times in triplicate and the results were expressed as mean percentage. Ferric Reducing Antioxidant Power (FRAP) assay was performed according to a previously described method (Erel, 2004). FRAP values were expressed as mmol of ferric reducing activity of the plant extract per gram of drv weight and Ferrous sulfate heptahydrate (FeSO4x7H2O) was used as a standard, based on the following equation: FRAP value of sample in mmol/L =(change in absorbance of sample from 0 to 4 min / change in absorbance of standard from 0 to 4 min) x FRAP value of standard.

2.3. Total Phenolic Compounds (TPC)

The total phenolic compounds (TPC) of aqueous plant extracts were determined by the Folin-Ciocalteu method (Miliauskas *et al.*, 2004), using gallic acid as a standard. Total phenolic content of the samples was determined, and the amounts of phenolic compounds in plant extracts were expressed in mg/g of extract and gallic acid equivalents (GAE), respectively. Each test was carried out three times in triplicates. Values were expressed as means.

2.4. Antimicrobial Activity Experiment

The ability to inhibit the growth of Gram-positive and Gram-negative bacteria, yeasts and filamentous fungi was

observed using an overlay method (Williams et al., 1993). Antibacterial screening utilized the agar dilution method as previously described (Afolayan and Meyer, 1997). The dried plant extracts were dissolved in methanol to a final concentration of 50 mg/mL and sterilized by filtration through 0.45 µm Millipore filters. The activity of this solution was compared with different standard antimicrobial agents. Discs of streptomycin (S, 10 µg) and tetracyciline (TE, 30 µg) were used as positive controls for bacteria, neomycin (N, 30 µg) and nystatin (NY, 100 µg) were used as positive controls for fungi. Sterilized paper discs without the extract or antimicrobial agents were used as negative controls for all microorganisms. Final dilutions of the extract (ranging between 0.1 and 10 mg/mL) were prepared in molten Müeller Hinton agar medium (Lab M., Bury, Lancashire, UK) maintained in a water bath at 50° C. The organisms were streaked in radial patterns on the agar surface. Plates were incubated under aerobic conditions at 37° C for 24 hrs for the bacteria or 28° C for 48 hrs for the fungi. The organisms used were: Bacillus subtitles, Staphylococcus aureus, Pseudomonas aeruginosa, Escherichia coli, Enterobacter aerogenes, Candida albicans, Salmonella enterica, Fusarium oxysporum, Cladosporium macrocarpum, and Fusarium solani. The bacteria were slanted on nutrient agar (Merck, Darmstadt, Germany), the yeast was slanted on Sabaroud's agar medium (Lab M., Bury, Lancashire, UK), and the fungi were slanted on potato dextrose agar medium (Lab M Limited, Bury, Lancashire, UK). Each test was conducted in triplicate. The lack of visible growth on the agar plates was used to indicate the inhibitory activity of the extracts.

2.5. MTS Assay

The cytotoxic activity of aqueous extract of A. kurdica was determined using Promega Cell Titer 96 AQueous Non-Radioactive Cell Proliferation (MTS) assay (Lestari et al., 2005). The MTS assay is a colorimetric test for the determination of cell viability in cytotoxicity assays. The assay utilized the human normal lung fibroblast cell line (Hs888Lu), purchased from American Type Culture Collection (ATCC, The Global Bioresource Centre, Manassas, VA, USA). Hs888Lu cells were cultured in Dulbecco's Modified Eagle's Medium (DMEM, Sigma, USA) with high glucose content, 1% non-essential amino acids (PAA Laboratory GmbH, Austria), 2% L-glutamine (200 mM) (Sigma, USA), 1% penicillin/streptomycin (100 x) (PAA Laboratories GmbH, Austria), 1% sodium pyruvate (1 mM) (Sigma-Aldrich, USA), and supplemented with 10% fetal bovine serum (FBS, PAA Laboratory GmbH, Austria). Cells (1 x 105 cells/mL) were seeded in a 96-well plate using 100 µL per well, and incubated at 37° C with 5% CO2 in a humidified atmosphere for 24 hrs before the addition of the plant extract. Dilutions of A. kurdica extract ranging in concentration from 125 µg/mL to 2000 µg/mL were added to the culture plate in triplicates, and then incubated for 24 hrs under the same conditions. Following the treatment, 20 µL of the MTS reagent (pre-warmed to 37° C) was added to each of the 96-wells and the plate was incubated at 37° C for 3 hrs. The absorbance was recorded using Glomax multi detection system (Promega, USA) at 492 nm. The experiment was conducted three times in

triplicates and the mean was calculated and expressed as percentage of the value observed with no plant extract treatment (control).

2.6. Statistical Analysis

The data were analyzed using One-way ANOVA test by Statistical Package for Social Sciences (SPSS) version 17.0 program. A p value less than 0.05 was considered statistically significant.

3. Results and Discussion

3.1. Antioxidant Experiments

The DPPH free radical scavenging abilities of the positive control and plant extracts are expressed as a percentage of inhibition. Based on the values calculated from the linear standard curves (y = 2.002x; R2 = 0.9819) as in Table 1, the aqueous extract of A. kurdica showed high free radical scavenging activity towards DPPH with $69.4\% \pm 1.19\%$ inhibition. The ferric reducing ability of A. kurdica was $258.33 \pm 0.97 \text{ mmol/g}$ (Table 1). The FRAP value was calculated from a standard calibration curve equation (y = 0.0011x; R2 = 0.9987) as in Table 1. The TPC of A. kurdica was 80 ± 0.98 mg gallic acid equivalents per g of extract (Table 1). The potent radical scavenging effect is positively associated with the high content of phenolic components consistent to what has been previously reported by Gorinstein and coworkers (Gorinstein et al., 2003; Qader et al., 2011). Furthermore, Scalzo and coworkers (Scalzo, 2005) and Giorgi and coworkers (Giorgi et al., 2005) have demonstrated a correlation between antioxidant activity and TPC. Therefore, the antioxidant capacity of A. kurdica could be related to its phenolic content.

 Table 1. The antioxidant activity and total phenolic compounds of aqueous extract of A. kurdica

| Antioxidant | Gallic | Vitamin | Quercetin | А. | Standard |
|-------------------------|------------|--------------|-----------|--------------|----------------|
| assay | Acid | С | | kurdica | Curve |
| | | | | | Equation |
| DPPH | $88.8 \pm$ | $87.5~\pm$ | - | 69.4± | y = 2.002x |
| (%) | 0.41 | 0.02 | | 1.19 | $R^2 = 0.9819$ |
| FRAP | 1216.67 | $432.67 \pm$ | - | $258.33 \pm$ | y = 0.0011x |
| (mmol.g ⁻¹) | ± 1.02 | 0.14 | | 0.97 | $R^2 = 0.9987$ |
| TPC | - | - | $118\pm$ | $80 \pm$ | y = 0.9917x |
| (mg GA | | | 0.37 | 0.98 | $R^2 = 0.9984$ |
| eq. g ⁻¹) | | | | | |
| D DDII at | 100.00 | • -1s | | | 0.5.1 |

DPPH % and FRAP (mmol.g⁻¹) values represent the mean \pm SEM of triplicate experiments. "-": not used.

3.2. Antimicrobial Activity of A. kurdica Extract

The aqueous extracts of A. kurdica exhibited modest antimicobial activity against different microbial organisms (Table 2). The extract did not inhibit the growth of Staphylococcus aureus, Bacillus subtilis, Enterobacter aerogenes, Salmonella enterica, and Fusarium solani. On the other hand, it demonstrated modest antimicrobial activity against Escherichia coli, Pseudomonas aeruginosa, Candida albicans, Cladosporium macrocarpum, and Fusarium oxysporium. Among the tested microorganisms, the filamentous fungi Cladosporium macrocarpum and Fusarium oxysporium, were the most affected by the extract, with inhibition zones of 15 mm. Therefore, the A. kurdica plant is a potential source of novel antimicrobial compounds especially against some fungal and bacterial pathogens (Gram negative). The antimicrobial activity of this plant extract has been previously reviewed by Sharifi (2012). Generally, phenolic compounds have been illustrated to possess different bioactivities including free radical scavenging. Furthermore, the antioxidant activities of phenolics provide important protective mechanisms in a variety of disease conditions (Alshawsh et al., 2012). Several studies have reported that phenolic compounds mediate the antimicrobial activities of various plant extracts (Dordevic et al., 2007; Alshawsh et al., 2012; Ebrahimabadi et al., 2010). Hence, this study has evaluated A. kurdica's antioxidant and phenolic contents as well as its antimicrobial activity.

| Organisms | Bacter | Bacteria | | | | | Fungi | | | |
|-----------------|--------|----------|---------------|------|-----|--------------|-------------|-----|-----|-----|
| | Gram | Positive | Gram Negative | | | Unice-llular | Filamentous | | | |
| | B.s | S.a | E.a | S. e | P.a | E.c | C.a | C.m | F.o | F.s |
| Inhibition Zone | | | | | | | | | | |
| (mm) | | | | | | | | | | |
| AKE | 00 | 00 | 00 | 00 | 12 | 12 | 13 | 15 | 15 | 00 |
| S 10µg | 14 | ND | ND | ND | ND | 12 | 00 | ND | ND | 00 |
| TE 30µg | 18 | ND | ND | ND | ND | 23 | 00 | ND | ND | 00 |
| N 30 µg | 0 | ND | ND | ND | ND | 00 | 16 | ND | ND | 15 |
| NY 100µg | 0 | ND | ND | ND | ND | 00 | 00 | ND | ND | 15 |

Table 2. The antimicrobial activity of A. kurdica aqueous extract

AKE A. kurdica extract, B.s: Bacillus subtilis. S.a: Staphylococcus aureus. E.a: Enterobacter aerogenes. S.e: Salmonella enterica. P.a: Pseudomonas aeruginosa. E.c: Escherichia coli). C.a: Candida albicans. C.m: Cladosporium macrocarpum. F.o: Fusarium oxysporum. and F.s: Fusarium solani. 00 = no inhibition zone. ND = not detected, S: streptomycin. TE: tetracycline (TE), N: neomycin, NY: nystatin.

3.3. MTS Assay

In this study, normal lung fibroblast cells (Hs888Lu) have been used for toxicity evaluation. The results of cytotoxic activity of aqueous extract of *A. kurdica* are summarized in Figure 1. Data were expressed as percentage of the value observed with no plant treatment (control). Cytotoxicity has been assessed using different concentrations of the extract. None of the extract concentrations had any cytotoxic effect as there were no significant differences (P < 0.05) between the cytotoxicity of the plant extract concentrations and the control. Previous studies have used normal lung cells as a model to evaluate toxicity (Najim *et al.*, 2010). This is the first time that the cytotoxic activity of *A. Kurdica* has been assessed against the human normal lung fibroblast cell line Hs888Lu.

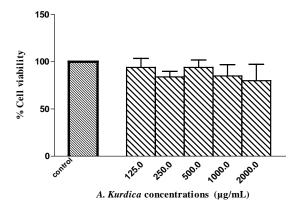


Figure 1. Cytotoxic activities of aqueous of *A. kurdica* in normal lung fibroblast Hs888Lu cell line at concentrations of 125-2000 μ g/mL and 24 hrs exposure times. Each bar represents the mean \pm SEM of triplicates. Control: no plant extract treatment.

4. Conclusion

In the present study, *A. kurdica* exhibited potent antioxidant activity which might be useful for the therapy or management of disorders involving ROS-mediated pathology. Further *A. kurdica* demonstrated interesting antimicrobial activity against growth of selected microorganisms. Notably, the plant extract did not have any cytotoxic effects against the normal lung fibroblast (Hs888Lu) cell line. Ultimately, this study confirmed that the aqueous extract of *A. kurdica* is able to scavenge free radicals and possessed modest antimicrobial activity.

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Conflict of Interest

The authors declare no conflicts of interest.

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Mating Frequency, Duration and Time in Baluchistan Melon Fly Myiopardalis pardalina (Bigot) (Diptera: Tephritidae)

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Abstract

Myiopardalis pardalina (Bigot) (Diptera: Tephritidae) is one of the injurious pests that damage melon fruits. The male sterility technique is one of the genetic methods that have been proposed for controlling fruit flies. This method is more effective in once-mated females. So mating frequency, starting time and mating duration by females and males of Baluchistan melon fly were studied in the laboratory (Department of Entomology, Institute of Plant Protection, Tehran, Iran). Mean number of matings/female was 5.83 ± 0.48 during the 8 day test period. The presence or absence of the host did not have any significant influence on mating frequency. The mean number of matings/male was 6.26 ± 0.45 . Mating predominantly occurred in early afternoon. Mating duration in female and male series was 4.95 ± 0.598 and 6.822 ± 0.378 hours, respectively. The first mating usually took longer in comparison with other matings.

Keywords: Mating frequency, Baluchistan melon fly, Myiopardalis pardalina, Mating duration, Mating time

1. Introduction

Insect reproduction involves two behaviors: mating and oviposition (Jimenez-Perez and Wang, 2003). In general, copulation is assumed to be costly for many reasons (Hunter *et al.*, 1993). Females of many diverse animal species mate multiple times in nature (Andersson, 1994; Johnson and Burley, 1997). Such multiple mating is performed with different male partners as in the fruit fly, *Drosophila melanogaster* (Fuerst *et al.*, 1973). However, sometimes females remate with the same male partner (repeated mating) (Hunter *et al.*, 1993). Repeated mating is only reported for a limited number of species (Petrie, 1992; Petrie *et al.*, 1992; Hunter *et al.*, 1993; Choe, 1995; Lens *et al.*, 1997; Andrade and Mason, 2000).

The frequency of mating in Tephritid fruit flies is an important aspect of their sexual behavior. It is relevant to the development of those pest control programs based in part on sexual interactions. For example, sex attractants developed for females may be more effective for species that remate frequently and may then repeatedly respond to male sex pheromone (Landolt, 1994). A multiple mating may increase the predation risks associated with searching for and mating with males, either because females have to search in risky areas(Koga *et al.*, 1998) or because during mating vigilance and mobility are reduced (Jennions and

Petrie, 2000). Females receiving multiple male contributions lay more eggs (Ridley, 1988) and often larger ones (Fox, 1993) than do once-mated females, indicating a large effect of male derived nutrients on females reproduction (Fox *et al.*, 1995). A number of hypotheses have been proposed to explain the occurrence of multiple mating, and there is a general empirical support for these (reviewed in Petrie *et al.*, 1992).

In many insects, females are receptive for much of their adults' life and so mate more than once. However, the evolution of patterns of female receptivity leading to multiple mating in short-lived animals is something of a mystery because the cost to females of mating more than once (increased risk of predation, time lost from feeding and oviposition) usually appear to out weight the benefits (Thornhill and Alcock, 1983; Jennions, 1997).

The potential or hypothesized benefits for females of multiple mating fall into two general classes: material benefits and/or genetic benefits (Reynolds, 1996). In general, material benefits enhance female fitness directly through increased numbers or size of eggs, whereas genetic benefits enhance female fitness indirectly through increased genetic quality of offspring (Zeh and Zeh, 1996). Material benefits may include nutritional resources from nuptial gift from males (Gwynne, 1997; Eberhard, 1996), a reduction in male harassment (Rubenstein, 1984; Arnqvist, 1989), and replenishment of sperms if one

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mating provides insufficient sperms to fertilize all the eggs a female which may produce in her lifetime (Thornhill and Alcock, 1983). Alternatively, genetic benefits of multiple mating may include opportunities to manipulate offspring paternity (Birkhead and Mollar, 1992; Ridley, 1993), and to avoid inbreeding (Brooker *et al.*, 1990; Madsen *et al.*, 1992). Also, it can decrease the chances of fertilization by sperm that are genetically defective due to their age (Halliday and Arnolds, 1987) or incompatible genotype (Zeh and Zeh, 1996). In some lepidopteran species the number of apyrene sperm in the spermatheca may influence female remating (He *et al.*, 1995).

The mating frequency varies among females of species of fruit infesting tephritids. Females of the apple maggot fly, Rhagoletis pomonella (Walsh) mate frequently, as often as weekly, possibly to maintain fertility levels (Prokopy and Roitberg, 1984). The Mediterranean fruit fly, Ceratitis capitata Wiedemann (Nakagawa et al., 1971), and Anastrepha suspense (Loew) (Sivinski and Heath, 1988), are thought to mate usually once, with rematings due either insemination failures at first mating or to sperm depletion following extensive oviposition. In papaya fruit fly, Toxotrypana curvicauda Gerstaecker, the most mature females mated more than once when held with immature papaya fruit (Landolt, 1994). The Baluchistan melon fruit fly, Myiopardalis pardalina is one of the important pests in Iran that attack melon varieties and peppo. The mean damage annually reaches 30-80% on melon varieties in Iran (Sirjanii, 1995; Eppo, 2013). However this study aimed at investigating the mating frequency of *M. pardalina*, in order to gather basic information needed for evaluating the possibility of using the male sterility technique or sex attractants for management and control of this pest.

2. Materials and Methods

Baluchistan melon fruit flies were obtained as mature larvae (3rd instar) from infested melon fruit collected from open fields in the Varamin area of Tehran province-Iran. After getting out of fruit, the larvae were pupated in potting soil. Pupae were screened and transferred to special cages for adult emergence. Newly emerged adult flies were daily sorted by sex (females have an obvious ovipositor) and kept in separate cages and fed with a solution of sucrose: protein hydrolysate in (5:1 w/w) ratio. The cages were kept under laboratory conditions of $28\pm2^{\circ}$ C temperatures, $50\pm10\%$ RH, and natural light conditions during July till August, nearly 16 L: 8 D h. The authors can do this easily.

Mating frequency was determined in the following series: A) mature female held with green immature melon (2-4 cm in diameter and 5-8 cm in length, as a preferred oviposition site (Sirjanii, 1995)), B) mature females without fruit, C) males without fruit, and D) paired females and males with fruit. In series (A), reproductively mature females (3-day-old) (Sirjanii, 1995) were separately kept per cage from 08:00 to 20:00 hours every day for a period of 8 days. Each morning at 08:30, a male (virgin and the same age as the female) was kept in each cage and observations were made at 30-min- interval until

20:00 hs, then the male was removed (if the mating was finished). Because matings on average take 264 min (Sirjanii, 1995), it was assumed that none would be missed if observations were made every 30 min. At each observation time, mating recorded and oviposition monitored of females held with fruit. All the matings that lasted less than 30 min were assumed to be followed by rejection and omitted from the results. After flies mated, the male was replaced. Twenty-five females were separately held with males and melon fruit within the cages that included a small cup of sugar and water on cotton. In the (B) series, the same number of females was separately held with males, without melon fruit. During the experiments conducted to determine mating frequency of females without fruit, melon was also excluded from the laboratory to avoid the host odor effects on mating behavior. In series (D) the mating frequency of a given pair with fruit was observed during the 8-day period in thirty-five series to determine the occurrence of repeated matings with the same male. In this experiment, the male was not excluded from the cage throughout the test. To assess mating frequency of males (series C), a similar protocol was followed. For eight consecutive days, at 08:00 hours, a mature virgin female was kept in each cage containing one male. Observations were made each 30 min, until 20:00 hs, when the female was removed (if mating was finished). The female was replaced after each copulation, with another mature virgin female. This was done for 17 mature individuals (≥ 3 days old). All the males were held without melon fruit. In addition, the time when mating began, copulation duration and the daily rhythm of mating (dN/dt) were also recorded and differences between various series were compared. The daily rhythm of mating was determined by dividing the number of matings that happened in all of replicates during each age to number of replicates.

2.1. Statistical Analysis

Mean mating frequencies for all the series were compared using Student t-test (Gomez and Gomez, 1984). Also, the mating frequencies, the time of mating initiation, copulation duration and dN/dt were compared in all the series using Duncan's Multiple Range test (SAS 9.1, SAS Institute, Inc). The data were analyzed at a probability level of 0.05.

3. Results

In series A, females, held in cages with melon fruit, mated more than 5 times, with most females mating more than once. Mean (\pm SE) number of matings/female was 5.83 \pm 0.48 (n=25) during the 8-day test period. In series B, all females, held in cages without fruit, showed multiple mating. Mean number of matings/female was 5.36 \pm 0.39 (n=25) during the test period. There were no significant differences between series A and B (P > 0.05). In series C, males mated more than six times over the course of the 8-day test period, with nearly all mating multiple times. Mean number of matings per male was 6.29 \pm 0.45 (n=17). Mean number of matings in series (D) (remating with the same male) was 5.63 \pm 0.38 (n=35), which did not reveal any significant difference with series (B) and (C). Also, the daily mean mating frequency (dN/dt) was determined

(Table 1). These results showed a significant decrease of dN/dt for the 8-9 days old females in (A) series (P <0.01). Matings by females in different test series were predominant during the early part of afternoon (14-18 hs) (Figure 1) and showed a significant difference with the other observational periods (P < 0.01). This time showed some variations based on different times of mating (Table 2). The mean mating duration in series A and C were 4.95±0.598 and 6.822±0.378 hs, respectively, and showed significant differences between series based on history of mating (Table 3). The first mating in series A showed longer duration and other arrangements showed significantly irregular fluctuations. Longer mating duration observed in second mating in series C. The duration of first and third mating in series A and C were similar but in other matings the copulation duration in series A was shorter than that in series C. Also it's revealed that the initial mating in each series lasted more than the final mating (Table 3).

Table 1. Daily mean(±SEM) mating frequency(dN/dt) in relation to adult age in *M. pardalina*.(N=10).

| Age(days) | Series A* | Series C | Series D | |
|-----------|------------|-----------|------------|--|
| 3 | 1±0.0001a | 0.9±0.1a | 0.9±0.1a | |
| 4 | 0.7±0.15b | 0.8±0.13a | 1±0.0001a | |
| 5 | 0.8±0.13ab | 0.9±0.1a | 0.9±0.1a | |
| 6 | 0.7±0.15b | 0.9±0.1a | 0.8±0.13ab | |
| 7 | 0.9±0.1a | 1±0.0001a | 0.8±0.13ab | |
| 8 | 0.2±0.13c | 1±0.0001a | 1±0.0001a | |
| 9 | 0.2±0.13c | 1±0.0001a | 0.6±0.16b | |

Series A: mature female held with fruit for determination of multiple mating in females , *Series C*: mature males without fruit , for determination of multiple mating in males , *Series D*: same pair for determination of repeated mating. * Means within columns followed by the same lower-case letter are not significantly different at the 5% level by Duncan's multiple range test.

Table 2. The mean $(\pm SE)(n)$ of starting time(h) of copulation in different series based on mating history in *M. pardalina*.

| Mating | Series A* | Series C | Series D | |
|-----------------|------------|-----------------|------------------|--|
| arrangement | | | | |
| 1^{St} | 14.27±0.54 | 15.14±0.6 | 14.61±0.36 | |
| | (18)b | 7 (30)a | (28)a | |
| 2^{nd} | 16.38±0.4 | 12.94±0.8 | 15.07±0.32 | |
| | (15)ab | 1 (28)a | (28)a | |
| 3 rd | 15.57±0.44 | 13.56±0.5 | 15.4 ± 0.36 | |
| | (18) ab | 5 (22)a | (25)a | |
| 4 th | 17.16±0.52 | 14.5 ± 0.51 | 15.83 ± 0.43 | |
| | (15)ab | (15)a | (23)a | |
| 5 th | 17.63±0.55 | 14.78±0.4 | 16.22±0.3 | |
| | (16)a | 8 (14)a | (23)a | |
| 6 th | 18.83±1.3 | 15.03±0.6 | 16.85±0.4 | |
| | (15)a | 1 (15)a | (23)a | |

Series A: mature female held with fruit for determination of multiple mating in females *Series C*: mature males without fruit, for determination of multiple mating in males *Series D*: same pair for determination of repeated mating *: Means within columns followed by the same lower-case letter are not significantly different at the 5% level by Duncan's multiple range test.

Table 3. The mean $(\pm SE)$ (n) of mating duration in different series based on mating arrangement in *M. pardalina*.

| Mating | Series A (Females) | Series C (males) |
|-----------------|------------------------------|------------------------------|
| arrangement | $M \pm SE$ | $M\pm SE$ |
| 1^{st} | 7.383 ± 0.51 (30) (a)A* | 6.861 ± 0.66 (18) (a) AB |
| 2^{nd} | 3.768 ± 0.49 (28) (a)C | 8.292 ± 0.74 (18) (b) A |
| 3 rd | 5.705 ± 0.57 (22) (a)B | 6.722 ± 0.66 (18) (a) AB |
| 4^{th} | 4.679 ± 0.56 (14) (a) BC | 7.833 ± 0.44 (16) (b) AB |
| 5 th | 4.563 ± 0.66 (14) (a) BC | 6.625 ± 0.35 (16) (b) AB |
| 6 th | 3.33 ± 0.35 (11) (a) C | $6.1 \pm 0.7 (15) (b)$ AB |
| $7^{\rm th}$ | - | $5.318 \pm 0.57 \ (15) \ B$ |

* Means within columns followed by the same upper-case letter or within rows followed by the same lower-case letter are not significantly different at the %5 level by Duncan's multiple range test.*Series A*: mature female held with fruit for determination of multiple mating in females *Series C*: mature males without fruit, for determination of multiple mating in males.

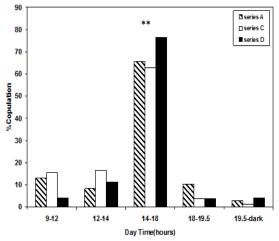


Figure 1. Daily rhythm of mating in *Myiopardalis pardalina* in different series.

Series A: mature female held with fruit for determination of multiple mating in females

Series C: mature males without fruit, for determination of multiple mating in males

Series D: same pair for determination of repeated mating

**: This time period was significantly different with others at the 1% level.

4. Discussion

During the course of the present study, experiments were conducted to investigate the female and male remating with respect to host fruit availability. These data indicate that the Baluchistan Melon fly typically mate more than once regardless of access to host fruit. This finding appears to be opposite to what is known for other species of frugivorous Tephritidae. In Caribbean fruit fly, *A. suspensa*, 60% of females can remate only when they have access to fruit as oviposition site (Sivinski and Heath, 1988). Sixty percent of Mediterranean fruit fly females held in cages with fruit for oviposition remated (Nakagawa et al., 1971) and 50% of the Mexican fruit fly, Anastrepha ludens (Loew) females provided wax oviposition domes remated (Robacker et al., 1985). In T. curvicauda, remating was observed only when females were kept in cages with both males and immature papaya fruit (Landolt, 1994). Multiple mating in tephritid fruit flies is thought to be due to: (1) forced matings by males controlling access to oviposition sites as in R. pomonella (Walsh) (Prokopy and Roitberg, 1984). (2) Poor sperm transfer in initial matings as suspected in part for C. capitata (Wiedemann) (Nakagawa et al., 1971), or (3) sperm depletion following extensive oviposition as in A. suspensa (Sivinski and Heath, 1988). As Baluchistan melon fly females showed multiple and repeated mating (Hunter et al., 1993) with or without access to host fruit, it is unlikely that multiple and repeated matings are the result of a forced copulation by males or sperm depletion following oviposition. The observed increased remating rates of females held with or without host fruit indicate that poor sperm transfer during matings may be contributed to multiple and repeated matings. An additional possibility is that females need nutrients that may be transferred by males in their ejaculates. In another study, radioactively labeled substances in the ejaculate of A. suspense were later recovered in the unfertilized eggs and tissues to mated females (Sivinski and Smittle, 1987). Male Baluchistan melon flies mated like females (P < 0.05) which is an indication of their potential for polygamy. These results are similar to those reported for males of C. capitata (Nakagawa et al., 1971) and T. curvicauda that males mated three times more often than females (Landolt, 1994). Copulation duration in series A was shorter than that in series C except for the first copulation (P < 0.03) (Table 3). It may be hypothesized that the first mating is longer in order to transfer sufficient number of gametes to fertilize all of the female eggs. The other matings may occur to compensate decreased sperm or to take a large number of accessory substances that are transferred with the ejaculate, and which may have a profound effect on female reproductive behavior (Chen, 1984; Gillott, 1988; Eberhard and Cordero, 1995; Eberhard, 1996; Klowden, 1999; Arnqvist and Nilsson, 2000). Also, the long mating duration may be a strategy that male selected for post insemination associations.

In some species, males maintain genital contact for beyond the time needed strictly for insemination of the female (Alcock, 1994). Prolonged copulation has been reported for insects in many orders, including the Odonata, Phasmida, Lepidoptera, Diptera, Coleoptera, Hymenoptera and Heteroptera (Alcock, 1994). In fruit flies mean mating times vary from 110 second in Anastrepha pseudoparallela to 24 hours in Euarestoides acutangulus (Headrick and Goeden, 1994; Sivinski et al., 2000). The extension of copulation beyond what is required for sperm transfer in related species of fruit flies are often interpreted in terms of sperm competition avoidance (Parker, 1970), protection from predators (Sivinski, 1981), or cryptic female choice (Eberhard, 1996; Belford and Jenkins, 1998; Sivinski et al., 2000). Furthermore if the mating continues into the night, beyond the sexual signaling period, when no other males

would be searching for mates. However, in some species (e.g., A. suspensa), females appear to have a considerable control over mating durations; because males have a difficult time maintaining their position when females become restless and move about (Sivinski et al., 2000). In M. pardalina, most of the copulation was observed in the 14-18 hours period in the afternoon (Figure 1). The first mating lasted at least five hours and may be continued into the night. But the following matings lasted shorter than the first (Table 3). So the mating duration can be due to three reasons: (1) compensation of sperm depletion, (2) to take a large number of accessory substances that are transferred with the male ejaculate and (3) post insemination association with maintained genital contact until the dark. The results clearly indicated that male sterility techniques (MST) may not be a successful way to control M. pardalina, because females mated more than 5 times during one week. But it seems that the sex attractants could be attractive several times to females and may be useful in their IPM.

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Relationship of Biometric Size-Weight, Nutritive Value, and Metal Concentrations in *Clarias lazera* (Cuvier and Valenciennes) Reared in Treated Wastewater

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Abstract

The objective of the present study was to investigate the nutritive value and heavy metals accumulation in the flesh of *Clarias lazera* (Cuvier and Valenciennes) reared in the discharge canal of Soba wastewater treatment station, south Khartoum, Sudan. A total of 57 fish were collected from the canal and 52 from the White Nile which served as the control. The proximate composition of fish and concentrations of eight hazardous heavy metals i.e. chromium (Cr), iron (Fe), copper (Cu), zinc (Zn), lead (Pb), robidium (Rb), strontium (Sr), and mercury (Hg) in the flesh of *C. lazera* were measured. The results which were statistically analyzed revealed insignificant differences in moisture, ash, fat contents, energy value, and fat: protein ratio (P>0.05) between the two studied sites. A significant difference (P<0.05) was evident in the protein content of fishes from both locations. Heavy metals accumulation in *Clarias* tissues differ from one element to another depending on each element characteristics and local environmental conditions e.g. Sr was higher in the White Nile fishes than in treated wastewater fishes (P<0.05). Accumulation of Pb and Hg was comparable in wastewater and White Nile (P<0.05). Cr was also higher in treated wastewater fishes (P<0.05). Nevertheless, the concentrations of most considered elements were lower than levels recommended by various international agencies.

Key words: Clarias lazera, Heavy metals, Accumulation, White Nile, Treated wastewater.

1. Introduction

Treated wastewater was used in 19th century in Europe to irrigate crops (Ensink and van der Hoek, 2007). Reuse of treated wastewater for fish aquaculture is practiced in many countries including India (Bunting, 2006), Egypt (Misheloff, 2010), and Netherland (Oberdieck and Verreth 2009). As water demand becomes an increasingly important concern in many places, and especially essential for the increasing human population, fish farming falls within the many options which exist for productive wastewater treatment design systems (WHO, 2006). Popular fish species suitable for fish farming in treated wastewater include catfish, tilapia spp. trout, carp, and many others. The annual production depends on fish species, local and environmental conditions. According to Girard (2011), there are many constraints to reusing treated wastewater for rearing fish, such as lack of knowledge, limited available sites; rapid urbanization, rapid eutrophication, improved sanitation, rapid industrialization contamination, social and cultural acceptance and climate. The pathogen transmission risk through treated wastewater fish farming represents a controllable risk; i.e., pathogen loads can be reduced to acceptable levels if adequate measures are adopted (Straus 1996). Microbial requirements for waste-fed aqua cultural schemes should be compatible with background levels in natural waters, since the harvesting of fish and other aquatic animals is generally unrestricted and socially accepted.

Fish is one of the most important available sources of animal protein in the tropics, and has been widely accepted as a good source of protein and other elements for the maintenance of a healthy body (Tidewell and Allan, 2001). Heavy metals are persistent contaminants in the environment that come to the forefront of dangerous substances such as cadmium, lead, mercury, copper and zinc that cause serious health hazards to humans and animals (Ahmed *et al.*, 1998). The agricultural and

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industrial wastes, partially treated or untreated regularly, are being discharged into surface water (Forstner and Wittmann, 2007). Heavy metals present in such polluted waters are absorbed through gills, skin and digestive tract of fish by bio-concentration and bio-magnification. Heavy metals are natural trace components of the aquatic environment, but their levels are increased due to domestic, industrial, mining and agricultural activities (Mance, 1987; Kalay and Canli 2000). At low levels, some heavy metals such as copper, cobalt, zinc, iron and manganese are essential for enzymatic activity and many biological processes. However, the essential metals may also become toxic at high concentrations (Bryan 1976 and Authman et al., 2012). Other metals, such as Cd, Hg, Pb play unknown essential roles in living organisms, and are toxic at even low concentrations (Authman et al., 2013).

Clarias lazera (Cuvier. and Valenciennes) is a freshwater fish which attracts attention as a potential fish for aquaculture (Babiker, 1984). According to Chervinski (1984), presence of a breathing apparatus enables the fish to withstand low level of oxygen and a wide range of temperatures. It is an omnivorous feeder found mainly in shallow waters; young ones feed on ostracods and aquatic insects while adults feed on any potential food like zooplankton and molluscs, but mainly on fish e.g. *Oreochromis niloticus* (Amirthalingam and Khalifa, 1965).

The aim of this study was to highlight the implications of the reuse of treated wastewater for fish culture, and to examine and compare the levels of toxic heavy metals accumulation in the muscle tissue of *C. lazera* from the polluted discharge canal of Soba wastewater treatment station and non-polluted of Jebel Aulia Reservoir on the White Nile, south Khartoum, Sudan. The proximate chemical composition and condition factor of fish were studied as complementary aspects. The present study is expected to shed light on the importance of the reuse of treated wastewater for fish farming and its promising role in contributing to provide a safe food for the increasing Sudanese population.

2. Materials and Methods

A total of 57 specimens of *C. lazera* (Arabic Garmouth) were collected from the effluent (discharge) canal carrying the treated wastewater from the maturation ponds, in addition to 52 specimens from the White Nile in the vicinity of Jebel Aulia Dam (control). Fish samples were collected from local fishermen during the period April 2012-April 2013. The canal (Figure 1) is located in the Southern part of Khartoum State ca. 15 Km, (15°29' 55"; 15°30' 25" N; 32°32' 36" – 32°36' 06" E).

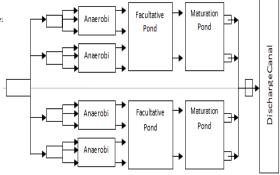


Figure 1: Ponds arrangement, flow pattern and the effluent discharge canal in Soba Wastewater Stabilization Station (Source: Ali and Hag Ibrahim, 2005).

The 2^{nd} site, Jebel Aulia dam on the White Nile, was built in 1937 ca. 50 Km south of Khartoum to store $3.5X10m^9$ of water (Rzoska *et al.* 1955). The dam length is 5 km and creates a large lake with a width ranging between 1-4 km and a maximum depth 22.5 m. As a result of the dam, a large shallow lake of about 12000 hectares was formed capable of storing 3.5 milliard m³. The maximum depth of the reservoir is ca. 15 m attained during high flood (August-mid September).

For each fish specimen, the total and standard lengths were measured, and then each fish was weighed. The condition factor (K) was calculated according to Le-Cren, 1951 equation:

$K = 100.W/L^3$

W is fish body weight (g) and L is fish total length (cm) $% \left({{{\mathbf{r}}_{\mathrm{m}}}} \right)$

Fishes were sexed and aged using vertebrae. Use of vertebrae for age determination was proved to be one of the reliable structures for fish ageing (Bishai and Abu Gideiri 1965, Mishrigi 1967, Bishai 1970, Gumaa 1974 and Tweddle 1975). Otolith was not used for aging C. lazera because its major advantage over other tissues e.g. scales and vertebrae is the presence of clearly visible daily lines (Pannella 1974). In addition, preparation of otoliths for light microscopy or scanning microscope (Liew 1974) is rather difficult and requires facilities not available in our institutes. Sexual maturity was determined according to Nikoliskii (1963). The stomach food content was investigated using the method described by Hynes (1950) where stomachs contents are examined and the individual food organisms was sorted and identified. The number of stomachs in which each item occurs is recorded and expressed as a percentage of the total number of stomachs examined. The collected fish were then skinned; the flesh was taken from different sites of the body to make sure that the examined sample is well representative to the whole body. Flesh samples were kept in air-tight plastic bags and frozen at 0.0-5.0°C till they were used for moisture determination. and ash contents

The frozen samples were then freeze-dried for 24 hrs using (Edwards High Vacuum 2507 Freeze Dryer). The dried samples were ground using a non metallic mortar. Powder samples were then kept in the air-tight plastic bags. All chemical constituents were determined according to Pearson 1976 and AOAC 1980. These include moisture; protein, fat and ash contents. Protein was evaluated by Micro-Kjeldahl Method; fat content by using soxhelt extraction method. The energy value was calculated from the fat and protein contents of samples using the values 9.02 Kcal./gm for fat content and 4.27 Kcal./gm for protein content as recommended by FAO (1989).

X-ray fluorescence spectroscopy (XRF) was used for qualitative and quantitative determination of heavy metals (Tertian and Claisse 1982). These are namely: Cr, Fe, Cu, Zn, Pb, Rb, Sr and Hg. According to Talbot (1987), XRF has the potential and capacity to give accurate linear response to a broad spectrum of elements in approximately 0.0-500 mg/Kg-1.

The data obtained was statistically analyzed using SPSS package (t-test for normal data and Mann Whitney u test for data not normally distributed).

3. Results and Discussion

The results of the present study (Table 1) showed greater sizes and weights of fishes in treated wastewater compared to those collected from the White Nile (P<0.05). The same applies to standard lengths although the difference was insignificant (P>0.05). According to Mason 1991, such results are possibly attributed to the availability of food in treated wastewater and the presence of organic matter which is rich in proteins, carbohydrates, and fats.

 Table 1: Weights and standard lengths of C. lazera in treated wastewater and White Nile

| Parameter | Treated Wastewater | White Nile | Р |
|-----------------|--------------------|------------|----|
| Weight (gm) | 528.96±38.9 | 360±45.90 | * |
| Standard length | 35.04±1.14 | 30.94±1.21 | NS |

The condition factor of fish reared in both study sites was calculated to evaluate fish situation. The mean condition factor of fish was found to be 1.23 g/cm³ and 1.22 g/cm³ in treated wastewater and White Nile, respectively. Both values were above 1.0 indicating good conditions of the fish (Barnham and Baxter 1998), however, they were below those obtained by Nwabueze 2013 for *Clarias anguillaris*. Furthermore, King (1995) attributed differences in condition factors of fish to food abundance, adaptation to the environment and gonadal development. According to Aloo (1999), the intensity of infection with *Contracaecum* was increased with the increase in the size of bass *Micropterus salmoides*, from Lake Naivasha and the Oloidien Bay, Kenya

Only two stages "I and IV" were observed out of Nikoliskii (1963) six stages for sexual maturity (Stage 1, Immature; Stage 11, quiescent; Stage 111, maturing: Stage 1V, mature: Stage V running; Stage V1, Spent).

Table 2 illustrates the difference in body weight according to sex, age and maturity stage and the results gave an insignificant difference with sex and maturity stage (P>0.5) in both localities. However, weights of mature fish were higher than immature fish. Regarding age, a significant difference was encountered (P<0.05) in weights of fish; older fish weights were higher than younger ones in both sites.

Figure 2 shows the moisture, ash, fat and protein contents which were examined to assess the fish flesh quality. The fat/protein ratio was calculated to indicate the nutritive value of flesh. Protein content in wastewater fish was higher than in the White Nile (P<0.05). Fat, moisture content and fat/protein ratio were almost similar (P>0.05) in the two sites (0.212 for Treated wastewater and 0.217 for the White Nile).

The food value of fish is normally estimated as the percentage of the edible portion to the total weight of fish and its contents of the basic nutrients i.e. fats and proteins (Karrar, 1997). In the present study, the energy values calculated were 0.0683 and 0.0629 for wastewater and White Nile fish, respectively. These figures indicate that the nutritive values of the fish from both study sites are comparable; however, freshwater fishes are slightly more nutritious due to their low fat/protein ratio.

Table 2: Variation in body weights of C. lazera in treated wastewater and White Nile according to sex, age group and maturity stage

| | Sex | | Age Groups | | | Maturity stage | | | |
|--------|--------------------------------|--------------|------------|-------------------|------------|--------------------|-----------------------|-------------|------------|
| | Treated wastewater | White Nile | | eated stewater | White Nile | | Treated Wastewater | | White Nile |
| Male | $459.38{\scriptstyle\pm}~63.5$ | 392.00±86.60 | 1 | 427.20±29.8 | 1 | 308.60±29.30 | А | 371.04±33.5 | 336.8±58.7 |
| Female | 575.35+63.50 | 333.28±42.20 | 2 | 936.03±53.1 | 2 | 1480.00 ± 10.0 | В | 714.40±53.7 | 426.4±10.0 |
| Р | NS | NS | * | | * | | * | | * |

*significant; NS insignificant

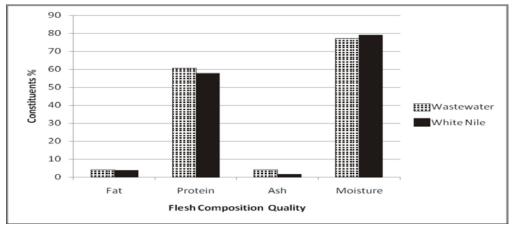


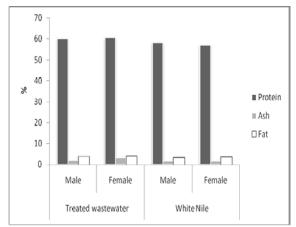
Figure2. Chemical composition of C. lazera in treated wastewater and White Nile

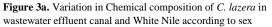
The energy value was higher in the White Nile fish (445.911+17.23 Kcal / 100 gm) than in wastewater $(414.540\pm8.394 \text{ Kcal} / 100 \text{ gm})$, but the difference was insignificant (*P*>0.05).

Figures 3a, 3b and 3c illustrate no significant difference in fat, protein and ash contents with sex, age and maturity stage, respectively (P>0.05). Exceptions were encountered in females' fat content in the White Nile that showed significantly higher values than in males (P<0.05).

Proximate composition showed no significant variation according to sex in both localities. This finding is in agreement with Mohammed *et al.* (1988) who assessed the chemical composition of *Mugil cephalus* along the Sudanese Red Sea Coast. Also proximate composition showed no significant variation with age. That result was in contrast to Dambergs (1963), but older fish reflected slight insignificant increase in fat and protein contents.

Protein and ash contents were insignificantly higher in mature fish in both study sites and that was also in contrast to Dambergs (1963), but fat content showed insignificantly higher levels in the immature fish. According to Hoar (1957), fat storage in the muscle tissue increased prior gonads maturation to provide energy for spawning activities.





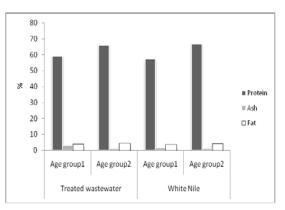


Figure 3b. Variation in Chemical composition of *C. lazera* in wastewater effluent canal and White Nile according to age group (age group 1: 1, 2 and 3 years; Age group 2: 4 and 5 years)

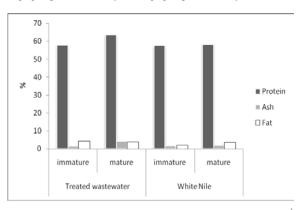


Figure 3c. Variation in Chemical composition of *C. lazera* in wastewater effluent canal and White Nile according to age

Concentrations of Fe, Cu, Zn and Rb (Table 3) were significantly higher in treated wastewater fishes than natural water fishes (P<0.05). In view of this, they were further analyzed with sex, age group, and maturity stage (Figures4a, 4b, 4c). Fe and Zn showed no variation with all the previously mentioned parameters in both study sites (P>0.05). Cr was also higher in treated wastewater fishes (P>0.05). Hg and Pb concentration was higher in treated wastewater than the White Nile. Statistically, the two heavy metal expressed insignificant difference ((P>0.05). Sr was significantly higher in the White Nile compared with treated wastewater (P<0.05).

 Table 3. Heavy metals concentrations in C. lazera in treated wastewater and White Nile

| Conc. (ppm) | Wastewater | White Nile | Р | Permissible limits (µg/g wet weight) |
|----------------|--------------------|--------------------|----|---|
| Cu | $4.86{\pm}0.56$ | $1.26{\pm}0.16$ | * | 3.280 "IAEA 2003; FAO 1983a"; 20 "MAAF 2000" |
| Rb | $177.63{\pm}23.18$ | $12.89{\pm}\ 1.54$ | * | 2.86 "IAEA 2003" |
| Cr | $0.05{\pm}\ 0.02$ | 0.03 ± 0.01 | NS | 0.730 "IAEA 2003" |
| Fe | $72.64{\pm}12.60$ | 6.94±0.93 | * | 146 "IAEA 2003" |
| Zn | 497.20± 44.7 | 37.83±7.04 | * | 30 FAO 1983a; 40 FAO/WHO 1989 |
| Hg | 60.03 ± 1.30 | 57.42±3.32 | * | 0.222 "IAEA 2003"; 0.50 "EC 2006" |
| Pb | $0.17{\pm}\ 0.02$ | $0.09{\pm}0.01$ | * | 0.2 "EC 2005" |
| Sr | $2.7\ 3\pm 2.46$ | 17.55 ± 10.35 | * | 130 "IAEA 2003" |

These results are in agreement with the findings of many authors e.g. Clement and Lovel (1994) and Gomez (2011). However, ash content was significantly higher in treated wastewater fishes (P<0.05). The concentrations of most elements considered in this study were lower than levels recommended by the international agencies e.g.EC (2006); EC (2005); IAEA (2003); FAO/WHO (1989); FAO (1983a). Rb showed significant variation with sex and age in both study sites but not with maturity stage. Cu concentration showed no variation with sex in both study sites (P>0.05). However, it gave significant differences with age in the two studied sites. With maturity stage, Cu was much higher in treated wastewater fish and expressing a significant difference (P<0.05).

Treated wastewater fish were found to accumulate considerable amounts of heavy metals compared with White Nile fish. This is likely because metals have certain properties which make them difficult to treat or remove from wastewater if not treated by certain chemical methods (Mubarak, 2014), and living organisms usually form an intimate relationship with the chemical composition of their environment (Elgobashy et al. 2001). According to Jezierska and Witeska (2006), fish living in polluted waters tend to accumulate heavy metals in their tissues. Generally, accumulation depends on metal concentration, time of exposure, way of metal uptake, environmental conditions (water temperature, pH, hardness, salinity), and intrinsic factors (fish age, feeding habits). Concentrations of Pb and Hg in treated wastewater fish were almost similar to fish of natural nonpolluted water possibly because surface water does not always reflect the real situation of heavy metals pollution. This is expected since the physico-chemical characteristics of water normally affect the distribution of metals in water. In addition, Karrar (1997) reported that some metals have the property of being rapidly adsorbed to particulate materials like detritus and suspended sediments. Moreover, some biological processes like uptake by planktons through assimilation can exert the same effect (Abu Gideiri, 1980).

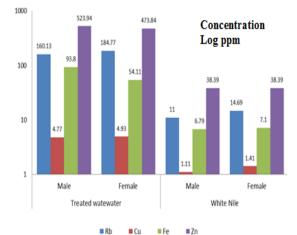
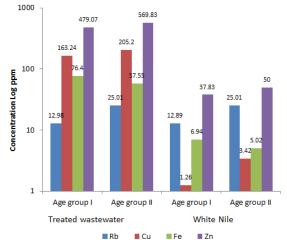
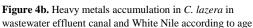


Figure 4a. Heavy metals accumulation in C. lazera in

wastewater effluent canal and White Nile according to sex





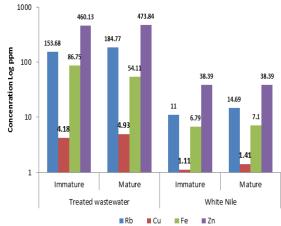


Figure 4c. Heavy metals accumulation in *C. lazera* in wastewater effluent canal and White Nile according to maturity stage

Cu, Rb, Fe and Zn showed significantly higher levels of accumulation in fish of treated wastewater than White Nile fish (P<0.05) probably because their concentration was lower in the latter site. However, except for Zn, the concentrations of other metals did not exceed the permitted international levels (FAO 1983a, b; Huss, 1994; Al-Wher, 2008). Cr, Hg and Pb reached the wastewater treatment plant with the wastewater transported from the Khartoum Industrial Area e.g. Khartoum Tannery, Printing facilities, paints factories and other industrial activities (Sabir et al. 2007). These metals were not subject to any biodegradation since the station depends mainly on natural micro-organisms which can only decompose organic matter. Zn, Fe and Cu concentrations were higher than Hg, Cr and Pb in both sites. Such situation could be attributed to the fact that Zn, Fe and Cu are essential micro-nutrients required in life processes, so most organisms have the ability to keep them at high concentrations in their bodies. This capacity is enhanced by certain feeding and metabolic processes which lead to high accumulation. Furthermore, many of these metals are capable of forming complexes with the available organic substances and hence have the tendency to be fixed in tissues rather than being excreted (Mara and Cairncross 1989). Deposition of heavy metals in fish tissues in treated wastewater seems to inflict no harmful effects on Clarias which survive successfully with increasing numbers and sizes. In conformity with this, Zaki (2007) stated that aquatic fauna are exposed to chronic substances i.e. pollutants that do not cause heavy mortalities but fishes survive and accumulate various amounts of microbial or chemical residues of heavy metals which might result, in extreme cases, in unpleasant tastes or are potentially dangerous. Saeed (2007) results on C. gariepinus in Lake Edku, Egypt, revealed that accumulation of heavy metals generally associated with specific tissues/organs of the fish e.g. Cu in liver, Cd in gills, liver and ovary and kidney and Pb in gills and ovary. Furthermore, Benamar and Zitouni (2013) reported that accumulation of Cu is higher than Cr in liver tissue compared with the muscle tissue of Sardinella aurita collected from Oran Coastline in Algeria. Das and Gupta (2013) concluded that Cu accumulation pattern in the Indian flying barb Esomus danricus was related to metal concentration and increased with exposure time. The findings of this study are also in agreement with Mason (1991) and Ebrahimi et al. (2007) who reported that consumption of edible tissue of mullet which is subjected to heavy metals pollution is not harmful to humans and that the heavy metals accumulation in fish tissues is below the Egyptian standards. Presence of some organic substances in treated wastewater may render heavy metals less toxic than they would be in pure uncontaminated conditions. The form of heavy metal to which aquatic organisms are exposed is important and determines its overall toxicity (Singh et al. 2011).

Cu, Rb, Fe and Zn showed slightly different pattern when analyzed according to sex. Values of Fe, Cu, and Zn showed insignificant variation between males and females in both study sites, while Rb showed significant increase in female specimens from both study areas which may be due to the high ash content of females. Patin (1982) however, reported a positive correlation between the ash content of the fish and its content of a certain metal. Authman and Abbass (2007) findings on heavy metals in *Tilapia zilli* and *Mugil cephalus* tissues indicated that accumulation was much higher than concentration of these heavy metals in their surrounding waters. The water characteristics for the two sites, obtained by Sabir *et al.* (2007) were in conformity with the results of the present study.

According to age, Cu, and Rb showed significantly higher accumulation in older fish in both localities, Zn insignificantly showed the same (Figure 4b). That is likely because fish accumulate elements throughout their life, so older fish would contain more of these substances (Connel 1975; Huss 1994). The previous finding is in agreement with Patin (1982) who found positive correlation between the actual metal content of a fish and its age, size and weight. Fe although showed no variation with age, the difference was not significant.

The pattern of variation of Cu, Rb, Fe and Zn with the stages of maturity of fish from both study sites did not follow certain models although Cu, and Rb showed insignificantly higher levels in mature fish in both study sites and Zn showed the same in treated waste water fish. According to Huss (1994), fish becomes mature when it reaches certain size not a certain age so mature fish with larger sizes are expected to contain more heavy metals as the actual metal content of a fish is positively related to its size and weight.

Insects, phytoplankton, zooplankton, weeds, molluscs and fish parts were detected as major food constituents in the stomach of Clarias lazera from both studied localities (Figure 5). Phytoplankton, fish parts and molluscs showed significant variations between the two sites whereas mean values of insects, zooplankton and weeds were almost similar (P>0.05). Fish, molluscs and zooplankton were much more detected in stomachs of freshwater fish because wastewater doesn't suit their growth. According to Jumaa (1974) the partially low oxygen, elevated CO_2 and the relatively high concentrations of nitrogen and nitrates create unfavorable conditions for zooplanktons growth. Besides, metals in both cationic and soluble complex forms can be toxic or inhibit zooplanktons growth (Biesinger and Christenser 1972). Superiority of phytoplankton and insects can be explained as due to presence of abundant organic matter in the treated wastewater which furnishes suitable conditions for their growth.

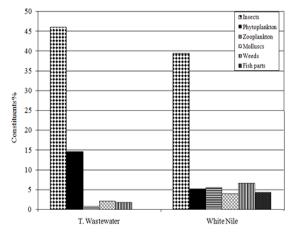


Figure 5. Food composition of *C. lazera* in treated wastewater effluent canal and White Nile

4. Conclusions

Insignificant variations were evident in proximate chemical composition of fish with age, sex, and maturity stages in both sites. However, fish collected from the treated effluent canal expressed higher sizes; weights and protein content are preferred by local consumers. Nutritive value of fishes reared in treated wastewater effluent was high and almost similar to that of natural habitat fish with significantly higher protein content. In spite of possible cultural bias against fish reared in treated wastewater effluents, the average concentrations of most hazardous heavy metals e.g. Hg and Pb are comparable to those obtained from fishes of the White Nile and are well below the values recommended by IAEA (2003), EC (2006) and other relevant agencies for human exceeded consumption. Zn concentrations the recommended level set by international agencies for human consumption and may constitute a potential health risk if ingested in large quantities.

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Microscopic Analysis of Extruded and Pelleted Barley and Sorghum Grains

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Abstract

Scanning Electron Microscopy (SEM) technique has been used in food and feed industry to characterize the final product with the main focus on changes that occur to starch material. This study demonstrates the use of SEM for examining the changes that occur to starch granules after exposing sorghum and barley grains to mild (pelleting) and intensive (extrusion) feed processing methods. In this study, SEM images analysis is proved to be a useful tool to recognize the changes that occur to grains after a different processing method. The present study showed that the swelling and melting of starch granules are influenced by the severity of the processing method. In case of pelleting process, oval shape appearance of starch granules remained intact after the pelleting process; however, absence of intact oval shape of starch granules occurred after the extrusion process.

Keywords: Grains, Scanning Electron Microscopy, Gelatinization, Starch, Feed Processing.

1. Introduction

Grains usually represent the main ingredient component in both ruminant and monogastric animals feed and are considered the primary energy source (Svihus et al., 2004). Before feeding animals, grains are ground to increase the digestibility and to improve mixing with other feed ingredients (Al-Rabadi et al., 2009). Due to the incomplete starch digestion, grains are further processed to enhance starch gelatinization and thus digestibility (Svihus et al., 2005). Excellent positive correlations have been reported between extent of starch gelatinization and digestibility among animal feed (Svihus et al., 2005). Extent of starch gelatinization is dependent on the processing method (pelleting, steam flaking, expanding, extrusion) and operating variables within the processing method (level of water addition, temperature and retention time) (Gilpin et al., 2002). The pelleting process is the most conventional method in producing animal feed where feed material is exposed to steam and then forced through a die (Thomas et al., 1997). The extrusion process is defined as a high temperature short time treatment where feed material is exposed to friction and shearing forces. Different microscopy techniques, such as scanning electron microscopy (SEM) have been reported to be applied into food and feed industry for quality control purposes and particularly in cereal products to determine the extent of starch gelatinization and characteristics in final product (Lee *et al.*, 2000; Srikaeo *et al.*, 2006; Srikaeo, 2008; Olav and Svihus, 2011). The objective of this study was to use microscopic analysis to examine the influence of two different feed processing methods (steam pelleting and extrusion) on starch structural changes of processed sorghum and barley grains used for animal feed.

2. Materials and Methods

2.1. Grain Processing (Steam Pelleting)

Sorghum and barley grains were obtained from the Queensland Department of Primary Industry and Fisheries, Australia. Grains were milled under steady state conditions using 4 mm hammer mill screen size (i.e., when there is no change in motor load or ampere meter reading) before being steam pelleted (Ring Die 520 diameter, Munch Edelstahl, Hilden, Germany) under constant motor load. For both barley and sorghum grains, steam conditioning temperature was 85 °C and moisture added as a steam at pre-conditioner at rate of 1.9 and 2.5%. Pellet diameter and length were 4.0 and 6.0 mm,

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respectively. After the pellets were prepared, they were sealed into 25 kg plastic bags and stored at 4 °C before examination using scanning electron microscopy.

2.2. Grain Processing (Extrusion)

High-temperature short-time (HTST) extrusion cooking was conducted using a co-rotating twin-screw model Prism Eurolab KX16 (Thermo Prism, Staffordshire, UK). The barrel diameter was 16 mm with a length/diameter ratio of 40:1. The die had two openings each 2 mm in diameter and 8 mm in length. Melt pressure was measured with a pressure transducer fitted to the die block (Terwin, Nottinghamshire, UK). Motor torque, screw speed, barrel temperatures and melt pressure were monitored with Prism software (Sysmac-SCS version 2.2; Omron Corporation, Milton Keynes, UK). Die temperature ranged from 90-100 °C and die pressure ranged 4.85-16.61 bar. Liquid feed rate and dry feed rate were recorded manually after being calibrated before processing. Dry feed was fed through a single screw volumetric feeder (KX16 Powder feeder; Brabender Technology, Duisburg, Germany). Water was injected through a port 150 mm from the start of the barrel using a peristaltic pump (L/S 7523) with a Tygon Lab tubing 13 (0.8 mm internal diameter, Masterflex; Cole-Parmer Instrument Company, Vernon Hills, IL, USA). The dry feed rate for barley and sorghum was 20 g/min and 25 g/min, respectively, and the amount of water added at the extruder barrel was adjusted to compensate for moisture differences in the samples to have a dough moisture content of 55% for barley and 50% for sorghum (wb). Barley fractions were extruded at lower feed rate and higher moisture content, compared to sorghum, to avoid any possible blockage during extrusion. High barrel temperature settings (140 °C) and constant screw speed of 200 r.p.m. were used.

Samples were collected when the extruder was running at a steady state (i.e., stable values for both torque and die pressure). The samples were collected over 15–20 min., placed in an aluminium tray, and dried in a hot air oven (50 °C for 24 h) (Ballogou *et al.*, 2011). After drying, they were sealed into plastic bags and stored at -18 °C pending visual examination by using scanning electron microscopy.

2.3. Scanning Electron Microscopy (SEM)

Specimens were mounted onto aluminium stubs with carbon tabs and sputter coated with a 10-15 nm layer of

platinum using an EIKO IB-5 Platinum Sputter Coater. Samples were viewed by field emission scanning electron microscope (JEOL 6300 or JEOL 6400, Japan). Representative Scanning Electron Micrographs were selected by taking many 5 to 10 pictures for the selected sample. The selected sample contains many grain fragments on the carbon tabs. For each grain fragment, many pictures were taken at different magnifications (range from 25-1500X) to explore any major structural difference at the grain fragment level and starch granule level. To solve the challenge of selecting the representative sample, a random micrograph from many micrographs with similar features and appearance was selected as a representative picture.

3. Results and Discussion

The SEM images for steam pelleted sorghum and barley samples are shown in Figure 1 and 2, respectively. These images show the difficulty of characterizing grain fragment borders in the pellet due to the union of fragments caused by the high compaction force between particles and the die surface during pelleting process. Union of grain fragments is considered extremely important in determining pellet quality (pellet durability) which has been reported to be related to the extent of starch gelatinization which enhances the binding properties of grain fragments (Thomas et al., 1996). When starch granules in pelleted grains are compared with unprocessed starch granules in sorghum (Figure 3) and barley grains (Figure 4), it seems that there was no swelling in starch granules after pelleting process has occurred. This may be due to low level of moisture addition during pelleting process. From a process prospective, Leaver (1988) reported that the maximum inclusion level of water during the pellet process should not exceed 6%. It has been reported that water addition above this level can cause die blockage and increase the energy required for the pelleting process (Thomas et al., 1996). Svihus et al. (2005) reported that the extent of starch gelatinization that occurs after pelleting process ranges from 1-20% of the total starch content. Stevens (1987) reported that conditioning the mash corn caused a limited gelatinization and that most of the starch gelatinization occurred when the feed material passed through the die.

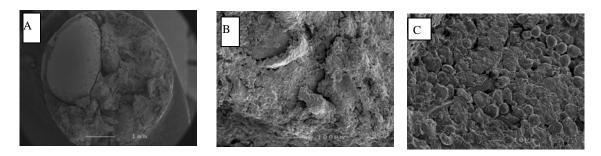


Figure 1. SEM image for sorghum pellets at different magnification levels Figure 1A show cross section of sorghum pellet. Figure 1B and 1C shows no changed occurred to starch granules after pelleting process.

These findings may suggest that starch gelatinization occurs on pellet surface when the feed material pass through the die which keeps the integrity of pellet after pressing through the die.

The SEM images of extruded sorghum and barley are shown in Figure 5 and Figure 6, respectively. The SEM images provide a clear view of changes of the intact starch granules in the extruded sorghum and barley samples. In raw unprocessed.

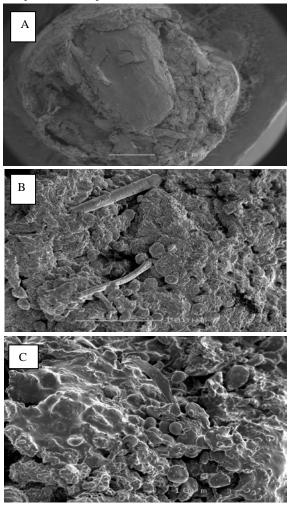


Figure 2. SEM image for barley pellets at different magnification levels. Figure 1A show cross section of barley pellet. Figure 1B and 1C shows no changed occurred to starch granules after pelleting process.

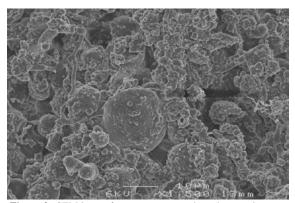


Figure 3. SEM image for raw unprocessed sorghum grain.

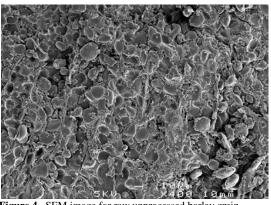


Figure 4. SEM image for raw unprocessed barley grain

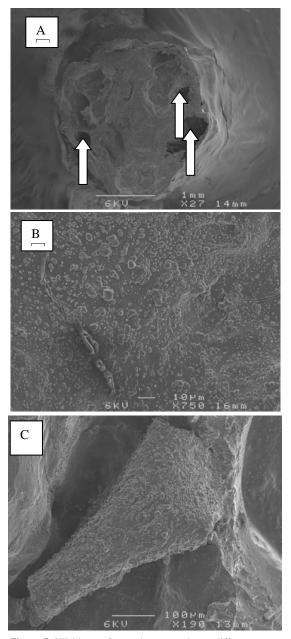


Figure 5. SEM image for sorghum extrudate at different magnification levels. White arrows in Figure 5A show formation of air sacs after extrusion process.

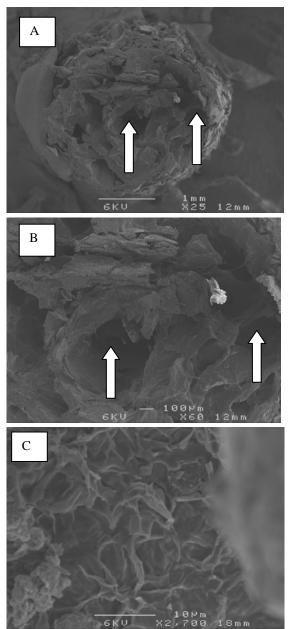


Figure 6. SEM image for barley extrudate at different magnification level. White arrows in Figure 6A and 6B indicate formation of air sacs.

grains, SEM images for sorghum (Figure 3) and barley grains (Figure 4) show clearly the oval-shaped and circular starch granules and protein matrix that is attached to starch granules. However, the extrusion process for both grain types resulted in swelling and melting of starch granules and consequently changed the microstructure of starch granules of being shapeless and mud-like structure as described previously by Srikaeo (2008) and to scatter protein matrix that surround starch granules as shown clearly and more pronounced in sorghum extruded samples micrograph (Figure 5-C). Due to high shearing force and thermal temperature, an extrusion process has been reported to achieve complete starch gelatinization and to completely rupture starch granules (Skoch et al., 1983). SEM images of cross sections of sorghum and barely extrudate showed the presence of small numbers of air sacs of irregular size

(Figure 5-A and Figure 6-A, respectively). These air sacs resulted from the rapid reduction in pressure once extrudate exposed to atmospheric pressure and consequently rapid evaporation of internal moisture (Berrios *et al.*, 2004).

In comparison to extrusion process, commercial processes (such as pelleting) are usually operated under less energy-intensive conditions and thus are considered as less expensive compared to extrusion process. In addition, nutrient digestibility (such as protein and starch digestibility) after extrusion process seems to be grain dependent (Ezeogu et al., 2005). For example, exposing sorghum to high thermal treatments has been reported to form disulphide bond cross-linked prolamin proteins and extensive polymerisation of the prolamins which limit protein digestibility (Ezeogu et al., 2005). The presence of tight protein matrix that surrounds starch granules within densely packed endosperm cells in sorghum can also reduce the extent of starch digestion (Hamaker et al., 1987; Rooney and Pflugfelder, 1986). A recent study showed that the extant and the rate of starch digestibility were higher in barley extruded grains compared to sorghum grains (Al-Rabadi et al., 2009). These factors may make the extrusion process as not the best processing method to adopt in feed industry for sorghum grains.

4. Conclusion

It can be concluded from micrograph images that starch granules in both grain types retain its integrity after the pelleting process. However, exposing grain fragments of barley and sorghum to extrusion process can eliminate the integrity of starch granules by inducing swelling and melting of starch granules. Scanning electron microscopy could be practical for feed industries for the quality control in cereal based diets where starch gelatinization is the most influential factor on starch digestibility.

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