Supplementary Materials and Methods

Fish collection

Specimens collected from Lake Fuxian in 1986 and 1988 and deposited in KIZ were used as wild populations in morphometric analysis. Recaptured fish were collected from the northwest (F northwest), west (F west), east (F east), and south (F south) coast of Lake Fuxian in 2017. The aquafarms around Lake Fuxian raising hatchery fish for reintroduction included Jiuxi, Huoyanshan, Niumo, Luchong and Haikou. Due to a lack of management, samples from Haikou were third generation (F3), whereas others were first generation (F1). Five populations (EFCC001-005) were collected from the Endangered Fish Conservation Center and cultured in separate ponds under the same conditions. EFCC001 and EFCC002 were wild populations introduced from Lake Fuxian as broodstock in 2000, and the population numbers have remained almost unchanged for 20 years. EFCC003 was derived from the Haikou aquafarm (F1) in 2004, and EFCC004 and EFCC005 were the offspring of EFCC003 produced in 2014 and 2015 at EFCC, respectively. Details on these 14 populations are shown in Table 1. All animal experiments were approved by the Ethics and Experimental Animal Committee of the Kunning Institute of Zoology, Chinese Academy of Sciences (Approval ID: SMKX-2016024; approved on 15 December 2016).

Body shape based on traditional measurements

Measurements were carried out using digital calipers on the left side of specimens, and data were recorded to the nearest 0.01 mm. At least 30 individuals, except for specimens collected in 1986 (29 individuals) and 1988 (26 individuals), were tested in each population. Morphometrics included standard length (SL), body depth (BD), caudal-peduncle length (CPL), caudal-peduncle depth (CPD), head length (HL), snout length (SnL), and eye diameter (ED), which were measured and expressed as mean \pm standard deviation (SD). To estimate whether body shape changed among populations, values of SL/BD, SL/HL, SL/CPL, SL/CPD, HL/SnL, HL/ED, and CPL/CPD were calculated. These seven variables formed the input data for principal component analysis (PCA) using SPSS 19.0 (SPSS for Windows, Chicago, IL, USA). Morphometrics changes were determined by one-way analysis of variance (ANOVA) of measured data, followed by Tukey's *post-hoc* test (P<0.05). Normality was evaluated before statistical analysis using the Kolmogorov-Smirnov test.

Skeletal deformity radiography

In addition to body shape measurements, all specimens were photographed to determine the incidence of skeletal deformity using the Digital Cabinet X-ray System (Xpeart 80, Kubtec, 270 Rowe Avenue, Unit E Milford, CT 06461, USA). Different settings were used according to different body size of the specimens. Skeletal deformities of the skull, vertebra, rib, neural arch and spine, and hemal arch and spine (Patterson & Johnson, 1995) were checked. Pearson correlation was used to test the correlation between skeletal deformity rates of recaptured fish and distance between recapture sites and release sites. The correlation coefficient (r) was used to determine the intensity of the association.

DNA extraction and genetic analysis of mtDNA Cytb and microsatellites

Total DNA was extracted from alcohol-preserved fish fins using standard methods (Sambrook et al., 1989). The DNA concentration was determined using a UV-Vis spectrophotometer (NanoDrop 2000c; Thermo Scientific, USA). Samples were diluted in ultrapure water as required for each molecular marker used (i.e., 10 $ng/\mu L$ for microsatellite markers and 5 $ng/\mu L$ for mtDNA *Cytb* markers). Fragments of the mitochondrial gene Cytb were amplified using primers L14724 (5'-GACTTGAAAAACCACCGTTG-3') and H15915 (5'-CTCCGATCTCCGGATTACAAGAC-3') (Xiao et al., 2001) with the following polymerase chain reaction (PCR) procedure: initial denaturing step at 95 °C for 4 min; 35 cycles of denaturing at 95 °C for 1 min, annealing at 56 °C for 1 min, and extension at 72 °C for 1 min; with a final extension step at 72 °C for 10 min (n=10 in each population). Sequences were aligned with ClustalW, with default gap penalties implemented as a tool in MEGA X (Kumar et al., 2018). Inter- and intraspecific mtDNA sequence divergences of Kimura's two-parameter (K2P) model were calculated by MEGA X with the transition/transversion ratio equally weighted. Genetic diversity parameters, i.e., haplotype diversity (H) and nucleotide diversity (Pi), were calculated using DnaSP v.5 (Librado & Rozas, 2009). Arlequin 3.5.1.3 (Excoffier et al., 1992) was used to determine haplotypes, estimate haplotype frequency, and test selective neutrality using the infinite sites model in Tajima (D)(Tajima, 1989) and Fu (Fs) (Fu, 1997).

Based on the recently annotated genome scaffolds of *A. grahami*, 11 loci for microsatellite analysis were identified (Supplementary Table S14) (Jiang et al., 2018).

PCR was first carried out in a 12.5 µL reaction volume using the following amplification profile: 4 min at 94 °C, 35 cycles of 30 s at 94 °C, 35 s at 57 °C, 40 s at 72 °C, followed by a final extension step of 10 min at 72 °C. The PCR procedures in the second and third steps were performed with the same conditions as those in the first step, except using fluorescent labeled reverse primers (6-FAM, HEX) instead of the regular primers, and using 1:(40-100) dilution of the first PCR product as the DNA template according to the brightness relative to standard DNA marker-referred electrophoretic stripes. All PCR products were then genotyped on an ABI 3730x1 genetic analyzer with Gene-Scan LIZ-500 (Applied Biosystems, USA) as the internal size standard, and scored with GeneMarker (SoftGenetics, USA). Genotyping errors associated with microsatellite analysis, such as stutter bands, large allele dropout, and null alleles, were detected using MICRO-CHECKER (v2.2.3) (Van Oosterhout et al., 2004). CERVUS (v3.0.7) (Kalinowski et al., 2007) was employed to find matching pairs of genotypes and calculate basic genetic parameters, including number of alleles (Na), number of effective alleles (Ne), polymorphism information content (PIC), observed and expected heterozygosities (Ho and He), and null allele frequencies. Inbreeding coefficient (Fis) tests and deviations from the Hardy-Weinberg equilibrium (HWE) were performed with GENEPOP (v4.7.0) (Rousset, 2008).

Arlequin v3.5.1.3 (Excoffier & Lischer, 2010) was used for AMOVA to estimate the partitioning of genetic variation within and between samples (or populations) applied to markers of *Cytb* and microsatellites. AMOVA was also used to calculate the genetic differentiation between populations (Excoffier et al., 1992) using the UST index (Weir & Cockerham, 1984) with pairwise comparisons. Estimates of significance were conducted based on 10 000 permutations.

To clarify the relationships of haplotypes for *Cvtb*, a median-joining (MJ) 1999) approach (Bandelt et al.. used in Network (v.5.0)was (http://www.fluxus-engineering.com/) with specific transition/transversion (Ti/Tv) ratios for each gene locus calculated from MEGA X. Genotypic clustering was performed using STRUCTURE (v2.2) (Pritchard et al., 2000) based on microsatellite data. The number of genetic groups (K) was set from 1 to 10. A total of $10\,000$ MCMC repetitions of burn-in and 20 000 MCMC subsequent replicates were employed. The optimum value of K was defined using the delta K approach (Evanno et al., 2005) by examining changes in Ln P(D).

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Supplementary Figures



Supplementary Figure S1 Scatter plots of first three principal components based on morphometric data of different populations of *A. grahami*



Supplementary Figure S2 Body shape of different populations of *A. grahami* A, B, and C are individuals collected in the 1980s and in 2017 from Lake Fuxian and Jiuxi aquafarm, respectively.



Supplementary Figure S3 Types of skeletal deformity in A. grahami

Normal skeleton is shown in (a), and deformities are shown in (b), jaw, (c), neural arch and spine, (d), hemal arch and spine, (e) vertebra, (f), rib, (g) and (h), multiple positions of skeleton.



Supplementary Figure S4 Skeletal deformity rate in each population of A. grahami



Supplementary Figure S5 Relationship between distance from release site and rate of skeletal deformity in *A. grahami*



Supplementary Figure S6 Pearson correlation between skeletal deformity rates in recaptured individuals and distance between recapture sites and release sites in A. *grahami*. r (correlation coefficient) and P values were used to verify the intensity of associations among variables and level of significance, respectively.



Supplementary Figure S7 Median network based on haplotypes showing relationships among *A. grahami* populations

Lake Fuxian, recaptured from coast of northwest, west, east, and south of Lake Fuxian. Endangered Fish Conservation Center, EFCC001, EFCC002, EFCC003, EFCC004, and EFCC005. Five aquafarms around Lake Fuxian, i.e., Jiuxi, Huoyanshan, Niumo, Luchong, and Haikou.

Supplementary Tables

Supplementary Table S1 Morphometric data for each population of A. grahami

Population name	SL (mm)	BD (mm)	HL (mm)	SnL (mm)	ED (mm)	CPL (mm)	CPD (mm)
Specimens in 1986	118.15±11.40	19.10±2.24	30.38±2.84	8.38±1.25	6.45±0.91	22.79±2.53	7.72±0.72
Specimens in 1988	120.17±36.36	20.40±6.84	30.56±8.22	8.71±2.52	6.72±1.14	23.45±6.02	8.08±2.36
EFCC001	175.51±17.55	33.19±5.27	40.14±3.51	11.53±1.41	9.16±0.74	33.06±4.89	12.05±1.17
EFCC002	176.13±17.46	33.84±5.42	40.59±3.49	11.75±1.64	9.00±0.81	33.17±5.28	12.18±1.40
EFCC003	152.99±20.43	30.00±3.11	37.89±4.61	10.23±1.39	9.03±1.41	25.55±5.58	11.50±1.30
EFCC004	76.30±18.48	13.11±3.85	18.95±3.86	5.03±1.18	5.17±0.97	15.88±3.83	5.75±1.62
EFCC005	135.65±15.98	24.88±3.30	33.19±4.33	8.96±1.68	7.71±1.11	21.80±3.11	9.78±1.19
F_Northwest	113.51±10.13	21.78±2.50	26.02±2.43	6.91±0.95	5.97±0.75	21.26±3.60	9.48±1.25
F_West	122.51±19.60	23.85±2.91	29.28±5.18	8.41±1.62	6.80±1.10	21.76±5.03	9.52±1.30
F_East	106.38±14.16	20.10±3.35	24.08±3.37	6.16±0.95	5.82±0.67	21.24±3.07	8.66±1.35
F_South	109.70±8.30	21.55±1.65	25.14±2.28	6.65±1.05	5.90±0.55	22.17±3.37	8.92±0.80
Jiuxi	76.29±4.80	14.57±1.57	18.91±1.29	4.96±0.87	4.71±0.39	14.01±1.72	6.35±0.64
Huoyanshan	75.60±8.89	13.58±2.25	18.44±1.89	5.27±0.57	5.39±0.86	12.14±2.26	5.99±0.91
Niumo	81.75±16.09	15.16±3.48	20.84±4.11	5.83±1.19	5.57±1.20	12.37±2.52	6.38±1.23
Luchong	98.81±11.59	19.45±2.97	23.93±2.28	6.47±0.82	6.36±0.84	16.23±2.54	7.74±1.17
Haikou	71.53±12.89	13.90±2.73	18.31±3.22	4.80±1.23	4.58±0.75	11.29±2.80	5.73±1.08

Standard length (SL), body depth (BD), caudal-peduncle length (CPL), caudal-peduncle depth (CPD), head length (HL), snout length (SnL) and eyes diameter (ED).

1 1	8						
Population name	ST/BD	ST/HL	ST/CPL	ST/CPD	HL/SnL	HL/ED	CPL/CPD
Specimens in 1986	6.22±0.43ª	3.89±0.22	$5.20{\pm}0.38^{\rm fg}$	15.35±1.08	3.67±0.40	4.76±0.43	2.96±0.26ª
Specimens in 1988	5.95±0.36 ^b	3.91±0.26	$5.10{\pm}0.54^{\rm fg}$	14.86±1.06	3.54±0.34	4.52±0.70	2.94±0.33ª
EFCC001	5.35±0.46 ^{de}	4.39±0.41	$5.36{\pm}0.43^{ef}$	14.61±1.06	3.51±0.33	4.40±0.35	2.74±0.22 ^b
EFCC002	5.26±0.46 ^{de}	4.35±0.40	$5.37{\pm}0.44^{\text{ef}}$	14.50±0.88	3.49±0.28	4.53±0.40	2.72±0.24 ^b
EFCC003	5.09±0.31°	4.05±0.35	6.11±0.70°	13.31±0.98	3.74±0.40	4.22±0.32	2.21±0.34 ^d
EFCC004	5.96±0.90 ^b	4.01±0.26	$4.84{\pm}0.51^{h}$	13.52±1.73	3.82±0.40	3.66±0.26	2.83±0.45 ^{ab}
EFCC005	5.48±0.39 ^{cd}	4.10±0.30	6.26±0.55 ^{bc}	13.89±0.77	3.77±0.41	4.32±0.29	$2.24{\pm}0.27^{d}$
F_Northwest	5.24±0.39 ^{de}	4.37±0.24	5.44±0.69 ^{de}	12.08±1.19	3.80±0.35	4.39±0.41	$2.26{\pm}0.37^{d}$
F_West	5.13±0.40 ^e	4.21±0.34	5.73±0.56 ^d	12.87±1.05	3.51±0.40	4.30±0.31	$2.28{\pm}0.34^{d}$
F_East	5.33±0.36 ^{de}	4.44±0.40	5.03±0.41 ^{gh}	12.37±1.03	3.94±0.43	4.15±0.38	2.47±0.27°
F_South	5.11±0.38e	4.38±0.36	5.02±0.56 ^{gh}	12.35±0.92	3.83±0.39	4.28±0.31	2.49±0.36°
Jiuxi	5.28±0.50 ^{de}	4.05±0.26	5.50±0.59 ^{de}	12.10±1.10	3.90±0.50	4.03±0.27	2.22 ± 0.30^d
Huoyanshan	5.61±0.30°	4.10±0.18	6.32±0.66 ^{bc}	12.70±0.78	3.52±0.32	3.47±0.35	2.02±0.19 ^{ef}
Niumo	5.43±0.31 ^{cd}	3.92±0.17	6.65±0.61ª	12.83±0.83	3.60±0.29	3.78±0.39	$1.94{\pm}0.18^{\rm f}$
Luchong	5.13±0.38e	4.12±0.19	6.15±0.54°	12.91±1.44	3.72±0.31	3.80±0.42	2.12±0.29 ^{de}

Supplementary Table S2 Ratios calculated by morphometric data for each population of *A. grahami*

Bars bearing different letters differ significantly from each other at P<0.05. Standard length (SL), body depth (BD), caudal-peduncle length (CPL), caudal-peduncle depth (CPD), head length (HL), snout length (SnL) and eyes diameter (ED).

12.55±1.04

 $3.93{\pm}0.57$

4.00±0.26

 $1.96{\pm}0.29^{\mathrm{ef}}$

 $6.51{\pm}0.89^{ab}$

Haikou

5.17±0.36e

 $3.92{\pm}0.39$

	Initial	Extraction
CPL/CPD	1	0.933
SL/SD	1	0.776
SL/CPL	1	0.733
SL/CPD	1	0.718
HL/SnL	1	0.689
HL/ED	1	0.651
SL/HL	1	0.624

Supplementary Table S3 Primary factor analysis results

Standard length (SL), body depth (BD), caudal-peduncle length (CPL), caudal-peduncle depth (CPD),

head length (HL), snout length (SnL) and eyes diameter (ED).

Component	Initial eiger	ivalues		Extraction sums of squared			Rotation sums of squared loadings			
				loadings	loadings					
	Total	% of	Cumulativ	Total	% of	Cumulativ	Total	% of	Cumulati	
		variance e %			variance	e %	e %		ve %	
1	2.542	36.31	36.31	2.542	36.31	36.31	2.088	29.824	29.824	
2	1.536	21.95	58.26	1.536	21.95	58.26	1.529	21.847	51.671	
3	1.045	14.926	73.186	1.045	14.926	73.186	1.506	21.516	73.186	
4	0.832	11.893	85.079							
5	0.617	8.819	93.898							
6	0.415	5.933	99.831							
7	0.012	0.169	100							

Supplementary Table S4 Total explained variance

Population	No. of checked	No. of deformity	Deformity rate (%)
Specimens in 1986	29	0	0
Specimens in 1988	26	0	0
EFCC001	30	0	0
EFCC002	30	0	0
EFCC003	32	0	0
EFCC004	36	0	0
EFCC005	30	0	0
F_Northwest	33	0	0
F_West	58	11	19
F_East	40	5	12.5
F_South	43	0	0
Jiuxi	45	2	4.4
Huoyanshan	41	2	4.9
Niumo	47	4	8.5
Luchong	30	15	50
Haikou	31	14	45.2

Supplementary Table S5 Skeletal deformities in each population of A. grahami

Population		Type of deformity											
	Jaw	Vertebra	Rib	Neural arch	Haemal arch and	United							
				and spine	spine								
F_west	0	2	1	3	1	4							
F_east	0	3	0	1	0	1							
Jiuxi	0	0	0	1	0	1							
Huoyanshan	0	0	0	1	0	1							
Niumo	1	0	1	1	1	0							
Luchong	1	2	0	1	1	10							
Haikou	0	4	0	0	0	10							

Supplementary Table S6 Details on deformity types in each population of A. grahami

Population	Н	Pi	D	Fs
EFCC001	0.733	0.00284	0.161	1.492
EFCC002	0.867	0.00283	-1.73	-3.033
EFCC003	0.778	0.00297	-0.158	-0.763
EFCC004	0.956	0.00459	-0.97	-2.127
EFCC005	0.911	0.00431	-0.873	-1.691
F_Northwest	0.956	0.00593	-0.096	-1.452
F_West	0.933	0.00449	0.049	-0.915
F_East	0.956	0.00466	-0.682	-2.088
F_South	0.933	0.00578	-0.515	-1.517
Jiuxi	0.911	0.00683	-0.226	0.072
Huoyanshan	0.844	0.007	0.116	1.287
Niumo	0.822	0.00601	0.464	2.164
Luchong	0.533	0.00352	-0.636	2.059
Haikou	0.778	0.00475	-0.035	0.346

Supplementary Table S7 Genetic diversity of 14 populations of *A. grahami* based on cyt *b*

	1	2	3	4	5	6	7	8	9	10	11
1	0.005										
2	0.005	0.003									
3	0.005	0.005	0.005								
4	0.005	0.004	0.004	0.003							
5	0.004	0.004	0.003	0.003	0.002						
6	0.005	0.004	0.004	0.003	0.003	0.003					
7	0.005	0.007	0.006	0.006	0.006	0.007	0.005				
8	0.006	0.007	0.006	0.007	0.006	0.007	0.006	0.007			
9	0.006	0.007	0.006	0.006	0.006	0.007	0.006	0.007	0.007		
10	0.006	0.008	0.006	0.007	0.006	0.007	0.004	0.006	0.005	0.004	
11	0.006	0.007	0.006	0.007	0.006	0.007	0.005	0.007	0.006	0.005	0.006

Supplementary Table S8 Inter- and intraspecific pairwise Kimura's two-parameter genetic distances among populations

1, Lake Fuxian, 2, EFCC001, 3, EFCC002, 4, EFCC003, 5, EFCC004, 6, EFCC005, 7, Haikou, 8, Huoyanshan, 9, Jiuxi, 10, Luchong, 11, Niumo.

Populations	Ν	Na	Ne	Но	Не	PIC	Fis	<i>P</i> (HWE)
F_west	30	2.818±0.936	1.605±0.379	0.418±0.172	0.353±0.129	0.300±0.111	-0.188±0.124	0.384
F_northwest	30	3.364±1.432	1.726±0.562	0.427±0.233	0.394±0.158	0.343±0.141	-0.057±0.201	0.000*
F_east	30	2.727±0.750	1.657±0.439	0.436±0.231	0.389±0.149	0.331±0.129	-0.084±0.241	0.008
F_south	30	2.818±0.833	1.686±0.563	0.458±0.232	0.373±0.163	0.322±0.145	-0.211±0.113	0.02
EFCC001	30	3.273±1.286	1.778±0.444	0.467±0.174	0.411±0.143	0.348±0.123	-0.138±0.117	0.075
EFCC002	30	3.000±1.128	1.680±0.427	0.473±0.233	0.376±0.149	0.318±0.127	-0.264±0.181	0.000*
EFCC003	30	2.636±0.643	1.682±0.407	0.382±0.192	0.366±0.154	0.308±0.125	-0.058±0.181	0.72
EFCC004	30	2.909±0.793	1.570±0.362	0.300±0.150	0.324±0.154	0.278±0.124	0.054±0.174	0.539
EFCC005	30	2.636±0.643	1.581±0.330	0.309±0.135	0.326±0.151	0.274±0.120	0.029±0.162	0.952
Jiuxi	30	2.545±0.498	1.652±0.321	0.476±0.191	0.377±0.126	0.314±0.099	-0.267±0.135	0.073
Huoyanshan	30	3.000±0.853	1.690±0.356	0.449±0.174	0.390±0.122	0.334±0.108	-0.153±0.144	0.835
Niumo	30	2.818±1.192	1.613±0.467	0.385±0.209	0.339±0.172	0.285±0.147	-0.137±0.182	0.094
Luchong	30	2.818±0.936	1.606±0.353	0.391±0.178	0.354±0.139	0.298±0.110	-0.009±0.190	0.687
Haikou	30	2.636±0.481	1.715±0.364	0.358±0.134	0.396±0.137	0.327±0.106	0.098±0.156	0.194

Supplementary Table S9 Information on genetic diversity of 14 populations of *A*. *grahami* based on microsatellites

*: P<0.001.

0										
Population	Locus	N	Na	Ne	Но	Не	PIC	Fis	P(HWE)	Null freq
F_west	SSR01	30	2	1.180	0.167	0.155	0.141	-0.074	1.000	-0.036
	SSR03	30	2	1.600	0.433	0.381	0.305	-0.139	0.640	-0.072
	SSR06	30	2	1.557	0.467	0.364	0.294	-0.289	0.295	-0.131
	SSR07	30	4	1.592	0.433	0.378	0.324	-0.149	0.011	-0.065
	SSR10	30	3	1.265	0.233	0.213	0.193	-0.097	1.000	-0.056
	SSR12	30	4	1.639	0.500	0.397	0.337	-0.266	0.579	-0.137
	SSR13	30	2	1.763	0.633	0.440	0.339	-0.450	0.028	-0.188
	SSR15	30	4	1.522	0.400	0.349	0.321	-0.150	1.000	-0.102
	SSR16	30	2	1.600	0.367	0.381	0.305	0.039	1.000	0.011
	SSR17	30	4	2.723	0.767	0.644	0.576	-0.195	0.265	-0.093
	SSR18	30	2	1.220	0.200	0.183	0.164	-0.094	1.000	-0.046
F_northwest	SSR01	30	3	1.394	0.267	0.288	0.251	0.074	0.592	0.024
	SSR03	30	2	1.514	0.433	0.381	0.305	-0.063	1.000	-0.072
	SSR06	30	3	2.096	0.433	0.532	0.448	0.188	0.134	0.098
	SSR07	30	2	1.342	0.300	0.259	0.222	-0.160	1.000	-0.078
	SSR10	30	3	1.307	0.267	0.239	0.214	-0.118	1.000	-0.066
	SSR12	30	6	3.000	1.000	0.678	0.606	-0.487	0.000	-0.224
	SSR13	30	2	1.471	0.333	0.364	0.294	0.183	0.307	0.035
	SSR15	30	4	1.363	0.400	0.349	0.321	-0.111	1.000	-0.102
	SSR16	30	6	1.800	0.333	0.452	0.401	0.266	0.003	0.144
	SSR17	30	4	2.561	0.767	0.637	0.566	-0.132	0.285	-0.098
	SSR18	30	2	1.142	0.167	0.155	0.141	-0.055	1.000	-0.036
F_east	SSR01	30	2	1.105	0.167	0.155	0.141	-0.036	1.000	-0.036
	SSR03	30	2	1.471	0.433	0.381	0.305	-0.025	1.000	-0.072
	SSR06	30	3	1.972	0.567	0.501	0.420	-0.133	0.529	-0.087

Supplementary Table S10 Details of 11 loci on genetic diversity in each population of *A. grahami*

	SSR07	30	3	1.484	0.400	0.332	0.283	-0.210	0.634	-0.108
	SSR10	30	3	1.350	0.300	0.264	0.233	-0.140	1.000	-0.076
	SSR12	30	3	2.597	0.967	0.625	0.545	-0.560	0.000	-0.260
	SSR13	30	2	1.514	0.367	0.381	0.305	0.133	0.589	0.011
	SSR15	30	4	1.416	0.333	0.299	0.278	-0.118	1.000	-0.083
	SSR16	30	2	1.835	0.233	0.463	0.351	0.500	0.012	0.322
	SSR17	30	4	2.267	0.767	0.644	0.576	-0.057	0.403	-0.093
	SSR18	30	2	1.220	0.267	0.235	0.204	-0.094	1.000	-0.067
F_south	SSR01	30	2	1.180	0.167	0.155	0.141	-0.074	1.000	-0.036
	SSR03	30	2	1.514	0.433	0.381	0.305	-0.063	1.000	-0.072
	SSR06	30	3	1.779	0.600	0.445	0.367	-0.356	0.121	-0.169
	SSR07	30	3	1.307	0.267	0.239	0.214	-0.118	1.000	-0.066
	SSR10	30	2	1.220	0.267	0.235	0.204	-0.094	1.000	-0.067
	SSR12	30	4	3.098	0.967	0.689	0.619	-0.413	0.000	-0.191
	SSR13	30	2	1.684	0.500	0.413	0.324	-0.215	0.376	-0.104
	SSR15	30	4	1.468	0.367	0.324	0.300	-0.133	1.000	-0.093
	SSR16	30	3	1.575	0.467	0.371	0.309	-0.263	0.444	-0.129
	SSR17	30	4	2.459	0.767	0.644	0.576	-0.107	0.225	-0.093
	SSR18	30	2	1.260	0.233	0.210	0.185	-0.115	1.000	-0.057
EFCC001	SSR01	30	2	1.180	0.167	0.155	0.141	-0.074	1.000	-0.036
	SSR03	30	2	1.835	0.433	0.463	0.351	0.065	1.000	0.024
	SSR06	30	5	2.835	0.667	0.658	0.585	-0.013	0.000	-0.018
	SSR07	30	3	1.638	0.467	0.396	0.335	-0.182	0.238	-0.080
	SSR10	30	2	1.220	0.200	0.183	0.164	-0.094	1.000	-0.046
	SSR12	30	4	2.110	0.733	0.535	0.466	-0.380	0.061	-0.198
	SSR13	30	4	1.496	0.400	0.337	0.295	-0.190	0.700	-0.106
	SSR15	30	5	1.743	0.467	0.433	0.387	-0.078	1.000	-0.071
	SSR16	30	2	1.980	0.633	0.503	0.372	-0.264	0.265	-0.123
	SSR17	30	5	2.011	0.600	0.511	0.455	-0.177	0.644	-0.091

	SSR18	30	2	1.514	0.367	0.345	0.282	-0.063	1.000	-0.039
EFCC002	SSR01	30	2	1.142	0.133	0.127	0.117	-0.055	1.000	-0.026
	SSR03	30	2	1.642	0.467	0.398	0.315	-0.177	0.638	-0.088
	SSR06	30	3	1.753	0.600	0.437	0.350	-0.383	0.089	-0.172
	SSR07	30	4	1.580	0.433	0.373	0.344	-0.164	1.000	-0.111
	SSR10	30	2	1.105	0.100	0.097	0.090	-0.036	1.000	-0.016
	SSR12	30	5	2.778	0.967	0.651	0.581	-0.498	0.000	-0.241
	SSR13	30	2	1.835	0.700	0.463	0.351	-0.526	0.004	-0.212
	SSR15	30	3	1.462	0.367	0.321	0.293	-0.143	1.000	-0.093
	SSR16	30	3	1.575	0.367	0.371	0.309	0.012	0.307	0.017
	SSR17	30	5	1.961	0.533	0.498	0.431	-0.072	0.308	-0.036
	SSR18	30	2	1.642	0.533	0.398	0.315	-0.349	0.075	-0.153
EFCC003	SSR01	30	2	1.260	0.167	0.155	0.141	-0.115	1.000	-0.036
	SSR03	30	2	1.800	0.367	0.440	0.339	0.117	0.682	0.083
	SSR06	30	3	2.220	0.733	0.559	0.465	-0.320	0.052	-0.163
	SSR07	30	3	1.575	0.233	0.371	0.309	0.375	0.025	0.241
	SSR10	30	3	1.269	0.233	0.215	0.199	-0.086	1.000	-0.055
	SSR12	30	3	2.062	0.500	0.524	0.424	0.046	1.000	0.016
	SSR13	30	2	1.867	0.600	0.472	0.357	-0.276	0.234	-0.127
	SSR15	30	3	1.312	0.267	0.242	0.221	-0.105	1.000	-0.065
	SSR16	30	2	1.427	0.300	0.305	0.255	0.015	1.000	-0.001
	SSR17	30	4	2.456	0.633	0.590	0.535	-0.108	0.666	-0.027
	SSR18	30	2	1.260	0.167	0.155	0.141	-0.115	1.000	-0.036
EFCC004	SSR01	30	2	1.180	0.100	0.097	0.090	-0.074	1.000	-0.016
	SSR03	30	2	1.600	0.267	0.364	0.294	0.216	0.327	0.146
	SSR06	30	3	2.299	0.433	0.575	0.482	0.249	0.093	0.151
	SSR07	30	3	1.226	0.133	0.188	0.175	0.293	0.028	0.152
	SSR10	30	3	1.226	0.167	0.158	0.147	-0.068	1.000	-0.035
	SSR12	30	4	1.946	0.500	0.482	0.401	-0.080	0.901	-0.026

	SSR13	30	4	1.911	0.500	0.473	0.384	-0.102	0.502	-0.032
	SSR15	30	3	1.361	0.300	0.269	0.247	-0.115	1.000	-0.075
	SSR16	30	2	1.514	0.233	0.345	0.282	0.328	0.101	0.185
	SSR17	30	4	1.824	0.500	0.459	0.416	-0.090	0.807	-0.042
	SSR18	30	2	1.180	0.167	0.155	0.141	-0.074	1.000	-0.036
EFCC005	SSR01	30	2	1.220	0.133	0.127	0.117	-0.094	1.000	-0.026
	SSR03	30	2	1.724	0.300	0.413	0.324	0.223	0.378	0.150
	SSR06	30	3	2.174	0.433	0.549	0.450	0.214	0.128	0.104
	SSR07	30	3	1.484	0.333	0.332	0.283	-0.005	1.000	-0.017
	SSR10	30	3	1.269	0.167	0.158	0.147	-0.086	1.000	-0.035
	SSR12	30	3	1.665	0.500	0.389	0.321	-0.320	0.180	-0.139
	SSR13	30	2	1.471	0.300	0.305	0.255	-0.025	1.000	-0.001
	SSR15	30	3	1.224	0.200	0.186	0.171	-0.077	1.000	-0.045
	SSR16	30	2	1.897	0.367	0.481	0.361	0.241	0.252	0.126
	SSR17	30	4	2.043	0.533	0.519	0.470	-0.028	1.000	-0.023
	SSR18	30	2	1.220	0.133	0.127	0.117	-0.094	1.000	-0.026
Jiuxi	SSR01	30	2	1.301	0.267	0.235	0.204	-0.137	1.000	-0.067
	SSR03	30	3	1.529	0.367	0.352	0.297	-0.043	1.000	-0.035
	SSR06	30	3	1.867	0.633	0.472	0.383	-0.349	0.057	-0.153
	SSR07	30	2	1.600	0.500	0.381	0.305	-0.318	0.144	-0.142
	SSR10	30	2	1.180	0.167	0.155	0.141	-0.074	1.000	-0.036
	SSR12	30	3	2.020	0.700	0.514	0.442	-0.372	0.037	-0.191
	SSR13	30	2	1.800	0.667	0.452	0.346	-0.487	0.011	-0.200
	SSR15	30	3	1.363	0.300	0.271	0.250	-0.111	1.000	-0.074
	SSR16	30	3	2.020	0.633	0.514	0.393	-0.238	0.182	-0.112
	SSR17	30	3	2.151	0.700	0.544	0.469	-0.293	0.168	-0.140
	SSR18	30	2	1.342	0.300	0.259	0.222	-0.160	1.000	-0.078
Huoyanshan	SSR01	30	3	1.394	0.267	0.288	0.251	0.074	0.592	0.024
	SSR03	30	3	1.484	0.400	0.332	0.283	-0.210	0.634	-0.108

	SSR06	30	4	1.791	0.467	0.449	0.395	-0.040	1.000	-0.030
	SSR07	30	2	1.557	0.467	0.364	0.294	-0.289	0.295	-0.131
	SSR10	30	2	1.301	0.267	0.235	0.204	-0.137	1.000	-0.067
	SSR12	30	4	2.270	0.800	0.569	0.499	-0.416	0.010	-0.215
	SSR13	30	3	1.665	0.467	0.406	0.332	-0.152	0.728	-0.084
	SSR15	30	4	1.818	0.533	0.458	0.412	-0.169	1.000	-0.096
	SSR16	30	2	1.684	0.367	0.413	0.324	0.114	0.655	0.051
	SSR17	30	4	2.403	0.700	0.594	0.520	-0.183	0.750	-0.095
	SSR18	30	2	1.220	0.200	0.183	0.164	-0.094	1.000	-0.046
Niumo	SSR01	30	2	1.034	0.033	0.033	0.032	0.000	-	-0.002
	SSR03	30	2	1.471	0.333	0.325	0.269	-0.025	1.000	-0.020
	SSR06	30	3	1.985	0.733	0.505	0.402	-0.465	0.006	-0.196
	SSR07	30	2	1.471	0.400	0.325	0.269	-0.234	0.560	-0.110
	SSR10	30	2	1.105	0.100	0.097	0.090	-0.036	1.000	-0.016
	SSR12	30	2	1.684	0.500	0.413	0.324	-0.215	0.376	-0.104
	SSR13	30	3	1.620	0.500	0.389	0.321	-0.291	0.259	-0.139
	SSR15	30	4	1.273	0.167	0.218	0.206	0.239	0.199	0.113
	SSR16	30	3	1.942	0.500	0.493	0.382	-0.014	1.000	-0.019
	SSR17	30	6	2.774	0.633	0.650	0.603	0.027	0.015	-0.003
	SSR18	30	2	1.385	0.333	0.282	0.239	-0.184	0.563	-0.088
Luchong	SSR01	30	2	1.105	0.100	0.097	0.090	-0.036	1.000	-0.016
	SSR03	30	2	1.684	0.300	0.413	0.324	0.277	0.179	0.150
	SSR06	30	2	1.763	0.633	0.440	0.339	-0.450	0.028	-0.188
	SSR07	30	5	1.147	0.133	0.130	0.126	-0.027	1.000	-0.025
	SSR10	30	2	1.385	0.267	0.282	0.239	0.057	1.000	0.020
	SSR12	30	3	1.909	0.600	0.484	0.390	-0.244	0.293	-0.114
	SSR13	30	2	1.600	0.500	0.381	0.305	-0.318	0.144	-0.142
	SSR15	30	3	1.514	0.367	0.345	0.313	-0.063	0.747	-0.027
	SSR16	30	3	1.603	0.367	0.382	0.333	0.042	0.778	0.025

	SSR17	30	4	2.456	0.633	0.603	0.511	-0.052	0.860	-0.032
	SSR18	30	3	1.504	0.400	0.341	0.303	-0.178	1.000	-0.104
Haikou	SSR01	30	2	1.105	0.100	0.097	0.090	-0.036	1.000	-0.016
	SSR03	30	2	1.642	0.267	0.398	0.315	0.333	0.148	0.189
	SSR06	30	3	2.062	0.500	0.524	0.434	0.046	0.041	0.016
	SSR07	30	2	1.600	0.233	0.381	0.305	0.392	0.048	0.233
	SSR10	30	2	1.342	0.233	0.259	0.222	0.102	0.505	0.044
	SSR12	30	3	1.732	0.433	0.430	0.357	-0.008	1.000	-0.022
	SSR13	30	3	2.096	0.500	0.532	0.417	0.061	0.028	0.008
	SSR15	30	3	1.514	0.367	0.345	0.313	-0.063	0.747	-0.027
	SSR16	30	3	1.972	0.400	0.501	0.387	0.205	0.431	0.103
	SSR17	30	3	2.397	0.567	0.593	0.494	0.045	0.796	0.017
	SSR18	30	3	1.407	0.333	0.294	0.267	-0.135	1.000	-0.084

Supplementary Table S11 Analysis of molecular variance (AMOVA) of 14 populations of *A. grahami*, showing percentage of variation within and between populations for 11 loci of simple sequence repeat (SSR)

Source of variation	Percentage of variation			
	Cytb	SSR		
Among population (%)	16.393*	6.624*		
Within population (%)	83.607	93.376		
Fixation Index	0.164*	0.066*		

*: P<0.01 (significance test using 1 000 permutations).

	EFCC001	EFCC002	EFCC003	EFCC004	EFCC005	F_Northwest	F_West	F_East	F_South	Jiuxi	Huoyanshan	Niumo	Luchong	Haikou
EFCC001	0.000													
EFCC002	0.200*	0.000												
EFCC003	0.160*	0.178*	0.000											
EFCC004	0.111*	0.080	0.116*	0.000										
EFCC005	0.009	0.102*	0.092	-0.014	0.000									
F_Northwest	0.156*	0.089*	0.125*	-0.017	0.048	0.000								
F_West	0.150*	0.011	0.080	-0.016	0.039	0.006	0.000							
F_East	0.156*	0.089*	0.133*	0.005	0.067*	0.005	0.016	0.000						
F_South	0.167*	0.100*	0.144*	-0.005	0.078*	-0.027	0.007	-0.016	0.000					
Jiuxi	0.178*	0.111*	0.156*	0.007	0.089*	-0.037	-0.002	0.007	-0.036	0.000				
Huoyanshan	0.211*	0.144*	0.189*	0.022	0.122*	0.022	0.034	0.022	-0.010	0.003	0.000			
Niumo	0.222*	0.156*	0.200*	0.034	0.133*	0.034	0.046	0.034	0.003	0.015	0.008	0.000		
Luchong	0.367*	0.300*	0.344*	0.134	0.278*	0.114	0.147*	0.134*	0.060	0.062	0.043	0.059	0.000	
Haikou	0.244*	0.178*	0.214*	0.037	0.156*	0.015	0.049	0.037	-0.031	-0.017	-0.014	0.000	-0.024	0.000

Supplementary Table S12 Pairwise genetic differentiation between each population of *A. grahami* base on cyt *b*

*: Significant values (P<0.05).

Supplementary	Table S	513	Pairwise	genetic	differentiation	between	each	popul	lation
of A. grahami ba	sed on n	nicr	osatellite	s					

	EFCC0	EFCC0	EFCC0	EFCC0	EFCC0	F_Nor	F_Wes	F_East	F_Sout	Jiuxi	Huoya	Niumo	Lucho	Haik
	01	02	03	04	05	thwest	t		h		nshan		ng	ou
EFCC001	0.000													
EFCC002	0.019*	0.000												
EFCC003	0.112*	0.091*	0.000											
EFCC004	0.150*	0.137*	-0.005	0.000										
EFCC005	0.108*	0.118*	0.006	0.002	0.000									
F_Northw	0.023*	0.010*	0.111*	0.159*	0.130*	0.000								
est														
F_West	0.025*	0.009*	0.105*	0.152*	0.122*	0.012*	0.000							
F_East	0.010*	0.008*	0.112*	0.154*	0.119*	-0.006	0.009*	0.000						
F_South	0.031*	0.002	0.120*	0.169*	0.145*	-0.005	0.013*	-0.006	0.000					
Jiuxi	0.006*	0.007*	0.107*	0.148*	0.112*	0.010*	0.001	0.000	0.014*	0.000				
Huoyansh	0.017*	0.007*	0.105*	0.148*	0.121*	-0.003	-0.005	-0.003	0.002	-0.003	0.000			
an														
Niumo	0.008*	0.012*	0.117*	0.159*	0.118*	0.016*	0.002	0.005	0.024*	-0.004	0.009*	0.000		
Luchong	0.039*	0.020*	0.127*	0.185*	0.153*	0.018*	0.011*	0.027*	0.022*	0.028*	0.017*	0.023*	0.000	
Haikou	0.109*	0.102*	0.016*	0.030*	0.023*	0.125*	0.100*	0.115*	0.128*	0.096*	0.104*	0.111*	0.111*	0.000

*: Significant values (P<0.05).

Supplementary Table S14 Details on 11 SSR markers used for preliminary genetic analysis of *A. grahami*

SSR	SSR position (Scaffold	Mot	Repeat	Forward primer	Reversed Primer	Excepted
loci	nostart_end)	if	numbe	sequence	sequence	length (bp)
			r			
SSR	scaffold68_cov128_9181378_	AC	7	CACCACAGCATTCTG	TCTGCCTGGAGGAAGA	120
4	9181391			GATCA	GAGA	
SSR	scaffold170_cov123_2693683	AC	6	ATTAGAGCTGGGCAC	CCCAACATCTGAGCAC	145
13	_2693694			TGTGG	ACAC	
SSR	scaffold328_cov125_1850929	TG	7	AATGCCTCCGTTGAC	AAAAAGCTGAAGCGG	108
19	_1850942			ACTTG	AGTCT	
SSR	scaffold333_cov128_8943508	AT	7	CCAAACACGGTGAAT	GGAAGAACTGCGTCG	139
22	_8943521			TTTTG	GTAAG	
SSR	scaffold509_cov124_1044342	CA	7	CCTTTTACCTGCTTGC	TGCAGTGTACGTGTGT	154
25	_1044355			TGGA	GGAA	
SSR	scaffold873_cov120_71963_7	GA	8	TTGCCATGAGATCCT	CCTTTCCCCGTTTTCTT	100
33	1978			GTGTC	СТС	
SSR	scaffold981_cov115_171340_	AC	6	GTGTATGTGCTGCAG	TTGTGCCTCTCCAGTT	151
34	171351			GGTGA	CTCC	
SSR	scaffold998_cov129_369584_	GA	7	GACAATCTCGCCTCC	TTCTGCCTCTATCGCTC	183
37	369597			CTTC	ACA	
SSR	scaffold6008_cov127_89219_	TG	6	CTGCCTGAGGTAACC	GACATGGCCACCTCCT	123
43	89230			GTGAT	TAAA	
SSR	scaffold9881_cov123_152027	TG	9	GAATTTGGCAAAGGA	TCCATCCACCTGCATCA	138
44	_152044			ACCAA	TAA	
SSR	scaffold14357_cov127_64431	CA	7	ACAGCGCTTTTTGGA	TGAATGTGAGCTTCAT	137
45	4_644327			CTGAT	TTCCAG	