Development a Set of 46 SNP Markers for the Yellow Catfish (*Tachysurus Fulvidraco*)

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Research Article

Keywords: Yellow catfish, SNP markers, Population genetic analysis, Whole genome resequencing

Posted Date: June 8th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-501513/v1>

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Abstract

The whole genome resequencing was used to develop single nucleotide polymorphisms (SNP) markers for the yellow catfish (*Tachysurus fulvidraco*). A total of 46 SNP markers were selected from 5550676 genotyping markers which distributed on 26 chromosomes. Of the 46 SNPs analyzed, 35 SNPs conformed to Hardy-Weinberg equilibrium. The observed and expected heterozygosity of these markers ranged from 0.2519 to 0.771 and from 0.265 to 0.5018, respectively. This set of markers will be of great useful for population genetics of the yellow catfish.

Introduction

The yellow catfish (*Tachysurus fulvidraco*), belonging to Bagridae (Nelson et al. 2016), is an important economic species of freshwater fish, widely distributed in China. Due to its delicious taste and high nutritional value, the yellow catfish was favored by the market. With the increasing market demand, this species has suffered over-exploitation and declined sharply of its natural stocks over the past few years (Guo et al. 2006; Yu et al. 2019). Therefore, it is essential to understand the population genetics of yellow catfish for the conservation and sustainable exploitation.

Precious genetic studies of this species has been explored using SSR markers (Feng et al. 2009; Hu et al. 2009; Zhang et al. 2009). However, the limitations of SSR markers motivated the development of more informative SNP markers for the population genetics of the yellow catfish (Meyer-Sand et al. 2018). Here we characterized a set of 46 SNP markers for the yellow catfish which were analyzed using whole genome resequencing.

Materials And Methods

The genomic DNA from 129 individuals was sequenced using Illumina HiSeq™ X Ten platform (Zhou et al. 2021). After reads quality filter and mapping to the reference genome (Gong et al. 2018), 46 SNP markers were randomly selected from 5550676 genotyping markers which distributed on 26 chromosomes. The genetic parameters of these markers, including observed heterozygosity, expected heterozygosity, and the Hardy–Weinberg equilibrium (HWE), were calculated using Popgene v 1.32 (Yeh et al. 1997).

The marker primers were designed by the flanking sequence using Oligo 7 (Rychlik 2007) software and examined for their amplification efficiency. PCR were conducted in 50 µL reaction mixtures containing 200 ng template DNA, 5 µL 10 × buffer (TaKaRa, Dalian, China), 4 µL MgCl₂ (2.5 mol/L), 2.5 µL dNTP (2.5 mmol/L), 2 µL of each primer (5 µmol/L), and 1 U Taq DNA polymerase (25 U/µL, TaKaRa). PCR conditions were as follows: initial denaturation (95°C, 2 min), then 34 cycles of denaturation (94°C, 40 s), primer annealing (55°C, 50 s), and elongation (72°C, 60 s) and a final extension (72°C, 10 min).

Results

All 46 SNP loci were amplified successfully. The observed heterozygosity of these markers varied from 0.2519 to 0.771, while the expected heterozygosity ranged from 0.265 to 0.5018 (Table 1). A total of 35 loci conformed to Hardy-Weinberg equilibrium ($p > 0.01$) after Bonferroni's correction, insuring the reliability of their application to evaluate larger groups.

Table 1
Characterization of 46 SNP markers in *Tachysurus fulvidraco*

SNP ID	Chr. NO.	Primer sequence (5'–3')	Size (bp)	SNP position (bp)	SNP type	H_o	H_e	HWEP
55823	1	AGGAGCTTTACAAACACTCAC CTGTTTGCCTAAAATGCTCCA	591	331	A/C	0.3664	0.3285	NS
2071	1	TTTAAATAAGCACAAATAGCAA AAACTTCCAGAATGTCCCC	571	87	A/C	0.4504	0.3586	NS
58894	1	CCAAATAATGAAGCGAAAGCC ACAATGCAGGAATGATAACCAG	681	310	C/A	0.3969	0.4661	NS
52924	1	CTGCCCATGGTCATAATTGGA TGCCACTACCTTATTATCACT	653	428	C/T	0.3817	0.4258	NS
560625	2	AACCGTTAAAATTAGAGATCACAC CAACTTAAGCACAACTCGGTA	586	393	G/T	0.4198	0.3966	NS
599487	2	GAATCTGATCACTGAGCTCGT TTTCAAGAACCAGCATGGAC	468	226	C/T	0.6870	0.4806	*
638351	2	AGTTCTGCCTTCAACACC TAGTGCCATAGAAAATAGCTT	877	378	T/C	0.2977	0.2955	NS
638434	2	TTCTTACCGTAACTCATGC CACGTCTATGAATCTACTGC	603	367	G/T	0.2519	0.3053	NS
760278	3	CCAACGTGCTATGGTCT ACAAACTGTCTTAAAGGGCTC	584	278	G/C	0.4351	0.5014	NS
938090	3	TCATTTTCCTCTTCATGCACT TAGCCAGACATCCCGAA	565	351	A/G	0.6947	0.4851	*
1149005	4	CAACTCCACAGATGCACT CAACATCCCCTAATTAATCCAC	364	99	A/T	0.6183	0.4790	NS
1149027	4	ATTTCAAGCCTTATTGCTC CTTTTACAACCAAGTGCAT	694	186	A/G	0.5802	0.4574	NS
1487601	5	AAATAGGCTTCATGTGT TCTTCTTTAACTGGCATC	501	275	T/G	0.6183	0.4756	NS
1798440	6	ACATATACATACGCACACGTT	498	367	T/C	0.5420	0.4990	NS

H_o represents the observed heterozygosity, H_e represents the expected heterozygosity, HWEP represents the results for Hardy–Weinberg equilibrium, NS represents non-significant, *p < 0.01.

SNP ID	Chr. NO.	Primer sequence (5'–3')	Size (bp)	SNP position (bp)	SNP type	H_o	H_e	HWEP
		CCATGTCTGTAATTTTCACGTT						
1855240	7	CAAGCTTATGTAAAGGCTCT AACTAACGATGTCACACGCTA	570	125	A/G	0.6641	0.4756	*
2265537	9	ATCGTCCATGACAAATCACC TCTGTTTATTCTCATAGTGCAA	620	149	C/T	0.5420	0.3966	*
2477173	10	TAGTGAATAATCATAGGGCTT TATTTCCACAACACGCTCA	540	231	G/T	0.3206	0.2906	NS
2597747	10	ATCCTAGCCAATGTATTGCTG TGTTAGGTATCGCCACT	603	398	C/T	0.2977	0.2650	NS
2676641	11	GCCTTTGTTCTTATAGTGCAT CACTGAGCTCCTGTTACACAC	603	337	A/G	0.5954	0.4836	NS
2941890	12	TTAGTTGCAGGTTTCCTC AAGTAAGCCTGTATTAGCC	658	154	A/C	0.5802	0.4701	NS
3171163	13	TTGCCACAAGGTATAACCGAA GGCTCTAGTATTTTATCAAACCC	419	327	A/T	0.4275	0.3931	NS
3171175	13	AATCAGAGCGTTTGAACCAT CAATTCCCTAATTTGCCCTT	403	119	T/G	0.6107	0.5012	NS
3171187	13	CAGAATCAGTTATGGCCCTC TTACTTCTGGCTAATTACTGG	693	317	A/G	0.5725	0.5014	NS
3171263	13	ATCACACTCATTCGGCTT AAGGCTATCATGCACCCAA	558	305	T/C	0.2672	0.3147	NS
3171347	13	CAGCCATTAAAATATAGGGAG CAACACAATTTGCTGGA	451	129	A/G	0.6260	0.4773	NS
3319329	14	GCCTCCACCTAGACTCC AGAATGCGATGTTTACTGCT	423	239	A/G	0.5344	0.4574	NS
3485859	14	CTAATTGTGCCTTGTATGCAG TGTAATAATCAGAGCGTGT	380	89	G/T	0.5649	0.4619	NS
3541374	15	ACGTGTACAACCTGTTATTACGC	405	233	G/C	0.5573	0.4756	NS
H_o represents the observed heterozygosity, H_e represents the expected heterozygosity, HWEP represents the results for Hardy–Weinberg equilibrium, NS represents non-significant, *p < 0.01.								

SNP ID	Chr. NO.	Primer sequence (5'–3')	Size (bp)	SNP position (bp)	SNP type	H_o	H_e	HWEP
		GTGTCCGCATCATAAACGAA						
3542145	15	CTAATCTCAGCACATCCG AATCAGATGAAAGGCACAC	450	157	C/T	0.5267	0.4228	NS
3706234	16	TATTGGCAACAACCACT GCATAAGACACATAACGCATC	537	372	G/T	0.5573	0.4756	NS
4029832	17	GTACTGCCAATTTACACAAC AAAATTAAAAGCCTTATTAGTCCA	576	385	G/C	0.6794	0.4720	*
4030097	17	ACGCTGTTGTCCTACCTG CCCATTTTCTAGGGGTCCTT	426	182	A/G	0.6336	0.4681	*
4057632	17	ATGCTTCATTTTCATCCGTTC ACCCGCCTTAAATTTGGAC	417	275	C/T	0.6794	0.5018	*
4174143	18	GTGACCCGATTTTACATGACC GCGTTGTGGAATTCTTATCACT	470	296	A/T	0.6183	0.4720	NS
4329563	19	CCTTCATCTTCTGGATTTTGCG TGA CTG CCAACAGATTACCCAA	561	291	C/T	0.5115	0.4102	NS
4540487	20	CTGTAGGAAAACACCGCTCT TGCCAATCAACCTACCATGC	653	330	A/G	0.6107	0.4701	NS
4590446	21	ACAGAGACATCAGTGCAA GACAAAACCTCCTTCGGAT	418	194	A/T	0.6947	0.4902	*
4931481	22	CCTTAAACACTAGGCTACCAC GAGAAAAGATTTACGCTGCT	659	392	C/T	0.6260	0.4914	NS
4931542	22	ATAAGTTGCACCAGCGTA GCTGGTCATTTAATAACTAACAC	522	105	G/T	0.5344	0.4528	NS
4931576	22	TCAGCCGTTACTAGGTT CCACAGACTGACGACCA	657	359	A/G	0.6947	0.4902	*
4931603	22	CTGCCTCTATGCCCGAT AACTGCTGCCTTTGAGACTG	531	310	G/T	0.4885	0.4069	NS
5028968	23	GAAAGCTGCTAGACACA	584	328	A/C	0.5344	0.4661	NS
H_o represents the observed heterozygosity, H_e represents the expected heterozygosity, HWEP represents the results for Hardy–Weinberg equilibrium, NS represents non-significant, *p < 0.01.								

SNP ID	Chr. NO.	Primer sequence (5'–3')	Size (bp)	SNP position (bp)	SNP type	H_o	H_e	HWEP
		GTTGGTAATTTTAGCCCTC						
5078926	23	ATGCTAACCACTAAGCCA CCAATTCACATATGCCTT	631	453	C/T	0.6031	0.4821	NS
5206582	24	ATCTTGGTGACTTTGCGCTT GCGGTTGCCACTATAATCTCA	539	246	A/G	0.6641	0.4790	*
5232887	25	GCAAATAAGAAGCACGA CAAGCACCAAGTTAGCTC	628	308	C/T	0.5725	0.4720	NS
5456365	26	TGGCTTACACCTGATATAGAGGAC CAGCGCAAAAGCTTAGCACCA	452	177	G/T	0.7710	0.4977	*
H_o represents the observed heterozygosity, H_e represents the expected heterozygosity, HWEP represents the results for Hardy–Weinberg equilibrium, NS represents non-significant, * $p < 0.01$.								

Declarations

Acknowledgements:

We would like to thank Huarun Technology Breeding Co. Ltd for the helping of sample collection. This study was funded by the Earmarked Fund of Anhui Fishery Research System (No.2016-84) and Anhui key research and development programs (202004a06020063, 201904f06020002).

Funding

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Conflicts of interest

The authors declare there are no competing interests.

Availability of data and material

The datasets analyses during the current study are available in the BioProject Database (Accession no. PRJNA683740).

Authors' contributions

All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Huaxing Zhou, Guoqing Duan, Huan Wang and Tingshuang Pan. The first draft of the manuscript was written by Huaxing Zhou and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

Ethics approval and consent to participate

The experimental protocol was established, according to the ethical guidelines of the Basel Declaration and was approved by the Experimental Animal Welfare and Ethical of Anhui Academy of Agricultural Sciences (NO. AAAS 2020-11)

Consent for publication

Not applicable.

References

- Feng XY, Li ZQ, Xie N, Li JL (2009) Isolation and characterization of twelve novel microsatellites in yellow catfish, *Pelteobagrus fulvidraco*. *Conserv Genet* 10: 755-757.
- Gong G, Dan C, Xiao S, Guo W, Huang P, Xiong Y, Wu J, He Y, Zhang J, Li X, Chen N, Gui J, Mei J (2018) Chromosomal-level assembly of yellow catfish genome using third-generation DNA sequencing and Hi-C analysis. *GigaScience* 7: 1-9.
- Guo J, Wang Y, Ma H, Yue Y (2006) Microsatellite marker analysis of genetic diversity and phylogenetic relationships in three populations of *Pseudobagrus fulvidraco*. *Amino Acids Biot Resour Sin* 28: 5-8.
- Hu GF, Liang HW, Li Z, Wang CZ, Wu QC, Liu XJ, Luo XZ, Zou GW (2009) Isolation and characterization of polymorphic microsatellite markers in the yellow catfish, *Pelteobagrus fulvidraco*. *Conserv Genet Resour* 1: 63.
- Meyer-Sand BR, Blanc-Jolivet C, Mader M, Paredes-Villanueva K, Tysklind N, Sebbenn AM, Guichoux E, Degen B (2018) Development of a set of SNP markers for population genetics studies of Ipe (*Handroanthus* sp.), a valuable tree genus from Latin America. *Conserv Genet Resour* 10: 779-781.
- Nelson JS, Grande TC, Wilson MV (2016) *Fishes of the World*. Hoboken: John Wiley & Sons Press.
- Rychlik W (2007) OLIGO 7 primer analysis software. *Methods Mol Biol* 402: 35–60.
- Yeh FC, Yang R, Boyle TB, Ye Z, Mao JX (1997) POPGENE, the user-friendly shareware for population genetic analysis. *Molecular Biology and Biotechnology Centre, University of Alberta, Canada* 10: 295-301.
- Yu JN, Kim SK, Sagong J, Ryu SH, Chae B (2019) Identification of microsatellite markers and their application in yellow catfish (*Pseudobagrus fulvidraco* Richardson, 1846) population genetics of Korea. *J Genet* 98: 2.
- Zhang X, Li Y, Gao Z, Wang W (2009) Isolation and characterization of polymorphic microsatellite loci from yellow catfish (*Pelteobagrus fulvidraco*). *Conserv Genet Resour* 1: 313-315.
- Zhou H, Duan G, Jiang H, Ling J, Hu Y, Zhang Y, Wang H, Pan T, Chen X (2021) High-density genetic map and QTL mapping for body color of the yellow catfish (*Tachysurus fulvidraco* × *T. vachelli*). *Anim Genet* 52: 246-248.