









The analysis of genetic data of the Amur tiger and Amur leopard samples from the field

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Outline:

1. Non-invasive samples collection;

2. How to treat with the samples;

3. Analysis results of the samples;

4. Summary.

Questions:

- 1 Of all the samples in field, which belong to Amur tiger and which belong to Amur leopard?
- 2. How many Amur Tigers and Amur leopards exist in China now?
- 3. How about genders of Amur tiger and population based on genectic analysis?

1. Non-invasive samples collection

① Number of samples

The 245 suspected samples of Amur tigers and leopards were colleted since 2010 across the range;

② Sample types

Including 169 fecal samples, 27 hair samples, 14 blood samples, 22 urine samples and 13 saliva samples.

DNA extraction

Blood samples:

DNA was extracted through the standard phenol: chloroform method (Sambrook et al., 1989).

Fecal samples:

All the DNAs of fecal samples were extracted through the modified QIAamp DNA Stool Mini Kit (Qiagen, Hilden, Germany) as described in Zhang et al. (2009).

- Improvements of DNA extraction methods of the fece samples
- 1) Make about 5g of feces (peeled from the surface of each fecal pellet)deactivated in 100% ethanol with volume ratio at room temperature for 12h.
- 2) Vortex the feces and ethanol at 2,200 rpm for 3 min.
- 3) Filtrate the mixture through a piece of sterile gauze.
- 4) Collecte the filtrate and centrifuge it at 3,500 rpm for 15 min.
- 5) Transfer the pellets at the bottom to a new tube for extraction.
- 6) The following can be done as the instructions.

Mitochondrial DNA Amplification

1) Amur tiger species identification(annealing60°C)

Pta-CbF (5-TTTGGCTCCTTACTAGGGGTG-3)

Pta-CbR (5-CCGTAAACAATAGCACAATCCCGATA-3)

2) Amur leopard species identification

Ppo-CbF (5'-GTAAATTATGGCTGAATTATCCGG-3')

Ppo-CbR (5'-CATAACCGTGAACAATAATACGAC-3')

Species identification

- ① 69 fecal samples,5 urine samples, 14 blood samples and 4 hair samples were confirmed to be Amur tigers;
- 2 55 stool samples and 4 urine samples were Amur leopards;
- 3 13 samples will be tested.

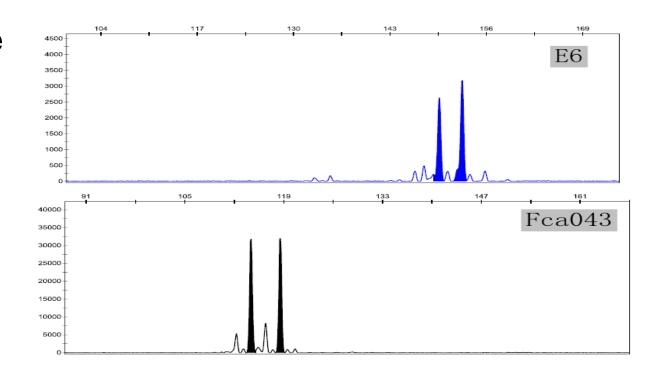
 Characterizations and conditions of polymerase chain reaction for 8 microsatellite loci

微卫星位点	引物 (5'-3')	重复单元	退火温度	PCR产物大小范围	
Microsatellite locus	Primers (5'-3')	Repeat motif	Annealing	PCR product size range (bp)	
			temperature		
			(°C)		
E6	CCTGGGGATAATAAAACTAGTA	(TAA),1	58	147-162	
	CATGAATGAATCTTTACACTGA				
E21B	GCGATAAAGGCTGGCAGAGG	(CA):1	62	154-168	
	CTTTGAGGGTCTGTTCTACTGTGA				
D10	CCCTCTCTGTCCCTCCCTTG	(GT) ₁₄	62	134-150	
	GCCGTTTCCCTCATGCTACA				
Fca304	TCATTGGCTACCACAAAGTAGG	$(GT)_{i}$ $\cdot (GG)_{i} (GT)_{i}$	58	120-134	
	CTGCATGCCATTGGGTAAC				
Fca043	GAGCCACCCTAGCACATATACC		58	116-130	
	AGACGGGATTGCATGAAAAG				
FCA391	GCCTTCTAACTTCCTTGCAGA	(ATGG): (GATA)::(TAGA):TGA(55	190-230	
	TTTAGGTAGCCCATTTTCATCA	TAGA):			
Fca152	TTTAGTCAGCTTAGGCTTCCA	(AC) ₀₁	58	129-147	
	CTTCCCAGCTTCCAGAATTG				
FCA441	ATCCGTAGGTAGGTAGATATAG	(ATAG) ₀ (GTAG) ₁ (ATAG) ₂ AG(AT	58	130-168	
	GCTTGCTTCAAAATTTTCAC	AG):			

PCR conditions

- 1 PCR was set up in a 20 μL system containing 1 × PCR buffer containing 50 mM Tris-HCl (pH 8.0), 25 mM KCl, 0.1 mM EDTA, 1 mM dTT 0.4 mM each of 4 dN; TP (TOYOBO), 0.2 uM each of forward and reverse primer, 0.4 U units of KOD FX Neo DNA polymerase (TOYOBO) and ~80 ng of total DNA.
- ②PCR amplification was performed on a Model 9700 Thermocycler (Perkin-Elmer) using the following program: 1 cycle of 2 min at 94° C, 35 cycles of 98° C for 20 s, annealing temperature (55–62° C, Table 1) for 30 s, 68° C for 20 s, and 1 cycle of 68° C for 20 min.

- •Amplification and analysis methods:
- 1) Ten microsatellite loci were selected for the amplification of field samples by using the fluorescence labeling technique of field sample in this experiment.
 - 2) Analysis the size of the amplified products by using 3100DNA sequencing



Multi-tube PCR-based standard for genotyping

Repeat every sample 3~5 times, when more than twice same cases occur, we regard it as correct.

		first		second		third		fourth		fifth		result	
8	tiger	148.3	150.49	148.32	150.49	148.32	150.59					148	150
9	tiger	148.3	150.49	133. 22	148.21	145.99	148.32	148.33	150.58	148. 23	150.49	148	150
A	В	C	D	E	F	G	H	I	J	K	L	M	N
		first		second		third		fourth		fifth		result	
102	lepord	179.96		126.53	154.13	156.27	158.1	150.67	154.19	150.2	152.15	0	0
106	lepord	156.25	158.22	156.33	162.01	153.85		154.3	156.31	154.17	156.07	0	0

●D10 and FCA391 sites for leopards were discarded due

to poor signal.

	<u>I</u>	D10		FCA391	
20B	lepord	0	0	206	210
21B	lepord	156	160	0	0
24B	lepord	156	158	210	214
28B	lepord	0	0	210	210
30B	lepord	0	0	0	0
33B	lepord	0	0	0	0
34B	lepord	158	160	0	0
35B	lepord	152	162	0	0
36B	lepord	152	162	0	0
63B	lepord	0	0	0	0
64B	lepord	0	0	0	0
65B	lepord	0	0	206	206
66B	lepord	0	0	0	0
67B	lepord	0	0	0	0
68B	lepord	156	158	206	214
69B	lepord	0	0	0	0
70B	lepord	0	0	0	0
71B	lepord	0	0	0	0
73B	lepord	0	0	0	0
74B	lepord	0	0	0	0
75B	lepord	0	0	0	0
76B	lepord	0	0	0	0
77B	lepord	152	162	0	0
79B	lepord	0	0	0	0
מחס	1 J	□	۸	0	0

Probability of Amur leopard individual identification

This is the P(ID) result, we can see from the table that the probability of identifing leopard individuals with 8 loci is quite high, reaching 9.564e-08, and even for sibs, the value can be 1.941e-03

locus	biased/loci	unbias./loc.	sibs/locus	Prod(biased)	Prod(unbias)	Prod(sibs)
E6	1.245e-01	1.087e-01	4. 214e-01	1.245e-01	1.087e-01	4.214e-01
E21	1.823e-01	1.629e-01	4.764e-01	2.270e-02	1.770e-02	2.008e-01
FCA304	1.006e-01	8.625e-02	3.980e-01	2.282e-03	1.527e-03	7.990e-02
FCA043	3.065e-01	2.957e-01	5.528e-01	6.996e-04	4.514e-04	4.417e-02
FCA152	4.222e-01	3.905e-01	6.765e-01	2.954e-04	1.763e-04	2.989e-02
FCA441	5.793e-02	4.553e-02	3.554e-01	1.711e-05	8.025e-06	1.062e-02
F53	8.698e-02	7.322e-02	3.850e-01	1.488e-06	5.876e-07	4.089e-03
F85	1.816e-01	1.628e-01	4.747e-01	2.703e-07	9.564e-08	1.941e-03

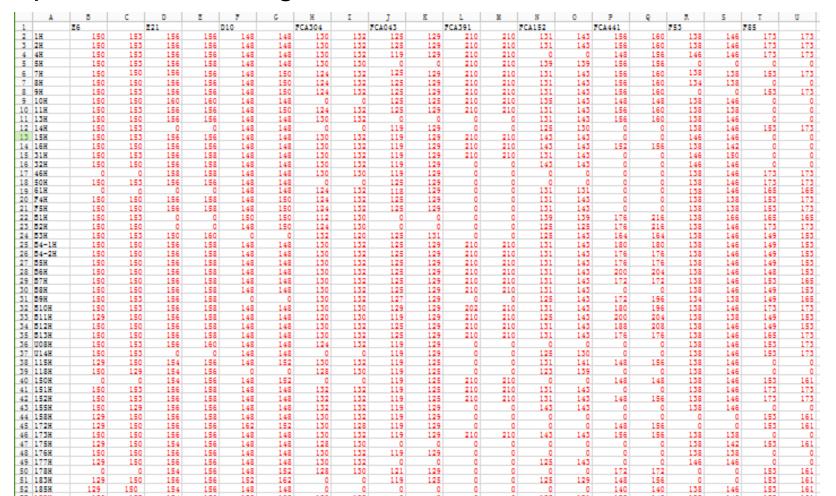
 Genotypes of 8 microsatellite loci of all samples for leopards.

A	В	С	D	E	F	G	Н	I	J	K	L	М	N	0	P	Q
1	E6		E21]	FCA304		FCAO43		FCA152		FCA441		F53	F	785	
2 21B	150	153	156	162	112	114	115	119	125	125	0	0	0	0	0	0
3 24B	0	0	156	162	0	0	115	119	125	125	140	148	0	0	149	153
4 28B	150	153	0	0	0	0	119	119	125	125	156	156	0	0	153	161
5 36B	0	0	156	166	112	114	115	119	125	125	0	0	126	134	149	153
6 63B	153	153	162	156	112	114	115	119	125	125	140	140	126	134	149	153
7 65B	153	150	0	0	112	114	115	119	125	125	148	148	126	134	149	153
8 66B	150	153	156	162	112	114	115	119	125	125	0	0	126	138	149	153
9 67B	0	0	0	0	0	0	115	119	125	125	140	152	122	122	153	157
10 68B	153	153	156	162	112	114	115	119	125	125	0	0	126	134	149	153
11 69B	0	0	156	158	112	114	115	119	125	125	140	152	122	122	153	157
12 70B	129	150	0	0	0	0	115	119	125	125	132	132	126	134	0	0
13 71B	150	147	154	156	0	0	115	119	125	139	148	148	0	0	153	153
14 74B	153	153	154	156	112	114	115	119	125	125	0	0	126	134	149	153
15 80B	150	153	0	0	0	0	115	115	121	123	140	148	126	138	0	0
16 88B	0	0	0	0	0	0	115	119	125	125	152	152	122	122	153	157
17 89B	153	159	156	158	112	114	115	119	125	125	148	148	122	122	153	157
18 90B	0	0	0	0	112	114	115	119	125	125	0	0	126	134	149	153
19 96B	129	132	0	0	112	114	115	119	125	125	0	0	146	138	149	153
20 98B	153	153	0	0	112	114	115	119	125	125	0	0	126	134	149	153
21 101B	153	153	156	162	112	114	115	119	125	125	140	148	126	134	149	153
22 106B	150	150	0	0	130	128	119	127	0	0	156	152	146	146	0	0
23 107B	153	153	156	162	112	114	115	119	0	0	0	0	126	134	149	153
24 V16B	153	159	156	156	0	0	115	119	125	125	0	0	126	138	0	0
25 V17B	153	159	0	0	0	0	115	119	125	131	156	156	138	126	0	0
26 121B	129	150	154	156	0	0	0	0	125	139	140	136	126	138	0	0
27 124B	0	0	0	0	132	128	119	115	0	0	140	152	138	146	149	153
28 125B	129	132	154	156	114	112	115	119	125	131	0	0	126	134	161	153
29 126B	150	153	0	0	128	130	0	0	123	129	172	176	0	0	153	161
30 161B	153	159	154	156	0	0	115	119	131	141	0	0	122	122	153	161
31 162B	129	150	154	156	130	132	119	125	0	0	140	156	0	0	153	161
32 163B	150	153	154	156	130	128	0	0	0	0	0	0	126	138	153	161
33 164B	129	150	154	156	130	132	0	0	0	0	140	148	126	138	153	161
34 166B	129	150	154	156	130	128	0	0	0	0	172	172	0	0	153	161
35 167B	129	150	154	156	130	132	0	ō	Ō	Ō		172	126	138	153	161
36 169B	129	132	0	0	0	0	119	125	Ō	Ō		156	138	146	153	161
37 171B	129	150	ō	Ō	128	130	0	0	125	129		0		138	153	161

● Probability of Amur Tiger individual identification This is the P(ID) result, we can see from the table that the probability of identifying tiger individuals with 10 loci is also high, reaching 7.714e-08, and for sibs, the value is 1.555e-03.

locus	biased/loci	unbias./loc.	sibs/locus	Prod(biased)	Prod(unbias)	Prod(sibs)
E6	3.408e-01	3.238e-01	6.057e-01	3.408e-01	3.238e-01	6.057e-01
E21	2.781e-01	2.614e-01	5.588e-01	9.476e-02	8.464e-02	3.384e-01
D10	4.722e-01	4.527e-01	7.050e-01	4.474e-02	3.831e-02	2.386e-01
FCA304	1.717e-01	1.605e-01	4.600e-01	7.681e-03	6.148e-03	1.097e-01
FCA043	1.708e-01	1.607e-01	4.560e-01	1.312e-03	9.883e-04	5.004e-02
FCA391	9.267e-01	9.230e-01	9.628e-01	1.216e-03	9.122e-04	4.818e-02
FCA152	1.593e-01	1.474e-01	4.525e-01	1.937e-04	1.344e-04	2.180e-02
FCA441	2.821e-02	2.062e-02	3.218e-01	5.465e-06	2.772e-06	7.016e-03
F53	2.895e-01	2.805e-01	5.439e-01	1.582e-06	7.777e-07	3.815e-03
F85	1.098e-01	9.920e-02	4.075e-01	1.737e-07	7.714e-08	1.555e-03

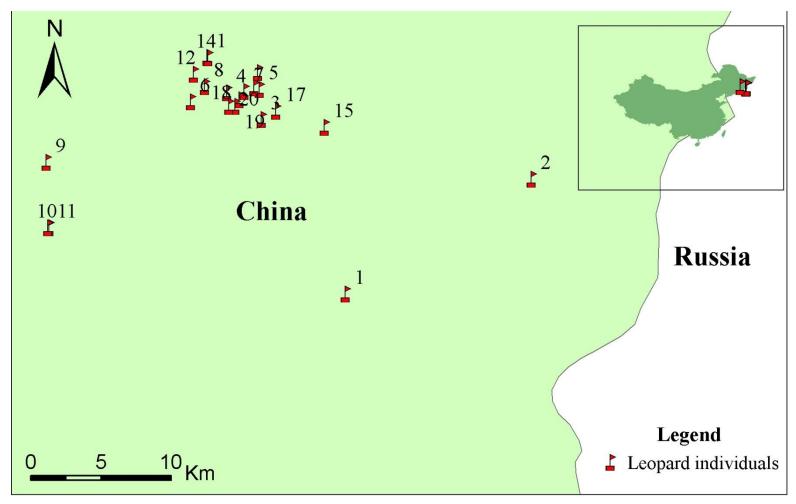
 The amplification result of the 10 locis of amur tiger is acceptable for Amur tigers.



Individualization determination principles

Using MStools to distinguish the samples with the same genotype, the main principle is to determine the same individual if all the locis of them are the same or only one loci is different at most.

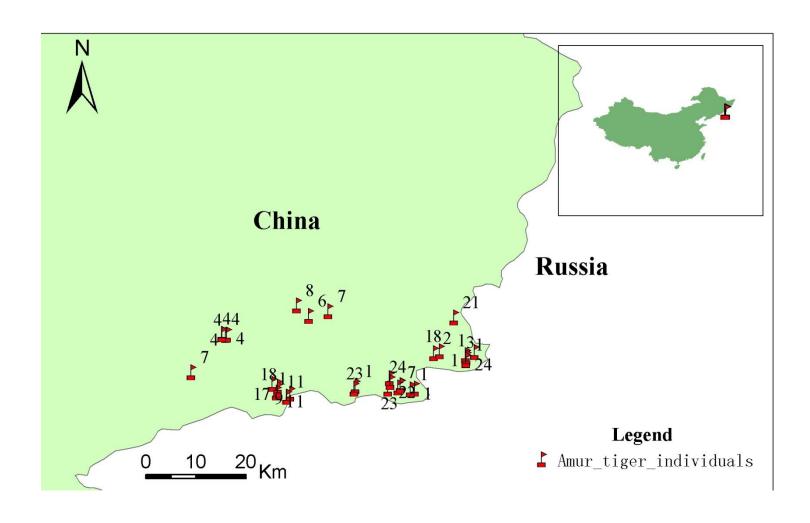
- 3. Analysis results of the samples.
- The 36 samples were determined to be 21
 Amur leopards and their spatial distribution.



- 3. Analysis results of the samples.
- Genetic diversity of Amur leopards
- The Characteristics of the 8 microsatellites in wild leopard population, and their overall HO is higher than the HE.
- 2 Most of the PIC values of microsatellites are above 0.5, which indicates that the microsatellite of leopard has a high polymorphism.

Locus E E2 FCA30 FCA04 FCA15 FCA44	k N 6 5 5 4 7	29 21 24 29 27 27	HObs 0.759 0.952 1.000 0.931 0.296 0.500	HExp 0.732 0.654 0.770 0.557 0.365 0.837	PIC 0.674 0.587 0.714 0.446 0.348 0.793
FCA44	8	22	0.500	0.837	0. 793
F5	5	29	0. 793	0.787	0. 738
F8	4	29	0.966	0.653	0.588

- 3. Analysis results of the samples.
- The 51 samples were determined to be 24 Amur tigers and their spatial distribution.



- The overall level of HO is greater than HE for Amur tigers.
- 2 The average value of PIC is 0.506, indicating that the loci of tiger has a high polymorphism.

Locus E E2 D1 FCA30 FCA39 FCA15 FCA44 F5	k N 3 5 4 7 6 2 8 16 6	47 47 48 45 40 40 33 45	HObs 0.596 0.596 0.271 0.867 0.953 0.038 0.775 0.636	HExp 0.464 0.527 0.330 0.673 0.681 0.038 0.884 0.563	PIC 0. 411 0. 472 0. 308 0. 606 0. 609 0. 037 0. 621 0. 859 0. 464
15 F8	ь 5	45 36	0.756 0.694	0.563 0.750	0.464 0.698
1- 0	•	00	V. VDI	V. 100	V. VDO

Sex determination

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Sex primer(56°Cannealing)

ZFX-PF (5'-TACCGAGCGATATAGCTCCAG-3')

ZFX-PR (5'-GTGTTCCTACGTTAAGCTATTG-3')

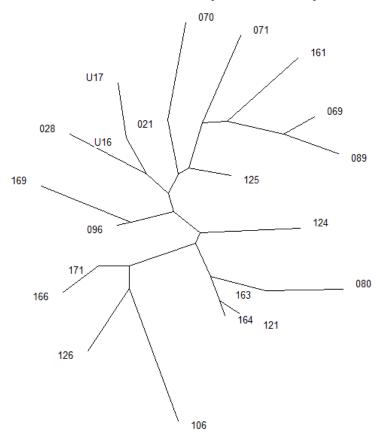
DBY7-PF (5'-CTCATGAAGCCCTATTTTTGGTTG-3')

DBY7-PR (5 '-ACGGCGTCCGTATCTTCCA-3')
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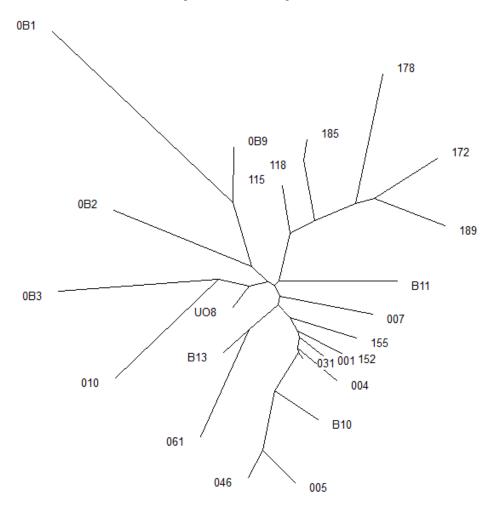
This is the results of tigers' and leopard's gender confirmed.

样品编号	物种	性别	样品编号	物种	性别
Samples	species	Sex	Samples	species	Sex
1	tiger	雄性	21	1eopard	雄性
7	tiger	雄性	67	1eopard	雄性
4	tiger	雌性	162	1eopard	雄性
31	tiger	雄性	166	1eopard	雌性
175	tiger	雄性	70	1eopard	雄性
B1	tiger	雌性	71	1eopard	雄性
B3	tiger	雌性	80	1eopard	雄性
B10	tiger	雄性	89	1eopard	雄性
B13	tiger	雄性	96	1eopard	雌性
B11	tiger	雄性	U16	leopard	雌性

 Tree of genetic relationship of wild Amur leopard individuals (n=21).



- 3. Analysis results of the samples.
- Tree of genetic relationship of wild Amur tiger individuals (n=24).



4. Summary

- 1) Based on this research, we can confirm that at least 21 Amur leopards and 24 Amur tigers are living in China until now;
- 2) According to the preliminary genetic information, we also know that the population of tiger and leopard have a high gene diversity;
- 3) Sex can be determined by non-invasive methods;
- 4) Relationships among individuals can be confirmed across the range;
- 5) Need to compare the individuals near the Sino-Russia border areas to confirm the corridor positon and continue to collect the samples in field for disease, gene and food habitat detections in future.

