

Research Article

Genetic Diversity and Genetic Structure Analysis of Introduced and Selectively Bred Generations in Largemouth Bass (*Micropterus nigricans*) Based on Microsatellite Analysis

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To assess the changes in genetic structure across generations of selectively bred largemouth bass (*Micropterus nigricans*) (F3, F4, F5, and F6), this study, in combination with an introduced population, utilized 15 pairs of microsatellite primers to analyze the genetic diversity and structure. The results revealed a total of 62 alleles (N_a), with an average of 4.160 alleles per locus. The average observed heterozygosity (H_o) was 0.559, and the average expected heterozygosity (H_e) was 0.529. The introduced population exhibited the highest genetic diversity parameters, including polymorphic information content (PIC), N_a effective number of alleles (N_e), H_o , H_e , and Shannon's information index (I). In contrast, the selectively bred populations showed a gradual decline, with PIC ranging from 0.398 to 0.494, N_a from 3.533 to 4.000, N_e from 2.008 to 2.387, H_o from 0.480 to 0.589, H_e from 0.457 to 0.550, and I from 0.794 to 0.990, indicating a moderate level of polymorphism. The F -test in different generations of selectively bred populations revealed that 10 loci had negative inbreeding coefficients (F_{is}), while 5 loci had positive values, suggesting a low level of inbreeding across generations. Overall, the introduced and selectively bred populations exhibited a moderate level of genetic differentiation, with low to moderate genetic differentiation observed. AMOVA revealed that 92% of the variation originated within individuals. UPGMA clustering and PCoA analysis demonstrated significant genetic differentiation between the selectively bred populations and the introduced population. In conclusion, the introduced population exhibited higher genetic diversity compared to the selectively bred populations. The genetic diversity of the selectively bred populations showed a declining trend as the selection process progressed, highlighting the importance of evaluating genetic diversity while improving target traits during selection. This study provides scientific guidance for the selection of new varieties and the evaluation and conservation of germplasm resources in largemouth bass.

Keywords: genetic diversity; introduced population; *Micropterus nigricans*; microsatellite markers; population structure; selective breeding

1. Introduction

Micropterus nigricans, taxonomically classified in *Perciformes*, *Centrarchidae*, and *Micropterus* [1]. Native to the Southeastern United States, it is an important game fish in its native range [2, 3]. Since its introduction to Guangdong, China, in 1983, the largemouth bass has been widely cultivated across the country [4]. It has become one of the most

important freshwater aquaculture species in China, with a production of 88.8×10^7 kg in 2023 [5]. Fan et al. [6] analyzed the quantitative traits and microsatellites of largemouth bass in China and concluded that the domestic cultured largemouth bass should be classified as the northern subspecies of *Micropterus nigricans*. Shengyan et al. [7] used the SSR markers to analyze the genetic diversity of introduced and domestic cultured populations of

largemouth bass and found that the genetic diversity of the introduced population was significantly higher than that of the domestic cultured population. Rong et al. [8] used microsatellite markers to analyze the genetic structure of different generations of selectively bred largemouth bass and found that the genetic structure of the population gradually became more homogeneous. Genetic diversity is a crucial factor in evaluating germplasm resources, as it is closely related to the survival, adaptability, and evolutionary potential of species populations [9]. Selective breeding is an effective approach for developing aquatic species with specific desirable traits, but it can also increase the likelihood of inbreeding and reduce the genetic diversity of breeding populations, leading to germplasm degradation [10]. Therefore, it is essential to evaluate the genetic diversity of populations during the breeding process, optimize traits, and maintain sufficient genetic diversity to avoid germplasm degradation [11]. It is essential to assess the genetic diversity of both the breeding and introduced populations to evaluate how breeding practices influence the population's genetic structure, thereby providing a scientific basis for guiding breeding programs.

The selectively bred populations in this study were developed from a natural breeding population introduced from Guangdong in the 1990s as the base population. Since 2017, through the mass selection technology and with a retention rate of less than 1% per generation, a new strain has been selectively bred to better adapt to the environmental and climatic conditions of the eastern China region. This strain has now reached the F6 generation and exhibits excellent growth rate and adaptability to summer heat tolerance. To understand the changes in genetic diversity and structure during the selective breeding process and to ensure the scientific progress of breeding work, it is necessary to evaluate the genetic changes across generations, thereby reducing the effects of selection and mitigating selection effects. Evaluating the genetic changes across breeding generations will guide the subsequent breeding of the new strain [12]. In addition, the genetic diversity of the introduced population should be assessed to provide a reference for improving the genetic traits of the selectively bred populations and formulating breeding strategies.

Microsatellite markers (simple sequence repeats [SSRs]) are widely used in genetic diversity analysis [12], family identification [13, 14], and germplasm analysis [15] of aquatic animals due to their widespread distribution, codominance, and high polymorphism. Fu et al. [16] used 18 microsatellite loci to construct a multiplex PCR system for genetic analysis of two largemouth bass populations and their hybrid offspring, validating the efficiency of the microsatellite system and the genetic structure of the populations. Microsatellite analysis of genetic diversity in selectively bred generations has been widely applied in various aquatic species, including the Pacific oyster (*Crassostrea gigas*) [10], the Babylon snail (*Babylonia areolata*) [17], common carp (*Cyprinus carpio*) [18], grass carp (*Ctenopharyngodon idella*) [19], and the Yangtze River anchovy (*Coilia nasus*) [20]. This study used microsatellite technology to analyze the genetic variation between the introduced

population and different generations of selectively bred largemouth bass populations, aiming to understand the impact of artificial selection on the genetic structure and diversity of largemouth bass and to provide a reference for continued selective breeding and germplasm improvement.

2. Materials and Methods

2.1. Sample Collection. The introduced population was purchased from the National Largemouth Bass Breeding Farm in Tongling, Anhui (Anhui Zhanglin Fisheries Co., Ltd.), and preserved at the Xiba breeding base of the breeding unit. The selectively bred generations (F3, F4, F5, and F6) were also obtained from the Xiba breeding base. Thirty individuals were randomly selected from each of the introduced and selectively bred populations, totaling 150 samples. Tail fins were clipped and fixed in anhydrous ethanol, and then stored at -20°C for DNA extraction.

2.2. Genomic DNA Extraction and Quality Detection. DNA was extracted using the TIANGEN Tissue Genomic DNA Extraction Kit (DP304). The integrity and purity of the extracted DNA were assessed using 1% agarose gel electrophoresis, and the concentration was measured using a NanoDrop spectrophotometer (GE, USA). Qualified DNA samples were diluted to $30\text{ ng}/\mu\text{L}$ and stored at -20°C for further use.

2.3. Polymorphic Microsatellite Primer Screening and Amplification Product Detection. Thirty pairs of microsatellite primers were randomly selected from published literature [4, 21–23], and 15 polymorphic primers were chosen after screening 15 individuals from each population (Table 1). The forward primers were labeled with FAM, TAMRA, and HEX fluorescent dyes at the 5' end for PCR amplification and capillary electrophoresis. The primers and fluorescent labels were synthesized by Shanghai Maipu Biotechnology Co., Ltd.

The PCR amplification system consisted of $10.0\ \mu\text{L}$ of $2\times$ Taq Master Mix (Vazyme), $0.1\ \mu\text{L}$ each of $10\ \mu\text{mol}/\text{L}$ forward and reverse primers, $1\ \mu\text{L}$ of $30\text{ ng}/\mu\text{L}$ genomic DNA, and ultra-pure water to make up a total volume of $20\ \mu\text{L}$. The PCR amplification program was as follows: 94°C for 5 min; 35 cycles of 94°C for 30 s, T_m for 30 s, and 72°C for 30 s; and a final extension at 72°C for 10 min. A $5\ \mu\text{L}$ aliquot of the PCR product was subjected to 1.5% agarose gel electrophoresis at 200 V for 15 min. Based on the brightness of the electrophoresis bands, samples were diluted, and unqualified samples were reamplified. Qualified samples were then subjected to capillary electrophoresis.

2.4. Data Statistics and Analysis. The capillary electrophoresis results were analyzed using GeneMapper 4.0 software to determine the allele sizes. GenAEx 6.5 software was used to calculate the number of alleles (N_a), effective number of alleles (N_e), observed heterozygosity (H_o), expected heterozygosity (H_e), Shannon–Wiener diversity index (I),

TABLE 1: Basic information of 15 microsatellite primers.

Locus	Repeat base	Primer sequence	Annealing temperature	Size (bp)	Reference
JZL114	(GA) ₁₁ (GT) ₁₇	CTACAGGTTAGGGAGTTACACG TGCTGAGGACACAACGAGGT	55	192~230	[20]
MiSaTPW001	(AC) ₁₆	AGTAAAGGACCACCCTTGTTCCA GCCTGGTCATTAGGTTTCGGAG	60	293~299	[21]
MiSaTPW117	(AC) ₂₄	TGTGAAAGGCACAACACAGCCTGC ATCGACCTGCAGACCAGCAACT	60	228~283	[3]
JZL85	(CA) ₁₇	GGGGCTCACTCACTGTGTTT GTGCGCAGACAGCTAGACAG	58	213	[3]
mod7	(CA) ₁₂	TCAAACGCACCTTCACTGAC GTCACCTCCATCATGCTCCT	53	156~172	[22]
JZL31	(CA) ₂₅	TGGACTGAGGCTACAGCAGA CCAAGAGAGTCCCAATGGA	60	202	[3]
JZL36	(CA) ₁₅	GCTGAGAGCCTGAAGACCAG ATGGAGGACAGCAGGAACAT	56	214	[3]
JZL43	(CA) ₂₁	GCTGCGAGTGCCTGTAACCTA GGGAAGCGAGAGTCAGAGTG	58	215	[3]
JZL59	(CA) ₂₁	CACAAGGCAAAACAGAACGTC TTGGCTACCCAGTGATGACA	55	183	[3]
JZL60	(CA) ₂₁	AGTTAACCCGCTTTGTGCTG GAAGGCGAAGAAGGGAGAGT	60	205	[3]
JZL84	(CA) ₂₀	GAAAACAGCCTCGGGTGTA CACTTGTGCTGCGTCTGTT	56	197	[3]
JZL106	(GT) ₃₅	GCAGGCAGTGAACCCAGATT TATGTATTGACGAGCGAGCAG	54	/	[20]
JZL111	(GT) ₂₇	TGTCTCAACTCCACCTACG CACCTGGCTTCATCTGC	52	/	[20]
JZL126	(AC) ₂₄	CAGGTAGCAGCGGTTAGGATG TCTGAAACACGGACTCACGAC	55	/	[20]
MiSaTPW184	(AC) ₁₄ (CT) ₁₀	TTGTATACCAAGTGACCTGTGG GGGAGTGCATCTTCTGAAGTGCC	55	247~272	[21]

inbreeding coefficient (F_{is}), genetic differentiation index (F_{st}), and gene flow (N_m) for the 15 microsatellite loci, as well as the N_a , N_e , H_o , H_e , and I for the five populations. Cervus 3.0 was used to calculate the polymorphic information content (PIC). GenAlEx 6.5 was used to test for Hardy–Weinberg equilibrium, perform molecular variance analysis (AMOVA) and principal coordinate analysis (PCoA), and calculate the F_{st} and N_m between populations, as well as Nei's standard genetic distance and genetic similarity coefficients. Bottleneck effect analysis was performed using BOTTLENECK 3.5. MEGA 11.0 was used to calculate genetic distances and construct a UPGMA dendrogram.

3. Results

3.1. Genetic Diversity Analysis of 15 Microsatellite Loci.

The genetic diversity parameters of the 15 microsatellite loci are shown in Table 2. A total of 62 alleles (N_a) were detected across the 15 loci, with the JZL111 locus having the highest number of alleles (6) and the MiSaTPW001 locus having the lowest (3.2), averaging 4.160 alleles per locus. The average effective number of alleles (N_e) was 2.395, with the lowest

TABLE 2: Genetic diversity parameters of 15 microsatellite loci.

Locus	N_a	N_e	I	H_o	H_e	N_m
JZL114	5.200	3.610	1.369	0.733	0.709	3.185
MiSaTPW001	3.200	1.765	0.645	0.360	0.369	1.128
MiSaTPW117	3.400	2.449	1.000	0.685	0.580	1.915
JZL85	4.400	2.519	1.048	0.633	0.548	2.935
mod7	3.800	2.313	1.010	0.341	0.556	4.032
JZL31	3.200	2.848	1.080	0.674	0.648	11.462
JZL36	5.800	3.053	1.270	0.632	0.640	2.821
JZL43	3.800	1.966	0.813	0.436	0.475	3.520
JZL59	3.800	2.086	0.871	0.832	0.518	2.825
JZL60	3.800	2.516	1.014	0.625	0.583	6.481
JZL84	4.200	2.168	0.943	0.660	0.518	3.404
JZL106	4.200	1.624	0.639	0.315	0.314	2.253
JZL111	6.000	3.354	1.322	0.544	0.662	2.923
JZL126	3.800	1.733	0.727	0.437	0.402	5.462
MiSaTPW184	3.800	1.922	0.745	0.472	0.411	1.789
平均值	4.160	2.395	0.966	0.559	0.529	3.742

value at JZL106 (1.624) and the highest at JZL114 (3.610). The Shannon–Wiener diversity index (I) ranged from 0.639 to 1.369, with an average of 0.966. The observed heterozygosity (H_o) ranged from 0.315 to 0.832, with an average of

0.559, while the expected heterozygosity (H_e) ranged from 0.314 to 0.709, with an average of 0.529. The gene flow (N_m) for each locus ranged from 1.128 to 11.462, with an average of 3.742.

3.2. Genetic Diversity Analysis of Introduced and Selectively Bred Populations. The genetic diversity parameters of the introduced and selectively bred populations are shown in Table 3. The introduced population exhibited the highest values for PIC, N_a , N_e , H_o , H_e , and I . In contrast, the selectively bred populations showed a gradual decline in genetic diversity across generations, with PIC ranging from 0.398 to 0.494, N_a from 3.533 to 4.000, N_e from 2.008 to 2.387, H_o from 0.480 to 0.589, H_e from 0.457 to 0.550, and I from 0.794 to 0.990, indicating a moderate level of polymorphism.

3.3. Genetic Variation and Differentiation Across Selectively Bred Generations. The F -test results for the 15 microsatellite loci across different generations of selectively bred populations are shown in Table 4. Among the 15 loci, 5 had positive values indicating a low level of inbreeding across generations, while 10 had negative inbreeding coefficients (F_{is}). Different generations of selectively bred populations showed varying degrees of heterozygote deficiency, with 5 loci exhibiting heterozygote deficiency and 10 loci showing heterozygote excess. The genetic differentiation index (F_{st}) for the 15 loci in the selectively bred populations ranged from 0.015 to 0.211, with 7 loci showing low genetic differentiation, 7 showing moderate differentiation, and 1 showing high differentiation (Table 4). Overall, the introduced and selectively bred populations exhibited a moderate level of genetic differentiation, while the selectively bred populations showed low to moderate genetic differentiation among themselves (Table 5).

3.4. Genetic Distance and Genetic Structure Analysis of Introduced and Selectively Bred Populations. The Nei's standard genetic distance and genetic similarity coefficients between the introduced and selectively bred populations are shown in Table 6. The genetic distance between the selectively bred generations and the introduced population ranged from 0.087 to 0.211, with the genetic distance gradually increasing across generations. The genetic similarity coefficients between the selectively bred generations and the introduced population ranged from 0.810 to 0.916, with a gradual decrease across generations.

AMOVA results (Table 7) showed that 8% of the variation originated between populations, while 92% of the variation originated within individuals, indicating that the majority of the variation was within individuals.

The UPGMA dendrogram based on genetic distance (Figure 1) showed that the introduced population formed a separate cluster, while the selectively bred generations clustered together. Within the selectively bred populations, F3 and F4 clustered together, while F5 and F6 formed another cluster. PCoA analysis (Figure 2) revealed a clear

distinction between the introduced and selectively bred populations, with the selectively bred populations forming a distinct cluster.

The bottleneck effect analysis reveals that under the IAM, all populations exhibit excess heterozygosity. In the sign test, AL and F3 show significant deviations from the mutation-drift equilibrium ($p < 0.05$), while others are nonsignificant. In the Wilcoxon test, AL demonstrates a highly significant deviation ($p < 0.01$), F3 shows a significant deviation ($p < 0.05$), and others remain nonsignificant. Under the two-phase model (TPM), all populations exhibit excess heterozygosity (Table 8).

4. Discussion

4.1. Diversity of Microsatellite Loci in Largemouth Bass. The 15 microsatellite loci screened in this study detected a total of 62 alleles, with an average of 4.160 alleles per locus (N_a). The average effective number of alleles (N_e) was 2.395, with an average expected heterozygosity (H_e) of 0.529 and an average observed heterozygosity (H_o) of 0.559. The microsatellite loci exhibited good polymorphism, providing effective information for the genetic analysis of largemouth bass populations. The diversity of different loci may be related to the type of repeat sequences and primer design [24]. Fu et al. [16] also observed significant differences in polymorphism among loci when analyzing largemouth bass populations using a multiplex PCR system. This suggests that incorporating more highly polymorphic loci in future studies could improve the accuracy of genetic analysis and enhance the reliability of population genetic assessments.

4.2. Genetic Diversity of Introduced and Selectively Bred Populations. The introduced population exhibited higher genetic diversity parameters compared to the selectively bred populations, consistent with the findings of Shengyan [7], Fu et al. [16], Jianfeng et al. [25], and Sun et al. [26]. The higher genetic diversity of the introduced population provides a larger breeding space and genetic potential, making it an excellent base population for largemouth bass breeding. It can also serve as a reference population for monitoring the genetic improvement of selectively bred populations and provide germplasm resources for further breeding.

The genetic diversity of the selectively bred populations showed a gradual decline across generations, consistent with the earlier findings of Rong et al. [8] on largemouth bass breeding. Similar trends have been observed in the selective breeding of other aquatic species, such as the Pacific oyster (*Crassostrea gigas*), where the PIC value decreased from 0.62 to 0.45 [11], and the Chinese shrimp (*Fenneropenaeus chinensis*), where the number of alleles (N_a) decreased by 30% [12]. These findings indicate that while artificial selection can improve specific desirable traits, it can also lead to the accumulation of inbreeding and a reduction in genetic diversity. Therefore, it is crucial to regularly evaluate the genetic diversity of selectively bred populations, incorporate molecular marker-assisted selection to balance target traits

TABLE 3: Genetic diversity of *M. nigricans*' bred and introduced populations.

Population	$N_a \pm SD$	$N_e \pm SD$	$I \pm SD$	$H_o \pm SD$	$H_e \pm SD$	PIC \pm SD
AL	5.800 \pm 0.641	3.225 \pm 0.328	1.292 \pm 0.097	0.694 \pm 0.040	0.649 \pm 0.031	0.600 \pm 0.133
F3	4.000 \pm 0.195	2.387 \pm 0.166	0.990 \pm 0.060	0.589 \pm 0.050	0.550 \pm 0.034	0.494 \pm 0.122
F4	3.800 \pm 0.279	2.236 \pm 0.158	0.916 \pm 0.067	0.540 \pm 0.052	0.515 \pm 0.039	0.457 \pm 0.136
F5	3.667 \pm 0.252	2.120 \pm 0.186	0.841 \pm 0.082	0.480 \pm 0.074	0.473 \pm 0.048	0.419 \pm 0.165
F6	3.533 \pm 0.215	2.008 \pm 0.166	0.794 \pm 0.079	0.490 \pm 0.071	0.457 \pm 0.047	0.398 \pm 0.160

TABLE 4: F -Statistics for the bred population of *M. nigricans* at 15 microsatellite loci.

Locus	F_{is}				The F_{is} of bred populations	The F_{st} of bred populations
	F3	F4	F5	F6		
JZL114	0.237	-0.104	-0.328	-0.347	-0.135	0.054
MiSaTPW001	0.024	0.122	0.140	-0.033	0.063	0.211
MiSaTPW117	-0.434	-0.183	0.016	-0.024	-0.156	0.140
JZL85	-0.332	0.027	0.048	-0.106	-0.091	0.061
mod7	0.304	0.354	0.652	0.794	0.526	0.045
JZL31	-0.055	-0.125	0.140	-0.176	-0.054	0.015
JZL36	0.156	0.180	-0.154	-0.008	0.044	0.091
JZL43	0.016	-0.093	0.421	-0.112	0.058	0.040
JZL59	-0.382	-0.682	-0.827	-0.773	-0.666	0.023
JZL60	-0.138	-0.102	-0.031	0.134	-0.034	0.016
JZL84	-0.375	0.031	-0.181	-0.262	-0.197	0.040
JZL106	0.006	-0.078	-0.040	0.076	-0.009	0.028
JZL111	0.200	-0.037	0.269	0.299	0.183	0.079
JZL126	-0.044	0.162	-0.189	-0.270	-0.086	0.055
MiSaTPW184	-0.297	-0.100	0.256	-0.039	-0.045	0.131

TABLE 5: Comparing pairwise values of F_{st} among bred and introduced populations.

Population	AL	F3	F4	F5	F6
AL	—				
F3	0.030	—			
F4	0.068	0.027	—		
F5	0.063	0.038	0.068	—	
F6	0.071	0.050	0.083	0.009	—

TABLE 6: Nei's genetic distance (above diagonal) and genetic similarity (below diagonal) among bred and introduced populations.

Population	AL	F3	F4	F5	F6
AL	—	0.087	0.211	0.156	0.169
F3	0.916	—	0.070	0.077	0.099
F4	0.810	0.932	—	0.160	0.190
F5	0.856	0.926	0.852	—	0.014
F6	0.844	0.906	0.824	0.986	—

TABLE 7: Analysis of molecular variances (AMOVAs).

Source of variation	Degrees of freedom	Sum of squares	Variance components	Percentage of variation (%)
Among populations	4	101.587	25.397	8
Among individuals	146	563.635	3.861	—
Within individuals	151	631.000	4.179	92
Total	301	1296.222	—	100

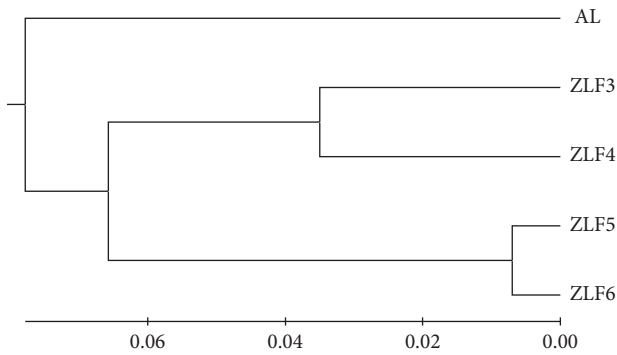


FIGURE 1: Bifurcation diagram by UPGMA cluster analysis of bred and introduced populations.

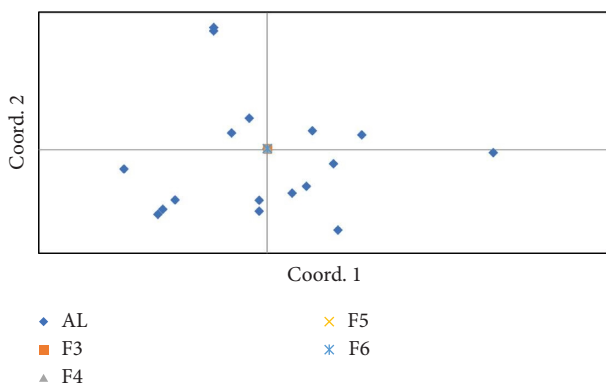


FIGURE 2: PCoA analysis of bred and introduced populations of *M. nigricans*.

TABLE 8: Sign test and Wilcoxon test to evaluate breeding and introduced populations.

Population	<i>p</i> value			
	Sign test		Wilcoxon test	
	IAM	TPM	IAM	TPM
AL	0.0165*	0.2390	0.0006**	0.4543
F3	0.1273	0.3644	0.0413*	0.4543
F4	0.0386*	0.4470	0.0730	0.5995
F5	0.2438	0.3440	0.2769	0.8040
F6	0.1041	0.5132	0.2078	0.7197

*Significant deviation from the equilibrium ($p < 0.05$).

**Highly significant deviation from the equilibrium ($p < 0.01$).

and genetic diversity, and avoid germplasm degradation in breeding populations.

4.3. Genetic Differentiation Between Introduced and Selectively Bred Populations. The introduced and selectively bred populations exhibited a moderate level of genetic differentiation across the 15 microsatellite loci, while the selectively bred populations showed low to moderate genetic differentiation among themselves. Most loci in the selectively bred populations had negative inbreeding coefficients, indicating a low level of inbreeding across generations. However,

different generations showed varying degrees of heterozygote deficiency, which may be related to the rapid changes in allele frequencies due to directional selection [27]. Compared to the introduced population, the selectively bred populations showed an increasing genetic distance and decreasing genetic similarity coefficients across generations, indicating a deepening genetic differentiation. This is consistent with the findings of FAN [28] on largemouth bass. Similar trends have been observed in the selective breeding of other aquatic species, such as common carp [18].

4.4. Genetic Structure Analysis and the Bottleneck Effect Analysis of Introduced and Selectively Bred Populations. AMOVA results showed that only 8% of the genetic variation originated between populations, while 92% of the variation originated within individuals, indicating that the majority of the variation was within individuals. The UPGMA dendrogram and PCoA analysis revealed significant genetic differentiation between the introduced and selectively bred populations, with the selectively bred generations also showing some genetic differentiation. This genetic differentiation may be due to the directional selection of specific traits and restricted gene flow between populations. Similar genetic differentiation has been reported in the selective breeding of other aquatic species, such as the Chinese mitten crab (*Eriocheir sinensis*) [15].

When a population experiences a bottleneck effect (a sharp decline in size), it often leads to excess heterozygosity [29]. Microsatellite loci, characterized by high heterozygosity and short repeat units, are employed in this study to analyze recent population trends. The IAM and TPM are more suitable than the SMM for analyzing long-term genetic dynamics in larger populations, as the latter is better suited for small populations [30]. In the sign test, AL and F3 show significant deviations from the mutation-drift equilibrium, and others are nonsignificant. This indicates that AL and F3 have recently experienced bottleneck effects of varying severity, likely due to their status as introduced breeding populations. While others that are nonsignificant suggest a gradual decline in population size.

5. Conclusion

This study used microsatellite markers to analyze the genetic diversity and structure of introduced and selectively bred populations of largemouth bass across different generations. The results showed that the introduced population had a higher genetic diversity compared to the selectively bred populations, and the genetic diversity of the selectively bred populations gradually declined across generations, indicating a significant impact of artificial selection. There was a moderate level of genetic differentiation between the introduced and selectively bred populations, as well as among the selectively bred generations. These findings provide important insights for the continued selective breeding and germplasm improvement of largemouth bass. In future breeding efforts, it is essential to balance the improvement of target traits with the maintenance of genetic diversity,

optimize breeding strategies, avoid germplasm degradation in selectively bred populations, and make full use of the genetic resources of the introduced population to further enhance the desirable traits of the selectively bred populations and achieve sustainable utilization of germplasm resources.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Ethics Statement

The animal study was approved by the Institutional Review Board of the Science and Technology Department of Zhejiang Province. The study was conducted in accordance with the local legislation and institutional requirements.

Conflicts of Interest

The authors declare no conflicts of interest.

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