УДК 575.21

GENETIC DIVERSITY AND POPULATION STRUCTURE OF SHAOXING AND SHANMA DUCKS BREEDS BY MICROSATELLITE LOCI

S. KOSTENKO, Doctor of Biological Sciences, Professor, Department of Genetics, Breeding and Biotechnology animals[1]
O. KONOVAL, Candidate of Biological Sciences, Postdoctoral researcher[1]
A. CHEPIHA, Post-graduate student[1]*
P. KOROL, Post-graduate student[3]*
M. DOROSHENKO, Post-graduate student[1]*
LIZHI LU, Director of Poultry Lab, Professor[2]
XINGCHEN BU, Post-graduate student[2**]
LINGLING HUANG, Post-graduate student[2**]
XUETAO HUANG, Post-graduate student[2**]
LIUMENG LI, Master student[2]
[1] National University of Life and Environmental Sciences of Ukraine
[2] Institute of Animal Husbandry & Veterinary Science Zhejiang Academy of Agricultural Science
[3] Institute of Animal Breeding and Genetics nd. a. M. V. Zubets of National Academy of Agrarian Science of Ukraine
E-mail: lulizhibox@163.com, svitlankostenko@i.ua

Abstract. *In the present study the genetic structure of Shanma and Shaoxing duck populations. One hundred ninety blood samples of ducks in south of China, Zhejiang province were collected. The genomic DNA was isolated and characterized genetically using nineteenth microsatellite markers. Species-specific alleles identified in the studied populations for 9 loci in the Shaoxing breed and 8 loci in the Shanma breed can be used to mark individual lines for constructing cross-breeding schemes.The information index in the Shaoxing breed ranged from 0.034 (SMO12) to 2.381 (APL2), in the breed of Shanma - from 0.032 (APL83) to 2.076 (APL12).*

The maximum actual heterozygosity was at the APL12 locus (0.897 in the Shaoxing breed, 0.848 in the Shanma breed). The minimum actual heterozygosity was 0.010 (APL83) in Shanma breed and 0.011 (SMO12) in the Shaoxing breed.

The obtained results at the present study indicated that characterization of genetic diversity by employing molecular tools is a prerequisite in developing strategies for conservation and utilization of duck genetic resources.

Keywords. Anas platyrhynchos, domestic duck, breeds specificity, Shanma and Shaoxing duck populations.

---

* Scientific Supervisor - Doctor of Biological Sciences, Professor – Kostenko S. O.

** Scientific Supervisor - Director of Poultry Lab, Professor – Lizhi Lu.

Introduction. The development of DNA based markers has had a revolutionary impact on gene mapping and more generally on all of animal and plant genetics. During the last two decades, different classes of molecular markers have become available for evaluation of genetic diversity within and between different populations.

Microsatellite markers are now been widely used for the detection and description of micropopulation processes occurring in the populations of domestic animals for the effects of various factors of breeding pressure [11].

Molecular genetic maps will provide insight into the genome organization and chromosomal localization of cloned genes, and also provide a framework for the identification and location of major genes associated with economically important traits [5]. Microsatellites or Simple Sequence Repeats (SSR) consist of a variable number of tandem repetitions of short DNA molecules found in all prokaryotic and eukaryotic genomes [21]. Microsatellites have been extensively used in forensics, genetic mapping, population genetics, evolutionary studies, migration [20, 4, 17, 2, 12, 8, 16, 19, 14]

Microsatellite loci distributed throughout eukaryotic genomes, making them the preferred genetic marker for high resolution genetic mapping [13, 1,7].

In recent years, rapid advances have been made in the development of molecular genetic maps. High-density linkage maps are now available for many farm animals, such as cattle, pigs, and goats. In contrast, mapping studies in avian species are much less advanced except in the chicken.

Asia is considered as the homeland for ducks holding 90 percentes of the world duck population. According to FAO (Food and Agriculture Organization) data for the year 2000, there were about 45 breeds in China, and in Europe in the meantime, there are only 36 [23]. 27 dairy ducks (China Agriculture Press 2004), which are predominantly distributed along the Yangtze River and the southern regions of China. Many of these local varieties of ducks have valuable genetic features. The populations of poultry in Asia, is an interesting model for population analysis. Because

F – Fixation Index**.**

$$F = \frac{H_E - H_O}{H_E}$$

Values close to zero are expected under random mating, while substantial positive values indicate inbreeding or undetected null alleles. Negative values indicate excess of heterozygosity, due to negative assortative mating, or eterotic selection.

Results. Table 2 represents the observed allele numbers, size range and frequency in 19 microsatellite loci in Shanma (population 1) and Shaoxing (population 2) duck populations.

Polymorphisms are important components for discrimination of populations and individuals. Based on this information, are shown in table 2, the 19 loci identified 114 alleles (population 2) and 128 alleles (population 1). The number of different alleles (Na) for each polymorphic locus ranged from 2 (APL82, APL81, APL83, SMO12, SMO13) to 17 (APL2). On average, one locus had 6.737 alleles in populations 2 and 6,000 of alleles in the population

1. The effective number of alleles (Ne) was 2.747 in Shanma and 3.202 in Shaoxing population, respectively (Table 2).

1. Describes the primers of microsatellite loci

Loci	Primer sequence(5′ - 3′)	Repetitive sequence	Annealing temperature, °C
1	2	3	4
APL 2	S01-F CGCTCTTGGCAAATGTCC S01-R GATTCAACCTTAGCTATCAGTCTCC	$(CA)_{15}GA(CA)_{32}AAA(CAA)_4$	60
APL 11	S02-F TTGCATCAGGGTCTGTATTTTC S02-R AACTACAGGGCACCTTATTTCC	$(GA)_{25}$	60
APL 12	S03-F AAGAGACACTGAGAAGTGCTATTG S03-R AGTTGACCCTAATGTCAGCATC	$(GA)_{27}$	60
APL 23	S04-F GCTGAGATGCTCCCAGGAC S04-R GAAGAGGCAGTGGCAACG	$(TG)_{13}(TC)_{)3}(TG)_2TCCG(TG)_3TCTN(TG)_7CG(TG)_2(TC_{)3}(TG_{)2}(TC)_3TG$	60
APL 26	S05-F TGAGCAGCTGTCTGGTATCTATTC S05-R AACAGGGATAACATGAGAAGTGG	$(CA)_{11}(GA)_9$	55
APL 36	S06-F TCCACTGGGTGCAAACAAG S06-R ATGCTTTGCTGTTGGAGAGC	$(CA)_{13}GA(CA)_3(GA)_2(CA)_2GA(CA)_{10}GA(CA)_7GA(CA)_2TA(CA)_5$	60
APL 83	S07-F CTGCTTGGTTTTGGAAAGT S07-R GAATAAAGTAACGGGCTTCTCT	$A_5GA_3T(CA)_7A(CA)_6$	55
APL 82	S08-F GCAGGCAGAGCAGGAAATA S08-R GGACCTCAGGAAAATCAGTGTA	$(CA)_9$	55
APL 81	S09-F GCAAGAAGTGGCTTTTTTC S09-R S09-F GCAAGAAGTGGCTTTTTTC	$(AC)_{12}$	55
APL 80	S10-F TTGCCTTGTTTATGAGCCATTA S10-R GGATGTTGCCCCACATATTT	$(AT)_4(GT)_{11}$	58

Continuation of Table 1

1	2	3	4
APL 79	S11-F CATCCACTAGAACACAGACATT S11-R ACATCTTTGGCATTTTGAA	$(TTCC)_{18}$	55
APL 78	S12-F GAACACAACTGCTTTGCTA S12-R AACCAAGACAGAATAATCCTTA	$(GT)_9(AT)_5$	55
APL 77	S13-F GTATGACAGCAGACACGGTAA S13-R TCACTTGCTCTTCACTTTCTTT	$(GT)_{10}$	55
CMO 11	S14-F CATCTTTGGCATTTTGAAG S14-R CTCCACTAGAACACAGACATT	$(GGAA)_{13}(GGGA)_{15}$	45
SMO 7	S15-F GATTCAAATTTGCCGCAGGATTA S15-R TTTTCACCCAGTTCACTTCAGCC	$(GT)_{12}$	55
SMO 10	S16-F CATTGTTCATTGTTTCTTCTTCA S16-R TCCTAGCGACAGCAATTCTAATG	$(TG)_{31}$	55
SMO 11	S17-F GCAGTTGTTTTGGAGGACAGACA S17-R AAATCAACCAAAGAGGCATAGCC	$(TG)_{12}GA(G)_{13}(AG)_5$	68
SMO 12	S18-F TGTTCATCAAAAGCAGAGAGGGG S18-R CCTGGTGGGATAGGTTTAAAATG	$(TG)_9T_{11}$	47
SMO 13	S19-F GGGCTTGAGGCATACACTCCCTA S19-R ACCATCTTCCTTTCCTCCCAACC	$(TG)_{13}(AC)_2(TG)_2$	58

Population 1 had polymorphic 94,74 % of loci, while population 2 - 89,47 % of the loci. A total of 19 loci examined in the species population Shanma, only one locus was monomorphism (SMO10), in a population of Shaoxing such monomorphic loci had two (SMO10, APL83). According to the results of 19 studies of the loci in population 1, there was only one locus of the monomorphism (SMO10), and population 2, two of these loci (SMO10, APL83).

The number of alleles and the expected heterozygosity (He) values can provide important information for the discrimination of individuals and breeds. The index of expected heterozygosity ranged from 0,011 (SMO12) to 0,892 (APL2) (population 2), and from 0.010 (APL83) to 0,824 (APL12) (population 2). The Wright's fixation index indicates a slight excess of heterozygotes at 7

loci in the population Shanma (APL11, APL12, APL13, APL83, APL82, APL80, SMO11, SMO13), and 5 loci in the population Shaoxing (APL11, APL12, APL13, APL82, SMO12).

2. The observed allele numbers, size range and frequency in 19 microsatellite loci in Shanma (population 1) and Shaoxing (population 2) duck populations

	Locus	Pop	Na	Ne	I	Ho	He	uHe	PIC	F
1	APL2	1	12	3,747	1,759	0,657	0,733	0,737	0,711	0,104
		2	16	9,120	2,359	0,846	0,890	0,895	0,880	0,050
2	APL11	1	8	3,375	1,395	0,737	0,704	0,707	0,660	-0,048
		2	5	3,737	1,432	0,791	0,732	0,736	0,688	-0,080
3	APL12	1	10	6,213	2,021	0,828	0,839	0,843	0,822	0,013
		2	16	6,365	2,134	0,879	0,843	0,848	0,825	-0,043
4	APL23	1	11	4,142	1,653	0,798	0,759	0,762	0,720	-0,052
		2	12	4,774	1,856	0,846	0,791	0,795	0,762	-0,070
5	APL26	1	4	3,757	1,350	0,465	0,734	0,738	0,684	0,367
		2	4	2,448	1,071	0,505	0,591	0,595	0,530	0,145
6	APL36	1	6	3,405	1,409	0,667	0,706	0,710	0,658	0,056
		2	8	4,360	1,718	0,736	0,771	0,775	0,744	0,045
7	APL83	1	2	1,010	0,032	0,010	0,010	0,010	0,010	-0,005
		2	1	1,000	-	-	-	-	-	-
8	APL82	1	2	1,246	0,349	0,202	0,198	0,199	0,178	-0,023
		2	2	1,092	0,180	0,088	0,084	0,085	0,081	-0,046
9	APL81	1	2	1,766	0,625	0,394	0,434	0,436	0,340	0,092
		2	2	1,565	0,547	0,341	0,361	0,363	0,296	0,056
10	APL80	1	9	4,865	1,713	0,818	0,794	0,798	0,765	-0,030
		2	8	4,085	1,614	0,703	0,755	0,759	0,721	0,069
11	APL79	1	8	2,105	1,177	0,394	0,525	0,528	0,503	0,250
		2	9	1,902	1,036	0,418	0,474	0,477	0,443	0,120
12	APL78	1	3	1,031	0,088	0,030	0,030	0,030	0,030	-0,012
		2	3	1,183	0,342	0,165	0,155	0,155	0,149	-0,066
13	APL77	1	4	2,616	1,043	0,596	0,618	0,621	0,544	0,035
		2	4	2,894	1,179	0,516	0,654	0,658	0,589	0,211
14	CMO11	1	9	2,281	1,271	0,455	0,562	0,564	0,539	0,191
		2	9	1,908	1,046	0,429	0,476	0,478	0,446	0,099
15	SMO7	1	5	2,048	0,944	0,576	0,512	0,514	0,448	-0,125
		2	4	1,901	0,831	0,429	0,474	0,476	0,410	0,096
16	SMO10	1	1	1,000	-	-	-	-	-	-
		2	1	1,000	-	-	-	-	-	-
17	SMO11	1	5	2,547	1,152	0,626	0,607	0,611	0,547	-0,031
		2	8	2,602	1,278	0,560	0,616	0,619	0,573	0,090
18	SMO12	1	2	1,198	0,305	0,141	0,165	0,166	0,152	0,144
		2	2	1,011	0,034	0,011	0,011	0,011	0,011	-0,006
19	SMO13	1	3	1,176	0,311	0,020	0,150	0,151	0,141	0,865
		2	3	1,080	0,179	0,077	0,074	0,075	0,072	-0,035

In our study the effective number of alleles (Na) ranged 6,000 in Shanma and 6,737 for the Shaoxing duck population (Table 2), which corresponds to the Hui-Fang L. study.. The average heterozygosity for the two breeds was 0.442.

Analysis of the allele frequencies of two populations for APL2 locus in animals of the two breeds identified 19 different alleles. Polymorphism in the population 1 due to of 11 different alleles, which occur with a frequency of from 0.010 0.485, and population 2 had 16 alleles of this locus with a frequency of from 0.005 to 0.154. Half of the population 1 carried the allele 119 distribution of frequencies it was characterized by asymmetry. In the population 1, alleles from 117 to 253, was represented with a frequency of 0.010 to 0.485. In population 2 were more uniform distribution of frequencies of different alleles (from 0.05 to 0,154) with a wide range (from 119 to 273). Alleles from 255 to 273 were characteristic only for the Shaoxing population. In the Shanma population also we did not find allele 243. The alleles of Shanma population were shorter, the distribution of their frequencies shifted to the left compared with the Shaoxing population. According to the obtained results the allele 243 and alleles from 255 to 273 can be considered as characteristic only for the population 2.

Hui-Fang L. et all, 2010 [9] found only 7 different alleles of this locus in 10 egg ducks in China. The locus APL11 has 8 alleles from 90 to 124. In population 1 all of these alleles had a frequency of from 0.005 to 0,449. Shaoxing's population had only 5 alleles APL11. According to the results of allele 122 was found with maximum frequency in Sanma (0,449) and Saoxing (0,368) duck populations. It is possible to assume that this locus is being attracted to performance selection.

The Locus APL11 is represented by 8 alleles from 90 to 124. In the Shanma population, all these alleles with frequencies from 0,005 to 0,44. Because populations are not linked their distribution not implies a founder effect. The locus APL12 belongs to one of the most polymorphic among the locuses we studied. It is represented by 18 different alleles. For the Shanma population, 12 alleles of this locus were characterized with a frequency of 0,005 to 0,293 and for the Shaoxing population it was founded 17 alleles with a frequency from 0.05 to 0.225. According to the obtained results the allele 156 was found in the both populations. The Shaoxing breed was more polymorphic in this allele.

The locus APL23 (S4) is represented by 15 alleles. In the population 1 were 11 alleles with frequency from 0.005 to 0.303. The population 2 had 12 alleles with a frequency of 0,005 to 0,324. In the two populations, the most frequent were three alleles: 144 (with a frequency of 0.303 in the Shanma and 0.225 in the Shaoxing populations), 198 (0.293 and 0.324) and 254 (0.242 and 0.214). Some alleles was characteristic only for the Shanma population (227, 252, 273) and other (148, 158, 188, 229) were found only in the Shaoxing population.

The locus APL26 (S5) is represented by 7 alleles that were encountered in both populations of investigated breeds. In the population 1 the frequency of

alleles was 0.020-0.303 and the population 2 was characterized by frequencies of 0.027-0.291. 7 alleles were detected at APL 26 of the MIAO Zhog-wei (effective number of alleles - 3,0452, RIS - 0,6239) [25].

The locus APL36 (S6) is represented by 9 alleles. In the Shanma population there were 7 alleles of this locus with a frequency from 0.015 to 0.333. The Shaoxing population had 9 alleles with a frequency from 0.022 to 0.308. Thus, the APL36 locus of the Shaoxing population turned out to be more polymorphic, only 157 (0.022) and 198 (0.022) alleles were found in it. The most frequent alleles were 175 (0.318 and 0.308) and 193 (0.333 and 0.165) alleles. The locus APL83 (S7) had only 2 alleles. The Shanma population has allele 154 with a frequency of 0.995, and an allele of 155 - 0.005. The Shaoxing population was monomorphic to allele 154. The locus APL82 (8) was represented by only two alleles, among which the allele 184 with a frequency of 0.889 (Shanma population) and 0.956 in the Shaoxing population. The animals studied by this locus differed from the results of the MIAO Zhog-wei research into four breeds of egg ducks, including Shanma breeds, which were characterized by 4 different alleles (effective number of alleles - 2.5159, RIS - 0.5202) [25]. The locus APL81 (9) had two alleles, among which the allele 136 was dominated by population 1(0.682) and population 2 (0.764).

The locus APL80 (10) presented with 10 alleles in Shanma and 8 alleles in the Shaoxing duck populations. Among these alleles, allele 120 had the highest frequency as a Shanma population (0.313) and in the Shaoxing population (0.379).

The effective number of alleles in two populations (4.964 and 4.085) was consistent with those of MIAO Zhog-wei with co-authors who found in four breeds of egg ducks, including Shanma breeds at the APL 80 locus identified 9 alleles (effective number of alleles - 4, 8827,Polymorphism Information Content Index (RIS) - 0.77701 [23]. The locus APL79 (11) is represented by 11 different alleles, among which the allele 227 (0.672 in the Shanma and 0.703 in the Shaoxing duck populations) are most commonly encountered. For the Shanma population 8 alleles were characteristic and 9 alleles for the Shaoxing population. The genus Shaoxing was more polymorphic in the locus of APL79, and there were alleles 219, 223, 258, which were not found in the Shanma population. In the Shanma population 262 and 266 alleles were present, which were not in the Shaoxing population. The polymorphism of locus APL79 can be used to determine the origin of ducks from these groups.

The locus APL78 (12) had 5 alleles, among which the allele 213 was found most often (with a frequency of 0.904 in the Shanma and 0.571 in the Shaoxing populations). The ducks of the population 2 have allele (210), which is not in the population 2. The Locus APL77 13 had 4 alleles, among which the Shanma population more often met alleles 196 (0.496) and 194 (0.328). The same alleles had a high frequency in the Shaoxing population (allele 194 - 0.412, allele 196 - 0.396). Breed-specific alleles for this locus were not detected in the studied groups.

The locus CMO11 (14) is represented by 13 alleles, of which the allele 228 was most common (0.631 in the Shanma and 0.698 in the Shaoxing duck populations). Breed-specific alleles 227, 264, 267 have been identified for the Shama population, which were not presented in the Shaoxing population. In the Shaoxing population the alleys of 220, 229 and 260 were specific for the breed.

The locus SMO7 (15) is represented by 6 alleles from 182 to 190. In the second population, the most frequent. Tables 3 and 4 describe the results of the analysis of private alleles and individual microsatellite loci.

3. Summary of Private Alleles by Population

Shanma *n* = 99								
APL2	116 (0,010)	118 (0,015)	132 (0,010)	143 (0,010)	-	-	-	-
APL11	90 (0,005)	104 (0,005)	118 (0,005)	-	-	-	-	-
APL12	146 (0,025)	-	-	-	-	-	-	-
APL23	226 (0,005)	252 (0,010)	272 (0,005)	-	-	-	-	-
APL83	156 (0,005)	-	-	-	-	-	-	-
APL80	98 (0,005)	-	-	-	-	-	-	-
APL79	262 (0,020)	265 (0,061)	-	-	-	-	-	-
CMO11	264 (0,020)	268 (0,066)	-	-	-	-	-	-
SMO7	188 (0,025)	-	-	-	-	-	-	-
Shaoxing *n* = 91								
APL2	243 (0,016)	255 (0,104)	257 (0,005)	259 (0,066)	261 (0,022)	263 0,011)	265 (0,005)	273 (0,005)
APL12	120 (0,011)	124 (0,005)	134 (0,016)	140 (0,005)	144 (0,011)	164 (0,027)	166 (0,022)	-
APL23	148 (0,038)	158 (0,033)	188 (0,016)	230 (0,005)	-	-	-	-
APL36	158 (0,022)	198 (0,022)	-	-	-	-	-	-
APL79	219 (0,005)	223 (0,016)	258 (0,022)	-	-	-	-	-
CMO11	220 (0,005)	260 (0,027)	-	-	-	-	-	-
SMO11	182 (0,033)	204 (0,005)	208 (0,022)	-	-	-	-	-

4. The Genetic Polymorphism of 19 SSR Loci

Locus	Size range (bp)	Na	Ne	I	Ho	He	uHe	PIC	F
APL2	117-273	20	6,996	2,259	0,747	0,857	0,859	0,844	0,128
APL11	90-124	8	3,667	1,459	0,763	0,727	0,729	0,686	-0,049
APL12	120-167	17	6,638	2,161	0,853	0,849	0,852	0,833	-0,004
APL23	144-275	15	4,484	1,803	0,821	0,777	0,779	0,744	-0,057
APL26	147-158	4	3,302	1,276	0,484	0,697	0,699	0,643	0,305
APL36	157-210	8	3,958	1,607	0,700	0,747	0,749	0,713	0,063
APL83	154-155	2	1,005	0,018	0,005	0,005	0,005	0,005	-0,003
APL82	184-186	2	1,170	0,276	0,147	0,145	0,146	0,135	-0,013
APL81	136-138	2	1,673	0,592	0,368	0,402	0,403	0,321	0,084
APL80	97-124	9	4,826	1,753	0,763	0,793	0,795	0,766	0,037
APL79	219-277	11	2,022	1,185	0,405	0,505	0,507	0,484	0,198
APL78	210-218	3	1,101	0,223	0,095	0,091	0,092	0,089	-0,037
APL77	190-197	4	2,790	1,135	0,558	0,642	0,643	0,572	0,130
CMO11	220-279	11	2,110	1,241	0,442	0,526	0,527	0,504	0,160
SMO7	182-190	5	1,977	0,901	0,505	0,494	0,496	0,431	-0,022
SMO10	96	1	1,000	-	-	-	-	-	-
SMO11	178-207	8	2,600	1,259	0,595	0,615	0,617	0,566	0,033
SMO12	70-72	2	1,105	0,199	0,079	0,095	0,095	0,090	0,169
SMO13	199-201	3	1,130	0,268	0,047	0,115	0,116	0,112	0,589
Mean	-	7,105	2,819	1,032	0,441	0,478	0,479	0,449	0,095
SE	-	1,282	0,427	0,166	0,069	0,070	0,071	0,70	0,036

Discussion. An analysis of the distribution of microsatellites by 19 loci in two populations of shaman and Shaoxing breeds indicates a high level of their polymorphism and a lack of close inbreeding. Species-specific alleles identified in the studied populations for 9 loci in the Shaoxing breed and 8 loci in the Shanma breed can be used to mark individual lines for constructing cross-breeding schemes.

The number of different alleles for each polymorphic locus ranged from 2 (APL82, APL81, APL83, SMO12, SMO13) to 18 (APL2). A total of 19 loci identified 114 alleles in the Shaoxing breed and 128 in the Shanma breed. In the middle of the population of the Shaoxing breed, 6 alleles accounted for one locus, and in the breed of Shanma - 6.74 alleles. The effective number of alleles (Ne) was 2.747 in the Chanma breed and 3.202 in the Shaoxing breed.

Polymorphous were 94.74% of loci in the Shanma population and 89.47% in the Shaoxing population. In total of 19 investigated loci in the Shanma breed population, only one locus was monomorphic (SMO10), in the population of Shaoxins of such monomorphic loci there were two (SMO10, APL83).

The information index in the Shaoxing breed ranged from 0.034 (SMO12) to 2.381 (APL2), in the breed of Shanma - from 0.032 (APL83) to 2.076 (APL12).

The maximum actual heterozygosity was at the APL12 locus (0.897 in the Shaoxing breed, 0.848 in the Shanma breed). The minimum actual

heterozygosity was 0.010 (APL83) in Shanma breed and 0.011 (SMO12) in the Shaoxing breed.

In the Shaoxian breed, the expected heterozygosity was in the range from 0.011 (SMO12) to 0.892 (APL2), in the breed of Shanma - from 0.010 (APL83) to 0.824 (APL12)

These results will provide useful information for genetic diversity studies in ducks and for the development of duck traceability systems in the market.

Reference

1. Abdelkrim, J., Robertson, B., Stanton, J.A., Gemmell, N. (2009). Fast, cost-effective development of species-specific microsatellite markers by genomic sequencing. Biotechniques, 46 (3), 185-191.

2. Abe, H., Gemmell, N. J. (2016). Evolutionary Footprints of Short Tandem Repeats in Avian Promoters. Sci Rep, 14 (6), 1-11.

3. China national commission of animal genetic resources. (2011). Animal genetic resources in china: Poultry. Beijing: China Agriculture Press, 404-406.

4. Choi, N. R., Seo D. W., Jemaa, S. B., Sultana, H., Heo, K. N., Jo, C., Lee, J. H.(2015). Discrimination of the commercial Korean native chicken population using microsatellite markers. Journal of Animal Science and Technology, 57 (5), 1-8.

5. Crittenden, L. B., Provencher, L., Levin, I., Abplanalp, H., Briles, R. W., Dodgson, J.B. (1993). Characterization of a Red Jungle Fowl by White Leghorn backcross reference population for molecular mapping of the chicken genome. Poultry Sci, 72, 334–348.

6. Denk, A. G., Gautschi, B., Carter, K., Kempenaers, B. (2004). Seven polymorphic microsatellite loci for paternity assessment in the mallard (Anas platyrhynchos). Molecular Ecology Notes, 4, 506–508.

7. Huang, Y., Haley, C.S., Wu, F., Hu, S., Hao, J., Wu, C., Li, N. (2007). Genetic mapping of quantitative trait loci affecting carcass and meat quality traits in Beijing ducks (Anas platyrhynchos). Anim Genet, 38 (2), 114-119.

8. Hui-Fang, L., Wei-Tao, S., Jing-Ting, S., Kuan-Wei, C., Wen-Qi, Z., Wei, H., Wen-Juan, X. (2010). Genetic diversity and population structure of 10 Chinese indigenous egg-type duck breeds assessed by microsatellite polymorphism. J. Genet, 89 (1), 65-72.

9. Hui-Fang, L., Wei-Tao, S., Jing-Ting, S., Kuan-Wei, C., Wen-Qi, Z., Wei, H., Wen-Juan, X. (2010). Genetic diversity and population structure of 10 Chinese indigenous egg-type duck breeds assessed by microsatellite polymorphism. J. Genet, 89, 65–72.

10. Kalinowski, S.T., Taper, M.L., Marshall, TC (2007) Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. Molecular Ecology, 16, 1099-1106.

11. Karabag, K., Balcıoglu, M. S., Karli T., Alkan S. (2016). Determination of genetic diversity using 15 simple sequence repeats markers in long term selected japanese quail lines. Asian-Australas J Anim Sci., 29 (12), 1696-1701.

12. Liu, Y., Keller, I., Heckel, G. (2012). Breeding site fidelity and winter admixture in a long-distance migrant, the tufted duck (Aythya fuligula). Heredity (Edinb), 109 (2), 108-116.

13. Mucha, S., Grajewski, B., Gornowicz, E., Lisowski, M., Radziszewska, J., Szwaczkowski, T. (2014). Mapping quantitative trait loci affecting some carcass and meat traits in duck (Anas platyrhynchos). J Appl Genet, 55 (4), 497-503.

14. Munoz-Fuentes, V., Green, A. J., Sorenson, M. D., Negro, J. J., Vila, C. (2006). The ruddy duck Oxyura jamaicensis in Europe: natural colonization or human introduction. Mol Ecol, 15 (6), 1441-1453.

15. Peakall, R., Smouse P. E. (2012) GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research – an update. Bioinformatics, 28, 2537-2539.

16. Qu, L., Liu, W., Yang, F., Hou, Z., Zheng, J., Xu, G., Yang, N. (2009). Origin and domestication history of Peking ducks deltermined through microsatellite and mitochondrial marker analysis. Science in China .Life Sciences, 52 (11), 1030-1037.

17. Sartore, S., Sacchi, P., Soglia, D., Maione, S., Schiavone, A., De Marco, M.1., Ceccobelli, S., Lasagna, E., Rasero, R. (2016). Genetic variability of two Italian indigenous chicken breeds inferred from microsatellite markeranalysis. Br Poult Sci, 57 (4), 435-443.

18. Shaoxing Ducks. (2012). Zhuji Quality and Technique Supervision Bureau: DB 33068/T 02.1-2012.-Zhuji (National Standard of China), 40.

19. Su, Y., Long, R., Chen, G., Wu, X., Xie, K., Wan, J. (2007). Genetic analysis of six endangered local duck populations in China based on microsatellitemarkers. J Genet Genomics, 34 (11), 1010-1018.

20. Tan, B, Zhao, Z, Zhang, Z, Li, S, Li, S.C. (2017). Search for more effective microsatellite markers for forensics with next-generation sequencing. Nanobioscience, 16 (5), 375-381.

21. Tautz, D. (1989). Hypervariability of simple sequences as a general source for polymorphic DNA markers. Nucleic Acids, 17 (17), 6463-6471.

22. Wu, F, Huang, Y, Ma, Y. (2009). Evaluation of genetic diversity and relationships within and between two breeds of duck based on microsatellite markers. Progress in Natural Science, 19 (11), 1581-1586.

23. Wucheng, B. (1988). The research on the origin of the house-duck in China. In The Satellite Conference for the18th World's Poultry Congress, 125-129.

24. Yinhua, H., Jianfeng, T., Xuebo, C. (2005). Characterization of 35 novel microsatellite DNA markers from the duck (Anas platyrhynchos) genome and cross-amplification in other birds. Genetics Selection Evolution, 37, 455- 472.

25. Zhong- wei, M., Sheng- lin, L.I., Xiao-ning, D., Hui, C., Nen-zhu, Z., Zhi-ming, Z., Hui-fang, L.I., Wei-tao, S. (2007). Genetic make -up of egg-laying duck breeds in Fujian determined by using microsatellite markers. 福建农业学报, 22 (4), 368-371.

ГЕНЕТИЧНЕ РІЗНОМАНІТТЯ ТА ПОПУЛЯЦІЙНА СТРУКТУРА ПОРІД КАЧОК ШАОСІНЬ ТА ШАНМА ЗА МІКРОСАТЕЛІТНИМИ ЛОКУСАМИ

С. Костенко, О. Коновал, А. Чепіга, П. Король, М. Дорошенко, Л. Лу, С. Бу, Л. Хуанг, Ц.Хуанг, Л. Лі

Анотація. *Проаналізована генетична структура популяцій качок Шанма та Шаосінь за використання дев'ятнадцяти мікросателітних локусів. Із крові качок на півдні Китаю, провінції Чжецзян було виділено та проаналізовано сто дев'яносто зразків геномної ДНК. Виявлені породоспецифічні алелі для 9 локусів у досліджуваних популяціях породи*

Шаосінь та 8 локусів породи Шанма можна використовувати для ідентифікації окремих ліній.

Інформаційний індекс у породі Шаосінь коливався від 0,034 (SMO12) до 2,381 (APL2), у породі Шанма - від 0,032 (APL83) до 2,076 (APL12). Максимальна фактична гетерозиготність була в локусі APL12 (0,897 у породі Шаосінь, 0,848 у породі Шанма). Мінімальна фактична гетерозиготність становила 0.010 (APL83) у породі Шанма та 0.011 (SMO12) у породі Шаосінь.

Отримані результати в даному дослідженні показали, що характеристика генетичного різноманітня за використання молекулярних інструментів є необхідною умовою розробки стратегій збереження та використання генетичних ресурсів качки.

Ключові слова. Anas platyrhynchos, качка свійська, породоспецифічність, Shanma, Shaoxing

ГЕНЕТИЧЕСКОЕ РАЗНООБРАЗИЕ И СТРУКТУРА ПОПУЛЯЦИЙ ПОРОД УТОК ШАОСИНЬ И ШАНМА ПО МИКРОСАТЕЛИТНЫМ ЛОКУСАМ

С. Костенко, О. Коновал, А. Чепига, П. Король, М. Дорошенко, Л. Лу, С. Бу, Л. Хуанг, Ц. Хуанг, Л. Ли

***Аннотация**. Использование девятнадцати микросателлитных локусов позволило проанализировать генетическую структуру популяций уток Шанма и Шаосинь. Из крови уток на юге Китая, провинции Чжэцзян было выделено и проанализировано сто девяносто образцов геномной ДНК. Выявленные породоспецифичные аллели для 9 локусов в исследуемых популяциях породы Шаосинь и 8 локусов породы Шанма можно использовать для идентификации отдельных линий при построении схем скрещивания.*

Выявлен информационный индекс породы Шаосинь предела от 0,034 (SMO12) до 2,381 (APL2), породы Шанма - от 0,032 (APL83) до 2,076 (APL12). Максимальная фактическая гетерозиготность была в локусе APL12 (0,897 у породы Шаосинь, 0,848 у породы Шанма). Минимальная фактическая гетерозиготность составила 0.010 (APL83) у породы Шанма и 0.011 (SMO12) у породы Шаосинь.

Полученные результаты в данном исследовании показали, что характеристика генетического разнообразия при использовании молекулярных инструментов является необходимым условием разработки стратегий сохранения и использования генетических ресурсов утки.

Ключевые слова. Anas platyrhynchos, утка домашняя, породоспецифичность, Shanma, Shaoxing