



Ecological and Taxonomical Characterizations of some Molluscan species in Irrigated Nile Channels, (Rayahs), Egypt

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ABSTRACT

Taxonomy and seasonal diversity of Nile molluscs are important to understand the ecological impact of these animals on sustainability of River Nile ecosystem dynamics. The present work aims to explore and evaluate the taxonomy and diversity of four benthic molluscan species; two gastropods and two bivalves, in three of Egyptian irrigated Nile channels (Rayahs). The specimens were collected seasonally during the period from spring 2014 to winter 2015. Taxonomy of specimens were studied from the views of morphology and 18S rRNA gene analysis. The Gastropod species -1 and -2 had 5-6 light or dark brown whorls, but the last whorl of Gastropod sp.-2 was larger than that in Gastropod sp.-1. The phylogenetic analyses of 18S rRNA gene showed that both of Gastropod species formed monophyletic cluster, which had paraphyletic lineage with species *Viviparus georgianus*, implicating two new species under the genus *Viviparus*. The shell of the Bivalve sp.-1 was ovoid with light greenish brownish or yellowish color, while the Bivalve sp.-2 had light brown to grayish elongated shell. Both of Bivalve spp.-1 and -2 showed 18S rRNA gene sequence identity; averages of 89% and 92%, respectively, with *Lampsilis cardium* suggesting new genera within the family Unionidae. Gastropod sp.-1 showed highest abundance, during winter in El-Rayah El-Tawfiky, while the lowest was recorded during spring in El-Rayah El-Behery. Gastropod sp.-2 was abundant during summer in El-Rayah El-Behery. The seasonal distribution of the two studied bivalves declared the highest abundance in both of El-Rayah El-Behery and El-Rayah El-Tawfiky during winter, while declined during spring in all Rayahs.

INTRODUCTION

The River Nile is recognized as the longest river, and can be considered as one of the most important rivers in the world. At Delta Barrage, North of Cairo at the River Nile bifurcates into two branches namely Damietta and Rossetta and four Rayahs (irrigated channels) namely El-Nassery, El-Behery, El-Monofiy and El-Tawfiky (Saad and Goma, 1994; Abdel Aziz, 2005; Ghannam *et al.*, 2015; Talab *et al.*, 2015 and Abd El-Karim *et al.*, 2016). These Rayahs are vital for irrigation,

navigation, fishing and other domestic uses in many Governorates of Egypt (Hossam and Ahmed, 2005). However, the Rayahs are filled with overlooked ecosystems that may play important roles in the dynamics of these environments.

Phylum Mollusca constitutes unusual interest, regarding diversity and the multitude of living species. The molluscs, greatly, vary in form, structure, habit and habitats. They are a highly adaptive and occupy all possible aquatic and terrestrial habitats.

Freshwater molluscs have been known to play significant roles in the public and veterinary health, and thus, needed to be scientifically explored more extensively (Supian and Ikhwanuddin, 2002). About 100 species of freshwater gastropods have been reported as intermediate hosts for many parasites (Subba-Rao, 1993). Physical factors, such as water current, temperature, turbidity, transparency and distribution of suspended solids, and some chemical parameters, such as ion concentration and dissolved gases in water, as well as biological factors, such as availability of food, competition and predator-prey interactions are from the main components, which affect the ecology of molluscs (Williams, 1970; Ofoezie, 1999; Orabi and Osman, 2015).

Population dynamics of molluscs depend on the physical geography of a given region, also land contours, soil composition; hydrograph and climate (El-Khayat *et al.*, 2011).

The taxonomy of class Gastropoda; snails and slugs, is changing rapidly, based on morphology and genetic barcoding (haszprunar 1988; Ponder and Lindberg, 1997; Bouchet and Rocroi, 2005). The freshwater snails found in Africa, including Egypt, are either prosobranchs or pulmonates (brown, 1994). Viviparids are freshwater snails. Their dextral shells are more than 10 mm high. The whorls are generally more numerous than in Neritidae. Moreover, the spire is higher and more conical. The operculum is entirely corneous and concentric. The animal is viviparous and the embryos develop in the lower oviduct. The right tentacle in males is modified as a copulatory organ. The radula is taenioglossate. The central tooth is wide and without basal denticles (Brown, 1994; Lotfy and Lotfy, 2015). Only a single species, *Bellamya unicolor* has been recorded in Egypt (Olivier, 1804).

African freshwater bivalves seem to be overlooked animal group; perhaps because they do not have a clear economic importance. These bivalves show great variations in morphology and colors that are coupled with relatively few constant characters, which rendered it a systematically group. The majority of the African freshwater clams belong to two superfamilies; Unionacea and Corbiculacea (Sphaeriacea) (Mandhal-Barlh, 1988). On the other hand, freshwater bivalves provide many ecological services to aquatic ecosystems including benthic–pelagic coupling and structure for other invertebrates (Strayer *et al.*, 1994; Spooner and Vaughn, 2006) and sediment stabilization (Zimmerman and de Szalay, 2007). Economic significance of the family Unionidae in Egypt is being ignored, although it constitutes a source of edible protein in east for Asia (Ibrahim *et al.*, 1999).

The rRNA genes have been considered as deeply phylogenetic markers, which have been used worldwide for studying the phylogeny of Mollusca. Bogan and Kevin (2008) studied the freshwater bivalve (Unioniformes) diversity, systematics, and evolution based on phylogenetic analysis of 18S rRNA gene. Also, Sengupta *et al.* (2009) investigated the phylogeny of family Viviparidae in the lakes of the Rift valley area of Africa.

The classification of freshwater Mollusca in Egypt is focusing only on traditional external morphology, mainly on the shape of shell, teeth and color of the

nacre, leaving a difficulty to identify species with similar morphometric parameters (Ibrahim *et al.*, 1999 ; Soliman, 2001). The objective of the present article is to study the ecology and taxonomy of molluscs inhabiting Nile Rayahs, based on a combination of both morphometric parameters and the genetic tool, 18S rRNA gene.

MATERIALS AND METHODS

Description of sampling sites:

El- Rayah El -Tawfiky

El-Rayah El-Tawfiky is a channel with length of about 180 km. It arises from Damietta branch of the River Nile in El Kanater city and extends towards northeastern of El Mansoura city and then branched into two sub- channels, (Fig.1). Seven stations were selected along El-Rayah to represent all types of habitats in this ecosystem, starting from El-Kanater El-khairia city (T1, 30°11'46.58" N-31° 7'55.98" E) to Manzalah city (T7 , 31°09'49.9 N - 31° 7'55.98" E).

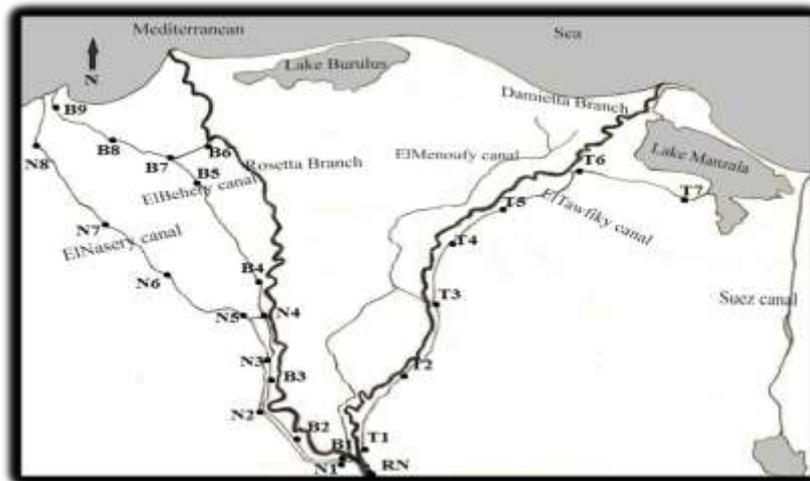


Fig. 1: Map of the River Nile Delta showing the sampling sites in the three studied channels.

El-Rayah El-Behery

Behery channel arises from Rossetta branch directed to northwestern of Alexandria city. Its length is about 220 km. Nine stations were selected along El-Rayah to represent all types of habitats in this ecosystem (Fig.1), starting from El-Kanater El-khairia city (B1, 30°10'47.36"N - 31°6'18.69"E) to El-Siuof ,Alexandria (B9, 31°13'6.67" N - 29°59'39.74" E).

El-Rayah El-Nassery

Nassery channel begins at Rossetta branch parallel to Behery channel, then directed to North West in direction of Nopareia city. It is connected with Noubria canal branched from Kanater Bolin then directed to North West till reaches Mediterranean Sea through Lake Mariut. Eight stations were selected along El-Rayah to represent all types of habitats in this ecosystem (Fig.1) , starting from El-Kanater El-khairia city (N1, 30°10'36.78" N - 31° 6'29.77" E) to end of Nubaria (N8, 30°59'54.76 N - 29°51'49.97" E).

Sampling

Four species of molluscs were collected from the studied Nile channels (Rayahs), seasonally during the period from spring 2014 to winter 2015 (Fig.1). The sediment samples, which contained the molluscs, were collected from investigated sites, using Ekman Grab Sampler. The samples were sieved by hand net, and then washed with drainage water to remove mud or other fine particles. The collected molluscs were preserved in plastic jar with 10% neutral formalin solution for counting, identification and classification according to Ibrahim *et al.* (1999). The live specimens were dissected and the shells were removed from the remaining body. The soft tissues were preserved in absolute ethanol and kept at 4°C for molecular analysis.

Morphometric analyses

The shells were cleaned from attached algae, fibers and calcareous deposits, using paraffin oil. The morphological study of molluscs species included shell color, measurements; operculum, presence or absence of nodules, tubercles, deep or shallow sutures, number of whorls and aperture height and width, using a digital caliper. Description of hinge ligament and Umbo were done on *Bivalvia* specimens. Sizes of gills and foot were measured with respect to body size (Ibrahim *et al.*, 1999; Thiam and Diallo, 2010; Desouky and Busais, 2012).

Molecular analyses

DNA was extracted from mantle of the studied species, using the method of Distel (2000) with a slight modification. Briefly, tissue was grounded in TE buffer, Tris 10 mM and EDTA 1mM and dissolved in a medium containing 5 M guanidinium thiocyanate. Tissue lysis was done at 70 °C for 20 minutes with shaking followed by centrifugation for 2 minutes at speed 100,000 rpm. Insoluble materials were discarded and the supernatant was moved into clean propylene tube. The DNA was purified from collected cell lysis suspension, using high pure PCR template preparation kit, Roche, Catalog no. 11796828001, Mannheim, Germany. The purified DNA was run on 0.9% agarose gel electrophoresis, followed by staining with ethidium bromide and UV visualization.

A PCR primer set, Euk-63F, 5' - ACG CTT GTC TCA AAG ATT A-3' and 1818R, 5' -ACG GAA ACC TTG TTA CGA-3' was used to amplify 18S rRNA gene (Lepere *et al.*, 2011). PCR reaction mixture, 50 µl, contained 10x EX taq buffer II (Mg²⁺ plus), 0.2 µM primer, 400 µM dNTP each, 2.25U Takara EX-Taq Polymerase (Takara, Japan) and 5–30 ng DNA template. PCR was performed with an initial denaturation step of 5 min at 95°C. The PCR reaction continued with 30 cycles of 1 min at 95°C, 40 sec. at the annealing temperature, 55 °C, and 1 min extension at 72°C. The PCR product was cut from the gel and eluted using QIAquick Gel Extraction Kit, catalogue no. 28704, Qiagen, USA. The purified 18S rRNA gene amplicon was analyzed directly by sequencing, through 3500 series genetic analyzer (Life Technology, CA, USA).

The 18S rRNA gene sequences were submitted to FASTA screening to determine their similarity to known molluscs sequences in the DNA database. Construction of phylogenetic tree was done through two bioinformatics processes. In the first process, the nucleotide sequences of the recovered 18S rRNA gene and homologue sequences, from the DNA database, were aligned using the online program “Clustal Omega”, <http://www.ebi.ac.uk/Tools/msa/clustalo/>. In the second process, the aligned sequences, including the sequence gaps, were submitted to the MEGA software, V. 6.06, <http://www.megasoftware.net/>, for drawing the phylogenetic tree. Bootstrap method, provided as a phylogeny test, in the MEGA

software, was performed using number of 500 Bootstrap replications. Consensus phylogenetic tree was constructed by applying the algorithms neighbor joining, maximum parsimony and maximum likelihood, in the same MEGA software.

The 18S rRNA gene sequences were registered at DNA database under accession numbers, LC383736, Bivalve-sp1; LC383737, Bivalve-sp 2; LC383738, Gastropod -sp1 and LC383739, Gastropod-sp 2.

RESULTS AND DISCUSSION

Morphometric characterization of studied gastropods

The comparison of shell morphometric characterization of studied Gastropod species is given in Table (1). Gastropod sp.-1 had thick, hard but smooth shell. It was mainly light in apex and light or dark brown in the base (Fig. 2). The shell had six conical to globose whorls, increasing slightly in the size towards the shell opening, with more or less pointed whitish apex and with deep or moderately deep sutures.

Table 1: Shell Morphometric characterizations of studied Gastropod molluscs.

Shell characteristics	Gastropod sp.-1	Gastropod sp.-2
Shell color	Light or dark brown and black	Dark brown with brown or black bands
Torsion	Dextral	Dextral
Whorls number	6	5-6
Shell height (cm)	0.4-1.6	0.9-2.6
Shell width (cm)	0.25-0.9	0.4-1.8
Spire height (cm)	0.13-0.45	0.0.2-0.95
Body whorl height (cm)	0.3-1.2	0.7-2.4
Aperture height (cm)	0.2-0.5	0.36-1.1
Aperture width cm	0.1-0.4	0.3-0.9
Shell thickness	8.75-143.8	14.5-277
Shell weight (g)	0.004-0.35	0.63-2.95
Columella	Axial and hollow	Axial and hollow
Umbilicus	Closed	Closed

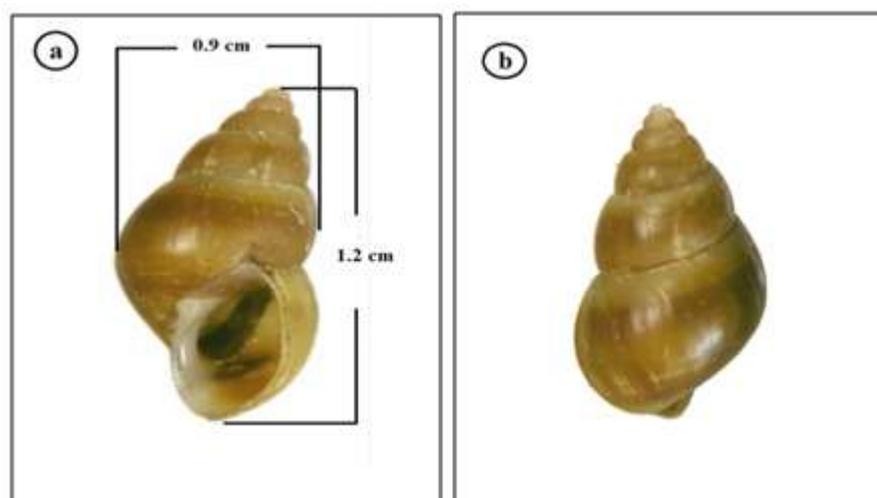


Fig. 2: Morphology of the shell of Gastropod sp. – 1, a .ventral view, b. dorsal view.

The height of the shell in full grown shell was 1.2 cm and the width of the shell was 0.9 cm, while the biomass was 0.165 gm. Lotfy and Lotfy (2015) reported that

the typical form measures 16×9 mm, while the slender form measures 22×9 mm. The typical form has lower whorls, evenly curved and smooth, carinations are confined to the apical whorls; usually with one or more dark brown bands. The shell of the Gastropod sp.-2 was thick, hard and conical and had long, dark brown spire with pointed apex and the last whorl was larger than that of Gastropod sp.-1 (Fig. 3).

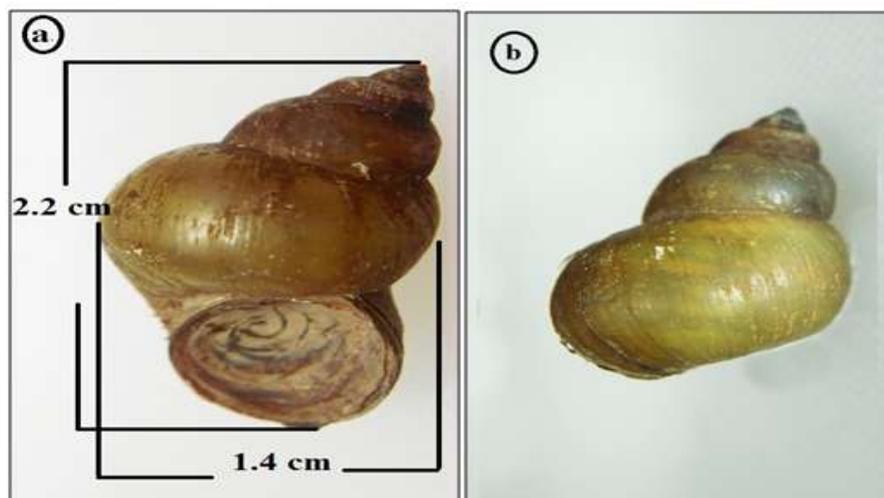


Fig. 3: Morphology of the shell of Gastropod sp.-2, a. ventral view, b. dorsal view.

Gastropod sp.-1 had an oval brown operculum, with horny and concentric shape. The height of the shell in full grown shell was 2.2 cm and the width of the shell was 1.4 cm, while the biomass was 2.58 gm. and the aperture height was 0.9 cm, while the aperture width was 0.8 cm. These results were explained by Orabi and Osman (2015) who mentioned that the average size is 25 mm (H) \times 20 mm (W). Regarding morphology of the operculum, both Gastropod spp.-1 and -2 were similar, but in Gastropod sp.-2 the operculum was thin and had corneous shape. The present results agree with Ibrahim *et al.* (1999) and (Lotfy and Lotfy, 2015).

Molecular characterization of studied gastropods

The Gastropods sp.-1 and -2 were linked with each other and formed paraphyletic cluster with the species *Viviparus georgianus*. However, the Gastropod sp.-1 was located more distantly than Gastropod sp.-2 (Fig. 6). Gastropod sp.-1 had sequence homology average 88% with all the species inside the cluster of family Viviparidae, implicating new family. Actually, family Viviparidae contains 16 known genera. Gastropod sp.-2 showed sequence homology percentage, 92.4% with *Viviparus georgianus*, representing a new genus under this family (Giribet and Weeler, 2002; Yazar *et al.*, 2014).

The Gastropod sp.-2 had morphology closely related to family Viviparidae than Gastropod sp.-1 and the whole shell morphology of Gastropod sp.-2 from Rayahs, described here, was very similar and corresponds to that of *Viviparus georgianus* (Giribet and Wheeler, 2002). Previous morphometric studies, suggested that Gastropod sp.-1 was belonged to family Thiaridae (Schutt, 1986; Sattmann and Kinzelbach, 1988; Brown, 1994; Ibrahim *et al.*, 1999; El-Kady *et al.*, 2000; Ibrahim *et al.*, 2006 and AbdEl-Wakeil *et al.*, 2013). These morphometric descriptions did not match with current genetic taxonomy, which suggested Viviparidae as the corresponding family of Gastropod sp.-1. However, morphology of the animal may be affected by environmental pressures, such as temperature, precipitation, and

salinity (Kato and Foltz, 1993) which may hinder the accurate description of the same animal from different localities. However, the taxonomy of Viviparid species have been suffered from, limitation of anatomical and molecular data, leaving gaps in taxon determination levels (Strong *et al.*, 2008; Sengupta *et al.*, 2009). Because of this lack of knowledge, no accurate evolutionary taxonomy for this Gastropod group, for example, how the subfamilies are phylogenetically related to one another, and what is the ancestor of early Viviparids (Starobogatov, 1992).

Morphometric characterization of studied bivalves

The Bivalve sp.-1, shell was ovoid and broader at posterior end than anterior one (Fig. 4, Table 2). The two valves were securely attached to each other by an elastic hinge ligament. The beak or umbo was a small swollen knob and considered as the point at which growth begins into the two valves. The outer surface of the valve was smooth, varying in colour through light greenish, brownish or yellowish.

The shell of Bivalve sp.-2 was elongated, more or less pointed posteriorly than anteriorly (Fig. 5). The two valves were securely attached to each other by an elastic brown hinge ligament. Both of Bivalves sp.-1 and -2, had a series of projecting and interlocking hinge teeth. The small cardinal teeth were located in the anterior part of the valve below the beak and there were very long narrow ridge-like lateral teeth in the posterior part.



Fig. 4: Morphology of the shell of Bivalve sp.-1. a, b outer shell valve and c, d inner shell valve.

Table 1: Shell Morphometric characterizations of studied *Bivalvia* molluscs

Shell characteristics	Bivalve sp.-1	Bivalve sp.-2
Shell color	Light greenish ,brownish or yellowish	Light brown to grayish brown
Length of valves (cm)	3-4	2.9-5.8
Height of valves (cm)	2.4-3.5	1.4-2.6
Width of valves (cm)	1.3-1.8	0.7-2.1
Shell weight (g)	2.5-7.6	2.3-9.4
Shell sculpture	Concentric smooth regular growth lines traversed by vertical faint rays from the umbo to the shell end	Concentric coarse regular growth lines
Umbo	Small	Small

The soft bodies of the two species had creamy white mantle, with light brown or brown edges. Dorsal mantle margin is presented a well expressed high angle with comb-shaped projections on the top and a muscular anterior margin. Gills were creamy white, dorsal margin was straight to sinuous and ventral margin was moderately convex. Inner gills were much longer and higher than outer ones; gill length was 40-45% of body length. The foot was massive, creamy white and darker distally. Labial palps were triangular, creamy white straight or slightly convex dorsally; straight or gently concave ventrally and bluntly pointed ventrally. These results are in agreement with those described by Olga *et al.* (2014) who analyzed the shell morphology and the whole soft body anatomy in detail for two *Cristaria* sp. additionally; a cytochrome oxidase subunit 1 (CO1) gene fragment was sequenced from foot tissue.

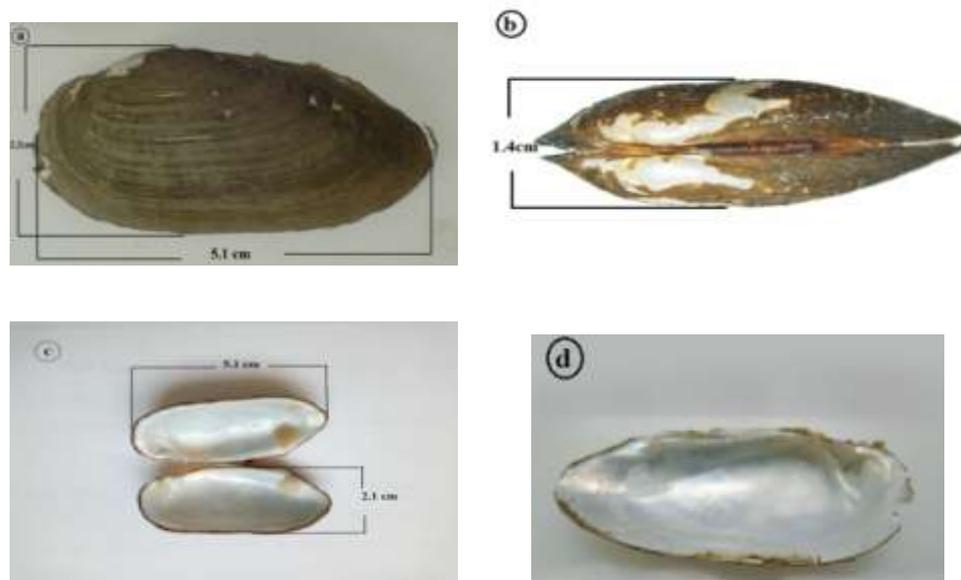


Fig. 5: Morphology of the shell of Bivalve sp.-2. a,b outer shell valve and c,d inner shell valve.

Molecular characterization of studied bivalves

Bivalve sp.-1 and -2, showed 18S rRNA gene sequence identity averages, 89% and 92%, respectively, with known species, which belonged to family Unionidae (Fig. 6). Hence, both of Bivalve sp.-1 and -2 formed a unique monophyletic clade, which was distant from other species belonging to family Unionidae (Fig. 6). On the other hand, Bivalve sp.-1 showed sequence identity percentage of 93.67% with Bivalve sp.-2. The sequence homologies of 18S rRNA genes between the known genera under the same family are between 99% and 96% (Giribet and Wheeler, 2002; Taylor *et al.*, 2007; Inoue *et al.*, 2013). Hence, both of Bivalve sp.-1 and -2 may represent two different genera, under a new family which has the same ancestor of family Unionidae (Yarza *et al.*, 2014). These genetic results were in parallel with morphological parameters of the studied Molluscan shells. The shell morphology of Bivalve sp.-2, described here, was similar to those of family Unionidae. On the other hand, the shell of Bivalve sp.-1 had some morphological variations from Unionidae family. However, the shell morphology of Bivalve sp.-1 was similar to that of *Lampsilis cardium*, but differs in color of shell, which was yellow to yellow-green with green rays and had pseudocardinal teeth and both showed 18S rRNA gene sequence identity of 90.26 % (Fig.6). On the other hand, Bivalve sp.-2 had sequence

identity of 92.03% with *Unio pictorum* and both have similar shell morphology that was the closet Bivalvia reference in the phylogeny tree (Taylor *et al.*, 2007).

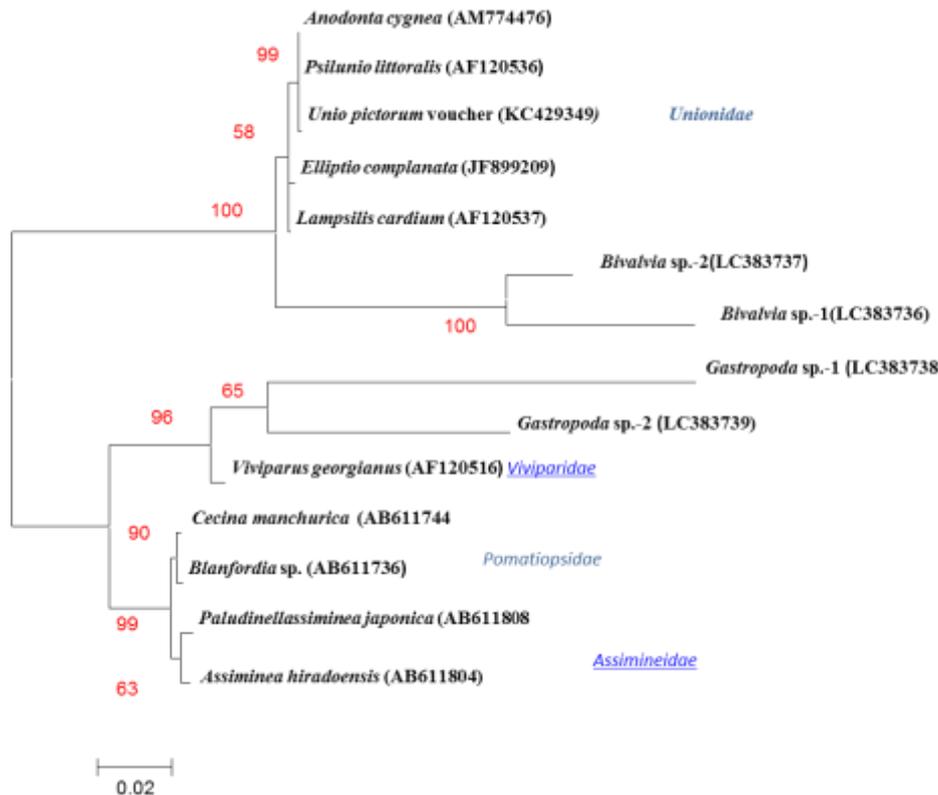


Fig. 6: A consensus phylogenetic tree based on 18S rRNA gene sequences of current molluscs; beside their corresponding sequences from database. Bootstrap values, more than 50%, of compared algorithms, are indicated at the branch roots. The bar represents 0.02 changes per nucleotide. Accession numbers of database extracted sequences are in brackets.

Biogeographic and seasonal distribution of studied Molluscan species

The abundance of species at studied Rayahs was identified as average number of individuals per station. Gastropod sp.-1 was recorded only in a single station of El-Rayah El-Tawfiky, in winter season, recording the highest abundance, 525 Org.m⁻² (Fig.7). The water in this station was more stagnant than other sampling sites (unpublished report). Moustafa (1995) had recorded this snail species crawling at the bottom of stagnant water of the River Nile and its branches. On the other hand, high vegetation in this station may explain the domination of Gastropod sp.-1. Hussein *et al.* (2011) recorded negative correlation between water depth and Gastropod sp.1, which occurred in the corresponding shallow water station.

Gastropod sp.-2 showed the highest abundance in summer at El-Rayah El-Behery, with an average of 163 Org.m⁻². This observation came in parallel with studies on reproduction cycle season was in summer of this gastropod (Brown, 1994; Karimi *et al.*, 2004)

The Bivalve sp.-1 showed highest abundance in autumn and winter at El-Rayah EL-Behery, with an average of 100 and 106 Org.m⁻², respectively. Abundance of bivalve population had been recorded during December, and completely disappeared from April to June at Gho-Manhasan stream, Chenab River, India (Sharma *et al.*, 2013). Although both of EL-Behery and El-Nassery are originated from the same Nile Rossetta branch, winter showed high abundance of Bivalve sp.-1 in EL-Behery, while disappeared in El-Nassery (Fig.7). Occurrence of suitable substrates, lack of

stratification of the overlying water, and good water flow in EL-Behery may optimize the occurrence of Bivalve sp.-1 (Johannsson *et al.*, 2000). On the other hand, winter is an optimized season for bivalve predators, such as migratory birds and others, at El-Nassery (Peterson *et al.*, 2000; Luzzatto and Penchaszadeh, 2001; Salas *et al.*, 2001).

Comparing with other studied molluscs, Bivalve sp.-2 had the lowest abundance, with completely disappearance in spring at all Rayahs (Fig.7). However, this disappearance may refer to deep burrowing, and consequently, hindering the process of sampling, especially in winter and spring (Sanders, 1958; McLachlan and Young, 1982). On the other, El-Ghobashy (2011) stated that the distribution and density of bivalves may be influenced by environmental changes and anthropogenic activities.

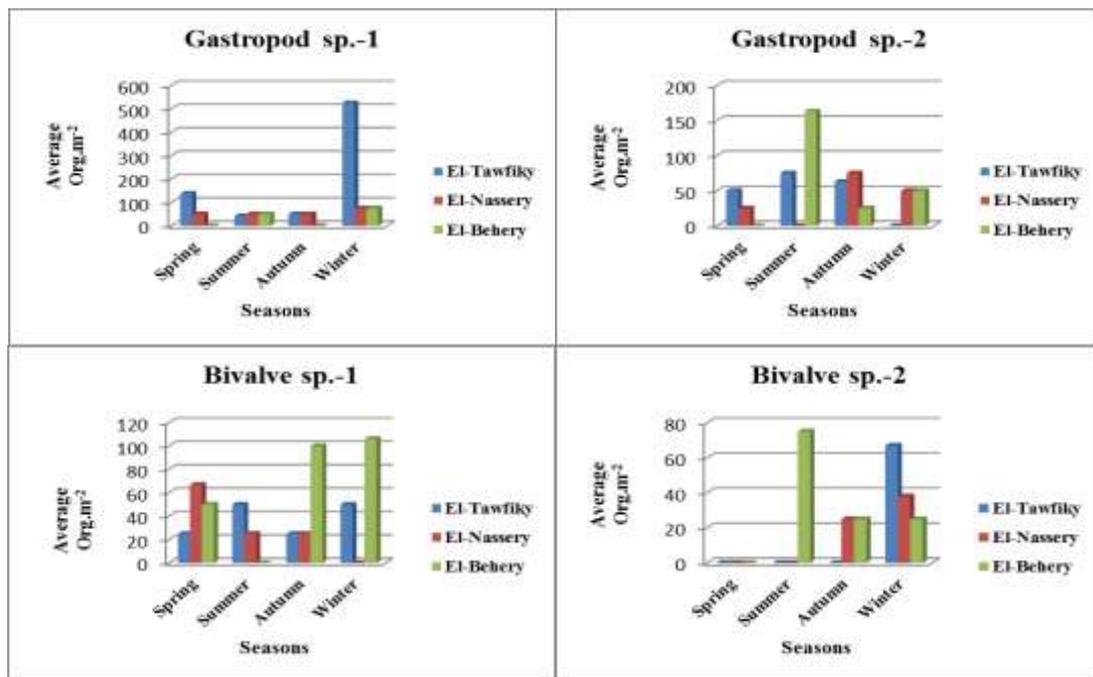


Fig. 7: Seasonal abundance variations of studied molluscs in the three Rayahs.

CONCLUSION

The present study highlighted the molecular taxonomy and biogeographic distribution of four Molluscan species in the main Egyptian irrigated River Nile channels; El-Rayah El-Tawfiky, El-Rayah El-Nassery and El-Rayah El-Behery. Both of morphometric and 18S rRNA gene analyses indicated that the Gastropod sp.-2 had characters similar to those of family Viviparidae. The whole shell morphology of Gastropod sp.-2 was very similar to that of *Viviparus georgianus*. The 18S rRNA gene analyses implicated that Bivalve sp.-1 and -2 may belong to overlooked family, having the same ancestor of the known family, Unionidae. Hence, the morphometric and molecular records of the present study suggested that the phylogeny of phylum Mollusca is still expanding to cover new taxa. The current molluscs showed wide variations in seasonal abundance at the studied Rayahs. This mollusc abundance fluctuation could be a response to the variations in temperature and habitat characteristics. However, this study is considered the base line towards exploring and evaluation of phylum Mollusca in Egyptian irrigated channels. Advanced studies, such as mollusc transcriptome and proteome analyses are needed to understand the ecological role and dynamics of studied molluscs in Egyptian irrigated channels.

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ARABIC SUMMARY

دراسات بيئية وتصنيفية لبعض أنواع من الرخويات فى قنوات الري بنهر النيل (الرياحات)، مصر.

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تهدف هذه الدراسة الى وضع اساس لتقييم وتصنيف لأربعة أنواع من رخويات المياه العذبة؛ نوعان من طائفة البطنقدميات والآخران من طائفة ذوات المصرعين. وقد تمت دراستهم فى ثلاث قنوات رى من رياحات نهر النيل وهم الرياح التوفيقي، الرياح الناصرى والرياح البحيرى، موسميا من الفترة ربيع ٢٠١٤ الى شتاء ٢٠١٥. وقد اشتملت هذه الدراسة على وصف الصفات الخارجية للاصداف وكذلك تحليل للمحتوى الجينى لهم بواسطة جينات الحمض النووى الريبوسومى (18s rRNA). وقد دلت النتائج على ان القوقعان لدهما من ٥-٦ لفات ولونهما بنى فاتح اوغامق ولكن النوع الثانى يتميز بكبراللفة الاخيرة للجسم عن القوقع الاول. وبدراسة المحتوى الجينى للقوقعين فقد وجدت الدراسة ان القوقعان من المرجح ان يكونا نوعان جديان ينتميان الى جنس قوقع يسمى فيفيپاروس (*Viviparus*). وبدراسة توزيعهما سنويا فى الرياحات فقد لوحظ ان اعلى توزيع للقوقع الاول كان خلال فصل الشتاء فى الرياح التوفيقي واقلها فى الرياح البحيرى بينما اعلى قيمة للقوقع الثانى كانت خلال فصل الصيف فى الرياح البحيرى.

اما بالنسبة للنوعين الاخرين اللذان ينتميان الى طائفة ذوات المصرعين فقد وجد ان النوع الاول بيضاوى الشكل ويتميز بلون اخضروربنى مصفر بينما النوع الثانى ممدود ولونه يميل الى البنى والرمادى. وبدراسة المحتوى الجينى للنوعين وجد ان النوعين من المرجح ان يكونا جنسان جديان ينتميان الى عائلة اليونيويدي (*Unionidae*). وبدراسة توزيعهما سنويا فى الرياحات فقد لوحظ ان اعلى توزيع للنوعان كان فى الرياحين البحيرى والتوفيقي خلال فصل الشتاء بينما اختفى النوعان تماما خلال فصل الربيع. اوصى البحث بمزيد من الدراسات المتقدمة مثل ترانسكربتوم (*transcriptome*) والبروتيوم (*proteome*) لفهم الدور البيئى والحيوى لهذه الرخويات فى رياحات نهر النيل.