Isolation and characterization of microsatellite loci in the Persian sturgeon (*Acipenser persicus*, Borodine, 1897) and cross-species amplification in four commercial sturgeons from the Caspian Sea

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Abstract
In order to have a sustainable management on Persian sturgeon as a highly commercial species in the South Caspian Sea, we need to identify its population structure and the level as well as its conservation status in their natural habitat. To develop a conservation program for this all Caspian Sea' sturgeon species it requires knowledge of its genetic diversity using reliable molecular marker to study population genetic structure. For these purposes, an enriched library was prepared based on a modified biotin-capture method. Approximately 1800 positive clones were screened for microsatellites in an *Acipenser persicus* genomic library. Of these 350 positively hybridizing clones were sequenced, and 81 clones were identified as having microsatellites with adequate flanking regions. We developed and tested 68 microsatellite primer pairs for Persian sturgeon. Out of 68 primer pairs developed, 11 pairs resulted in poor or no amplification, 13 were ambiguous, 6 were monomorphic, 20 were tetrasomic and 18 were octosomic in Persian sturgeon. While none of the markers showed disomic inheritance in Persian sturgeon and Russian sturgeon (*A. gueldenstaedtii*). Several of the markers appeared useful for studies stellate sturgeon (*A. stellatus*), ship sturgeon (*A.nudiventris*) and beluga (*Huso huso*). Nearly all the polymorphic pattern for ship, stellate and beluga displayed the simple banding patterns characteristic of disomic loci, while those for Russian sturgeon displayed banding patterns characteristic of tetraploid or higher polyploid levels. These markers may prove useful in a variety of future sturgeon population genetic studies in the Caspian Sea.

Keywords: Persian sturgeon, *Acipenser persicus*, Caspian Sea, Microsatellite, Population genetic
Introduction

The Persian sturgeon is an anadromous species living in the Caspian Sea, but it mainly inhabits in the southern Caspian region along the Iranian coast. Persian sturgeon enters the rivers for spawning, mainly the Sefid-Rud, Tajan and Gorganrud rivers in Iran and Kura river in Azerbaijan, less-the Volga, Ural, Samur, Terek, Lenkoranka and Astara rivers (Berg, 1948). Its population, after collapse in 1970’s, has risen in the 1990 decade and comprises the largest proportion of the total Iranian sturgeon commercial catch in recent years (Pikitch et al., 2005; Moghim et al., 2006). While in 1980-s its catch did not exceed 5% of the total sturgeon catches at the Volga and the Ural rivers, the share of this species decreased to 0.03%, in the year of 2000 (Khodorevskaya et al., 2000). Persian sturgeon is listed as a critically endangered species by the International Union for Nature Conservation (IUCN 2011), due to continued overexploitation, illegal catch spawning habitat loss and pollution.

Persian sturgeon stocks are recovered mainly by artificial propagation and Iranian Fisheries, release millions of 3-5 g fingerlings to the adjacent rivers of Caspian Sea annually (Abdolhay and Baradaran Tahori, 2006; Moghim et al., 2006). The sustainable management and conservation plan of this unique species requires knowledge of its genetic structure and levels of each stock in its natural habitat. Several population genetic studies were conducted on five sturgeon species in the Caspian Sea using microsatellite markers (Pourkazemi, 2007; Safari et al., 2008; Noruzi et al., 2008; Khoshkholgh et al., 2008).

Cross-species amplification using microsatellite primers of Scaphirhynchus were applied in the Persian sturgeon by Moghim et al., (2009) but none of the loci exhibited disomic inheritance. While microsatellites are expensive to develop initially, because of the higher degree of statistical power associated with codominant markers - microsatellite loci were developed for the Persian sturgeon to find disomic loci. The objective of the present research was to develop the Persian sturgeon specific microsatellite primers, and compare its application on other four sturgeon species in the Caspian Sea.

Materials and methods

An enriched library was prepared following a modification of the protocols of Hamilton et al., (1999) and Glenn et al., (2000) as described in Heist et al., (2003). Total genomic DNA from a single Persian sturgeon was digested with Rsal. Complementary linkers for use as polymerase chain reaction (PCR) primer sites were designed to contain an Rsal site when double-stranded (Linker-F: 5’-CTAAGGCTTGGATCGAAGGC-3’; phosphorylated Linker-R: 5’-pGCTTCTGCGATCAAGGGCTTAGAA AA-3’) and ligated to genomic DNA fragments. Biotinylated (GT)$_{15}$, (GA)$_{15}$, (GATA)$_{5}$ and (GACA)$_{5}$ probes were hybridized to linker-ligated DNA fragments and microsatellite containing DNA was selectively retained by binding biotinylated DNA fragments to streptavidin coated MagneSphere paramagnetic particles (Promega, Madison, WI, USA). Microsatellite-containing fragments were then amplified using PCR reactions containing approximately 10 ng microsatellite-enriched genomic DNA and 1× PCR buffer (200 mM KCl, 100 mM Tris), 200 µm of each dNTP, 2 mM MgCl$_2$, 1 µm Linker-F as primer, and 2 units Taq DNA polymerase. PCR amplifications consisted of 94 °C for 5 min, followed by 40 cycles of 94 °C for 45 s, 62 °C for 1 min, and 72 °C for 1 min using an Quanta Biotec master cycler gradient thermocycler (Quanta Biotec Ltd, Surrey, United Kingdom). The PCR product was ligated
into a pUC19 cloning vector and used to transform DH5α competent cells (Invitrogen, Carlsbad, CA, USA). Colonies were transferred to a nylon membrane and probed with 32P labeled (GT)15, (GA)15, (GATA)5 and (GACA)5. We isolated plasmid DNA from positive colonies using the Wizard miniprep kit (Promega). The positive clones were sequenced using M13 (F and R) universal sequence primers. Plasmid DNA was isolated from positive clones and sequenced with the ABI PRISM BigDye terminator cycle sequencing ready reaction kit using an ABI 377 automated sequencer (PE Applied Biosystems, Weiterstadt, Germany). Approximately 1800 positive clones were screened for microsatellites in an Acipenser persicus genomic library. Of these 350 positively hybridizing clones were sequenced, and 81 clones were identified as having microsatellites with adequate flanking regions. In total 68 microsatellite PCR primers were designed after omitting 13 clones with the same sequences. Microsatellite PCR primers were designed using the Primer3 (http://www.genome.wi.mit.edu/cgi-in/primer/primer3.cgi) or the MacVector (Oxford Molecular) software package. These loci were tested in Persian sturgeon (n=12) to identify optimal annealing temperatures and to determine if disomic polymorphic products could be reliably amplified. Additional individuals (n=24) from different populations were used to confirm the ploidy status.

Amplification was performed using a gradient thermocycler at annealing temperatures ranging from 52 °C to 64 °C. The ten microlitre PCRs reactions containing approximately 1-10 ng genomic DNA, 0.1 units Taq DNA polymerase, 0.5 mM of each primer, 200 mM of each dNTP, 2 mM MgCl2, and 1× PCR buffer. Amplification consisted of a 5 min denaturing step at 95 °C, 40 cycles of 95 °C for 30 s, 56 - 64 °C for 30 s, and 72 °C for 30 s, followed by a single five-minute extension step at 72 °C. PCR products were suspended 1:1 in 98% formamide/loading dye, denatured at 95°C for 5 min, and separated in a 6% denaturing polyacrylamide gels on a BIO-RAD gel sequencer running at 70 W for 45 - 60 min and visualized via Silver staining (An et al., 2009). Allele sizes were estimated using a 50-bp ladder molecular size standard (Invitrogen).

Amplification results were characterized as monomorphic if a single band of the same size was observed in all individuals, disomic if one or two bands were seen in every individual, tetrasomic if some individuals exhibited three or four bands, octosomic if more than four bands were observed in some individuals, weak if products were too faint to resolve, and ambiguous if banding patterns were too complex for us to interpret.

All primer pairs (except Ape-01 to Ape-18) were tested for cross-species amplification efficiency with four sturgeon species of the Caspian Sea, under the same PCR conditions used for Persian sturgeon including; the Stellate sturgeon, Russian sturgeon, Ship sturgeon and Beluga. Six individuals from each species were screened for polymorphism at these loci.

Results
In total 68 microsatellites PCR primers were designed after omitting 13 clones with the same sequences. Out of 68 primer pairs developed, 10 resulted in poor or no amplification, 13 were ambiguous; six of loci that amplified successfully were monomorphic, 21 were tetrasomic and 18 were octosomic in Persian sturgeon. None of the loci exhibited disomic inheritance (Figure 1). Locus name, clone size, GenBank accession number, repeat motif, PCR annealing temperature, and primer sequences are listed for these loci in Table 1.
Table 1: Characterization of 68 microsatellite loci in Persian sturgeon (*Acipenser persicus*), including repeat motifs, primer sequences and GenBank accession numbers, and cross-amplification in Russian (*A. gueldenstaedtii*), stellatus (*A. stellatus*), ship (*A. nudiventris*) sturgeon and beluga (*Huso huso*).

<table>
<thead>
<tr>
<th>Prime</th>
<th>Repeat type and length</th>
<th>primer sequences (5’ to 3’)</th>
<th>GenBank accession no.</th>
<th>A. persicus</th>
<th>A. gueldenstaedtii</th>
<th>A. stellatus</th>
<th>A. nudiventris</th>
<th>H. huso</th>
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<td>Ape-01</td>
<td>(CAGA)$_{14}$</td>
<td>F:CAATGTCACAAACACACACACGCG R:TTTCCTTCGAGTTGTCAATGTC</td>
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<td>171</td>
<td>tetrasomic</td>
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<td>octosomic</td>
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<td>(CT)$_{11}$</td>
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<td>JF77384</td>
<td>202</td>
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| Ape-19 | (CA)$_{34}$ | R:GGGAAGATTTCCAGAGGAGCACACTC F:GGGTTAGTAAAGACAGATGA CATGAGCACTGAC
| Ape-20 | (GACA)$_{13}$ | R:CAAGGTGGCACAGTGGACTA EU483155 172 octosomic octosomic ambiguous disomic disomic |
| Ape-21 | (GACA)$_{13}$ | R:ATTCGAGACCTGAGACCATAT F:CAAGAAAACCCAGCCCCACAGT EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-22 | (GACA)$_{15}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-23 | (CA)$_{25}$ | R:GGGGTTAGTAAAGACAGATGA CATGAGCACTGAC |
| Ape-24 | (GA)$_{18}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-25 | (GA)$_{18}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-26 | (GA)$_{18}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-27 | (GA)$_{18}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-28 | (CTGT)$_{10}$ | R:RTGCAGACCTGAGACCATAT F:CAAGAAAACCCAGCCCCACAGT EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-29 | (GT)$_{11}$ | R:RTGCAGACCTGAGACCATAT F:CAAGAAAACCCAGCCCCACAGT EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-30 | (GT)$_{11}$ | R:RTGCAGACCTGAGACCATAT F:CAAGAAAACCCAGCCCCACAGT EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-31 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-32 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-33 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-34 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-35 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-36 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-37 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-38 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-39 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-40 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-41 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-42 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |
| Ape-43 | (CT)$_{25}$ | R:CAAGGTGGCACAGTGGACTA EU483155 176 tetrasomic tetrasomic disomic mono disomic |

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| Ape-46 | (GA)27 | F: TGTGCCACAATTACAGTCA  
R: CAGAGAAGGTCAAGGCTCT | JF773790 | 245 | octosomic | octosomic | no amplify | disomic | mono |
| Ape-47 | (GA)34 | F: ATCTCAGCCAGAAGAGCA  
R: GCCCTTGTGACTGTCTTTT | JF773791 | 180 | octosomic | tetrasomic | disomic | disomic | disomic |
| Ape-48 | (GA)32 | F: TGTGCCACAATTACAGTCA  
R: CCACTTATTTAACCCAAATCAG | JF773792 | 201 | ambiguous | no amplify | no amplify | no amplify |
| Ape-49 | (GA)38 | F: ATCTCAGCCAGAAGAGCA  
R: GCCCTTGTGACTGTCTTTT | JF773793 | 188 | octosomic | tetrasomic | disomic | disomic | no amplify |
| Ape-50 | (CA)24 | F: CCTGCTGCTGATATAAAC  
R: CGGACTGTGTCTGTCTGTTC | JF773794 | 249 | mono | mono | disomic | mono | mono |
| Ape-51 | (GA)27(GA)32 | F: ATCTCAGCCAGAAGAGCA  
R: GCCCTTGTGACTGTCTTTT | JF773795 | 189 | tetrasomic | tetrasomic | disomic | disomic | mono |
| Ape-52 | (CAGA)6 | F: CACTGCTGCTGATATAAAC  
R: TATTAACCCATCGGTCTCAC | JF773796 | 151 | no amplify | no amplify | mono | no amplify | mono |
| Ape-53 | (CA)14 | F: GCACACACACAGACATA  
R: ACGGCATATACGCAAA | JF773797 | 196 | ambiguous | weak | weak | weak | weak |
| Ape-54 | (GA)25 | F: ATCTCAGCCAGAAGAGCA  
R: CCCGTGTCTGTCTGTCTTTT | JF773798 | 165 | tetrasomic | disomic | disomic | mono |
| Ape-56 | (CA)11 | F: TCCTCGCTGAGGAGGAAT  
R: CTGCTGACTGAGGACATGA | JF773799 | 146 | tetrasomic | octosomic | ambiguous | tetrasomic | ambiguous |
| Ape-57 | (CA)15 | F: CCATGCACACGCACTAGTTT  
R: ATTGTCATGCCCGTTTCAGT | JF773800 | 218 | mono | mono | no amplify | no amplify |
| Ape-58 | (CA)28 | F: GGACCTCAGAGACATGCAG  
R: GGCGACACATATTGCTCTCT | JF773801 | 155 | ambiguous | ambiguous | disomic | ambiguous | disomic |
| Ape-59 | (CA)11 | F: CGTCTGCTGAGGAGGAGGAAT  
R: CTGCTGACTGAGGACATGA | JF773802 | 110 | no amplify | no amplify | no amplify | no amplify |
| Ape-60 | (CT)25 | F: TTCAGGGATCCTGTCTCCAG  
R: GGGGAGCAGTCACAAAGAGT | JF773803 | 231 | mono | mono | no amplify | no amplify |
| Ape-62 | (CA)15(CA)6 | F: GACTTGCCCTACAGCAGCTC  
R: TACAGGAAAGAACATGTCAG | JF773804 | 385 | octosomic | tetrasomic | disomic | disomic | disomic |
| Ape-63 | (GACA)6 | F: GCCCTTGTGCTCAGAGCAG  
R: GACAGGAAGGAAATGCTGGAA | JF773805 | 360 | mono | tetrasomic | weak | mono | disomic |
| Ape-64 | (CAGA)12 | F: GAGAGAGGGAGGAGGACAACTCT  
R: TAGCTGAGTGGTGGTGGATG | JF773806 | 213 | mono | mono | weak | disomic |
| Ape-65 | (GA)17CA(GAGA)9(GA)6 | F: TTAGACCTTCATCACTGTA  
R: CCAAGGACCTACAGTCGC | JF773807 | 154 | ambiguous | disomic | ambiguous | weak |
| Ape-66 | (GACA)5 | F: CAGAAAAACCGGCCCCAGCT  
R: GAGAGAAGGAGGGGAGGACAA | JF773808 | 225 | ambiguous | octosomic | disomic | mono | disomic |
| Ape-68 | (GACA)5 | F: AGTTCGACACTGATAGGATTC  
R: TTCGCAATTAAGGTTAAAAAAGA  
R: GTTCGCAATTAAGGTTAAAAAAGA | JF773809 | 300 | ambiguous | mono | weak | weak | weak |
| Ape-70 | (CA)11 | F: AGTGAAGAGGAACAGATGGT  
R: GTTCAAGGAGGAAATGCTGGAA | JF773810 | 166 | tetrasomic | mono | mono | mono |
| Ape-71 | (GACA)15 | F: GAGAGAGGGAGGAGGACAACTCT  
R: CAGAAAAACCGGCCCCAGCT | JF773811 | 296 | tetrasomic | mono | mono | |
| Ape-73 | (GACA)7G2(CAGA)6 | F: GAGAGAGGGAGGAGGACAACTCT  
R: CAGAAAAACCGGCCCCAGCT | JF773812 | 221 | octosomic | disomic | disomic | no amplify |
<table>
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<tr>
<th>Locus</th>
<th>Repeat Unit</th>
<th>Forward Primer</th>
<th>Reverse Primer</th>
<th>Accession No.</th>
<th>Chr 1</th>
<th>Chr 2</th>
<th>Chr 3</th>
<th>Chr 4</th>
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<td>Ape-76</td>
<td>(GACA)(_{15})</td>
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<td>JF773814</td>
<td>171</td>
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Because no loci exhibited disomic inheritance in Persian sturgeon, standard tests for deviations from Hardy–Weinberg equilibrium and linkage disequilibrium could not be determined. Fifty two microsatellite primer pairs developed for Persian sturgeon were tested to generate polymorphic genetic markers for four Caspian Sea sturgeon species. In Russian sturgeon, forty six loci were screened in initial screening of samples. Only 32 (83%) of these primer pairs amplified successfully. Of these, 25 loci (54%) were found to be polymorphic in Russian sturgeon. Seven loci were monomorphic while eight loci failed to amplify. Of the 25 polymorphic loci identified, 18 loci were tetrasomic while seven loci were octosomic.

Of the 49 microsatellite loci that were tested in Stellate sturgeon, 39 loci (84%) amplified successfully of which 27 (69%) were polymorphic and seven loci (18%) were monomorphic. All polymorphic loci exhibited disomic banding patterns in stellate sturgeon. Ten loci failed to produce any bands. Forty six loci were tested for cross-species amplification in ship sturgeon. Thirty nine loci (85%) amplified successfully producing 18 polymorphic loci (39%), 13 loci were monomorphic and 8 loci failed to produce any bands. In addition, ambiguous bands were produced at eight loci. All polymorphic loci exhibited disomic banding patterns in Ship sturgeon.

Forty nine loci were screened in Beluga samples. Only 29 loci (83%) amplified successfully. 18 loci (37%) were polymorphic. 11 loci (24%) were monomorphic while 8 loci failed to amplify. All polymorphic loci showed disomic banding patterns. Thus all loci that amplified successfully and that were shown to be polymorphic in ship, stellate and beluga sturgeon species showed simple banding patterns characteristic of disomic loci, while those for Russian sturgeon (like Persian sturgeon) displayed banding patterns characteristic of tetraploid or higher polyploid karyotypes. Examples of electrophoretic banding patterns at polymorphic loci in the four sturgeon species are presented in Figure 2. Detailed results of cross-species amplification efficiency of the SSR primer pairs developed for Persian sturgeon tested on four Caspian Sea sturgeon species are presented Table 1. Due to the polysomic nature of these loci and the small sample sizes screened in each species, it was considered not possible to test for conformation to hardy-Weinberg equilibrium or heterozygosity per locus. These data will require a more extensive study of larger populations per species.

Discussion

Traditionally, microsatellite marker are developed by extensive screening for microsatellite containing clones through repetitive hybridizations of a repeat motif probe to a large number of random clones (Rassmann et al., 1991). Such an isolation strategy resulted in low rate of the number of positive clones (containing microsatellites) detection. This traditional method usually that can be obtained by means of ranges from 12% to less than 0.04% (Zane et al., 2002).

Using modified protocols of Hamilton et al., (1999) and Glenn et al., (2000) to construct and clone genomic libraries increased proportions of inserts that contained tandem repeat arrays. Thus, a greater number of microsatellite repeat regions detected, sequenced and subsequently used to design species-specific flanking primers for microsatellite amplification. This technique reduced the time and effort as well as cost required for microsatellite isolation from Persian sturgeon. To date there has been no species specific microsatellite primers developed for the Caspian Sea sturgeon species and this is the first report for Persian sturgeon.
Developing microsatellite markers for sturgeon species can be challenging particularly in species that have experienced multiple polyploid events (i.e., 4n, 8n and 16n species) for example, Welsh and May (2006) found only nine reliable disomic microsatellites among 254 primer pairs tested in lake sturgeon (*A. fulvescens*), a species with the same ploidy level as Persian sturgeon.

Amplification results for Persian sturgeon and cross-species amplifications in four Caspian Sea sturgeon species were consistent with the reported ploidy levels of each species. Ship, Stellate and Beluga sturgeon are considered to be functional diploids (2n=120), while Persian and Russian sturgeon are considered to be functional tetraploids (2n=240) that are undergoing rediploidization (Ludwig et al., 2001; Fontana, 2002; Fontana et al. 2008).

While none of the markers that amplified in Persian sturgeon were disomic, they may still prove to be useful as dominant markers (e.g. Israel et al., 2009) for this species. Several markers appear to show codominant inheritance patterns in ship, stellate, and beluga sturgeon and may prove useful in a variety of future population genetic applications, ranging from stock assessment to mapping of quantitative trait loci in culture stocks. Testing more individuals and fine tuning optimization of PCR reactions, is likely to identify new alleles at polymorphic loci, as well as the possibility of detecting polymorphisms in loci that were recorded as being monomorphic in small test populations here. Results of these studies suggested that SSR DNA markers developed for Persian sturgeon were candidates for application in other sturgeon species in the Caspian Sea. This proved to be the case and suggests a high level of sequence homology among related species in the Caspian Sea, a result that is consistent with the results from studies on other sturgeon species (May et al. 1997; McQuown et al., 2000).

To eliminate the inherent difficulties associated with tetrasomic loci, future Persian sturgeon genetic marker development required identifying nuclear microsatellite loci that are disomic.

Figure 1: Electrophoretic banding pattern for locus Ape_19 in Persian sturgeon that exhibited octosomic inheritance. Relative allele’s density would correspond to gene doses.
Lane M: 50 bp DNA step ladder.

1-A: Persian sturgeon

1- B: Russian (lanes1-5) and Ship (lanes 6-10) Sturgeon.

Figure 2: Electrophoretic banding pattern for locus Ape_20 in Persian (A), Russian (B: 1-5) and ship sturgeon (B: 6-10). This locus exhibited tetrasomy in Persian and Russian sturgeon but was monomorphic inheritance in ship sturgeon. Lane M: 50 bp DNA step ladder

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References


شناختی و جداسازی گانه‌های ریز ماهوار تاسمهای ایرانی
و بررسی امکان تکثیر آنها در زنوم چتر گونه

ماده‌های خاویاری دریای خزر

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چکیده

به منظور مدل‌برداری بازدارنده‌ای ماهی ایران که یک گونه با ارزش تجاری در جنوب دریای خزر است، ما نیاز به شناسایی

جعبه‌های ساختار جمعیتی و معمولی و وضعیت حفاظتی آنها در زیستگاه طبیعی شان داریم. معمولاً رای توسعه یک برنامه

حفاظتی برای تاس ماهی ایران در دریای خزر نیاز به آگاهی از نوع زنبیلی آن داده‌ها با استفاده از نشانگر

مولکولی قابل اعتماد جمع آوری شده باشد. نشانگر مولکولی ریزماهوارهای میکروستایت، نشانگر مناسب برای این منظور می

باشد. برای این منظور، یک کتابخانه الف. می‌شود از DNA تاس ماهی ایران بر اساس روش ژن‌بندی آبی آماده شد. حدود 1800

کلون سفید از کتابخانه زنومی تاس ماهی ایران جدایی کرد و برای مدل جمع کردن مقاوم تولیدی تو کلونید ها با ریزماهوارهای

شریایی. از این تعداد 525 کلونی شناسایی و تیون‌نمایی شدند، از این 74 کلونی با داشتن ریزماهواره و میکروستایت

PCR مناسب (با مناطق (flanking) شناسایی و ۴۲ جفت آغازگر ریزماهواره توسعه (develop) یافت. نتایج آزمایش آغازگرها

با نمونه‌های DNA تاس ماهی ایران نشان داد که از 27 جفت آغازگر، 6 آغازگر گانه‌های مونومورف با نک شکلی

tetrasomic (oka somic) ) و 18 آغازگر گانه‌های چند شکلی ترسومورف (monomorphic)

اکتا گانه‌ای (octosomic) ) 24 آغازگر هیچ گانه‌ای را تکثیر نکردند، یک مرکز بنویسی داگ لانه‌ها ضعیف و مهم

A. (disomic) ) در تاس ماهی ایران و تاس ماهی روس (A. stellatus) نشان دادند. تعیین حاصل از نشانگرها برای مطالعات

یافته‌ها از آغازگرها با ارزون رون در شیپ و فیل (Huso huso) (A. nudiventris) (gueldenstaedtii)

و فیل ماهی (A. nudiventris) مناسب ظاهر شدند. با زیاده‌های حاصل از آغازگرها از ارزون رون شیپ و فیل

گانه‌های چند شکلی ساده که مشخصه گانه‌ای دیسومیک (disomic) است، نشانگر داده‌ها، در حالی که

برای تاس ماهی ایران و تاس ماهی روس الگوی اول حاصل گانه‌های پلی سومیک چهار نایی با بیشترها را نمایش دادند. این

نشانگرها برای مطالعات زنبیلی گانه‌های انواع مختلف ماهیان خاوری دریای خزر مفید خواهد بود.

واژگان کلیدی: تاس ماهی ایران، DNA، ماهواره، ریزماهوار، ژنتیک، جمعیت، Acipenser persicus