

## Comparative Phylogenetic Perspectives on the Evolutionary Relationships in the Brine Shrimp *Artemia* Leach, 1819 (Crustacea: Anostraca) Based on Secondary Structure of *ITS1* Gene

Alireza Asem<sup>1,2</sup>, Pu Wang<sup>3</sup> and Shi-Chun Sun<sup>2\*</sup>

<sup>1</sup> College of Life Sciences and Ecology, Hainan Tropical Ocean University, Yucai Rd, Sanya 572000, China

<sup>2</sup> Institute of Evolution and Marine Biodiversity, Ocean University of China, 5 Yushan Road, Qingdao 266003, China

<sup>3</sup> Department of Ecology, Evolution and Behavior, University of Minnesota, MN 55108, USA

### ARTICLE INFO

#### Article history:

Received 05 March 2018

Accepted 11 May 2018

Available online 31 August 2018

#### Keywords:

Phylogenetic

Primary sequence

Secondary structures

Internal transcribed spacer 1

*Artemia*

#### \*Corresponding author:

✉ S.C. Sun

[sunsc@ouc.edu.cn](mailto:sunsc@ouc.edu.cn)

p-ISSN 2423-4257

e-ISSN 2588-2589

### ABSTRACT

This is the first study on phylogenetic relationships in the genus *Artemia* Leach, 1819 using the pattern and sequence of secondary structures of internal transcribed spacer 1 (*ITS1*). Significant intraspecific variation in the secondary structure of *ITS1* rRNA was found in *Artemia tibetiana*. In the phylogenetic tree based on joined primary and secondary structure sequences, *Artemia urmiana* and parthenogenetic populations displayed new lineages, and two New World species (*Artemia franciscana* and *Artemia persimilis*) were located in a basal clade that was not detected in previous studies. The close evolutionary relationship between *A. franciscana* and *A. persimilis* are expressively supported by the previous empirical and experimental investigation on the ability of hybridization (in natural habitats and lab conditions) and analysis on allozyme markers.

© 2015 UMZ. All rights reserved.

**Please cite this paper as:** Asem A, Wang P, Sun Sh. 2018. Comparative Phylogenetic Perspectives on the Evolutionary Relationships in the Brine Shrimp *Artemia* Leach, 1819 (Crustacea: Anostraca) Based on Secondary Structure of *ITS1* Gene. *J Genet Resour* 4(2): 72-84. doi: 10.22080/jgr.2018.14623.1109

### Introduction

Phylogenetics is the study of evolutionary history and relationships of biological taxa using mostly morphological, genetic and molecular characters. Sometimes the results due to different phylogenetic methods are paradoxical. The genus *Artemia* leach, 1819 (Crustacea: Anostraca) is one taxon representing this kind of paradox. *Artemia* includes three bisexual species in the New World (*Artemia franciscana* Kellogg, 1906, *Artemia persimilis* Piccinelli & Prosdocimi, 1968 and *Artemia monica* Verrill, 1869), four bisexual species in the old world (*Artemia salina* (Linnaeus, 1758), *Artemia urmiana* Günther, 1899, *Artemia sinica* Cai, 1989 and *Artemia tibetiana* Abatzopoulos *et al.*, 1998) (Asem *et al.*, 2010), and a large number of parthenogenetic populations including di-, tri-, tetra-, penta- and also heteroploids or even mixtures of different ploidies (Sun *et al.*, 1999; Abatzopoulos *et al.*, 2002a,b; Amat *et al.*, 2007;

Zheng and Sun 2013). Although recent analyses based on mitochondrial DNA data confirmed that Asian bisexual species had a common ancestor (Maniatsi *et al.*, 2011; Asem *et al.*, 2016), a previous morphological study demonstrated that *A. urmiana* significantly distinguished from the other Asian species as well as the Mediterranean *A. salina* and the American *A. franciscana* (Triantaphyllidis *et al.*, 1997). Baxevanis *et al.* (2005) claimed there was no consistency between results of genetic distance and morphometric characters of bisexual *Artemia*. They proved that *A. urmiana* and *A. tibetiana* were genetically close but significantly dissimilar in the morphology, while *A. urmiana* and *A. persimilis* had obvious genetic differentiation but were close in morphometric patterns. On the other hand, different genetic methods also showed inconsistent results for evolutionary relationships of genus *Artemia*. Analysis using the sequence of the nuclear internal transcribed spacer 1 (*ITS1*) region confirmed that *A.*

*persimilis* formed a distinct clade and was well differentiated from the others, and *A. franciscana* was placed as a clade sister to Asian bisexuals and parthenogenetics. (Baxevanis *et al.*, 2006; Hou *et al.*, 2006; Kappas *et al.*, 2009; Vikas *et al.*, 2012; Eimanifar *et al.*, 2014). According to the results of 16S rDNA RFLP analyses (Unrooted NJ), *A. franciscana* located in a cluster, and *A. salina* + *A. persimilis* and three Asian bisexual species in two others separately (Baxevanis *et al.*, 2005). Maniatsi *et al.* (2011) confirmed that *COI* (Cytochrome *c* Oxidase subunit I) data displayed the similar result with *ITS1* data. Moreover, the analysis on *COI* sequences of 541 individuals showed that the Mediterranean *A. salina*, rather than the South American *A. persimilis*, was placed in a separate phylogenetic clade (Eimanifar *et al.*, 2014). These consequences indicate that systematics of *Artemia* is still puzzling and therefore a comprehensive review is needed.

In the past decade, several studies have demonstrated the application of nuclear rRNA secondary structure models (mostly *SSU-rRNA*, *ITS1* and *ITS2*) could clarify the evolutionary history of taxa (Gottschling & Plotner 2004; Campbell *et al.*, 2005; Sun *et al.*, 2010; Reblova *et al.*, 2013; Yosefzadeh *et al.*, 2012; Coleman, 2013; Hodac *et al.*, 2014; Wang *et al.*, 2015; Hosseinzadeh Colagar *et al.*, 2016). For example, Wang *et al.* (2015) proved that using the sequence of secondary structure of *SSU-rRNA* gene could give different information than its primary sequence to better understand phylogenetic relationships among members of family Pseudokronopsidae in the ciliates.

In this study, the secondary structures of the first partial *ITS1* region of bisexual/parthenogenetic *Artemia* are predicted and compared. Phylogenetic trees are constructed based on the primary and primary+secondary sequences. The aims of this study are to model *ITS1* secondary structures and examine the contribution of secondary sequence in understanding the evolutionary relationships in the genus *Artemia*.

## Materials and Methods

### Taxa and sequences

Sequences of the internal transcribed spacer 1

(*ITS1*) region were downloaded entirely from GenBank (<http://www.ncbi.nlm.nih.gov/genbank/>). Our dataset contained 313 *ITS1* sequences including seven bisexual species and parthenogenetic populations with different ploidy degrees (i.e. di-, tri-, tetra- and pentaploidy) (Table 1). Sequences were aligned using Muscle in MEGA ver. 6.00 with default parameters (Tamura *et al.*, 2013). The total sequences (including 111 haplotypes) were collapsed by DNAsp ver. 5.00 (Librado and Rozas, 2009). *Streptocephalus proboscideus* (AY519840) was used as an outgroup (Baxevanis *et al.*, 2006; Eimanifar *et al.*, 2014).

The first partial *ITS1* region which ranged from 294 bp to 340 bp (started with a conserved sequence of GTTT and stopped with TCKC) was chosen for secondary structure analysis followed by secondary structure model for *ITS1* suggested by Gottschling and Plötner (2004), using  $\Delta G$  minimization, similarity and constraint folding (Mathews *et al.*, 1999; Reuter and Mathews, 2010) using mfold onlen software (Zuker, 2003). Additionally, tree topology from the primary sequence of this part was the same as that from the whole *ITS1* sequence (for more information see results and discussion sections).

### Secondary structure prediction

The secondary structures were predicted for each haplotype with respect to same shapes for conserved parts between species/populations and minimum free-energy optimization (Zuker, 1989, Hofacker *et al.*, 2002) using the mfold web server (<http://unafold.rna.albany.edu/?q=mfold/RNA-Folding-Form>) (Zuker, 2003). The structures were aligned and further edited by 4SALE ver. 1.7 (Seibel *et al.*, 2006). The sequence alignments were manually edited via comparison between primary and secondary positions to find the best homogeneous arrangements. 4SALE ver. 1.7 (Seibel *et al.*, 2006) was used to draw the general patterns of secondary structure based on the results of conservation rates. The lengths of helices and single strands and the number of paired nucleotides were counted for each general pattern (Table 2).

**Table 1.** Sampling information of *Artemia* specimens/sequences (all downloaded from GenBank) used in the present study.

Species/Population	Abbreviation	Haplotype names	Accession numbers	References
<i>Artemia urmiana</i>	URM	URM1	DQ201275	Baxevanis et al., 2006
		URM2	DQ201276	Baxevanis et al., 2006
		URM3	DQ201277	Baxevanis et al., 2006
		URM4	KF736251	Maccari et al., 2013
		URM5	KF736252	Maccari et al., 2013
		URM6	KF703810-15	Eimanifar et al., 2014
		URM6	KF703820	Eimanifar et al., 2014
		URM6	KF703822-23	Eimanifar et al., 2014
		URM7	KF703816	Eimanifar et al., 2014
		URM8	KF703817	Eimanifar et al., 2014
		URM9	KF703818	Eimanifar et al., 2014
		URM10	KF703819	Eimanifar et al., 2014
		URM11	KF703821	Eimanifar et al., 2014
		URM12	KF703824	Eimanifar et al., 2014
		URM13*	DQ069926	Hou et al., 2006
		URM13*	DQ084193	Hou et al., 2006
<i>Artemia tibetiana</i>	TIB	URM13*	KF736249-50	Maccari et al., 2013
		TIB1	DQ201269-70	Baxevanis et al., 2006
		TIB2	KF736290-95	Maccari et al., 2013
		TIB3	KF703778	Eimanifar et al., 2014
		TIB4	KF703785	Eimanifar et al., 2014
<i>Artemia sinica</i>	SIN	TIB5	KF703798	Eimanifar et al., 2014
		SIN1	DQ069929	Hou et al., 2006
		SIN1	DQ069930	Hou et al., 2006
		SIN2	DQ069931	Hou et al., 2006
		SIN3	DQ084196	Hou et al., 2006
		SIN4	DQ084197	Hou et al., 2006
		SIN5	DQ084198	Hou et al., 2006
		SIN6	DQ201285	Baxevanis et al., 2006
		SIN7	DQ201286	Baxevanis et al., 2006
		SIN8	DQ201287	Baxevanis et al., 2006
		SIN9	FJ004945	Kappas et al., 2009
		SIN10	KF736296-97	Maccari et al., 2013
<i>Artemia sp.</i> <i>Artemia salina</i>	SP SAL	SIN11	KF703766	Eimanifar et al., 2014
		SIN11	KF703790	Eimanifar et al., 2014
		SIN12	KF703796	Eimanifar et al., 2014
		SP1	DQ084194	Hou et al., 2006
		SAL1	DQ201302	Baxevanis et al., 2006
		SAL2	DQ201303	Baxevanis et al., 2006
		SAL3	DQ201304	Baxevanis et al., 2006
		SAL4	DQ201305	Baxevanis et al., 2006
		SAL5	DQ201306	Baxevanis et al., 2006
		SAL6	DQ201307	Baxevanis et al., 2006
		SAL7	DQ201308	Baxevanis et al., 2006
		SAL8	DQ201309	Baxevanis et al., 2006
<i>Artemia persimilis</i>	PER	SAL9	FJ004946	Kappas et al., 2009
		SAL10	KF703762	Eimanifar et al., 2014
		PER1	DQ069925	Hou et al., 2006
		PER2	DQ084192	Hou et al., 2006
		PER3	DQ201263	Baxevanis et al., 2006
		PER4	DQ201264	Baxevanis et al., 2006
		PER5	DQ201265	Baxevanis et al., 2006
		PER6	DQ201266	Baxevanis et al., 2006
		PER7	DQ201267	Baxevanis et al., 2006
		PER8	DQ201268	Baxevanis et al., 2006
<i>Artemia franciscana</i>	FRA	PER9	FJ004922-23	Kappas et al., 2009
		PER10	FJ004924	Kappas et al., 2009
		FRA1	DQ069923	Hou et al., 2006
		FRA1	DQ084190	Hou et al., 2006
		FRA1	DQ201297	Baxevanis et al., 2006
		FRA2	DQ069924	Hou et al., 2006
		FRA2	FJ004935-36	Kappas et al., 2009
		FRA2	FJ004938-39	Kappas et al., 2009
		FRA2	FJ004941-42	Kappas et al., 2009
		FRA2	GU252106	Maniatsi et al., 2009
		FRA2	GU323291	Vikas et al., 2012
		FRA2	GU323293-94	Vikas et al., 2012
		FRA2	GU323296-97	Vikas et al., 2012
FRA2	GU323309-12	Vikas et al., 2012		
FRA2	GU323314	Vikas et al., 2012		
FRA2	GU323316	Vikas et al., 2012		
FRA3	DQ084191	Hou et al., 2006		

**Table 1.** Continued

Species/Population	Abbreviation	Haplotype names	Accession numbers	References
<i>Artemia franciscana</i>	FRA	FRA3	DQ201298	Baxevanis et al., 2006
		FRA4	DQ201289	Baxevanis et al., 2006
		FRA4	DQ201291	Baxevanis et al., 2006
		FRA4	DQ201295	Baxevanis et al., 2006
		FRA4	FJ004933-34	Kappas et al., 2009
		FRA4	GU252102-04	Maniatsi et al., 2009
		FRA4	GU323298	Vikas et al., 2012
		FRA4	GU323301-02	Vikas et al., 2012
		FRA4	GU323304-06	Vikas et al., 2012
		FRA4	GU323308	Vikas et al., 2012
		FRA4	GU323315	Vikas et al., 2012
		FRA4	GU323317	Vikas et al., 2012
		FRA5	DQ201290	Baxevanis et al., 2006
		FRA6	DQ201292	Baxevanis et al., 2006
		FRA7	DQ201293	Baxevanis et al., 2006
		FRA8	DQ201294	Baxevanis et al., 2006
		FRA9	DQ201296	Baxevanis et al., 2006
		FRA9	FJ004925-31	Kappas et al., 2009
		FRA9	GU323299	Vikas et al., 2012
		FRA10	DQ201299	Baxevanis et al., 2006
		FRA11	DQ201300	Baxevanis et al., 2006
		FRA12	DQ201301	Baxevanis et al., 2006
		FRA13	FJ004932	Kappas et al., 2009
		FRA14	FJ004937	Kappas et al., 2009
		FRA15	FJ004940	Kappas et al., 2009
		FRA16	GU252105	Maniatsi et al., 2009
		FRA17	GU252107	Maniatsi et al., 2009
		FRA18	GU323289	Vikas et al., 2012
		FRA19	GU323290	Vikas et al., 2012
		FRA19	GU323292	Vikas et al., 2012
		FRA20	GU323295	Vikas et al., 2012
		FRA21	GU323300	Vikas et al., 2012
		FRA22	GU323303	Vikas et al., 2012
		FRA23	GU323307	Vikas et al., 2012
		FRA24	GU323313	Vikas et al., 2012
		FRA25	KF703763	Eimanifar et al., 2014
		FRA26	KF703765	Eimanifar et al., 2014
		FRA26	KF703770	Eimanifar et al., 2014
		FRA26	KF703781	Eimanifar et al., 2014
		FRA26	KF703787-88	Eimanifar et al., 2014
		FRA26	KF703808	Eimanifar et al., 2014
		FRA27	KF703767	Eimanifar et al., 2014
		FRA27	KF703795	Eimanifar et al., 2014
		FRA28	KF703771	Eimanifar et al., 2014
		FRA28	KF703773	Eimanifar et al., 2014
		FRA28	KF703777	Eimanifar et al., 2014
		FRA28	KF703801	Eimanifar et al., 2014
		FRA28	KF703826	Eimanifar et al., 2014
		FRA28	KF703836	Eimanifar et al., 2014
		FRA29	KF703776	Eimanifar et al., 2014
FRA30	KF703779	Eimanifar et al., 2014		
FRA31	KF703784	Eimanifar et al., 2014		
FRA32	KF703786	Eimanifar et al., 2014		
FRA33	KF703791	Eimanifar et al., 2014		
FRA34	KF703797	Eimanifar et al., 2014		
FRA35	KF703799	Eimanifar et al., 2014		
FRA35	KF703827	Eimanifar et al., 2014		
FRA35	KF703834	Eimanifar et al., 2014		
FRA36	KF703800	Eimanifar et al., 2014		
FRA37	KF703806	Eimanifar et al., 2014		
FRA36	KF703800	Eimanifar et al., 2014		
FRA38	KF703848	Eimanifar et al., 2014		
FRA38	KF703854	Eimanifar et al., 2014		
Parthenogenetic populations	PART	PART1	DQ201271-72	Baxevanis et al., 2006
		PART1	DQ201274	Baxevanis et al., 2006
		PART2	DQ201273	Baxevanis et al., 2006
		PART3	DQ201278	Baxevanis et al., 2006
		PART4	DQ201279	Baxevanis et al., 2006
		PART5	DQ201280	Baxevanis et al., 2006
		PART6	DQ201281-83	Baxevanis et al., 2006
		PART6	KF703804	Eimanifar et al., 2014
PART6	KU183830-36	Asem et al., 2016		
PART7*	FJ004943-44	Kappas et al., 2009		

**Table 1.** Continued

Species/Population	Abbreviation	Haplotype names	Accession numbers	References
Parthenogenetic populations	PART	PART7*	KF736253-73	Maccari et al., 2013
		PART7*	KF736276-89	Maccari et al., 2013
		PART7*	KF703764	Eimanifar et al., 2014
		PART7*	KF703803	Eimanifar et al., 2014
		PART7*	KF703807	Eimanifar et al., 2014
		PART7*	KF703809	Eimanifar et al., 2014
		PART7*	KF703825	Eimanifar et al., 2014
		PART7*	KF703830	Eimanifar et al., 2014
		PART7*	KF703832-33	Eimanifar et al., 2014
		PART7*	KF703835	Eimanifar et al., 2014
		PART7*	KF703837-39	Eimanifar et al., 2014
		PART7*	KF703844	Eimanifar et al., 2014
		PART7*	KF703851	Eimanifar et al., 2014
		PART7*	KF703853	Eimanifar et al., 2014
		PART7*	KU183800-04	Asem et al., 2016
		PART7*	KU183815-19	Asem et al., 2016
		PART7*	KU183820-24	Asem et al., 2016
		PART7*	KU183825-29	Asem et al., 2016
		PART7*	KU183805-09	Asem et al., 2016
		PART7*	KU183810-14	Asem et al., 2016
		PART7*	KU183843-47	Asem et al., 2016
		PART8	KF736274-75	Maccari et al., 2013
		PART9	KF703768	Eimanifar et al., 2014
		PART10	KF703769	Eimanifar et al., 2014
		PART10	KF703774-75	Eimanifar et al., 2014
		PART10	KF703780	Eimanifar et al., 2014
		PART10	KF703782	Eimanifar et al., 2014
		PART10	KF703828	Eimanifar et al., 2014
		PART10	KF703840	Eimanifar et al., 2014
		PART10	KF703843	Eimanifar et al., 2014
		PART10	KF703845-46	Eimanifar et al., 2014
		PART11	KF703772	Eimanifar et al., 2014
		PART12	KF703783	Eimanifar et al., 2014
		PART13	KF703792	Eimanifar et al., 2014
		PART14	KF703805	Eimanifar et al., 2014
		PART15	KF703831	Eimanifar et al., 2014
		PART16	KF703841	Eimanifar et al., 2014
		PART17	KF703802	Eimanifar et al., 2014
		PART17	KF703852	Eimanifar et al., 2014
		PART18	DQ201284	Baxevanis et al., 2006
		PART19	DQ201288	Baxevanis et al., 2006
		PART20	KF703789	Eimanifar et al., 2014
PART21	KU183838-42	Asem et al., 2016		
PART22	KU183837	Asem et al., 2016		

\* URM13 and PART7 share the same haplotype.

**Table 2.** A statistic for the composition of the secondary structures proposed in this study. Data shown as number of nucleotides (L and S) or number of Nucleotide pairs (P). H<sub>x</sub>: The xth helix; L: Length; P: Paired nucleotides; S<sub>x-y</sub>: Single strand between the xth and yth helix. Abbreviations of species/populations are defined in Table S1.

Sp./P.	H <sub>I</sub>		S <sub>I</sub>	H <sub>II</sub>		S <sub>II</sub>	H <sub>III</sub>		S <sub>III</sub>	H <sub>IV</sub>		S <sub>IV</sub>	H <sub>V</sub>		S <sub>V</sub>	H <sub>VI</sub>		S <sub>VI</sub>	H <sub>VII</sub>		S <sub>VII</sub>	H <sub>VIII</sub>	
	L	P		L	P		L	P		L	P		L	P		L	P		L	P		L	P
FRA	18	7	3	46	17	16	58	22	7	28	10	2	27	8	4	20	8	1	62	22	1	24	7
PER	22	7	1	22	8	14	65	23	3	28	7	3	30	9	2	20	5	3	81	27	3	13	4
SAL	51	19	2	27	7	4	57	18	6	29	10	2	29	7	3	19	6	0	58	22	2	25	7
TIB <sup>1*</sup>	51	17	2	27	11	1	56	19	6	29	10	2	27	11	3	21	7	0	55	20	4	24	8
TIB <sup>2*</sup>	49	17	1	10	3	3	56	19	6	29	10	2	27	11	3	21	7	0	55	20	4	24	8
SIN	50	18	2	27	9	1	56	19	6	29	10	2	26	9	3	21	8	0	55	22	4	24	8
URM	48	17	2	27	11	1	51	20	6	29	10	2	27	9	2	20	7	0	51	17	4	24	8
SP	51	17	2	27	11	1	56	21	6	29	10	2	27	9	3	21	7	0	55	20	4	24	8
PART	51	17	2	27	11	1	56	19	6	29	10	2	27	9	3	21	7	0	55	20	4	24	8

Sp.: Species, P.: Populations

\* TIB<sup>1</sup>: Haplotypes TIB2-5; TIB<sup>2</sup>: Haplotype TIB1

## Phylogenetic analyses

Phylogenetic analyses were performed based on the alignment of primary sequences for both the first partial and whole *ITS1* region, as well as the alignment consisting of sequence information of joined primary and secondary structure. Phylogenetic trees of haplotypes were designed by Maximum Likelihood (ML) in RAxML-HPC BlackBox 8.2.3 on XSEDE (Miller *et al.*, 2010), Bayesian Inference (BI) as implemented in MrBayes 3.2.2 on XSEDE (Miller *et al.*, 2010), and Neighbor-Joining (NJ) in MEGA ver. 6.00 (Tamura *et al.*, 2013). For ML and NJ, the robustness of branches was assessed by default setting and 1000 bootstrap replicates, respectively. For BI the best nucleotide substitution model of DNA was selected based on MrModeltest 2.2 (Nylander, 2004). Phylogenetic trees based on the primary sequences and sequences of secondary structures (hereinafter referred to as 'sequence-structure') of the partial *ITS1* region were constructed via ProfDistS 0.9.9 (Wolf *et al.*, 2008) with 1000 bootstrap replicates. All trees were visualized using FigTree v 1.4.0 (Rambaut, 2012). For the Maximum Likelihood and Neighbor-Joining bootstraps, the values <70 were regarded as low, 70-94 as moderate, and  $\geq 95$  as high (Hillis & Bull, 1993). For the Bayesian posterior probabilities, the values <0.94 were considered as low, and  $\geq 0.95$  as high following (Alfaro *et al.*, 2003).

## Results

### Secondary structure

All the analyzed *Artemia* shared a similar fingers-pattern of secondary structure with eight helices (Fig. 1), contrast *Streptocephalus proboscideus* (out group) in the same alignment length have a significant difference in secondary structure with six helices (Fig. 2). According to the rate of conservation, a significant intraspecific difference was only observed in the second helix of *A. tibetiana* (Fig. 3).

Statistics of the numeric characters of the general secondary structure are shown in Table 2. Helices IV and VI were conservative in length (28 to 29 bp and 19 to 21 bp, respectively), while helices II and I showed high variability (10 to 46 bp and 18 to 51 bp, respectively). The substitution rate of paired

nucleotides had almost same pattern with the variation of helical length; the lowest substituted numbers of paired nucleotides were observed in Helices IV and VI (7 to 10 bp and 5 to 8 bp, respectively), but the highest rate belonged to helices II and I (3 to 17 bp and 7 to 19 bp, respectively). The highest length variations of the single strand between helix were present in S<sub>II-III</sub> (1 to 16 bp; with the longest ones appearing in FRA (16 bp) and PER (14 bp), respectively). TIB displayed highly intraspecific variation in the length of helix II (27 bp vs 10 bp) and paired nucleotides (11 bp vs 3 bp) (Figs. 1 and 3).

### Comparison of phylogenies based on primary and secondary structure sequences

All methods of ML, NJ, and BI demonstrated uniform tree topology for primary sequences of the first partial *ITS1* region (Fig. 4a). The genus *Artemia* was divided into two distinct and well-supported clusters. Cluster I was further divided into four clades, with either of the Mediterranean *A. salina* and American *A. franciscana* constituting a separate clade, and the Asian bisexual species and parthenogenetic populations constituting the other two clades. The South American *A. persimilis* is placed in a basal position with long branch (Fig. 4a). In addition, the ML (Baxevanis *et al.*, 2006; Eimanifar *et al.*, 2014), BI (Baxevanis *et al.*, 2006; Eimanifar *et al.*, 2014) and NJ (this study, result not shown) analyses based on the complete primary sequence of *ITS1* also generated correspondent tree topologies. Therefore, the first partial region, which ranged from 294 bp to 340 bp, was likely to have the same evolutionary pattern as the total sequence of *ITS1*.

The sequence-structure tree, by the profile neighbor-joining (PNJ) method, displayed same general pattern for parthenogens, Asian and Mediterranean bisexual *Artemia*; whereas *A. franciscana* and *A. persimilis* were clustered into a basal clade in the tree (Fig. 4b). While no significant intra-specific variation was determined with primary sequences for the bisexual species (Fig. 4a), the results of sequence-structure showed markedly intra-specific variation within *A. urmiana*, which was divided into two different sub-clades (support values = 95) (Fig. 4b). For the parthenogenetic *Artemia*, PART<sub>19,20</sub> were collected with SINS; the others were collected

with Asian bisexual species in trees based on primary sequence (Fig. 4a). In contrast, they were divided into four major groups in the sequence-structure tree, with the PART<sub>6,15,16,18,22</sub> placed with *A. tibetiana*, PART<sub>1-5,7-14,17</sub> placed with *A. urmiana*, PART<sub>19,20</sub> placed with *A. sinica*, and PART<sub>21</sub> located separately (Fig. 4b).

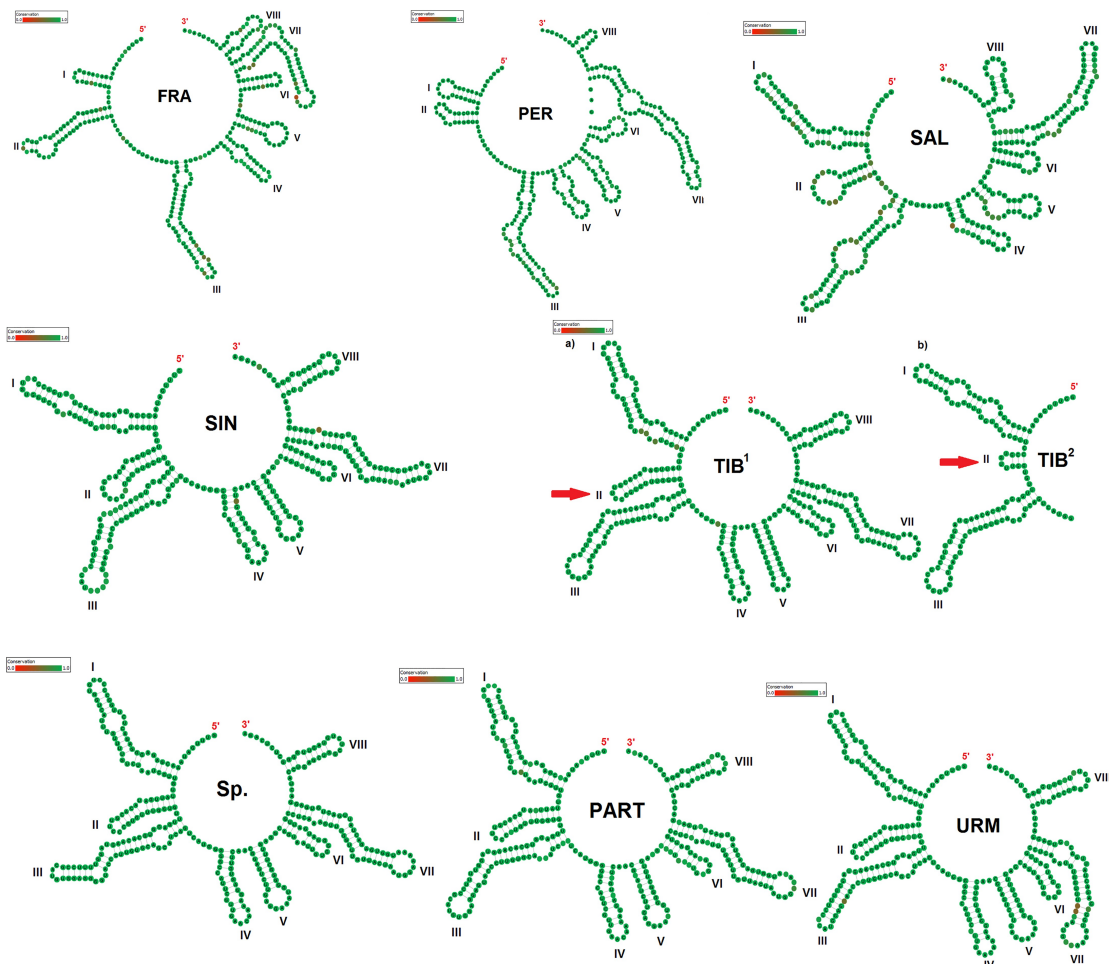
**Discussion**

This study provides the first evidence of phylogeny of the Anostraca *Artemia*, using the sequence of RNA secondary structure.

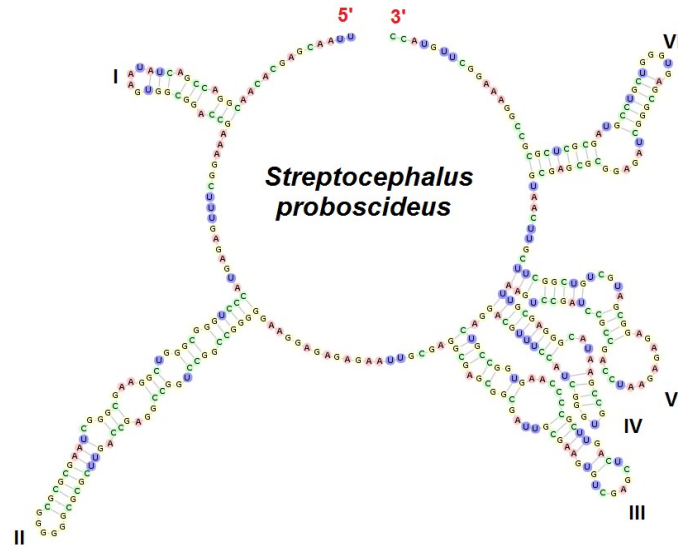
Even if the general secondary structure of *ITS1* shows a fingers-pattern in all the studied species, interspecific variation is considerable in the length of helices, the paired structure and the length of single strands (Fig. 1). Though phylogenetic trees of total primary

sequence of *ITS1* (Baxevanis *et al.*, 2006, Hou *et al.*, 2006; Kappas *et al.*, 2009; Vikas *et al.*, 2012, Eimanifar *et al.*, 2014), partial primary sequence (Fig. 4a) and sequence-structure (Fig. 4b) showed a single collection for *A. tibetiana*, a remarkable intraspecific variation was detected in the second helix of *A. tibetiana* (Figs. 1 and 3).

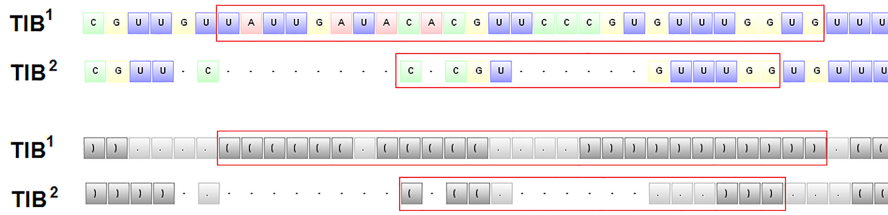
Asem *et al.* (2016) proved that the nuclear marker *ITS1* could not clearly sort *A. urmiana*, *A. tibetiana* and parthenogenetic populations in phylogenetic trees (see also Maccari *et al.*, 2013; Eimanifar *et al.*, 2014; this study Fig. 4a); but the phylogenetic tree based on sequence-secondary of *ITS1* displayed an appreciable differentiation for these groups in this study (Fig. 4b). *Artemia tibetiana* clearly located in a separated clade.



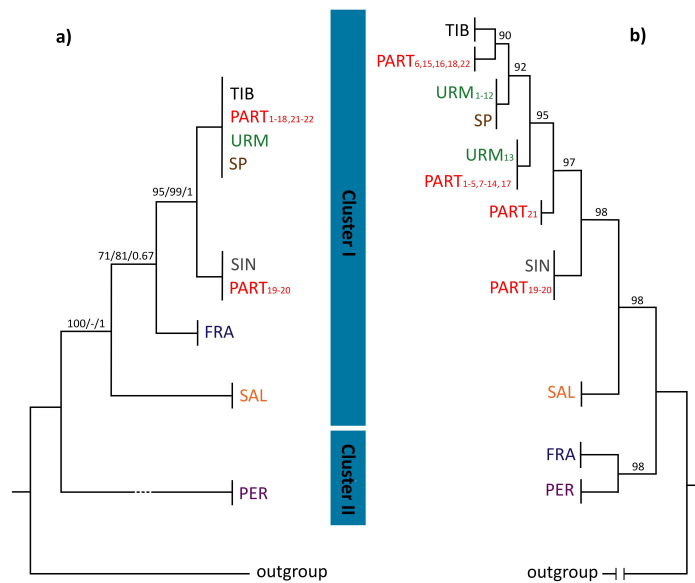
**Fig. 1.** Predicted general secondary structure for the *ITS1* partial regions of genus *Artemia*: TIB<sup>1</sup>; Haplotypes TIB2-5; TIB<sup>2</sup>; Haplotype TIB1; Arrows point to the region with different patterns between two secondary structures of TIB. (Abbreviations of species/population are defined in Table 1).



**Fig. 2.** Predicted general secondary structure for the *ITS1* partial regions of *Streptocephalus proboscideus* (outgroup).



**Fig. 3.** The primary (upper) and secondary (lower) sequences in Helix II of *ITS1* of *Artemia tibetiana* (boxes show the position of Helix II). TIB<sup>1</sup>: Haplotypes TIB2-5; TIB<sup>2</sup>: Haplotype TIB1. (Abbreviations of species/population are defined in Table 1).

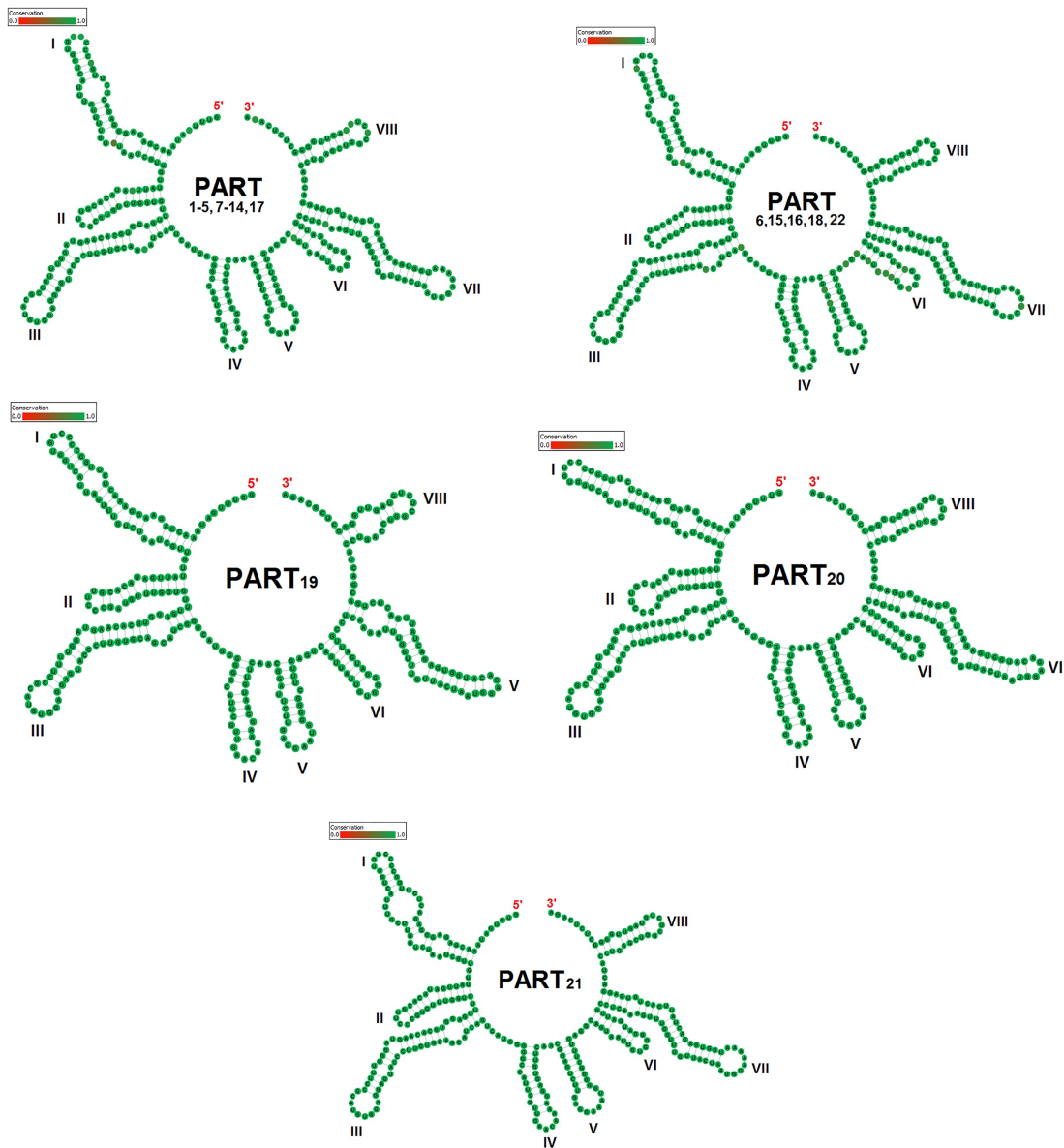


**Fig. 4.** Simplified phylogenetic trees of the genus *Artemia* based on 313 *ITS1* sequences. *Streptocephalus proboscideus* was used as an out-group. **a)** ML/BI/NJ trees inferred from primary sequence. Numbers on the nodes are: the bootstrap value from maximum-likelihood / that of neighbor-joining / the Bayesian posterior probability values. **b)** PNJ tree based on sequence-structure. Numbers at the nodes represent the bootstrap values from profile neighbor-joining. (Abbreviations of species/population are defined in Table 1).



The highest intra-population variation was shown in the parthenogenetic *Artemia* with four lineages which two ones (PART<sub>1-5,7-14,17</sub> and PART<sub>19-20</sub>) shared same subclades with *A. urmiana* and *A. sinica* respectively, and two others (PART<sub>6,15,16,18,22</sub> and PART<sub>21</sub>) located in unique separated platforms. In addition, *A. urmiana* presented a level of intraspecific variation in two subclades (Fig. 4b). Our findings showed the secondary structure shapes could not support the observed intra-specific/population differentiation by

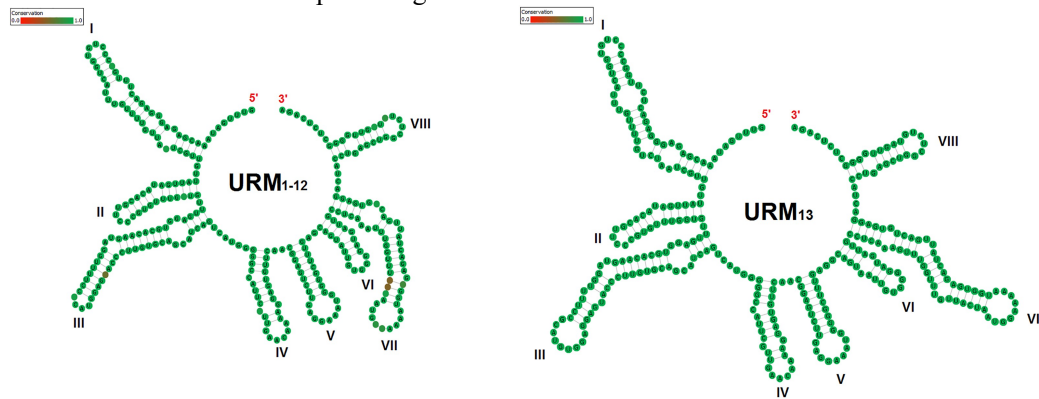
sequence-secondary tree among variants of PART and URM (Figs. 4b, 5, and 6), so that different lineages of parthenogenetic populations and *A. urmiana* in the phylogenetic tree (Fig. 4b) have same secondary structures with their general predicted patterns (Figs. 1, 5, and 6). This finding confirmed that phylogenetic analysis by combined primary and secondary sequences can display remarkable diversification in comparison of using only secondary structure.



**Fig. 5.** Predicted secondary structure for partial *ITS1* regions of parthenogenetic *Artemia*, based on four separated lineages by sequence-structure from profile neighbor-joining (See Fig. 4b). (Abbreviations of population are defined in Table 1).

With regards to the results of mitochondrial markers, parthenogenetic *Artemia* is a polyphyletic group, a fact which, di- and tetraploid parthenogenetic *Artemia* originated from *A. urmiana* and *A. sinica*, and tri- and pentaploids divided from diploid and tetraploid *Artemia*, respectively (Maniatsi et al., 2011; Asem et al., 2016). Contrary to the primary sequence of *ITS1*, sequence-structure was also able to differentiate parthenogenetic

populations into different lineages, but not able to distinguish ploidy levels. The members of two major groups (i.e. PART<sub>1-5,7-14,17</sub> and PART<sub>6,15,16,18,22</sub>) include all ploidy degrees, besides that two other lineages (PART<sub>19,20</sub> and PART<sub>21</sub>) keep only tetraploids (Table 1, for more information about ploidy levels, see Baxevanis et al., 2006; Kappas et al., 2009; Maniatsi et al., 2011; Asem et al., 2016).



**Fig. 6.** Predicted secondary structure of *ITS1* partial regions for *Artemia urmiana* based on two separated lineages by sequence-structure from profile neighbor-joining (See Fig. 4b).

Different genetic methods showed almost opposed evolutionary history for taxa of genus *Artemia*, especially regarding the position of *A. salina* and *A. persimilis* (see Introduction section). While all genetic studies indicated that there was no close phylogenetic relationship between *A. franciscana* and *A. persimilis* (Baxevanis et al., 2005; 2006; Hou et al., 2006; Kappas et al., 2009; Maniatsi et al., 2011; Vikas et al., 2012; Eimanifar et al., 2014), phylogenetic analysis based on allozyme markers showed that *A. franciscana* and *A. persimilis* were located in the basal clade together (Beardmore and Abreu-Grobois, 1983). This finding agrees with the occurrence of natural hybridization between *A. persimilis* and *A. franciscana*. Several morphologic, genetic and cytogenetic studies have documented the existence of occasional degrees of natural hybridization and/or introgression between *A. franciscana* and *A. persimilis* in the Las Tunas Lagoon population (Córdoba Province, Argentina) (Papeschi et al., 2000; Amat et al., 2004; Cohen, 2012). Morphometric analyses of adults (Papeschi et al., 2000; Amat et al., 2004) and phylogenetic analyses using genetic markers including *16S*, *COI*, *ITS1* and *p26* (Ruiz et al., 2008; Maniatsi et al., 2009) grouped Las Tunas with *A.*

*franciscana*. Meanwhile, the cytogenetic study proved that most meiotic cells of adult males had 21 haploid chromosomes; others had 22 or 23 chromosomes with irregular meiosis. This abnormality was attributed to a hybridization/introgression between *A. franciscana* ( $n = 21$ ) and *A. persimilis* ( $n = 22$ ) (Papeschi et al., 2000). Another controversial case was documented for the population of Pichilemu saltworks (Cardenal Caro Province, Chile). Based on allozymes (Gajardo et al., 1995), morphometric data of adults (Zuñiga et al., 1999) and 42 diploid chromosomes (Parraguez et al., 2009), this population has been imputed to *A. franciscana*, whereas analyses referring to chromocenter numbers (Gajardo et al., 2001a), *16S* rRNA RFLP patterns (Gajardo et al., 2004), and *ITS1* sequence (Baxevanis et al., 2006) referred this population to *A. persimilis*. The possibility of hybridization between *A. franciscana* and *A. persimilis* has previously been observed in cross-fertility laboratory experiments (Gajardo et al., 2001b). Since natural hybridization usually take place between very closely related species or sister taxa (Coyne and Orr, 1997; Agatsuma et al., 2000; Price and Bouvier 2002; Seehausen, 2004; Mallet, 2005; Mallet et al., 2007; Kovalev et al., 2016), the existence of

natural hybridization between *A. franciscana* and *A. persimilis* further emphasizes that these species might have close evolutionary relationship. Moreover, in the *ITS1* primary sequence trees, *A. franciscana* was sorted as a sister clade of the Asian bisexual species, but laboratory cross-breeding tests have documented complete infertility between *A. franciscana* and Asian bisexual species (Pilla & Beardmore, 1994; Abatzopoulos *et al.*, 2002a). Therefore, phylogenetic analysis using both primary and secondary sequences may better reveal the relationships of these taxa than using only primary sequences.

In conclusion, the secondary structure and sequence-structure of *ITS1* DNA in the genus *Artemia* could be a powerful tool for understanding phylogenetic relationships among taxa. The secondary structure shows a considerable intraspecific variation in *Artemia tibetiana*, and sequence-structure reveals new lineages for parthenogenetic populations and *A. urmiana*. The New World species in the same cluster by sequence-structure analysis agrees with the ability of natural hybridization and the result from allozyme markers.

#### Acknowledgements

This study was funded by the Fundamental Research Funds (201562029) for the Central Universities (China). The help of Prof. Okazaki (Weber State University, USA) with the English text is highly appreciated.

#### References

- Abatzopoulos TJ, Beardmore JA, Clegg JS, Sorgeloos P. 2002b. *Artemia*: basic and applied biology. Kluwer Academic Publishers, Dordrecht, the Netherlands.
- Abatzopoulos TJ, Kappas I, Bossier P, Sorgeloos P, Beardmore JA. 2002a. Genetic characterization of *Artemia tibetiana* (Crustacea: Anostraca). *Biol J Linnean Soc* 75: 333-344.
- Agatsuma T, Arakawa Y, Iwagami M, Honzako Y, Cahyaningsih U, Kang Sh-Y, Hong SJ. 2000. Molecular evidence of natural hybridization between *Fasciola hepatica* and *F. gigantica*. *Parasitol Int* 49: 231-238.
- Alfaro ME, Zoller S, Lutzoni F. 2003. Bayes or bootstrap? A simulation study comparing the performance of Bayesian Markov Chain Monte Carlo sampling and bootstrapping in assessing phylogenetic confidence. *Mol Biol Evol* 20: 255-266.
- Amat F, Cohen RG, Hontoria F, Navarro JC. 2004. Further evidence and characterization of *Artemia franciscana* (Kellogg, 1906) populations in Argentina. *J Biogeogr* 31: 1735-1749.
- Amat F, Hontaria F, Navarro JC, Vieira N, Mura G. 2007. Biodiversity loss in the genus *Artemia* in the Western Mediterranean Region. *Limnetica* 26: 177-194.
- Asem A, Eimanifar A, Sun SC. 2016. Genetic variation and evolutionary origins of parthenogenetic *Artemia* (Crustacea: Anostraca) with different ploidies. *Zool Scr* 45: 421-436.
- Asem A, Rastegar-Pouyani N, De los Rios P. 2010. The genus *Artemia* Leach, 1819 (Crustacea: Branchiopoda): true and false taxonomical descriptions. *Lat Am J Aquat Res* 38: 501-506.
- Baxevanis AD, Kappas I, Abatzopoulos TJ. 2006. Molecular phylogenetics and asexuality in the brine shrimp *Artemia*. *Mol Phylogenet Evol* 40: 724-738.
- Baxevanis AD, Triantaphyllidis GV, Kappas I, Triantafyllidis A, Triantaphyllidis CD, Abatzopoulos TJ. 2005. Evolutionary assessment of *Artemia tibetiana* (Crustacea, Anostraca) based on morphometry and 16S rRNA RFLP analysis. *J Zool Sys Evol Res* 43: 189-198.
- Beardmore JA, Abreu-Grobois FA. 1983. Taxonomy and evolution in the brine shrimp *Artemia*. In: Oxford GS, Rollinson D (eds) Protein Polymorphism: Adaptive and Taxonomic Significance. Academic Press, London, pp. 153-164.
- Campbell CS, Wright WA, Cox M, Vining TF, Major CS, Arsenault MP. 2005. Nuclear ribosomal DNA internal transcribed spacer 1 (ITS1) in *Picea* (Pinaceae): sequence divergence and structure. *Mol Phylogenet Evol* 35: 165-185.
- Cohen RG. 2012. Review of the biogeography of *Artemia* Leach, 1819 (Crustacea: Anostraca). *Int J Artemia Biol* 2: 9-23.
- Coleman AW. 2013. Analysis of mammalian rDNA internal transcribed spacers. *PLoS One* 8(11): e79122.
- Coyne JA, Orr HA. 1997. Patterns of speciation in *Drosophila* revisited. *Evolution* 51: 295-303.

- Eimanifar A, Van Stappen G, Marden B, Wink M. 2014. *Artemia* biodiversity in Asia with the focus on the phylogeography of the introduced American species *Artemia franciscana* Kellogg, 1906. *Mol Phylogenet Evol* 79:392-403.
- Gajardo G, Beardmore JA, Sorgeloos P. 2001a. International study on *Artemia* LXII. Genomic relationships between *Artemia franciscana* and *A. persimilis*, inferred from chromocentre numbers. *Heredity* 87:172-177.
- Gajardo G, Conceicao DM, Weber L, Beardmore JA. 1995. Genetic variability and inter populational differentiation of *Artemia* strains from South America. *Hydrobiologia* 302:21-29.
- Gajardo G, Crespo J, Triantafyllidis A, Tzika A, Baxevanis A, Kappas I, Abatzopoulos TJ. 2004. Species identification of Chilean *Artemia* populations based on mitochondrial DNA RFLP analysis. *J Biogeogr* 31:547-555.
- Gajardo G, Parraguez M, Beardmore JA, Sorgeloos P. 2001b. Reproduction in the brine shrimp *Artemia*: evolutionary relevance of laboratory cross-fertility tests. *J Zool* 253:25-32.
- Gottschling M, Plotner J. 2004. Secondary structure models of the nuclear internal transcribed spacer regions and 5.8S rRNA in Calciodinelloideae (Peridiniaceae) and other dinoagellates. *Nucleic Acids Res* 32: 307-315.
- Hillis DM, Bull JJ. 1993. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. *Syst Boil* 42: 182-192.
- Hodac L, Scheben AP, Hojsgaard D, Paun O, Horandl E. 2014. ITS Polymorphisms shed light on hybrid evolution in apomictic plants: A case study on the ranunculus auricomus complex. *PLoS One* 9: e103003.
- Hofacker IL, Fekete M, Stadler PF. 2002. Secondary structure prediction for aligned RNA sequences. *J Mol Biol* 319: 1059-1066.
- Hosseinzadeh Colagar A, Yousefzadeh H, Shayanmehr F, Jalali SG, Zare H, Tippery NP. 2016. Molecular taxonomy of Hyrcanian *Alnus* using nuclear ribosomal ITS and chloroplast trnH-psbA DNA barcode markers. *Syst Biodiver*, 14: 88-101.
- Hou L, Bi X, Zou X, He C, Yang L, Qu R, Liu Z. 2006. Molecular systematics of bisexual *Artemia* populations. *Aquacult Res* 37: 671-680.
- Kappas I, Baxevanis AD, Maniatsi S, Abatzopoulos TJ. 2009. Porous genomes and species integrity in the branchiopod *Artemia*. *Mol Phylogenet Evol* 52: 192-204.
- Kovalev SY, Golovljova IV, Mukhacheva TA. 2016. Natural hybridization between *Ixodes ricinus* and *Ixodes persulcatus* ticks evidenced by molecular genetics methods. *Ticks Tick-borne Dis* 7: 113-118.
- Librado P, Rozas J. 2009. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. *Bioinformatics* 25: 1451-1452.
- Maccari M, Amat F, Gómez A. 2013. Origin and genetic diversity of diploid parthenogenetic *Artemia* in Eurasia. *PLoS One* 8: e83348.
- Mallet J, Beltrán M, Neukirchen W, Linares M. 2007. Natural hybridization in heliconiine butterflies: the species boundary as a continuum. *BMC Evol Biol* 7:1-16.
- Mallet J. 2005. Hybridization as an invasion of the genome. *Trends Ecol Evol* 20:229-237.
- Maniatsi S, Baxevanis AD, Kappas I, Deligiannidis P, Triantafyllidis A, Papakostas S, Bougiouklis D, Abatzopoulos TJ. 2011. Is polyploidy a persevering accident or an adaptive evolutionary pattern? The case of the brine shrimp *Artemia*. *Mol Phylogenet Evol* 58: 353-364.
- Maniatsi S, Kappas I, Baxevanis AD, Farmaki T, Abatzopoulos TJ. 2009. Sharp Phylogeographic Breaks and Patterns of Genealogical Concordance in the Brine Shrimp *Artemia franciscana*. *Int J Mol Sci* 10: 5455-5470.
- Mathews DH, Sabina J, Zuker M, Turner DH. 1999. Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. *J Mol Biol* 288: 911-940.
- Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees Gateway Computing Environments Workshop (GCE), IEEE 1-8.
- Nylander JAA. 2004. MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.
- Papeschi AG, Cohen RG, Pastorino XI, Amat F. 2000. Cytogenetic proof that the brine shrimp *Artemia franciscana* (Crustacea,

- Branchiopoda) is found in Argentina *Hereditas* 133: 159-166.
- Parraguez M, Gajardo G, Beardmore JA. 2009. The New World *Artemia* species *A. franciscana* and *A. persimilis* are highly differentiated for chromosome size and heterochromatin content. *Hereditas* 146: 93-103.
- Pilla EJS, Beardmore JA. 1994. Genetic and morphometric differentiation in old world bisexual species of *Artemia* (the brine shrimp). *Heredity* 73: 47-56.
- Price TD, Bouvier MM. 2002. The evolution of F1 postzygotic incompatibilities in birds. *Evol* 56: 2083-2089.
- Rambaut A. 2012. FigTree (version 1.4.0). Available at <http://tree.bio.ed.ac.uk/software/figtree/>.
- Reblova M, Untereiner WA, Reblova K. 2013. Novel evolutionary lineages revealed in the chaetothyriales (Fungi) based on multigene phylogenetic analyses and comparison of ITS secondary structure. *PLoS ONE* 8: e63547
- Reuter JS, Mathews DH. 2010. RNA structure: software for RNA secondary structure prediction and analysis. *BMC Bioinformatics* 11: 129.
- Ruiz O, Amat F, Saavedra C, Papeschi A, Cohen RG, Baxevedis AD, Kappas I, Abatzopoulos TJ, Navarro JC. 2008. Genetic characterization of argentinean *Artemia* species with different fatty acid profiles. *Hydrobiologia* 610: 223-234.
- Seehausen O. 2004. Hybridization and adaptive radiation. *Trends Ecol Evol* 19: 198-206.
- Seibel P, Muller T, Dandekar T, Schultz J, Wolf M. 2006. 4SALE-a tool for synchronous RNA sequence and secondary structure alignment and editing. *BMC Bioinformatics* 7: 498.
- Sun P, Clamp C, Xu D. 2010. Analysis of the secondary structure of ITS transcripts in peritrich ciliates (Ciliophora, Oligohymenophorea): Implications for structural evolution and phylogenetic reconstruction. *Mol Phylogenet Evol* 56: 242-251.
- Sun Y, Zhong YC, Song WQ, Zhang RS, Chen RY. 1999. Detection of genetic relationships among four *Artemia* species using randomly amplified polymorphic DNA (RAPD). *Int J Salt Lake Res* 8: 139-147.
- Tamura K, Stecher G, Peterson D, Filipski A, Kuma, S. 2013. MEGA6: Molecular evolutionary genetics analysis version 6.0. *Mol Biol Evol* 30: 2725-2729.
- Triantaphyllidis GV, Criel GRJ, Abatzopoulos TJ, Sorgeloos P. 1997. International study on *Artemia*. LIII. Morphological study of *Artemia* with emphasis to old world strains. I. Bisexual populations. *Hydrobiologia* 357: 139-153.
- Vikas PA, Sajeshkumar NK, Thomas PC, Chakraborty K, Vijayan KK. 2012. Aquaculture related invasion of the exotic *Artemia franciscana* and displacement of the autochthonous *Artemia* populations from the hypersaline habitats of India. *Hydrobiologia* 684: 129-142.
- Wang P, Gao F, Huang J, Strüder-Kypke M, Yi Z. 2015. A case study to estimate the applicability of secondary structures of SSU-rRNA gene in taxonomy and phylogenetic analyses of ciliates. *Zool Scr* 44: 574-585.
- Wolf M, Ruderisch B, Dandekar T, Schultz J, Muller T. 2008. ProfDistS: (profile-) distance based phylogeny on sequence-structure alignments. *Bioinformatics* 24: 2401-2402.
- Yosefzadeh H, Hosseinzadeh Colagar A, Tabari M, Sattarian A, Assadi M. 2012. Utility of ITS region sequence and structure for molecular identification of *Tilia* species from Hyrcanian forests, Iran. *Plant Syst Evol* 298: 947-961.
- Zheng B, Sun SC. 2013. Review of the biogeography of *Artemia* Leach, 1819 (Crustacea: Anostraca) in China. *Int J Artemia Biol* 3: 20-50.
- Zuker M. 1989. On finding all suboptimal foldings of an RNA molecule. *Science* 244: 48-52.
- Zuker M. 2003. Mfold web server for nucleic acid folding and hybridization prediction. *Nucleic Acids Res* 31: 3406-3415.
- Zuñiga O, Wilson R, Amat F, Hontoria F. 1999. Distribution and characterization of Chilean populations of the brine shrimp *Artemia* (Crustacea, Branchiopoda, Anostraca). *Int J Salt Lake Res* 8: 23-40.