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’s 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 Scaphirhynchos 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'-CTAAGGACTTGGATCGAAGGC-3'; phosphorylated Linker-R: 5'-pGCTTCTGCGATCAAGGCCTTAGAA 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 $^{32}$P 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 MgCl$_2$, and 1× PCR buffer. Amplification consisted of a 5 min denaturing step at 95 °C, 40 cycles of 95 °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>Product size (bp)</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>(CAGA)$_{14}$</td>
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<td>JF773783</td>
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<td>JF773784</td>
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<td>R: GGAAGATTTTCAGAGAGCAGCACTC</td>
<td>GGGGTAGGAAGACACAGATTGA</td>
<td>EU483155</td>
<td>172</td>
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<td>GAGGGCGAGCTGGGTGGTCAG</td>
<td>EU531732</td>
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<td>ATGGGACCTGGACACAGACAT</td>
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<td>EU531734</td>
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<td>GCCACGGGGGAGAAGACAG</td>
<td>EU531736</td>
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<td>EU531737</td>
<td>237</td>
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<td>disomic</td>
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<td>disomic</td>
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<td>Ape-26</td>
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<td>TCTGACCCAGAGAACAG</td>
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<td>Ape-27</td>
<td>(GA)_{3}</td>
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<td>CCCTGTCCTCTGTGCTGCTG</td>
<td>EU531740</td>
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<td>EU531741</td>
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<td>R: CTTGTCCTGCTGCTGCTG</td>
<td>EU531744</td>
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<td>GCCTGTCCTGCTGCTGCTG</td>
<td>EU531745</td>
<td>227</td>
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<td>GCATGTCTTTTTGTTTAC</td>
<td>EU531746</td>
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<td>tetrasomic</td>
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<td>(CA)_{10}</td>
<td>F: GCCACAACCATCCTCTTTC</td>
<td>R: GGGCAAATATGCTGCTG</td>
<td>EU531747</td>
<td>162</td>
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<td>(GACA)_{6}</td>
<td>F: ACTGGCTGCTGCTGCTGCTAAACA</td>
<td>CTGGAGCAGGGAGGAAGAACGA</td>
<td>EU531748</td>
<td>231</td>
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<td>CTTGACCCAGAGAACAGA</td>
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<td>no amplify</td>
<td>no amplify</td>
<td>no amplify</td>
<td>no amplify</td>
</tr>
<tr>
<td>Ape-49</td>
<td>(GA)$_{38}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77393</td>
<td>188</td>
<td>octosomic</td>
<td>tetrasomic</td>
<td>disomic</td>
<td>disomic</td>
<td>no amplify</td>
</tr>
<tr>
<td>Ape-50</td>
<td>(CA)$_{24}$</td>
<td>F: CTCGTCAGCTGATATACCAGAAGGCTTT</td>
<td>JF77394</td>
<td>249</td>
<td>mono</td>
<td>mono</td>
<td>disomic</td>
<td>mono</td>
<td>mono</td>
</tr>
<tr>
<td>Ape-51</td>
<td>(GA)$<em>{33}$, (GA)$</em>{32}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77395</td>
<td>189</td>
<td>tetrasomic</td>
<td>tetrasomic</td>
<td>disomic</td>
<td>disomic</td>
<td>mono</td>
</tr>
<tr>
<td>Ape-52</td>
<td>(CAGA)$_{6}$</td>
<td>F: CACGTCCGCTGATCAGAAACACCAC</td>
<td>JF77396</td>
<td>151</td>
<td>no amplify</td>
<td>no amplify</td>
<td>mono</td>
<td>no amplify</td>
<td>mono</td>
</tr>
<tr>
<td>Ape-53</td>
<td>(CA)$_{14}$</td>
<td>F: GCACACACACACACATA R: ACGGCACTATACGCCAAAATT</td>
<td>JF77397</td>
<td>196</td>
<td>ambiguous</td>
<td>weak</td>
<td>weak</td>
<td>weak</td>
<td>weak</td>
</tr>
<tr>
<td>Ape-54</td>
<td>(GA)$_{25}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77398</td>
<td>165</td>
<td>tetrasomic</td>
<td>tetrasomic</td>
<td>disomic</td>
<td>disomic</td>
<td>mono</td>
</tr>
<tr>
<td>Ape-55</td>
<td>(CAGA)$_{6}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77399</td>
<td>146</td>
<td>tetrasomic</td>
<td>octosomic</td>
<td>ambiguous</td>
<td>tetrasomic</td>
<td>ambiguous</td>
</tr>
<tr>
<td>Ape-56</td>
<td>(CA)$_{11}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77400</td>
<td>218</td>
<td>mono</td>
<td>_</td>
<td>no amplify</td>
<td>_</td>
<td>no amplify</td>
</tr>
<tr>
<td>Ape-57</td>
<td>(CA)$_{15}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77401</td>
<td>155</td>
<td>ambiguous</td>
<td>ambiguous</td>
<td>no amplify</td>
<td>disomic</td>
<td>ambiguous</td>
</tr>
<tr>
<td>Ape-58</td>
<td>(GA)$_{28}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77402</td>
<td>110</td>
<td>no amplify</td>
<td>no amplify</td>
<td>no amplify</td>
<td>no amplify</td>
<td>no amplify</td>
</tr>
<tr>
<td>Ape-59</td>
<td>(CA)$_{11}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77403</td>
<td>231</td>
<td>ambiguous</td>
<td>mono</td>
<td>no amplify</td>
<td>disomic</td>
<td>no amplify</td>
</tr>
<tr>
<td>Ape-60</td>
<td>(CT)$_{25}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77404</td>
<td>385</td>
<td>tetrasomic</td>
<td>tetrasomic</td>
<td>disomic</td>
<td>disomic</td>
<td>disomic</td>
</tr>
<tr>
<td>Ape-61</td>
<td>(GA)$<em>{20}$, (GA)$</em>{21}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77405</td>
<td>360</td>
<td>mono</td>
<td>tetrasomic</td>
<td>weak</td>
<td>mono</td>
<td>disomic</td>
</tr>
<tr>
<td>Ape-62</td>
<td>(CAGA)$_{12}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77406</td>
<td>213</td>
<td>mono</td>
<td>mono</td>
<td>weak</td>
<td>mono</td>
<td>weak</td>
</tr>
<tr>
<td>Ape-63</td>
<td>(GA)$<em>{17}$CA, (GA)$</em>{9}$GCA, (GA)$_{6}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77407</td>
<td>154</td>
<td>ambiguous</td>
<td>ambiguous</td>
<td>ambiguous</td>
<td>weak</td>
<td>weak</td>
</tr>
<tr>
<td>Ape-64</td>
<td>(GA)$<em>{17}$CA, (GA)$</em>{9}$GCA, (GA)$_{6}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77408</td>
<td>225</td>
<td>ambiguous</td>
<td>octosomic</td>
<td>disomic</td>
<td>mono</td>
<td>disomic</td>
</tr>
<tr>
<td>Ape-65</td>
<td>(CAGA)$_{15}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77409</td>
<td>300</td>
<td>ambiguous</td>
<td>mono</td>
<td>weak</td>
<td>disomic</td>
<td>disomic</td>
</tr>
<tr>
<td>Ape-66</td>
<td>(CAGA)$_{15}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77410</td>
<td>166</td>
<td>tetrasomic</td>
<td>mono</td>
<td>monono</td>
<td>mono</td>
<td>mono</td>
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<tr>
<td>Ape-67</td>
<td>(CAGA)$_{15}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77411</td>
<td>296</td>
<td>tetrasomic</td>
<td>mono</td>
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<td>mono</td>
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<tr>
<td>Ape-68</td>
<td>(CAGA)$_{15}$</td>
<td>F: ATCTCAAGCGAGAGGACGA R: GGCCTGCTTGTCTGCTT</td>
<td>JF77412</td>
<td>221</td>
<td>tetrasomic</td>
<td>mono</td>
<td>mono</td>
<td>disomic</td>
<td>no amplify</td>
</tr>
</tbody>
</table>
| Ape-76 | (GACA)15 | F: GAGAGAGAGGGAGCGACAAA  
R: CAGAAAAACCACAGCCACAGT | JF773813 | 225  
octosomic  
tetrasomic  
disomic  
disomic  
disomic  |
|--------|----------|-------------------------------------------------|---------|---------|
| Ape-77 | (GA)28   | F: ATCTCAGCCAGGAAGAAGGA  
R: CCGTGTCTGTCTGTCTGTGT | JF773814 | 171  
tetrasomic  
disomic  
disomic  
disomic  
ambiguous  |
| Ape-78 | (CAGA)6  | F: CACTGCTGCTGCTAAAAC  
R: TATTAACCCATCGGCTCCAC | JF773815 | 151  
tetrasomic  
tetrasomic  
disomic  
disomic  
disomic  |
| Ape-80 | (CTGT)14 | F: GGGGTTCAGGGAGCTTCTA  
R: GCACTTTGTCAGGCAGACA | JF773816 | 228  
ambiguous  
disomic  
_  
mono  
mono  |
| Ape-81 | (GA)28   | F: GGTCCAATGTATCAGGCCAAA  
R: GCCGAGCAGCTCCATTAG | JF773817 | 152  
tetrasomic  
_  
ambiguous  
_  
ambiguous  |
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 (lanes 1-5) 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


شناسایی و جداسازی چاپگاه‌های ریز ماهوار تاسماهی ایرانی
و بررسی امکان تکثیر آنها در زنون چهار گونه

مراهقبازاری دریای خزر

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سراج ۵؛ جووی مالک پانادام ۶؛ رضا پورغلام ۱؛ داور کر ۱؛ فرامرز لالنی ۱؛ محمد جواد تقوی ۱

چکیده

به منظور مدلبرداری پایداری ذخیره‌ی بی‌ویژه شناسایی ماهی در جنوب دریای خزر است، ما نباید به شناسایی
جیبیت، ساختار جمعیتی و همچنین وضعیت هفاظتی آنها در زیستگاه‌های طبیعی شناساری نمودم. همچنین برای توسعه یک برنامه
هفاظتی برای تاس ماهی‌ای از دریای خزر به آگاهی از نوع زنیکی آن دارد که داده‌های آن با استفاده از نشانگر
مولکولی قابل اعتباری جمع آوری شده است. نشانگر مولکولی ریز‌ماهوار ایکسپرسیونی، نشانگر مناسب برای این منظور می
باشد. برای این منظور، یک کتابخانه گنی شده از DNA تاس ماهی ایران بر اساس روش جذب بیوین آماده شد. حدود ۱۸۰۰
کلونی میفید از کتابخانه ژنومی تاس ماهی ایران چهار سالیانه و برای کنترل وجود تکرار متوالی تولکلی‌های ریز‌ماهوار غیر
بلند، از تعداد ۱۲۰ کلونی شناسایی و تغییر توافقی شدن، از آن ۱۳ کلونی با داشتن ریز‌ماهوار و مکان پدیدارگیری
PCR مناسب (بایاٗ (flanking) شناسایی شدند و ۶۸ جفت آغازگر ریز‌ماهوار توسه (develop) یافت. نتایج آزمایش
آغازگرها با نمونه تاس ماهی ایران دان که از ۶۸ جفت آغازگر، ۶ آغازگر جایگاه مونومورفی بنا شکل DNA را داشتند
و ۲۳ آغازگر جایگاه چند شکلی پراگتیکی (tetrasomic)، (monomorphic) اکستالیکی (octosomic) را داشتند. ۱۲ آغازگر هیچ جایگاهی را نکنترنیدن یا الگوی بنده ضعیف و مهم
A. (disomic) در تاس ماهی ایران و تاس ماهی روس (A. stellatus) (gueldensasti) شبیه نمی‌شوند. آغازگرها برای مطالعات ماهی‌های خوارای آزون برون (Huso huso) (A. nudiventris)
و فیل ماهی (H. stellatus) نشان دادند، تعدادی از نشانگرها برای مطالعات ماهی‌های خوارای آزون برون فیل
ماهی‌گونگی جایگاه متناسب این شکل‌سازه که مشخصه جایگاه دیسومیک (disomic) است را نمایش دادند، در حالتی که
برای تاس ماهی ایران و تاس ماهی روس گونگی بنده‌ای حاصل گیاهانه جایزه حیاتی سومنگی جیب چهار مفید که خواهد بود.

واژگان کلیدی: تاس ماهی ایران،
برای خزر، ریز‌ماهوار، جایگاه جمعیت.

(Acipenser persicus, Borodine, 1897)