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The Effect of Environmental Condition on Genetic Background in Nile Tilapia (*Oreochromis niloticus)*

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ABSTRACT

Random samples from three different natural populations were caught from three different localities i.e., Polluted Drainage Canal, Faculty Fish Farm and Edku Lake. Different heavy metal concentrations in water and in different fish organs (i.e., liver, head and muscles) were estimated to identify the residues of such pollutants in fish tissues in relation to water quality resources. Water analyses indicated that Polluted Drainage Canal performed the significant higher level of heavy metal concentrations in relation to the other two localities. Such trend affects drastically the concentrations of heavy metal in fish organs. The results clearly indicated that Drainage Canal fish sample showed the highest concentration of heavy metal in there organs specially in liver in relation to the samples of the other two localities. The effect of environmental adaptation of these natural populations on their genetic constitutions was estimated by applying biochemical and molecular genetic analysis. Esterase isozyme, SDS PAGE as the biochemical genetic markers showed significant genetic variation among the three different samples of fish. The same trend was confirmed at the DNA level (RAPD analysis). Combined statistical genetic analysis including biochemical and molecular tests indicated that the similarity index among the three different populations was 45.31. These genetic variations among these three different populations are almost due to the effect of environmental stresses on the genetic constitutions of such populations. Due to the genetic differences among these

different populations, it is expected to get some source of heterosis in the offspring produce from the crosses among these different populations. Such expected response was found in the offspring produced from the reciprocal crosses between Edku and Drainage Canal samples.

Keywords: Esterase - SDS PAGE - RAPD analysis – Heterosis - Nile tilapia

INTRODUCTION

Tilapia species are currently the second most farmed group of fish (behind carps) with an annual world production of 2.5 million tons (FAO, 2008). Tilapia species are an increasingly important group of cultured fish for several reasons e.g. {rapid growth, high tolerance to low water quality, efficiency food conversion, resistance to disease and good consumer acceptance}. Water pollution is the most important factor affecting quality and quantity of fish production either in natural habitats or culture bonds. Heavy metal ions in water considered as the most dangerous source of water pollution. The contamination of heavy metals and other pollutants is a serious threat because of their toxicity, long persistence, bioaccumulation and biomagnification in the food chain (Eisler, 1988). It is well known that genetic adaptation under different environmental condition leads to changes in gene frequencies, leading to changes in genetic background of different isolated populations. Biochemical and molecular genetic analysis are commonly used to identify the effect of different environmental condition and genetic environmental interaction on genetic background of different isolated population and to measure the degree of similarity and the genetic distance between different populations. Estimates of additive and non-additive genetic effects provide information on the choice of a breeding strategy and may also assist in the choice of parental and/or maternal in a crossbreeding program. A review of literature on the estimates of additive genetic and heterosis effects shows that most of the breeding and genetic selection work in aquaculture has concentrated on estimating these effects from diallel cross experiments involving F_1 populations (Gjerde *et al*., 2002). The aim of the present study is the identification of heavy metals concentration in water and fish tissues in relation to different natural water habitats, phylogenetic analysis by using biochemical and molecular genetic approach of identify the genetic variation among the three different populations and the estimation of the magnitude maternal and paternal heterosis effects for harvest body weight and length of *Oreochromis niloticus*.,

MATERIALS AND METHODS

Sampling location and preparation

Three different natural populations from three different localities of Nile Tilapia were presented by three different random samples. The three different locations were; Polluted Drainage Canal "in front of Village No 10", Faculty Fish Farm (Abeice Region, Alexandria Governorate) and Edku Lake (Behayra Governorate). The live fish stocks were transported to the Faculty fish genetic aquarium. Each stock was separated to two parts, The First one was killed to obtain the internal organs i.e., liver, head and muscles. These organs were dried in an oven at 70 ^{0}C for 48 h; and homogenized separately in a mortar. The fine samples were preserved in clean and dry polyethylene bottles. These samples were used for chemical analysis for the identification of heavy metal concentration in different preserved organs. The same analysis were performed for the water resources from the three different localities.

The second part was used to establish the live broods stock of aquarium according to El-Dahhar (2000). The live stocks were used for biochemical and molecular genetic analysis and for the estimation of heterosis in the offspring produced from the reciprocal crosses between different localities.

Chemical analysis

Accurately weighted 1 g from each grouped dried sample of each organ was homogenized separately in a mortar and treated with 4 ml of H_2O_2 and 4 ml of H_2SO_4 in a flask. Finally, the solution was transferred to a 100 ml volumetric flask and diluted to 100 ml volume with demineralized pure water. After filtration the elemental concentrations in the solution were measured with a Perkin Elmer AAnalyst-400 flame atomic absorption spectrophotometer with hollow cathode lamp (zinc (Zn), copper (Cu), cadmium (Cd), lead (Pb), manganese (Mn), iron (Fe), nickel (Ni), and chromium (Cr). Concentration of the same heavy metals in water samples were estimated with the same technique.

Biochemical analysis

Electrophoretic techniques and esterase analysis

Agar-starch-polyvinyl pyrolidine (P.V.P) gel electrophoresis was carried out according to the procedures described by Shaw and Kaen (1967). Electrode buffer was prepared according to Ahmed, (1994). Staining procedure was prepared according to Youssef *et al*., (1989).

Protein electrophoresis

Sodium dodecyl sulfate polyacrylamide gel (SDS-PAGE) was used to compare between the three

populations of tilapia by their protein patterns. Water soluble protein fractions was separated exclusively on a vertical slab gel (19.8 cm x 26.8 cm x 0.3 cm) using the gel electrophoresis apparatus (Manufactured by Biorad, USA) according to the method of Laemmli, (1970).

Extraction of protein samples

Muscle samples of three fish from each population were finely ground with 1ml extraction buffer (2x) and left in eppendorf tube in refrigerator overnight, then vortexed for 15 second and centrifuged at 10000 rpm at 5°c for 15 min. The supernatants containing total proteins were transferred to new eppendorf tubes and kept at deep-freezer until use for electrophoretic analysis.

Molecular analysis

DNA isolation

DNA was extracted from muscle following the method described by Hillis and Moritz (1990).

RAPD analysis

Five arbitrary 10 mer oligonucleotide primers (Table1) were used in this study. Reaction volume (25 µl) containing 25 ng genomic DNA, 0.2 uM oligonucleotide primers (Bioron, Germany), 200 uM of each dNTP (Promega, USA), 1.5 units of Taq DNA polymerase (Promega, USA), 2.5 µl 10x buffer, Steril d.d. H_2O up to 25µl. Amplification was performed in a thermal cycler (Biometra, Germany). Thermal cycler program was 1 cycle at 95°C for 5min., 40 cycles of 95°C for 1min., 37 °C for 1min. and 72 °C for 2min. Final extention cycle at 72 °C for 15 min.

Table (1) ***Primer Sequences.***

Primer No.	Sequences	GC%	Annealing temperature
1	TTCGAGCCAG	60%	37 °C
2	GGGGGTCTTT	60%	37 °C
3	CCGCATCTAC	60%	37 °C
4	CCCAGTCACT	60%	37 °C
5	CCACGGACTC	70%	37 °C

Agarose gel electrophoresis

The amplified DNA fragments were separated on (2% agarose gel in 1x TBE buffer) and stained with ethidium bromide. 100 bp DNA Ladder marker was used in this study. The amplified pattern was visualized on an UV transilluminator and photographed by Gel Documentation system.

Data analysis

Analysis of isozyme

Gene frequency

A simple method of calculating gene frequency of S (allele coding for

slow migrating band) and F (for fast) uses the following equations:

$$q(S) = m(S) + 1/2\ H$$

$$q(F) = m(F) + 1/2\ H$$

Where q (S) and q (F) are the gene frequencies of S and F alleles, respectively, m (S) and m (F) are the frequencies of SS and FF homozygotes, respectively, and H is the frequency of heterozygotes.

Analysis of RAPD and protein

DNA as well as protein bands were scored for their presence and absence in the RAPD and SDS-PAGE profile, respectively. The index of similarity among the three genetic variants was calculated using the formula: $B_{ab}= 2N_{ab}/ (N_a+N_b)$, where N_{ab} is the number of common fragments observed in individuals a and b and N_a and N_b are the total number of fragments scored in a and b respectively, similarity plus polymorphic equal one (Lynch, 1990).

Phylogenetic relationships

Isozymes, Protein and RAPD banding patterns were scored for presence (1) or absence (0). Similarity coefficients were estimated using TREE from the program NTSYS-pc version 2.10 (Applied Biostatistics, Setauket, New York, USA) according to (Rohlf, 2000).

Fish culture and heterosis

Brood stocks were first separated into males and females for about 2 weeks. Aquariums management was made according to El-Dahhar (2000). After the acclimatization period, 4 breeding aquaria were stocked with one male and one female (1 male and 1 female) per aquarium. The four studied lines were {parental lines (Edku x Edku) and (Drainage Canal x Drainage Canal) hybrids (♂Edku x ♀ Drainage Canal and (♂Drainage Canal x ♀ Edku)}. The experimental procedure was organized in three consecutive phases: mating, spawning and fry rearing.

Quantitative traits measurements

All quantitative traits were measured for offspring produced from parental lines and the offspring produced from crosses between Edku x Drainage Canal.

Growth rate

Individual weight and length of all fish were recorded every two weeks. Growth rate of the offspring was measured for 6 month by mean of calculated average weight of the 90 offspring from each family.

Phenotypic correlations

Phenotypic correlations between the two parameters; (weight and length) were estimated by apply the equation

$$r = \frac{\sum x_1 x_2 - \frac{(\sum x_1)(\sum x_2)}{n}}{\sqrt{[(\sum x_1^2 - \frac{(\sum \times_1)^2}{n}][\sum \times_2^2 - \frac{(\sum \times_2)^2}{n}]}}$$

Which x_1 represents weight variable and x_2 for length variable and n the offspring produced from the reciprocal crosses between them.

RESULTS AND DISCUSSION

Water ionic characteristics

The pH and heavy metals concentration values for the water from the three different studied localities (Drainage Canal, Fish Farm and Edku Lake) are given in Table (2). Decreases in pH values have been found to aggravate toxicity in aquatic organisms (Licata *et al*., 2003). The mean water pH value for Fish Farm (9) is higher than the World Health Organization (WHO) limit of 6.50–8.50 for drinking water (World Health Organization [WHO] 1996). The pH of the water from the other two localities was within the WHO limit.

Table (2) indicates heavy metals concentrations in different ecosystems in relation to the permissible concentration, which were advised from WHO (1996). Data clearly indicated that the levels of Cd in the water samples collected from Drainage Canal, Fish Farm and Edku Lake were 0.021 mg/L, 0.017 mg/L and 0.009 mg/L, respectively, which exceed the limit of 0.005 mg/L set by World Health Organization (WHO 1996).

Contamination of aquatic ecosystems can be confirmed by determining levels of contaminants in water, sediment and organisms (Usero *et al*., 2005; Altindag and Yigit, 2005; Yilmaz, 2003). Metals transferred through the aquatic food webs to fish and humans are of environmental and health concern (Chen *et al*., 2000).

Table (2): ***Concentrations (ppm) of heavy metals and pH in water samples collected from different ecosystems, compared with the permissible limits.***

Location	pH	Metal							
		Zn	Cu	Cd	Pb	Mn	Fe	Ni	Cr
Drainage Canal	**7.66**	**0.606**	**0.138**	**0.021**	**0.157**	**0.250**	**0.970**	**0.147**	**0.328**
Fish Farm	**9**	**0.081**	**n.d.**	**0.017**	**0.141**	**0.249**	**0.641**	**0.072**	**0.326**
Edku Lake	**7.65**	**0.074**	**n.d.**	**0.009**	**0.052**	**0.232**	**0.541**	**0.052**	**0.081**
WHO limits (mg / L)	**6.50–8.50**	**5.00**	**1.0**	**0.005**	**0.05**	**0.10**	**0.30**	**0.005**	**0.1**

n.d. = ***no values determined in this study.***
WHO World Health Organization limits.

Heavy metals in different fish organs

Table (3) shows the concentrations of heavy metals in different organs of the fish body (e.g. liver, head and muscle). In general concentrations of heavy metals (Zn, Cu, Cd, Pb, Mn, Fe, Ni and Cr) in different organs were higher in Drainage Canal in relation to the other two localities.

It's important to note that the average of heavy metal concentrations for the grouped organs performed highly significant differences between different localities in which Drainage Canal exposed the higher concentration.

For instance some of such heavy metal as Cu in Drainage Canal (14.23 ppm) exceeded the other two localities with 4.6 fold for Fish Farm (3.07 ppm) and with 6.9 fold for Edku Lake (2.05 ppm).

Table (3) shows heavy metals accumulation in different organs of different fish samples in relation to the permissible concentration. Data clearly indicated that Edku Lake had concentrations zinc, copper, lead, iron and chromium below the permissible limits (ppm) However, all of different localities contained cadmium at concentrations above the permissible limit (0.20 ppm; FAO, 1983).

The most important point observed was the accumulation of heavy metal ions in liver tissue that significantly exceeded accumulation in the other two fish tissues i.e., head and muscle as shown in Figure (1).

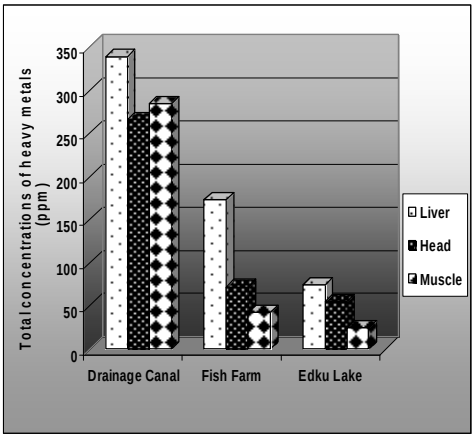

Figure (1) ***Total Concentrations (ppm) of heavy metals in Bolti fish (Oreochromis niloticus).***

From the population genetics point of view, the natural population which existed in the polluted Drainage Canal is adapted to pollutant stresses by natural selection. However, this adapted fish population may represent a serious effect on the health of the local inhabitants where high concentrations of heavy metals implicate fish tissues affecting its quality and hence become a threat to man health.

Table (3): ***Concentrations (ppm) of heavy metals in Bolti fish (Oreochromis niloticus.)[a] organs, compared with the permissible limits.***

Metal	Drainage Canal				Fish Farm				Edku Lake				Permissible limits (ppm) FAO (1983)
	Distribution in different parts			Mean (ppm)	Distribution in different parts			Mean (ppm)	Distribution in different parts			Mean (ppm)	
	Liver	Head	Muscle		Liver	Head	Muscle		Liver	Head	Muscle		
Zn	180.3	164.6	157.8	67.57	153.3	69.1	39.6	87.33	64.6	48.3	21.0	44.63	150
Cu	15.6	14.3	12.8	14.23	9.2	n.d.	n.d.	3.07	4.2	1.95	n.d.	2.05	10
Cd	10.4	6.1	9.0	8.5	0.23	0.07	0.08	0.13	0.22	0.06	0.07	0.12	0.20
Pb	51.5	44.2	78.4	58.03	0.31	0.39	1.55	0.75	0.32	0.45	0.38	0.38	1.5
Mn	0.28	0.41	0.17	0.29	0.30	0.62	0.17	0.36	0.21	0.25	0.12	0.19	n.l.
Fe	78.40	35.27	26.04	46.57	8.59	1.39	0.71	3.56	3.92	3.53	2.75	3.4	5.6
Ni	0.48	0.43	0.33	0.41	0.40	0.36	0.34	0.37	0.29	0.27	0.26	0.27	n.l.
Cr	2.85	0.94	0.84	1.54	0.69	0.56	0.50	0.48	0.37	0.33	0.30	0.33	1.0
Total	339.81	266.25	285.38	-	173.02	72.49	42.95	-	74.13	55.14	24.88	-	-

n.d. = no values determined in this study.
n.l = no information about maximum permissible limit in fish tissue.
[a] ***Each value represents an average of ten samples collected in May 3, 2008 and May 4, 2008.***

Biochemical genetic analysis

Esterase system profile and gene frequency

Figure (2) shows the anodic esterase isozyme pattern of liver tissue of the three populations of *O. niloticus.* The banding patterns activity of esterase isozymes was most pronounced in the liver tissue of different loci (EST.1 and EST. 2). There was no migration to cathodal direction.

Data clearly indicated that, EST.1 was consistently monomorphic expressing "FF" genotype for Edku Lake while it was polymorphic for Drainage Canal and Fish Farm. EST.2, however was polymorphic for there populations (Drainage Canal, Fish Farm and Edku Lake) as shown in Table (4).

Feresu and Howard (1998) found that 27 loci were polymorphic, 5 were monomorphic but had fixed allele differences among species and 6 were monomorphic for the same allele in all tilapia species in Zimbabwe.

Heterozygotes rate

Table (5) shows the precantage of heterozygote genotypes for esterase isozymes in liver of the three *Oreochromis niloticus* populations for the two different loci EST.1 and EST.2.

Cadmium may interact with other metals such as iron, copper and zinc and may influence the enzyme activities of metabolic patterns (Katakura and Sugawara, 1995).

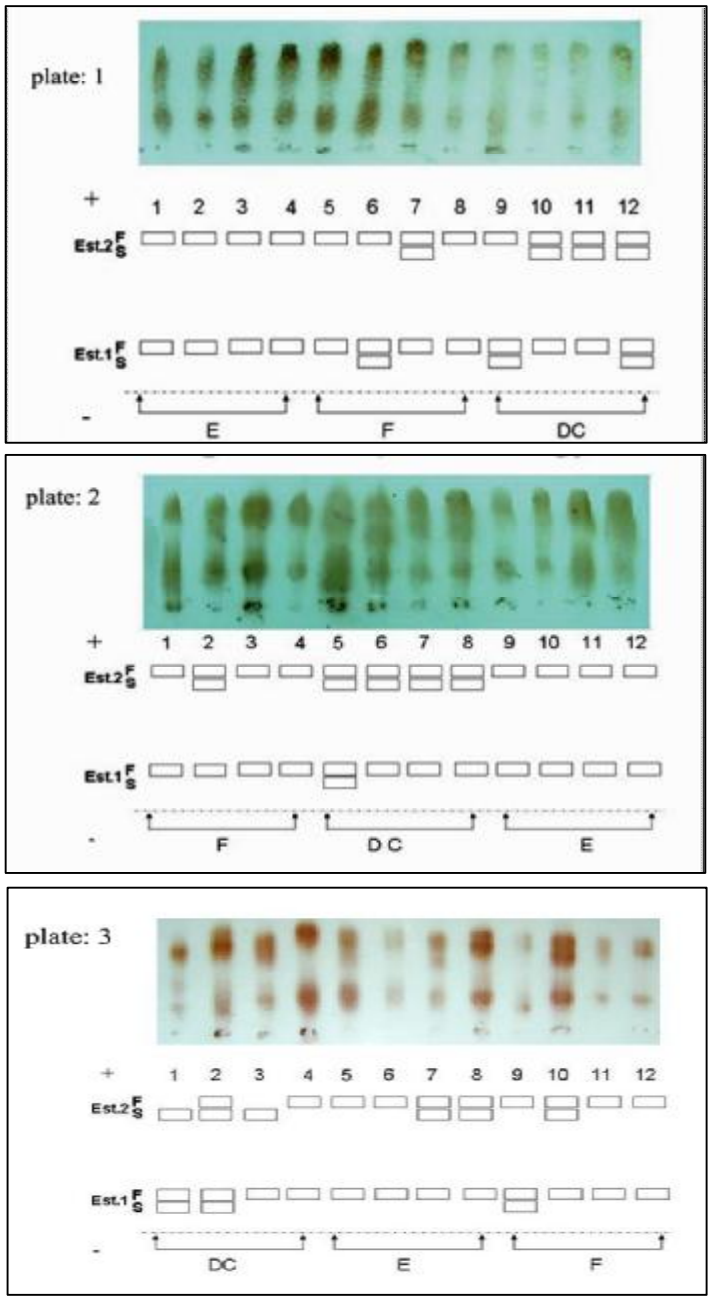

Figure (2) ***Zymograms showing electrophoretic profiles of esterase in liver of different Oreochromis niloticus populations. Lane F: Fish Farm; Lane E: Edku Lake; Lane DC: Drainage Canal, respectively.***
Resulted from the 12 fish for each population.

Table (4) ***Gene frequency estimates for alleles segregating at different loci coding for esterase isozymes in liver of the three Oreochromis niloticus populations.***

Loci	Populations	Drainage Canal	Fish Farm	Edku Lake
EST.1	F	0.79	0.91	1
	S	0.21	0.09	0
EST.2	F	0.50	0.88	0.91
	S	0.50	0.12	0.09

Table (5) ***Heterozygotes rate for esterase isozymes in liver of the three Oreochromis niloticus.***

Loci	Drainage Canal	Fish Farm	Edku Lake
	% of heterozygotes		
EST.1	42	17	0
EST.2	67	25	17

From population genetics point of view, the natural population which existed in the polluted Drainage Canal is adapted to pollutant stresses through highly heterozygotes rate.

Protein electrophoresis

SDS-PAGE

Qualitative analysis by SDS-PAGE generated a total number of 39 protein bands. Out of this number 5 unique bands and 10 common bands have been generated as shown in Tables (6 and 7).

Semi-quantitative analysis via SDS-PAGE

Because the total protein concentration extracted from each genetic variant has been standardized, equal concentration of total protein contents (78 µg/µl) have been loaded in the PAGE. Therefore, the variation of the intensity of any protein could be used as an indicator of a variation on the gene expression level among the studied genetic variants. As shown in Figure (3), protein bands of molecular weights 406, 330, 49, 29, 11 Kda. Showed a different band intensities. This variation could be attributed to gene expression variation due to the environmental stresses that affects these genetic variants.

Table (6) Number of bands of each isolate with six different characterization tool.

Characterization Tool ⇓	Genetic ⇒ populations				
	Total Amplified Bands	**Total unique bands**	**Unique bands %**	**Total common bands**	**Similarity index %**
1	**35**	**11**	**31.43**	**4**	
2	**22**	**3**	**13.64**	**3**	
3	**25**	**7**	**28**	**6**	
4	**21**	**7**	**33.33**	**1**	
5	**25**	**5**	**20**	**5**	
SDS-PAGE	**39**	**5**	**12.8**	**10**	
Total	**167**	**38**		**29**	**45.31**

Table (7): ***Number of unique bands of the studied genetic variant with each characterization tool.***

Variety ⇓	primer ⇒						
	1	2	3	4	5	SDS-PAGE	Total
Fish farm	7	3	4	2	3	2	21
Edku Lake	2	0	2	0	2	1	7
Drainage Canal	2	0	1	5	0	2	10

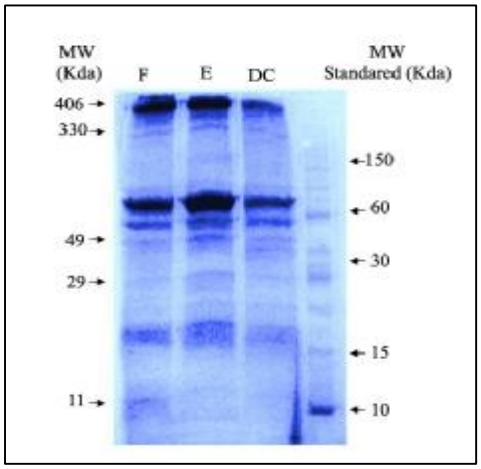

Figure (3): ***SDS-PAGE of muscle protein from the different Oreochromis niloticus populations. Arrows indicate major protein bands discussed in the text; MW are indicated in kda. Lane F: Fish Farm; Lane E: Edku Lake; Lane DC: Drainage Canal, respectively.***

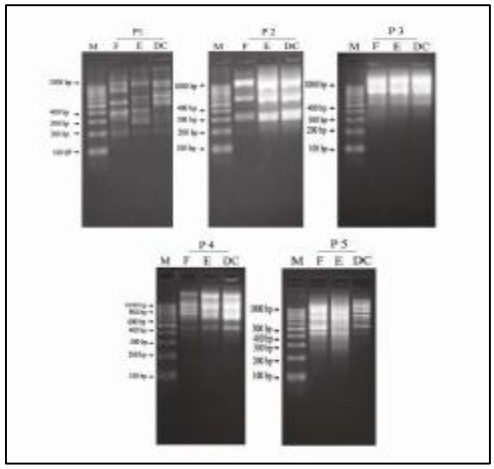

Figure (4): ***RAPD amplification products generated from different Oreochromis niloticus populations using five random primers (P1-P5). M: DNA marker; Lane F: Fish Farm; Lane E: Edku Lake; Lane DC: Drainage Canal, respectively.***

Exposure to heavy metals could affect protein concentration either by increase the in soluble or structure protein such as Cu (Hilmy *et al*., 1987), Zn and Cu (El-Sarha, 1986) and Zn and Ni (Sornaraj *et al*., 1995).

RAPD-PCR analysis

The five primers generated a total of 128 bands within the three different populations (Drainage Canal, Fish Farm and Edku Lake).

Figure (4) and Tables (6 and 7) show a total of 128 bands by 5 random primers. These primers identifying and differentiating the three different samples of fish based on DNA amplification using their template DNA.

In general, the number of PCR products generated for every primer varied between 21 to 35 bands. Arrangement of primers depending on the number of generated DNA fragments was 1> 3> 5> 2> 4. Furthermore, the highest number of common bands was generated by primer 3 which produces 6 bands, while the lowest number was 1 band generated by primer 4. Also the highest number of unique bands produced by primer 1 (11 bands) and lowest number was 3 bands produced by primer 2. Moreover, the five primers were reacted and produced PCR fragments with all studied varieties.

The RAPD technique was used by Bardakci and Skibinski (1994) to differentiate between species and subspecies of the Nile tilapia and three other species of the genus *Oreochromis* in aquaculture similarty. This study represents the application of RAPD technique to the assessment of variation between natural populations of Nile tilapia.

Similarity and dissimilarity analysis

According to the formula mentioned in the materials and methods using the results from protein and RAPD analysis, the similarity index among the studied genetic variants were 45.31. Hence, the polymorphism among the three genetic variants by the use of these characterization tools is 54.68. These results indicated that there are clear variations among the studied genetic variants in response to the environmental stresses. Moreover, Similarity between the genetic variant Edku Lake and Drainage Canal has the highest value (18.1%) and the similarity between Fish farm and Edku Lake was (12.5 %) as shown in Table (8). While the similarity between Fish farm and Drainage Canal was the lowest (5 %). These results indicated that the there are a gradual accumulation of variation in response to the exposure to the environmental stress (heavy metal pollution). Therefore, these genetic variations among the studied genetic variants could be attributed to the environmental stress (heavy metal pollution).

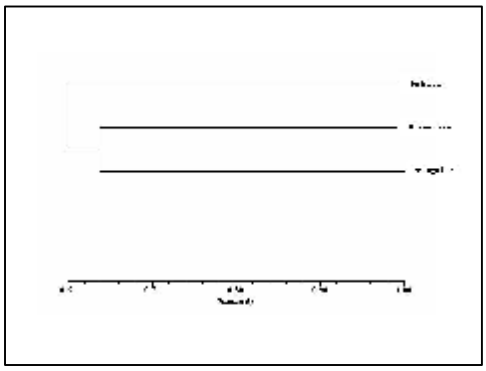

Figure (5): ***Dendrogram of genetic similarity among the different Oreochromis niloticus populations (Drainage Canal, Fish Farm and Edku Lake).***

Table (8): ***Number of shared bands between each two genetic variants.***

Genetic variant	Number of shared bands	Total number of shared bands	Similarity index %	Genetic variant
Fish farm	3	120	5	Drainage Canal
Edku Lake	7	112	12.5	Fish farm
Drainage Canal	10	110	18.1	Edku Lake

According to the formula mentioned in the materials and methods by grouping the obtained results from isozyme, protein and RAPD analysis. Similarity between the genetic variant Edku Lake and Drainage Canal has the highest value (65%) and the similarity between Fish farm and Edku Lake was (61%) as shown in Dendrogram (5). While the similarity between Fish farm and Drainage Canal was (61%).

Quantitative traits and heterosis

Growth rate in relation to weight and length

Figures (6 and 7) demonstrate the mean values of weight and length a long a twenty four weeks for the two parental lines (Edku Lake (E) and Drainage Canal (DC)) and the offspring produced from the reciprocal crosses between them. The obtained results clearly indicated that offspring produced from the reciprocal crosses between the two parental lines from the two localities had significant higher growth rate characteristic.

The same trend was observed for body length (Figure 7). At the twenty four week of development the average of survival rate were 80% and 93.33% for the parental lines and 100% and 100% for the hybrids as shown in Figure (8). (Hulata, 2001) reported that Intraspecific crossbreeding often increases growth rate of aquacultured species, although specific heterotic combinations need to be experimentally identified. Only a few commercially aquacultured species have been improved by crossbreeding. Variable proportions of crossbreds showing heterosis for growth rate have been obtained in the channel catfish; rainbow trout; common carp and the Pacific oyster. Heterosis was also found in survival, disease resistance and intraspecific crossbreeding often increases growth rate of aquacultured species, although specific heterotic combinations need to be experimentally identified.

Phenotypic correlations

Table (9) presents phenotypic correlation values between weight and length characteristics. Estimates of correlation using covariance analysis indicated highly significant values of correlation in two tested weeks of growth i.e. twelve week and twenty four week. These estimates indicate that the transferable genes from parents to offspring are almost the same for both characters.

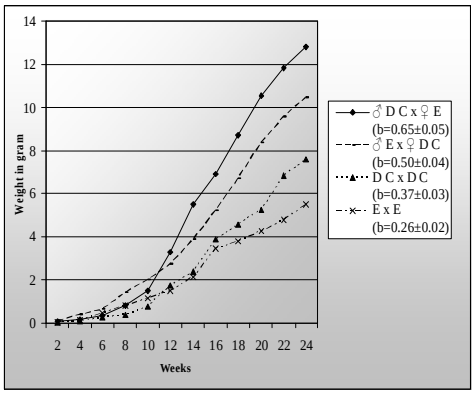

Figure (6): ***Mean weight values of offspring produced from different families of Nile tilapia in grams in relation to age in weeks.***

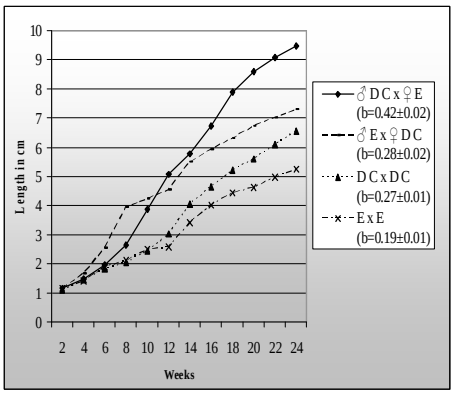

Figure (7) Mean length values of offspring produced from different families of Nile tilapia in centimeters in relation to age in weeks.

All studied lines indicated that genetic improvement by selection for one of the characters will improve significantly the other. The phenotypic correlations found among body weight and body length were very high and significant and ranged from 0.94 to 0.99 (El-Wakil *et al*., 2005).

In conclusion, it could be postulated from this study that the cross between different populations is better than cross between same populations in growth rate, survival rate and feed conversion ratio and *O. niloticus* could be considered as an accurate and sensitive organism to monitor the toxicity of the environmental pollutants on different levels i.e., genotoxicity, molecular and biochemical abnormalities.

Table (9) Estimates of phenotypic correlation for weight and length of Nile tilapia offspring.

Family	E x E	♂ E x ♀ D C	♂ D C x ♀ E	D C x D C
Age In Weeks	Phenotypic correlations			
12	0.97	0.95	0.97	0.94
24	0.99	0.93	0.98	0.98

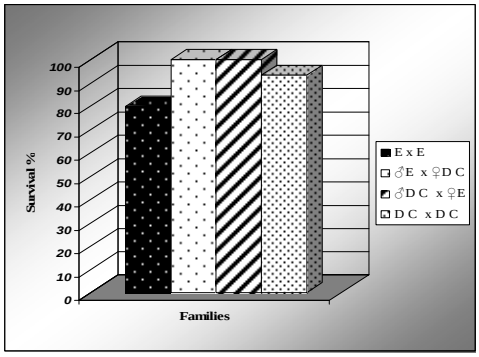

Figure (8) The percent survival % of offspring produced from different families of Nile tilapia in centimeters according to fish genotype, at the end of the experiment.

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تأثير الظروف البيئية علي الخلفية الوراثية لأسماك البلطي النيلي

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تم جمع ثلاث عينات منفصلة عشوائية من ثلاث عشائر طبيعية من أسماك البلطي النيلي من ثلاث مناطق مختلفة وهي: بحيرة ادكو (محافظة البحيرة), المزرعة السمكية لكلية الزراعة-سابا باشا بمنطقة أبيس, المصرف الزراعي الملوث إمام القرية العاشرة مقابل المزرعة السمكية (محافظة الاسكندرية) و ذلك للمقارنة بين الثلاث عشائر في درجة تراكم العناصر الثقيلة في أنسجة أجسامها اعتمادا على درجة تلوث البيئة المائية لكل عشيرة و لقد أظهرت النتائج أن ماء المصرف الزراعي هو الأكثر تلوثا بالعناصر الثقيلة معنويا مقارنة بنتائج التحليل الكيميائي للمصدرين الآخرين ونتيجة لذلك فإن درجة تراكم أيونات العناصر الثقيلة في كلا من الرأس و الكبد و العضلات كانت أكثر معنوية في أسماك ماء المصرف و من الملاحظ إن درجة التراكم لهذه العناصر كانت أعلى ما يمكن في نسيج الكبد. لقد تم دراسة أثر الأختلاف البيئى بين هذه المناطق اعتمادا على درجة تلوثها على الخلفية الوراثية لعشائر الأسماك الطبيعية المتوجدة فى هذه البيئات و ذلك بإجراء التحليل الوراثى البيوكيميائى و الجزيئى على أنسجاتها و لقد أظهرت النتائج وجود أختلاف وراثيا واضحا فكانت similarity index بين الثلاث عائلات ٤٥.٣١ و عند إجراء التلقيح العكسى بين أسماك بحيرة أدكو و أسماك المصرف الزراعى تم الحصول على قوة هجين لبعض الصفات الأقتصادية الهامة فى البلطى النيلى مثل الوزن و الطول.