

Genetic diversity and differentiation in different geographic populations of black carp (*Mylopharyngodon piceus*) based on the whole mitochondrial genome

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Introduction

At present, there are few studies on the genetic variation of *M. piceus*, which can not fully reflect the current germplasm distribution characteristics. Therefore, for the first time, we selected the whole mitochondrial genome of *M. piceus* from different geographical populations as the research object, aiming to more comprehensively reveal the genetic variation of *M. piceus* germplasm resources in China and provide the latest information and scientific guidance for the protection and sustainable utilization of *M. piceus* germplasm resources.

Materials and methods

90 *M. piceus* from 9 different geographical groups were collected from Original seed farm and improved seed farm. *M. piceus* mitochondrial DNA variation, *M. piceus* genetic differentiation and genetic diversity are analyzed.

Results

1. Nucleotide mutations of mtDNA

A total of 245 polymorphic sites and 247 nucleotide mutations were detected, with a mutation rate of 1.47%, including 74 singleton variable sites and 171 parsimony informative sites, regardless of insertion and deletion. There exit three variants in parsimony informative sites in D-loop region., which were A/T/G and A/T/C variants types. Mutation sites are mainly concentrated in the protein-coding gene region and D-loop control region (15690bp - 16616bp), among which the rate of evolution was D-loop> ND5> ND4> COII> COI>16S rRNA> ND2, COIII, Cytb >12S rRNA> ND1> ND6> ATP6> ND3> ND4L> ATP8.

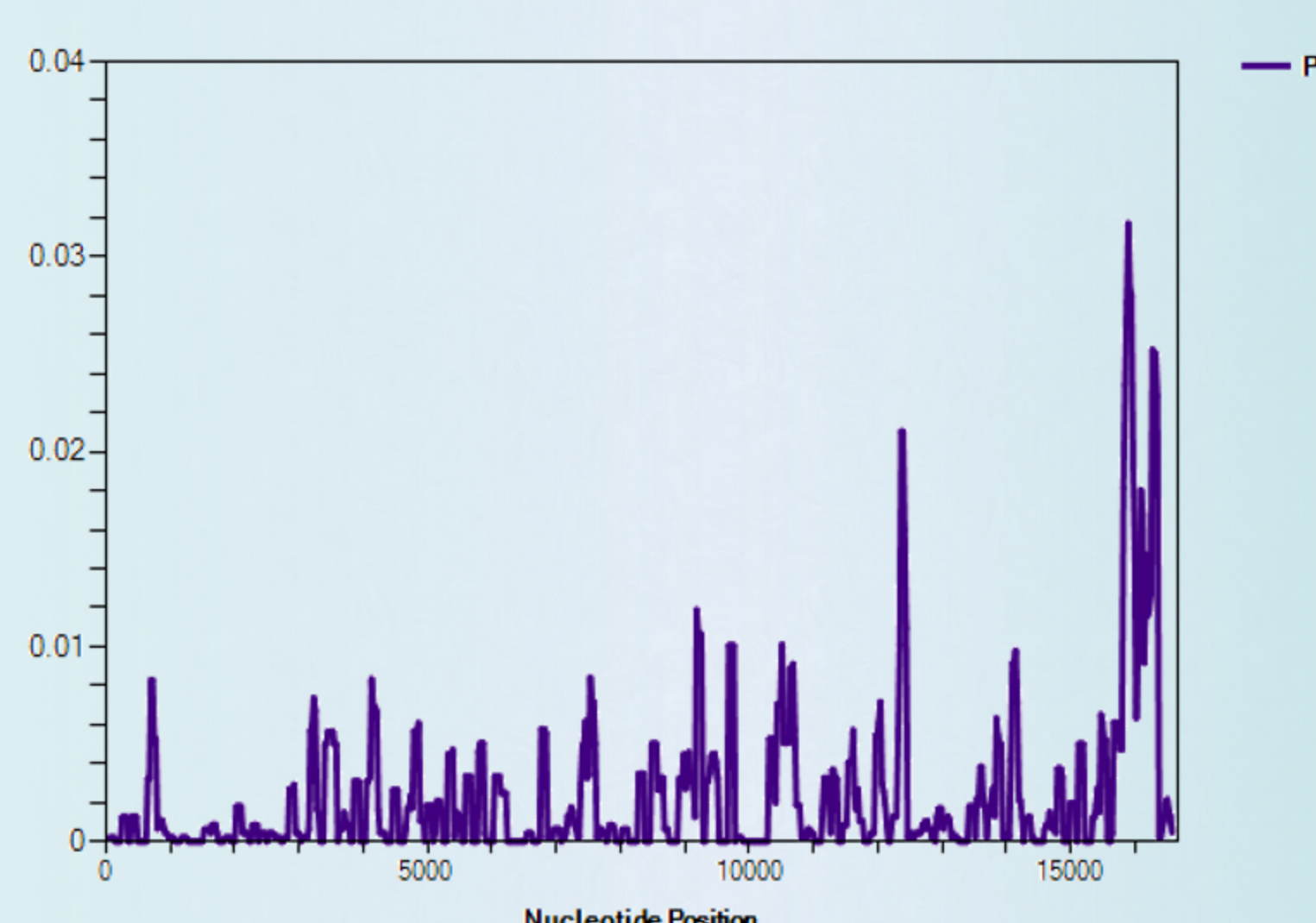


Figure1. Nucleotide diversity (Pi) distribution of mtDNA

2. Genetic diversity and genetic differentiation of *M. piceus* population

Table 1 Genetic diversity of nine populations of *M. piceus*

Population	H	S	H _d	Pi	K
JSSZ	10	99	1	0.0023	33.9
JSYZ	10	130	1	0.0020	39.4
ZJJX	10	73	1	0.0020	33.4
HNCS	10	87	1	0.0021	35.8
HBSS	10	91	1	0.0019	32.4
SXWN	10	106	1	0.0024	40.2
JXRC	10	90	1	0.0018	30.5
GDFS	9	62	0.978	0.0010	17.4
GXYL	10	78	1	0.0018	31.3

H: Number of Haplotypes; S: Number of polymorphic sites; H_d: Haplotype diversity; Pi: Nucleotide diversity; K: Average number of pairwise nucleotide difference.

Table 2 Pairwise genetic differentiation and gene flow among populations

	JSSZ	JSYZ	ZJJX	HNCS	HBSS	SXWN	JXRC	GDFS	GXYL
JSSZ		2.29	1.52	1.18	0.62	1.42	0.43	0.88	1.44
JSYZ	0.09		2.79	1.14	0.90	3.45	0.60	0.85	2.22
ZJJX	0.14	0.08		1.05	0.95	2.14	0.52	0.53	1.77
HNCS	0.17	0.17	0.19		2.73	1.99	1.34	0.42	0.94
HBSS	0.28	0.21	0.20	0.08		2.30	1.46	0.30	0.65
SXWN	0.14	0.06	0.10	0.11	0.09		2.03	0.56	1.69
JXRC	0.37	0.29	0.32	0.15	0.14	0.10		0.20	0.42
GDFS	0.22	0.22	0.32	0.37	0.45	0.30	0.55		0.77
GXYL	0.14	0.10	0.12	0.20	0.27	0.12	0.37	0.24	

Note: The genetic fixation index (F_{st}) is in the upper triangle and the gene flow (Nm) is in the lower triangle.

3. Population historical dynamics and Phylogenetic tree

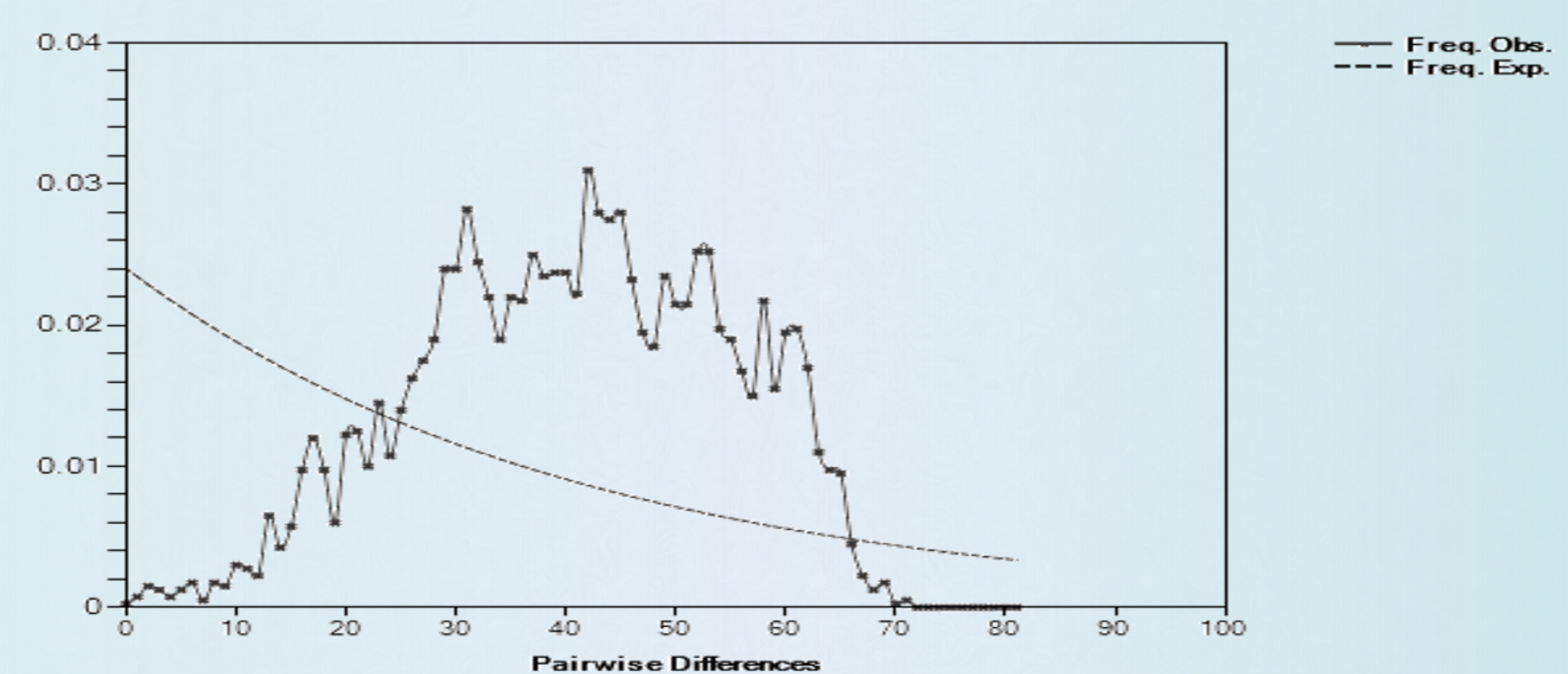


Figure 2. Nucleotide mismatch distribution curve of mtDNA

Note: Freq.Obs. is the expected frequency of nucleotide mismatch distribution, and Freq.Exp. is the observed frequency of nucleotide mismatch distribution.

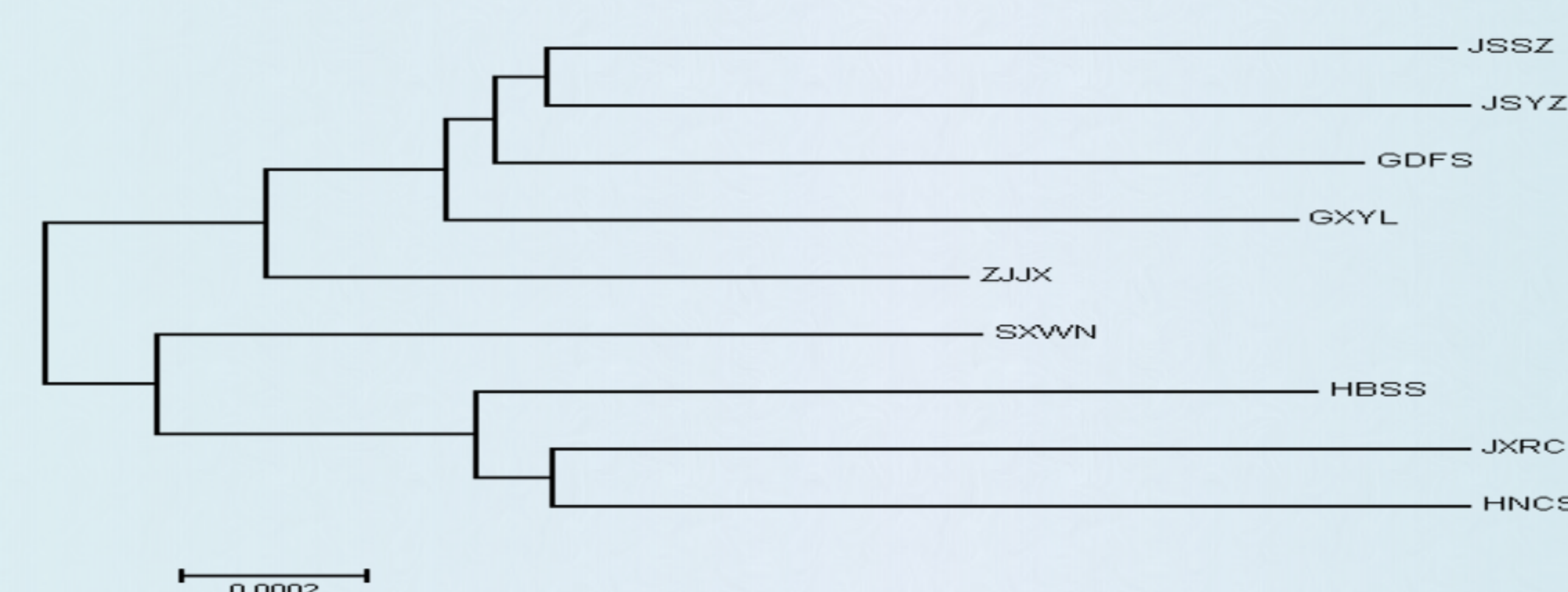


Figure 3. Neighbor-joining phylogenetic tree of nine populations of *M. piceus* based on genetic distance of the whole mitochondrial genome

Conclusion

Our results showed that the D-loop control region of the mtDNA had the highest degree of genetic variation, and ATP6, ATP8, ND3 and ND4L genes were the most conserved. The overall genetic diversity of *M. piceus* is low, but the haplotype diversity is high, and rapid population expansion events have occurred in history. The genetic differentiation among populations was at a moderate to high level. Our study comprehensively revealed the genetic variation of *M. piceus* germplasm resources, provided the latest information and scientific guidance for the conservation and sustainable utilization of *M. piceus* germplasm resources, and contributed to the development of genetic breeding.