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RESEARCH PAPER

Population Structure of *Acanthopagrus latus* from the Northern Persian Gulf and Gulf of Oman Based on Microsatellite Markers

Ahmad Ghasemi[1,*], Ahmad Shadi[2]

[1] Persian Gulf University, Persian Gulf Research Institute, Bushehr, Iran.
[2] Persian Gulf University, Faculty of Marine Science and Technology, Department of Marine Biotechnology, Bushehr, Iran.

* Corresponding Author: Tel.: +98.936 4855956
E-mail: aqasemi@gmail.com

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Abstract

Yellowfin seabream is reproduced both naturally and semi-artificially and is one of the most probable candidates for coastal aquaculture in Iran. Genetic structuring of wild *Acanthopagrus latus* populations from the Northern Persian Gulf and Gulf of Oman was analyzed using microsatellite markers. Allelic diversity was estimated in 180 organisms (3 sample sites in the Persian Gulf and 3 in Gulf of Oman) in 8 microsatellite loci. Results showed a high level of polymorphism (H_E=0.81, Ho=0.89), the number of alleles in polymorphic loci ranged from 9 to 14. High level of diversity between individuals but moderate diversity rate between populations was observed. AMOVA analysis showed low to medium but significant genetic differentiation between populations (p= 0.001) and significant genetic differentiation between Gulf of Oman and the Persian Gulf populations was detected. Results from this study differentiate four populations in the region: two in the Persian Gulf and two in Gulf of Oman. No evidence for recent population bottleneck was detected; however low allelic rate may relate to high fishing pressure on this species. This suggests that care should be taken for fisheries managers, for aquaculture and restocking programs.

Keywords: Yellowfin seabream; genetic differentiation; Hardy-Weinberg Equilibrium; Persian Gulf; Gulf of Oman.

Introduction

The yellowfin sea bream *Acanthopagrus latus* is widely distributed in warm coastal waters throughout the Indo-Pacific, where it is fished both recreationally and commercially (Allen, 1997; Hussain & Abdullah, 1980; Lee & Al-Baz, 1989). Yellowfin Sea bream (*Acanthopagrus latus*) is an important benthic commercial fish in the Persian Gulf and Gulf of Oman. *Acanthopagrus latus* stocks in the Persian Gulf have been variably estimated from about 758 tons in 2003, 649 tons in 2005 to about 1055 tons in 2010 while total catch for sea breams estimated 2731 tons in 2010 (Valinasab Dehghani, Kamali, & Khorshidian, 2011). Many of commercial fish stocks were declined gradually in the Persian Gulf and Gulf of Oman as a result of overfishing. Furthermore, in recent years, habitat alteration as a consequence of military activities, oil pollution, industrialization and heavy transportation affected most of fish stocks substantially. Therefore, appropriate knowledge on population structure and differentiation is essential for conservation of yellowfin sea bream in the Persian Gulf and Gulf of Oman.

The understanding of genetic diversity is one of the most important steps in management of fisheries resources and aquaculture selective breeding programs (Beaumont & Hoare, 2003; Dunham, 2011; Ward, Elliott & Grewe, 1995).

In order to investigate the population genetic structure and provide guidelines for artificial propagation and resource conservation of the yellowfin sea bream, microsatellite markers were used.

Microsatellites are highly variable nuclear genetic markers, which are inherited co-dominantly following Mendelian rules (Liu & Cordes, 2004). Microsatellites have been found suitable for a variety of applications in fisheries and aquaculture research, particularly where genetic differentiation within and between populations may be limited (Davis & Hetzel, 2000). Potential applications in aquaculture include monitoring changes in genetic variation as a consequence of different breeding strategies (Liu & Cordes, 2004), the investigation of interactions between wild and cultured populations, parentage assignment and estimation of relatedness between potential breeding pairs (Norris, Bradley, & Cunningham, 2000). Yellowfin sea bream is from the most important wild and cultured fish species and

providing a valuable source of protein in many developing countries. Microsatellite loci of *Acanthopagrus latus* were characterized and isolated by Xia, Xia, & Jiang, (2006). In the present study, genetic diversity of yellowfin sea bream in Iran is investigated using eight microsatellite loci. The results of this study provide important new insights into the management of yellowfin sea bream populations and the selective breeding and dissemination programs for this species in the country.

Materials and Methods

Sample Collection

Fish samples were collected from six sampling sites, 3 in the north Persian Gulf and 3 in the Gulf of Oman including: Khur-Musa, Genaveh, Bushehr and Asalouyeh in the Persian Gulf , Bandar Abbas , Jask and Chabahar in Gulf of Oman (fig.1.).

A total of 180 specimens were sampled. All fish were captured by local fishermen at all locations. Tissue samples (about 2 grams of muscle tissue) were preserved in 96% ethanol until DNA extraction.

DNA Extraction and Amplification

Whole genomic DNA was extracted from all samples using CTAB method (Jaferian, *et al*., 2013). Amplification of 8 microsatellite loci (Table 1) was performed using polymerase chain reaction (PCR). For this, 16 primers which had been isolated previously from the same species were used (Xia *et al.*, 2006).

The polymerase chain reaction was carried out in final volume of 12.5 µl containing: 50ng of template DNA, 1× PCR buffer, 2.5ml of 1.5 mM $MgCl_2$, 0.2mM dNTPs, 10 pmol of each primer and 0.5 unit of Taq polymerase. The thermal cycling

Figure 1. Sampling sites of the yellowfin sea bream *Acanthopagrus latus* located in north Persian Gulf and Gulf of Oman**.**

Table1. Characteristics of the yellowfin sea bream microsatellite loci (reference: Xia et al., 2006)

Locus	Repeat motif	Primer sequences (5′–3′)	*R* (bp)	*A*	*P*	T_a (°C)	GenBank Accession no.
S15	$(GT)_{20}$	F: GCGGGAAAACATGTCATT R: AATTGAAGGGTGAGGGGTCA	146 –158	5	0.000	58	DQ222444
S16	$(CA)_{21}$	F: GAGCAGAGCAGCGGACATC R: TGCATGTTTATGTACCGCATAC	180 –250	6	0.000	58	DQ222445
S18	$(GT)_{19}$	F: CGTTTCACTGGAAAACACC R: TCTGTGACAGGATGCTGACTTA	210-260	6	0.000	58	DQ222446
S19a	$(CA)_{20}$	F: GATATAATAGAGGGGTTGACA R: CACTGAGCGCTTGCTT	250-268	7	0.000	58	DQ222447
S30	$(CA)_{38}$	F: GCGCTTTATTGTTCTGGGTTAC R: GAATAGACTGGTGAGGCGTCA	196-230	9	0.570	58	DQ222448
S32	$(GT)_{20}$	F: GCCAGCGCACTGTGTTGTTATT R: GCGCTGAAGCTCCGTTACTTTA	175 –231	6	0.032	58	DQ222449
S34	$(GT)_{30}$	F: GAAGGATAGAGGAGGTGTGG R: ATCACATGCACACGCAGAC	156 –190	10	0.026	58	DQ222450
S35a	$(GT)_{20}$	F: CGCATACATGTTACAAGTCAC R: CGGACATCATTATGATTCTA	160 –192	6	0.000	58	DQ222451

Repeat motif, primer sequences, range of observed alleles (*R*), number of alleles (*A*), annealing temperature (T_a) , probability value (P) and GenBank Accession no. were provided.

parameters were consist of an initial denaturing at 95 °C for 2min, 35 cycles at 94 °C for 60s, 40 sec primer specific annealing temperature (see Table 1.) and extension for 40 s at 72 °C, followed by one final extension for 7 min at 72 °C.

PCR products were size-fractionated by electrophoresing on denaturizing 8% polyacrylamide gel, at 150V for 3 h. Then gels were visualized by silver nitrate staining and analyzed by using gel documentation system (Bio-Rad). Microsatellite alleles were sized relating to a 50 bps ladder (DNA Ladder RTU Sinaclone, Iran) using Bio-Rad's Quantity One software.

Statistical Analyses

Levels of genetic variability, expressed in number of alleles (N_A), observed heterozygosity (H_O) and expected heterozygosity (H_E) were obtained for each locus from every population using the software GENEPOP (Rousset, 2008).

Micro-checker 2.2.1 software was used to detect allelic errors (Van Oosterhout, Hutchinson, Wills, & Shipley, 2004).

Deviations from the Hardy–Weinberg equilibrium were estimated for each population at each locus with 10,000 dememorizations and 1000 iterations. Calculating the fixation index F_{IS} and Allele richness were performed by FSTAT 2.9.4 software (Goudet, 1995).

Levels of genetic differentiation between all sampling sites were achieved by calculating Wright's pairwise F_{ST} statistics (Weir & Cockerham, 1984) using Arlequin 3.5 software (Excoffier & Lischer, 2010). A global AMOVA test was conducted to obtain the global F_{ST} value. Hierarchical genetic structuring of the samples was undertaken by assessing the relative contribution among groups, within groups, and within populations (AMOVA). Pairwise estimate of the fixation index F_{ST}(Weir & Cockerham, 1984) as a measure of genetic differentiation(Hedrick, 1999) was calculated and tested for significant departure from zero using permutation procedures in FSTAT(Goudet, 1995). Inbreeding coefficient(FIS)(Weir & Cockerham, 1984) was also calculated in FSTAT.

Estimation of deviations from Hardy–Weinberg equilibrium and linkage disequilibrium evaluation performed using software Arlequin 3.0 by 10,000 permutations in each case. Principal coordinate analysis (PCA) was performed based on the standardized genetic distance matrix between populations using GENALEX 6.41 (Peakall & Smouse, 2006) to visualize population differentiation.

Results

Genetic Diversity

All eight tested microsatellite loci were polymorphic and showed levels of diversity in all sampling sites. The mean number of alleles (N_a) ranged from 9 to 14. Levels of observed heterozygosity (H_o) were high, ranging from 0.37 to 1 and expected heterozygosity (H_e) were between 0.50 and 0.89 (Table 2). The results of linkage disequilibrium analysis revealed that no loci were in disequilibrium after the sequential Bonferroni correction ($P > 0.05$). This indicates that the assortment of alleles is independent at eight loci.

Analysis of homozygote size classes by MICROCHECKER software revealed no null alleles affected the results of the present study. Results of Hardy–Weinberg equilibrium tests (after Bonferroni correction) for six sampled sites with eight loci (6×8=48) showed that 16 tests from 48 were in disequilibrium (Table 2). All localities under study showed some extent of deviation from the HWE ($P<0.05$).

Levels of expected heterozygosity were different among loci and among localities (table2). Mean expected heterozygosity were lower than observed heterozygosity in all sampling sites from Persian Gulf and Gulf of Oman. Mean expected heterozygosity (H_e) was calculated between 0.76-0.86.

Population Genetic Structure

The degree of allelic differentiation was tested among six localities (Khur-Musa, Genaveh and Bushehr, Bandar-Abbas, Jask and Chabahar) as well as between Persian Gulf and Gulf of Oman.

F_{ST} estimates showed low to moderate but significant differentiation between investigated populations of *Acanthopagrus latus* (except between Jask and Bandar Abbas samples) (Table 4). Genetic distances among pairs of populations showed considerable significant variation ($P < 0.05$) (Table 3). Jask population showed highest genetic distances (0.12-0.33) in relation to other populations (Table 3).

The analysis of molecular variance (AMOVA) partitioned most of the genetic variance (78%) within individuals and the variation among populations and within populations were 13% and 9% respectively (table 5).

Fixation indices' based on allelic frequencies (F_{st}) were low but significant among all localities (table 6).

Low but mostly significant levels of fixation indices were estimated between pairs of populations leading to a significant overall F_{ST} of 0.054 and R_{ST} of 0.131 (Table 4-5). The pairwise F_{st} ranged from 0.01(Chabahar versus Genaveh) to 0.048 (Bushehr versus Jask); whereas pairwise Rst ranged from 0.00 (Jask versus Chabahar) to 0.258 (KhueMusa versus Jask).

Pairwise population matrix of Nei genetic distances depicted the underlying structure of population differentiation (Table 3). The genetic distances based on Nei (1972), calculations revealed

Table 2. Summary statistics for eight microsatellite loci in 6 sampling sites (Persian Gulf and Gulf of Oman) of *Acanthopagrus latus*

Pop		S15	S30	S16	S18	S19a	S34	S32	S35a	mean	SD
Khurmusa	N	30.00	28.00	30.00	30.00	30.00	30.00	30.00	30.00		
	Na	8.00	8.00	5.00	8.00	6.00	5.00	6.00	6.00	6.50	0.46
	Ne	5.11	5.60	2.87	3.67	4.93	4.56	3.52	5.07	4.42	0.34
	Ar	7.93	8	4.93	7.86	6.00	5.00	5.93	6.00		
	I	1.79	1.87	1.21	1.57	1.66	1.56	1.43	1.69	1.60	0.07
	Ho	0.87	0.93	1.00	0.73	1.00	1.00	0.77	0.97	0.91	0.04
	He	0.80	0.82	0.65	0.73	0.80	0.78	0.72	0.80	0.76	0.02
	uHe	0.82	0.84	0.66	0.74	0.81	0.79	0.73	0.82	0.78	0.02
	F	-0.08	-0.13	-0.54	-0.01	-0.25	-0.28	-0.07	-0.20	-0.20	0.06
	HWE	*	ns	ns	ns	*	*	ns	ns		
Genaveh	N	30.00	30.00	30.00	30.00	30.00	29.00	30.00	30.00		
	Na	9.00	8.00	5.00	9.00	7.00	9.00	6.00	6.00	7.38	0.56
	Ne	6.79	5.49	3.57	5.52	5.13	6.32	2.94	3.30	4.88	0.51
	Ar	8.99	7.86	5.00	8.92	6.93	8.99	5.86	5.93		
	I	2.05	1.82	1.40	1.89	1.74	2.01	1.27	1.38	1.70	0.11
	Ho	0.90	0.93	1.00	0.97	1.00	0.76	0.40	0.97	0.87	0.07
	He	0.85	0.82	0.72	0.82	0.81	0.84	0.66	0.70	0.78	0.03
	uHe	0.87	0.83	0.73	0.83	0.82	0.86	0.67	0.71	0.79	0.03
	F	-0.06	-0.14	-0.39	-0.18	-0.24	0.10	0.39**	-0.39	-0.11	0.09
	HWE	*	ns	ns	ns	**	*	ns	ns		
Bushehr	N	30.00	30.00	30.00	30.00	30.00	29.00	30.00	30.00		
	Na	8.00	8.00	2.00	10.00	9.00	10.00	6.00	6.00	7.38	0.94
	Ne	5.52	5.79	2.00	6.41	4.75	7.16	3.69	4.40	4.96	0.58
	Ar	8.00	7.93	2.00	9.99	8.86	9.96	6.00	5.99		
	I	1.88	1.87	0.69	2.06	1.79	2.11	1.50	1.59	1.69	0.16
	Ho	0.93	1.00	1.00	0.73	0.97	0.93	0.37	1.00	0.87	0.08
	He	0.82	0.83	0.50	0.84	0.79	0.86	0.73	0.77	0.77	0.04
	uHe	0.83	0.84	0.51	0.86	0.80	0.88	0.74	0.79	0.78	0.04
	F	-0.14	-0.21	-1.00	0.13	-0.22	-0.08	0.50**	-0.29	-0.17	0.15
	HWE	**	*	*	ns	*	**	*	ns		
Bandarabas	N	30.00	30.00	30.00	30.00	30.00	30.00	30.00	30.00		
	Na	9.00	11.00	9.00	12.00	11.00	12.00	7.00	9.00	10.00	0.63
	Ar	8.92	10.79	8.93	11.92	10.92	11.73	6.99	8.92		
	Ne	5.56	6.32	7.06	7.89	8.29	7.35	5.22	6.08	6.72	0.39
	I	1.90	2.05	2.04	2.24	2.23	2.16	1.77	1.94	2.04	0.06
	Ho	0.87	1.00	0.93	0.97	0.87	1.00	0.83	1.00	0.93	0.02
	He	0.82	0.84	0.86	0.87	0.88	0.86	0.81	0.84	0.85	0.01
	uHe	0.83	0.86	0.87	0.89	0.89	0.88	0.82	0.85	0.86	0.01
	F	-0.06	-0.19	-0.09	-0.11	0.01	-0.16	-0.03	-0.20	-0.10	0.03
	HWE	ns	ns	ns	ns	ns	ns	ns	ns		
Jask	N	30.00	30.00	30.00	30.00	30.00	30.00	30.00	30.00		
	Na	8.00	12.00	9.00	11.00	9.00	12.00	7.00	7.00	9.38	0.73
	Ar	8.00	11.92	8.99	10.93	9.00	11.85	7.00	7.00		
	Ne	6.55	7.56	5.54	8.65	7.44	7.09	6.41	6.19	6.93	0.34
	I	1.98	2.23	1.95	2.25	2.10	2.16	1.90	1.88	2.06	0.05
	Ho	0.83	0.97	0.97	0.87	0.77	0.93	0.90	0.87	0.89	0.02
	He	0.85	0.87	0.82	0.88	0.87	0.86	0.84	0.84	0.85	0.01
	uHe	0.86	0.88	0.83	0.90	0.88	0.87	0.86	0.85	0.87	0.01
	F	0.02	-0.11	-0.18	0.02	0.11	-0.09	-0.07	-0.03	-0.04	0.03
	HWE	**	*	ns	*	ns	ns	ns	ns		
Chabahar	N	30.00	30.00	30.00	30.00	30.00	30.00	30.00	30.00		
	Na	9.00	13.00	9.00	11.00	9.00	12.00	7.00	8.00	9.75	0.73
	Ne	6.27	8.57	6.77	8.70	8.45	7.03	6.16	6.08	7.25	0.40
	Ar	8.93	12.79	9.00	10.93	9.00	11.85	7.00	7.93		
	I	1.98	2.32	2.05	2.26	2.17	2.15	1.88	1.91	2.09	0.06
	Ho	0.87	0.93	0.97	0.93	0.80	0.90	0.80	0.87	0.88	0.02
	He	0.84	0.88	0.85	0.89	0.88	0.86	0.84	0.84	0.86	0.01
	uHe	0.85	0.90	0.87	0.90	0.90	0.87	0.85	0.85	0.87	0.01
	F	-0.03	-0.06	-0.13	-0.05	0.09	-0.05	0.05	-0.04	-0.03	0.02
	HWE	*	ns	ns	ns	ns	ns	ns	ns		

Population abbreviations as in Table 2; N= number of specimens Na=number of alleles; Ne=effective number of alleles per locus; Ar=allelic richness; I = Shannon's Information Index; H_o=observed heterozygosity; He=expected heterozygosity; UHe = Unbiased Expected Heterozygosity, F= F_{IS}=inbreeding coefficient. HWE=deviation from Hardy-Weinberg equilibrium

Table 3. Pairwise Population Matrix of Nei Genetic Distance (below), Genetic identity (above)

	KhM	Gen	Bush	BA	Jas	Chb
KhM	000	0.867	0.875	0.790	0.720	0.768
Gen	0.141	000	0.919	0.775	0.725	0.731
Bush	0.133	0.081	000	0.691	0.715	0.755
BA	0.235	0.225	0.309	000	0.869	0.936
Jas	0.280	0.375	0.285	0.131	000	0.963
Chb	0.263	0.269	0.280	0.064	0.037	000

Table 4. Pairwise Population Fst, Rst, and gene flow (Nm) Values between station pairs based on microsatellite data

Pop1	Pop2	Fst	Rst	Nm	P(rand >= data)
KhM	Gen	0.023	0.148	10.25	0.000
KhM	Bush	0.022	0.175	10.72	0.000
Gen	Bush	0.008	0.039	30.17	0.007
KhM	BAb	0.038	0.179	6.24	0.000
Gen	BAb	0.036	0.121	6.51	0.000
Bush	BAb	0.047	0.041	5.00	0.000
KhM	Jas	0.047	0.258	4.97	0.000
Gen	Jas	0.047	0.219	4.97	0.000
Bush	Jas	0.048	0.108	4.91	0.000
BAb	Jas	0.016	0.025	17.84	0.009
KhM	Chab	0.041	0.224	5.75	0.000
Gen	Chab	0.038	0.198	6.30	0.000
Bush	Chab	0.042	0.090	5.62	0.000
BAb	Chab	0.015	0.009	15.21	0.050
Jas	Chab	0.011	0.005	57.11	0.050

Table5. Pairwise population differentiation values between six populations based on microsatellite data

Sources of Variation	Percentages Variation	of Fixation indices	Pvalue
Among groups(one)	0	Rst= 0.131	P<0.01
Among Populations	13	Ris= 0.10	P<0.01
Among Individuals within population	9	Rit= 0.218	P<0.01
Within Individuals	78		
Among groups(four groups Khurmusa, Genavh+Bushehr, Bandarabas, Jask and Chabahar)	14	Rrt= 0.146	P<0.01
Among Populations within group	1	Rsr=-0.003	P>0.54
Among population	9	Rst= 0.10	P<0.01
Within Individuals	76		
Among groups(four groups Khurmusa, Genavh+Bushehr, Bandarabas, Jask and Chabahar)	13	Fst=0.054	P<0.001
Among Populations within group	1.14	Fsc=0.007	P<0.05
Within Individuals	85.77	Fct=0.046	P>0.05

Table 6. Results of three mutational models, the infinite alleles model (IAM), the two phase model (TPM), and the stepwise mutation model (SMM) and allele frequency distribution mode.

Pop name	P_{IAM}	P_{SMM}	P_{TPM}	Mod-shift
KhM	0.014	0.571	0.097	L-shaped
Gnv	0.015	0.572	0.102	L-shaped
Bsh	0.012	0.085	0.011	L-shaped
BAb	0.017	0.511	0.016	L-shaped
Jas	0.018	0.556	0.017	L-shaped
Chb	0.019	0.881	0.016	L-shaped

high genetic distances from 0.037 (Jask and Chabahar) to 0.330 (Jask and Genaveh. Genetic identity between sites was in the range of 0.71 (between samples of Jask and Genaveh) to 0.96 (between Jask and Chabahar samples).

The principal coordinate analysis based on population genetic distance revealed that samples from Khure-Musa, Genaveh and Bushehr clustered seperately from Chabahar, Jask and Bandar Abbas samples (Fig. 2). Chabahar samples are distinct from Bandar Abbas samples. There was evidence for correlation between genetic and geographic distances based on Mantel tests (R^2=0.80).

Results of the analysis using Bottleneck software revealed no evidence of recent population bottleneck (table6).

Discussions

Microsatellites are molecular markers widely used in population genetics of farmed as well as wild fish species (Liu *et al.*, 2009). In spite of high importance of yellow fin sea bream in local fisheries, no research has been conducted to evaluate genetic diversity and population differentiation of the species in the Persian Gulf and Gulf of Oman. The aim of this study was to estimate genetic differentiation in yellowfin sea bream populations from Persian Gulf and Gulf of Oman using microsatellite loci.

Of the 8 microsatellite loci analyzed in the 180 individuals among six sampling sites, all loci were polymorphic (Table 2). The total number of alleles per locus (N_a) across all populations in the present study was lower than that reported in other studies on Sparidae (Blanco Gonzalez & Umino, 2009; Dal-Sang et al., 2003; Dal-Sang et al.,2007; Perez-Enriquez Takemura, Tabata, & Taniguchi, 2001; Syazni *et al.*, 2015).

DeWoody & Avise (2000) reviewed microsatellite data from 40000 individuals from about 80 species and found that the mean H_e for microsatellite markers in marine species was 0.79. Molecular genetic diversity in marine species has been reported to be associated with their lifecycle reflecting their habitat types. Marine fish generally possess significantly high heterozygosity (average He=0.79) than freshwater species (average He=0.46) (DeWoody & Avise, 2000). Therefore the high heterozygosities found in *Acanthopagrus latus* in the present study (average He=0.82) are not uncommon.

No previous microsatellite studies was performed on Sparidae in the studied area, however the range of H_e for two Sparidae in Japan *P. major* and *A. schlegelii* (Jeong *et al.*, 2003; Perez-Enriquez, Takagi, & Taniguchi, 1999) was between 0.69-0.92 and 0.77-0.83 respectively, and for *A.Latus* from Japan was 0.911– 0.920 which was consistent with the range of values in our study (He: 0.76 - 0.86).

Altogether, Based on these observations, the microsatellite markers for *A. latus* in the present study showed a sufficient power of resolution.

Sixty of 48 (33%) loci departed from H_{WE}. Deviations from H_{WE} have been reported in marine fishes and Sparidae species such as yellowfin sea bream *A. latus* (Syazni *et al*., 2015), gilthead sea bream *Sparus aurata* (De Innocentiis *et al*., 2004).

Furthermore the Fis values among populations of *A.latus* in the Persian Gulf and Gulf of Oman did not suggest the occurrence of significant levels of inbreeding (table 1).

The low differentiation across all loci between localities is in consistency with estimated high gene flow. Jask population (Gulf of Oman) was more genetically differed from the other populations especially from the Persian Gulf samples. This is also consistent with the expectations, since Persian Gulf populations are more distant geographically to Gulf of Oman samples.

According to Thorpe (1982) the mean range of genetic identity among populations of the same species is between 0.80-0.90 which is close to the range of the populations of the present study.

Several theories has been germane to deviations from the H_{WE}, including inbreeding, intrapopulation

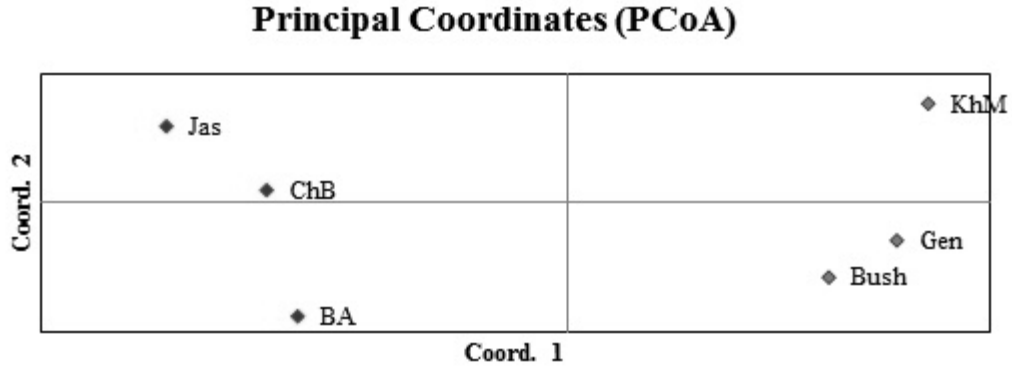

Figure 2. Plot of principal coordinate axes for six populations of yellowfin sea bream (*Acanthopagrus latus*) from Persian Gulf and Gulf of Oman based on population genetic distance.

structure (Wahlund effect), non-random sampling, selection against heterozygotisity and fishing pressure (De Innocentiis, Sola, Cataudella, & Bentzen , 2001; Xia *et al*., 2006). Many species of commercial fish suffering from overfishing in the Persian Gulf, thus H_{WE} deviation could be attributed to fishing pressure. Departure from H_{WE} in the present study may be due to other factors such as migration as supported by high Nm values between stations. Comparing Fst and Nm values between stations low genetic differentiation and high gene flow between studied stations from Persian Gulf and Gulf of Oman was detected, and the values are in consistency with geographical distances between stations.

High gene flow of *A.latus* in the present study may be caused by random dispersal of their pelagic eggs and larvae. This species spawns floating eggs which moves freely, resulting in high gene flow in its range, whereas some studies reported a single population with a low degree of geographic divergence (Jean, Lee, & Chen, 2000; Jeong Gonzalez, Morishima, Arai, & Umino , 2007; Syazni *et al.*, 2015). Syazni *et al.*, (2015) concluded that *A. latus* adults extensively migrate, but only within a limited range of their habitat and the high gene flow of the species is due to random dispersal of eggs and larvae. This is consistency with high gene flow observed in the present study. On the other hand, unlike other studies on *A.latus (*Jeong *et al*., 2007; *et al.*, 2015) which reported no significant differentiation (single population), some significant differentiation was observed the present study, which might be due to the large scale of the studied area (North Persian Gulf and Gulf of Oman).

Genetic distances, results of AMOVA and the pairwise estimates of F_{ST}, suggest significant differentiation between samples from northern Persian Gulf and Gulf of Oman, and in conclusion at least four different populations of *A.latus* (1: northwest Persian Gulf population: Khurmusa, 2:north Persian Gulf population including: Genaveh and Bushehr stations, 3:northwest Gulf of Oman population including Bandar-Abbas,3:north Gulf of Oman population including: Jask and Chabahar stations) exist in the northern coasts of Persian Gulf and Gulf of Oman.

This type of partitioning was found in other fish species populations in the northern Persian Gulf and Gulf of Oman (Khaledi *et al.*, 2012; Salari Rezvani Savari, & Nabavi, 2008).

Genetic bottleneck occurs when the effective size of the population experiences some temporary reduction. This may affect inter and intrapopulation genetic variations. Loss of genetic diversity may lead to reduced potential of small populations for responding to selective pressure (Allendorf & Leary, 1986). The L-shaped curve obtained indicates that studied *A.latus* populations have not undergone any recent bottleneck.

In conclusion, low but significant differentiation was observed among populations of *Acanthopagrus latus* in the north Persian Gulf and Gulf of Oman and these populations have not undergone any recent bottleneck. However fishing pressure is a threating issue as reported by other authors which should be considered in management programs.

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