Polymorphism analysis of 3 quail groups by using microsatellite marker

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Abstract: This study was using 12 microsatellite markers do the polymorphism analysis of 3 quail groups, which is on the purpose of offering scientific evidence for the comment, protection and utilization of our country's quail genetic resources. The result of this study show: the observation of the number of alleles which was checked by the 12 microsatellite markers is between 4 and 7. The average polymorphism information content 12 microsatellite marked at Chinese yellow quail, Chinese black quail, Korean quail are respectively: 0.6853,0.6401,0.6565; the average heterozygosity are respectively: 0.7333,0.6957,0.7111. From the data, we learn that genetic polymorphism of Chinese yellow quail is most abundant. Cluster analysis show, the minimum genetic distance of Chinese black quail and Korean quail is 0,0628, and it also show the genetic relationship between Chinese black quail and Korean quail is closest. Next, the genetic distance between Chinese yellow quail and Korean quail is 0.0951, so it shows Chinese black quail and Korean quail get together first, later get together with Chinese yellow quail.
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Introduction

Microsatellite marker is a good genetic marker applied to study the genetic variance within the breed or among the breed, it has some character in the genome, such as: large quantities, wide and well distributed, abundant polymorphism, and the character of simple and convenience, fast about dominant inheritance and analysis method. Therefore, it is a molecular marker which is the widely used for evaluating livestock and poultry genetic resources so far. Microsatellite marker is mainly used in the following aspect for quail genetic breeding: 1. the structure of quail genetic map: in 2004, Kayang *et al*., on the basic of finding 100 microsatellite markers in the quail's genome, they established the first generation of microsatellite markers linkage map which contains 72 microsatellite markers. 2. fix position of quail functional gene and QTL: in 2005, Miwa *et al*., put the three blood protein site Tf, Hb-1 and Pa-1 respectively fix on the chromosome QL08, CJA14, QL13 by using three microsatellite primers GUJ0071, GUJ0097 and GUJ0061. 3. The analysis of quail genetic diversity: both here and abroad using microsatellite marker do the polymorphism analysis for the wild quail and domestic quail, which accumulate amount of data for evaluating quail genetic resources, analyzing population genetic variation and evolutionary relationship and it plays an positive role in the analysis (Wang *et al*.,2004; Chang *et al*., 2007; Olowofeso *et al*., 2006; Amirinia, 2007).

Quail is an age-old bird, it is also called Japanese quail, and it mainly has the wild quail and domestic quail the two kinds. While the wild quail is mainly be divided into wild common quail and wild Japanese quail. Although our country did not feed quail for a long time, in 1970s, the quail was grown rapidly not only increased in quantity, but also increased the varieties of quail. In our country, we have the two kinds of wild quail, the number of the wild Japanese quail more than the other wild quail（Chang *et al*., 2005）. Korean quail is an age-type cultivating breed which was cultivated by Japanese quail by Korean. According to the growing district, it can be divided into Longcheng quail and Huangcheng quail. After the Korean Longcheng quail was introduced to China, we cultivated Chinese yellow quail and Chinese wheat quail one after another. Chinese yellow quail is recessive quail which was successfully cultivated by a young teacher Yue Genhua from Nanjing Agricultural University（Yue *et al*., 1994）. Chinese black quail is a feather color's mutation new discovered by the research man of this subject (Pang 2009). It is the hybrid between Chinese yellow male quail and Korean female quail, the verification of hybridization was to be confirmed that the mutation of feather color is coursed by euchromosome incompletely occurring recessive mutation（Yu *et al*., 2009）.

Due to there is a little research report about Chinese black quail, and in order to discuss the evolution extent of Korean quail, Chinese yellow quail and Chinese black quail, as well as providing scientific

evidence for the comment, protection and utilization of our country's quail genetic resources, this study was using 12 microsatellite markers do the polymorphism analysis of 3 quail groups (Korean quail, Chinese yellow quail and Chinese black quail)

Materials And Methods

Sample collection: The quails to test came from the test farm of Henan University of Science and Technology. 100 Chinese black quail mutants were randomly selected, 75 Chinese yellow quails and 75 Korean quails. There were a total of 250 quails. In Chinese black quails half are male and half female, in Chinese yellow quails and Korean quails, there were 40 males and 35 females. 2ml of heart blood was taken and ACD anticoagulant was used. Blood: ACD is 6:1. The blood sample was stored in refrigerator at -20℃. Genomic DNA was extracted with the blood tissue genomic DNA extraction kit (Tiangen, Beijing, China).

The selection and synthesis of primers:12 microsatellite primers were synthesized by Shanghai Sangon Biological Engineering Technology Co., primer sequences are shown in Table 1.

PCR reaction condition: The total size of the PCR reaction system was 12.5μL, including 8.65μL of ddH_2O, 1.25μL of 10×buffer, 0.75μL of Mg^{2+}(25 mmol/L), 0.5μL of DNA template, 0.5μL (10 mmol/L) of upstream and downstream primers, 0.25μL of dNTPs, and 0.1μL of Taq enzyme. The PCR amplification process was as follows: denaturation for 3 min at 95°C; denaturation for 45 s at 94°C, annealing for 60s at X°C, extension for 60s at 72°C, and 30 cycles, extension for 12 min at 72°C and preserving at 4°C. The annealing temperature is shown in Table 1.

Table 1. Relational information for microsatellite locus

Locus name	Primer sequence (5'→ 3')	T_A (℃)
UBC0004	F:TCCTTGGGCAGTAGTTTCAA R:CTCCCATGTTGCTTCTTTAG	49
UBC0005	F:GGAACATGTAGACAAAAGC R:AGTAGTCCATTTCCACAGCCA	55
UBC0006	F:TTTCTATCCTTCATCTCCAG R:AGACATCCTGCTTTCTCGTG	46
GUJ0001	F:GAAGCGAAAGCCGAGCCA R:CAGCACTTCGGAGCACAGGA	55
GUJ0013	F:ACCAAACCCGAGATCCGACA R:AGCGTTCGCGTTCCTCTTTC	54
GUJ0034	F:CGTAACGGTCCAATATGGAT R:TCCACGATGCAGAGGTATTT	55
GUJ0049	F:GAAGCAGTGACAGCAGAATG R:CGGTAGCATTTCTGACTCCA	55
GUJ0054	F:GTGTTCTCTCACTCCCCAAT R:ATGTGAGCAATTGGGACTG	56
GUJ0055	F:GCATACTGCAATATACCTGA; R:TTGACATACTTGGATTAGAGA	56
GUJ0070	F:AAACCCCAAAGAAGCTGTCC R:ACGTTGTCACCATCAGCTTG	54
GUJ0071	F:AGATCCTGCTCCTGGAATTG R:CAGCTGCACTTAATACAGGC	58
GUJ0086	F:AGCTGCCATATCTACTGCTC R:TGGCTTAGTGCTTTCAGAGG	55

Polyacrylamide gel electrophoresis: A 1% agarose gel prepared using a 1.0×TBE electrophoresis buffer was used to test the existence of PCR amplification products. Approximately 3μL of the PCR amplification products and the isometric loading buffer were mixed for sample application and electrophoresis. DNA marker I was used as the control sample to observe the availability of the needed bands on the UV transmittance analyzer. If the specific bands are bright and if the hybrids are insignificant, they can be tested using 8% non-denaturing acrylamide gel electrophoresis at 120V for about 2h. The bands were then stained by silver nitrate and photographed using optical coherence tomography for reservation and analysis. The allele size was detected to identify the individual genotype of each microsatellite marker based on the standard of the pBR322DNA/Msp I marker.

Statistical analysis: The molecular biology software POPGENE (Version1.32) was used to analyze polymorphism information content (PIC), effective number of alleles (Ne), and miscellaneous

heterozygosity (H) of each marker.

$$H = 1 - \sum_{i=1}^{n} p_i^2$$

Heterozygosity:

Where p_i was the frequency of ith allele of a microsatellite DNA.

Effective number of allele: Effective number of allele (Ne) is the reciprocal of genetic homozygosity, which reflects the mutual influence among alleles, so it is used to detect population genetic variation.

$$N_e = 1 / \sum_{i=1}^{n} p_i^2$$

Where p_i was the frequency of ith and jth allele of a microsatellite DNA

Polymorphic information content: Polymorphic information content (PIC) is employed to assess whether the effective information of some locus is suitable for the linkage analysis probability and reflects the degree of genetic polymorphism of microsatellite locus.

$$PIC = 1 - (\sum_{i=1}^{n} p_i^2) - (\sum_{i=1}^{n-1} \sum_{j=i+1}^{n} 2p_i^2 p_j^2)$$

Where p_i and p_j were the frequency of ith allele of a microsatellite DNA, and n is allele number.

Genetic differentiation coefficient: Genetic differentiation coefficient is an indicator evaluating the genetic differentiation in many loci among populations and the function of whole population's average heterozygosity (H_t) and average sub-population heterozygosity (H_s).

$G_{st}=1-H_s/H_t$

Where H_t is total population average heterozygosity, H_s is average heterozygosity of different quail populations, and G_{st} is coefficient of gene differentiation.

Cluster analysis: Cluster is based on Nei's genetic distance (1978): method = cluster.

Results

The allele frequency of 12 microsatellite markered at the 3 quail groups see table 2. From the table 2, we learn that observed the range of the numbers of allele is 4 to 7, and in total we checked the number of observed allele is 197 from the 12 microsatellite markered at the 3 quail groups. Among them, the maximum number of observed allele of GUJ005 and GUJ0071 in Chinese yellow quail and Chinese black quail is 7, and the maximum number of allele of GUJ0086 in Korean quail is 7.

Table 2. Allele frequencies of microsatellite loci

Populations	Locus name	Allele frequencies						
Chinese yellow Quails	UBC0004			0.0169	0.3475	0.5678	0.0678	
	UBC0005	0.0169	0.2458	0.2458	0.0254	0.4661		
	UBC0006	0.0764	0.3983	0.1186		0.1525	0.2542	
	GUJ0001	0.0847	0.3644	0.1441	0.1441	0.1695	0.0932	
	GUJ0013	0.0848	0.1186	0.2288	0.1610	0.1949	0.2119	
	GUJ0034	0.0508	0.2119	0.2458	0.0508	0.1610	0.2797	
	GUJ0049	0.0169	0.1695	0.4407	0.2288	0.1102	0.0339	
	GUJ0054	0.1017	0.1864	0.4746	0.0932	0.0932	0.0509	
	GUJ0055	0.0169	0.0339	0.3814	0.1017	0.0932	0.2966	0.0763
	GUJ0070	0.3983	0.1017	0.0508	0.3475	0.1017		
	GUJ0071	0.0847	0.1864	0.2034	0.1271	0.1780	0.1864	0.0340
	GUJ0086		0.4492	0.0678		0.1525	0.2458	0.0847
Chinese black quails	UBC0004		0.0156	0.1641	0.5625	0.2578		
	UBC0005		0.3125	0.1953	0.0078	0.4844		
	UBC0006	0.3672	0.3516	0.0469		0.0781	0.1562	
	GUJ0001	0.1094	0.3047	0.3047	0.2812			
	GUJ0013	0.0391	0.2656	0.1484	0.0547	0.1016	0.3906	
	GUJ0034		0.0469	0.4062	0.0469	0.0859	0.4141	
	GUJ0049		0.0938	0.5312	0.0391	0.2109	0.1250	
	GUJ0054	0.0312	0.2188	0.3437	0.0156	0.1719	0.2188	
	GUJ0055	0.0234	0.0547	0.2969	0.1406	0.0859	0.3047	0.0938
	GUJ0070	0.0547	0.4531		0.2578	0.2344		
	GUJ0071	0.0156	0.1719	0.2969	0.2031	0.2266	0.0781	0.0078
	GUJ0086	0.0078	0.5625	0.0312	0.0235	0.0078	0.1094	0.2578
Korean quails	UBC0004	0.0096	0.0192	0.0096	0.4712	0.4327	0.0577	
	UBC0005		0.2692	0.2308	0.0385	0.4615		
	UBC0006	0.1634	0.3558	0.0288		0.0962	0.3558	
	GUJ0001	0.1154	0.4231	0.1827	0.1441	0.1250	0.0097	

	GUJ0013	0.0481	0.2981	0.1923	0.1442	0.0288	0.2885	
	GUJ0034	0.0288	0.1155	0.3558	0.0288	0.1538	0.3173	
	GUJ0049		0.1635	0.3942		0.2115	0.2308	
	GUJ0054	0.0577	0.1731	0.4807	0.0385	0.0769	0.1731	
	GUJ0055		0.0577	0.3749	0.0962	0.0769	0.2981	0.0962
	GUJ0070	0.1250	0.4231		0.1442	0.3077		
	GUJ0071		0.1058	0.4904	0.0577	0.2596	0.0865	
	GUJ0086	0.0192	0.4135	0.1346	0.0192	0.0769	0.2404	0.0962

Table 3. Polymorphism information content (PIC) of microsatellite loci

Locus name	Populations	Number of alleles locus (Na)	Effective number of alleles (Ne)	Fixation index (F)	Polymorphism information content (PIC)	I
UBC0004	Chinese yellow Quails	4	2.2321	0.3245	0.4698	0.9402
	Chinese black quails	4	2.4388	0.8941	0.5271	1.0346
	Korean quails	6	2.4208	0.6068	0.5005	1.0469
UBC0005	Chinese yellow Quails	5	2.9500	-0.5128	0.6006	1.2081
	Chinese black quails	4	2.6992	-0.5637	0.5583	1.0715
	Korean quails	4	2.9391	-0.5157	0.5975	1.1738
UBC0006	Chinese yellow Quails	5	3.7531	-0.0629	0.6927	1.4508
	Chinese black quails	5	3.4348	0.4269	0.6582	1.3681
	Korean quails	5	3.4490	-0.2729	0.6588	1.3589
GUJ0001	Chinese yellow Quails	6	4.5682	-0.2803	0.7526	1.6573
	Chinese black quails	4	3.6136	-0.1234	0.6703	1.3230
	Korean quails	6	3.8138	-0.3554	0.7031	1.5075
GUJ0013	Chinese yellow Quails	6	5.4819	0.0257	0.7914	1.7411
	Chinese black quails	6	3.8460	-0.2880	0.7013	1.5204
	Korean quails	6	4.2921	-0.0280	0.7293	1.5639
GUJ0034	Chinese yellow Quails	6	4.6600	-0.2516	0.7518	1.6270
	Chinese black quails	5	2.8714	-0.5344	0.5872	1.2288
	Korean quails	6	3.7608	-0.3622	0.6903	1.4736
GUJ0049	Chinese yellow Quails	6	3.4620	-0.0487	0.6691	1.4263
	Chinese black quails	5	2.8356	-0.1586	0.6050	1.2728
	Korean quails	4	3.5696	-0.2289	0.6711	1.3300
GUJ0054	Chinese yellow Quails	6	3.4448	0.0208	0.6776	1.4932
	Chinese black quails	6	4.0878	-0.0756	0.7149	1.5080
	Korean quails	6	3.3137	-0.1017	0.6625	1.4465
GUJ0055	Chinese yellow Quails	7	3.8507	-0.3050	0.7019	1.5619
	Chinese black quails	7	4.5360	-0.2828	0.7478	1.6782
	Korean quails	6	3.8879	-0.2686	0.7046	1.5408
GUJ0070	Chinese yellow Quails	5	3.3042	-0.4340	0.6457	1.3503
	Chinese black quails	4	3.0330	-0.4686	0.6112	1.2071
	Korean quails	4	3.2248	-0.3380	0.6354	1.2658
GUJ0071	Chinese yellow Quails	7	5.9862	-0.2006	0.8105	1.8435
	Chinese black quails	7	4.6152	-0.2367	0.7494	1.6254
	Korean quails	5	3.0314	-0.2340	0.6239	1.3135
GUJ0086	Chinese yellow Quails	5	3.3649	-0.3746	0.6594	1.3828
	Chinese black quails	7	2.5222	-0.3981	0.5510	1.1872
	Korean quails	7	3.8058	-0.1738	0.7012	1.5522
Mean	Chinese yellow Quails	5.6667	3.9215	-0.1750	0.6853	1.4735
	Chinese black quails	5.3333	3.3778	-0.1507	0.6401	1.3354
	Korean quails	5.4167	3.4591	-0.1894	0.6565	1.3811

The Number of alleles locus, Effective number of alleles, polymorphism information content and fixation index of 12 microsatellite markered at the 3 quail groups see table 3, and from the table 3, we learn that the number of average observed allele of Chinese yellow quail, Chinese black quail and Korean quail respectively are 5.6667, 5.3333, 5.4167. Among the 12 microsatellite markers, the minimum marker of efficient allele is UBC0004(Chinese yellow quail, 2.2321), and the maximum is GUJ0071(Chinese

yellow quail, 5.9862); the average efficient allele of Chinese yellow quail, Chinese black quail and Korean quail respectively are 3.9215, 3.3778, 3.4591. The average polymorphism information content of Chinese yellow quail, Chinese black quail and Korean quail respectively are 0.6853, 0.6401, 0.6565, and from that we learn Chinese yellow quail's polymorphism information content is little higher than the two other quail's.

The hepx and average heterozygosity of the 3 quail groups see table 4. The average heterozygosity of 12 microsatellite markered at Chinese yellow quail, Chinese black quail and Korean quail respectively are 0.7333, 0.6957, 0.7111, which shows that the 3 quail groups all have high polymorphism, and Chinese yellow quail's genetic polymorphism is most abundant, Chinese black quial's polymorphism is lower than the two others. When we did the genetic research of a group, we must check the Hardy-weinberg state of equilibrium of this group for assuring whether it has the condition of genetic Balance within a population. From table 4, we learn that only GUJ0054 in Korean quail group obey the Hardy-weinberg law ($p>0.05$), all other markers distinct or extremely distinct deviate from the law, that is to say, the gene distribution of other markers are all in the Hardy-weinberg's non-equilibrium state.

Table 4. Heterozygosity of microsatellite loci

Locus name	Populations	Obs.Hom.	Obs.Het.	Exp.Hom.	Exp.Het.	Chi-square
UBC0004	Chinese yellow Quails	0.6271	0.3729	0.4433	0.5567	126.0020**
	Chinese black quails	0.9375	0.0625	0.4054	0.5946	235.5987**
	Korean quails	0.7692	0.2308	0.4074	0.5926	138.3258**
UBC0005	Chinese yellow Quails	0.0000	1.0000	0.3333	0.6667	78.8815**
	Chinese black quails	0.0156	0.9844	0.3655	0.6345	62.3844**
	Korean quails	0.0000	1.0000	0.3338	0.6662	51.0510**
UBC0006	Chinese yellow Quails	0.2203	0.7797	0.2602	0.7398	65.0606**
	Chinese black quails	0.5938	0.4062	0.2856	0.7144	125.2977**
	Korean quails	0.0962	0.9038	0.2830	0.7170	92.7116**
GUJ0001	Chinese yellow Quails	0.0000	1.0000	0.2122	0.7878	51.0140**
	Chinese black quails	0.1875	0.8125	0.2710	0.7290	18.1220**
	Korean quails	0.0000	1.0000	0.2550	0.7450	39.1210**
GUJ0013	Chinese yellow Quails	0.2034	0.7966	0.1754	0.8246	27.3916*
	Chinese black quails	0.0469	0.9531	0.2542	0.7458	38.0336**
	Korean quails	0.2115	0.7885	0.2255	0.7745	47.8137**
GUJ0034	Chinese yellow Quails	0.0169	0.9831	0.2079	0.7921	165.9295**
	Chinese black quails	0.0000	1.0000	0.3431	0.6569	126.9049**
	Korean quails	0.0000	1.0000	0.2588	0.7412	130.6089**
GUJ0049	Chinese yellow Quails	0.2542	0.7458	0.2828	0.7172	169.8493**
	Chinese black quails	0.2500	0.7500	0.3476	0.6524	53.0964**
	Korean quails	0.1154	0.8846	0.2732	0.7268	51.4800**
GUJ0054	Chinese yellow Quails	0.3051	0.6949	0.2842	0.7158	49.7565**
	Chinese black quails	0.1875	0.8125	0.2387	0.7613	200.4585**
	Korean quails	0.2308	0.7692	0.2950	0.7050	21.6544ns
GUJ0055	Chinese yellow Quails	0.0339	0.9661	0.2534	0.7466	171.8327**
	Chinese black quails	0.0000	1.0000	0.2143	0.7857	192.3515**
	Korean quails	0.0577	0.9423	0.2500	0.7500	212.6933**
GUJ0070	Chinese yellow Quails	0.0000	1.0000	0.2967	0.7033	175.0000**
	Chinese black quails	0.0156	0.9844	0.3244	0.6756	73.5027**
	Korean quails	0.0769	0.9231	0.3034	0.6966	36.1802**
GUJ0071	Chinese yellow Quails	0.0000	1.0000	0.1599	0.8401	205.4907**
	Chinese black quails	0.0312	0.9688	0.2105	0.7895	83.1230**
	Korean quails	0.1731	0.8269	0.3234	0.6766	77.7222**
GUJ0086	Chinese yellow Quails	0.0399	0.9661	0.2912	0.7088	75.2757**
	Chinese black quails	0.1562	0.8438	0.3917	0.6083	32.8646*
	Korean quails	0.1346	0.8654	0.2556	0.7444	170.6024**
Mean	Chinese yellow Quails	0.1412	0.8588	0.2667	0.7333	
	Chinese black quails	0.2002	0.7982	0.3043	0.6957	
	Korean quails	0.1554	0.8446	0.2887	0.7111	

Genetic differentiation coefficient (Gst) can reflect the extent of genetic variation between groups. The variety of Gst among groups is from 0 to 1. When groups' all allele is nearly same, and the value of Gst is closed to 0, it shows there is no differentiation between the groups. When the value of Gst is closed to 1, it shows there is distinct differentiation between the groups. From the table 5, we learn that the Gst among the 3 quail groups is between 0.0103 and 0.0773, which shows the differentiation degree among the 3 quail groups is not high, it also shows the 3 quail has higher homology. From the table 6, we learn that, the minimum genetic distance between Chinese yellow quail and Korean quail is 0.0628, which shows the genetic relationship between Chinese black quail and Korean quail is closest. Next, the genetic distance between Chinese yellow quail and Korean quail is 0.0951, and from Figure 1 we also can learn Chinese black quail and Korean quail get together first, later get together with Chinese yellow quail.

Table 5. Genetic differentiation coefficient (G_{st}) of microsatellite loci

Loci	Total population average heterozygosity (Ht)	Average heterozygosity of different quail populations (Hs)	Genetic differentiation coefficient (Gst)
UBC0004	0.6094	0.5813	0.0461
UBC0005	0.6626	0.6558	0.0103
UBC0006	0.7449	0.7237	0.0284
GUJ0001	0.7683	0.7539	0.0187
GUJ0013	0.7964	0.7816	0.0185
GUJ0034	0.738	0.7301	0.0107
GUJ0049	0.7153	0.6988	0.0231
GUJ0054	0.7386	0.7274	0.0152
GUJ0055	0.7699	0.7608	0.0119
GUJ0070	0.7498	0.6918	0.0773
GUJ0071	0.7918	0.7687	0.0291
GUJ0086	0.6992	0.6872	0.0172
Mean	0.7320	0.7134	0.0255

Table 6. Genetic distance of four quail populations

Populations	Chinese yellow Quails	Chinese black quails	Korean quails
Chinese yellow Quails		0.8585	0.9092
Chinese black quails	0.1526		0.9391
Korean quails	0.0951	0.0628	

Note: Nei's genetic identity (above diagonal) and genetic distance (below diagonal).

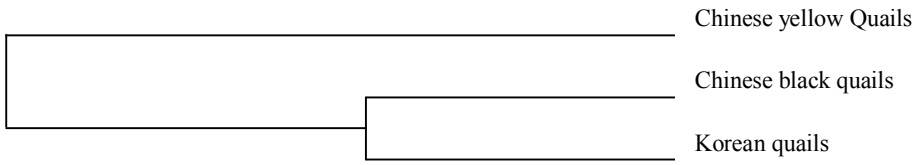

Figure 1. Dendrogram of quail populations

Discussion

PIC shows that the possibility of offspring obtained one same allelic marker from its father or mother's allelic marker, is a statistical quantity for using to describe the variation degree of microsatellite loci and PIC is an ideal index measuring the allele fragment's polymorphism. When PIC>0.5, it shows this gene locus is highly polymorphic gene locus; when 0.25<PIC>0.5, it shows the locus is moderate gene locus; when PIC<0.25, it shows the locus is minuend gene locus (Botstein *et al*.,1980). In this study, except the minimum PIC of mircosatellite marker UBC004 is 0.4698 which is moderate polymorphism, the others markers are highly polymorphism. The average PIC of 12 microsatellite markered at Chinese yellow quail, Chinese black quail and Korean quail respectively are 0.6853, 0.6401, 0.6565, which are all over 0.5, and among them, Korean quail's average PIC is similar to the Meng Qingmei's research result (0.6945) (Meng *et al*., 2007).

The size of heterozygosity can nearly reflect the genetic variation degree. Higher heterozygosity shows higher genetic diversity in groups and higher genetic

variation degree; otherwise, it will have smaller genetic variation degree. The value of groups heterozygosity is generally in 0.3 to 0.8 which was calculated by microsatellite marker. In this research, except that the average heterozygosity of UBC0004 in the 3 groups is low, the other 11 microsatellite markered in 3 quail groups has high heterozygosity. It shows that all the 3 quail groups have high polymorphism and the genetic diversity of yellow feather quail is most abundant.

Gst shows the differentiation degree between the groups, but it is only a relative indicators, more often than not doing some qualitative explanation. Due to the size of Gst is related to the amount of gene locus, polymorphism of gene locus and the size of sample we chose, so far there is no a unified quantified standard, how large of the Gst means high differentiation degree, and how small means the low differentiation degree. Due to the different factors, such as the number of microsatellite, different locus and different size of sample people chose, we can not compare the different people's research report. Chang et al., analyzed the genetic diversity of two kinds of wild quail (wild Japanese quail and common wild quail) and domestic quail in our country, and the gene differentiation rate of 3 quail groups are respectively 0.0109, 0.0439, 0.0548 (Chang et al., 2005) The data means the gene differentiation rate of the whole quail group is 0.0365. The research by analyzing the gene differentiation, shows the differentiation degree between the 3 quail groups is not high, which confirmed the 3 quail groups have high homology.

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