

Did genetic lineage divergence or spatial environmental variance lead to global subspecies differentiation of northern goshawk (*Accipiter gentilis*)?

Un-Hyang Ho* and Sam-Rang Song

Faculty of Life Science, Kim Il Sung University, Pyongyang +850, Democratic People's Republic of Korea

*) Corresponding author; e-mail: uh.ho@ryongnamsan.edu.kp

Supplementary material

Table S1.

Sample data of northern goshawk tissues collected from northern forests in the Korean peninsula.

Region	Sample site	Number of samples	Tissue source ^a
Hamgyong Province	Doksong county	11	B
	Yonsa county	9	B, MF, PF
	Hoaryong county	8	B, MF
Ryangang Province	Pochon county	11	B, MF
	Pungso county	7	PF
	Pungsan county	9	PF
Jagang Province	Jasong county	10	B
	Rangrim county	9	PF

^a B = blood, MF = molted feathers, PF = plucked feathers

Table S2.

Mitochondrial DNA control region haplotypes of northern goshawk populations.

Country index	Accession number*
K-1	-
K-2	-
K-3	-
K-4	-
K-5	-
J-I	AB436743
J-J	AB436744
J-K	AB436745
R-L	AB436746
J-M	AB436747
R-L	AB436748
U-A	AY699828
U-B	AY699829
U-C	AY699830
U-D	AY699831
U-E	AY699832
U-F	AY699833
U-G	AY699834
U-H	AY699835
U-9	JQ794588
C-11	JQ794589
U-12	JQ794590
U-13	JQ794591
C-16	JQ794592
C-18	JQ794593
U-19	JQ794594
U-20	JQ794595
U-21	JQ794596
U-22	JQ794597
C-23	JQ794598
U-24	JQ794599
U-26	JQ794600
U-29	JQ794601
U-35	JQ794602
C-37	JQ794603
C-38	JQ794604

U-I	KC662186
U-N	KC662187
U-O	KC662188
U-P	KC662189
U-Q	KC662190
U-R	KC662191
U-S	KC662192
U-U	KC662193
U-W	KC662194
C-X	KC662195
U-Y	KC662196
G	KC662197

*) -, not accessed.

Table S3.

Morphological traits of individuals of northern goshawk populations in the Korean peninsula.

Sex	Region	No	Body weight/g	Body length/mm	Nip length/mm	Wing length/mm	Tail length/mm	Haplotype
male	Hamgyong	1	525	482	25	290	215	1
		2	650	490	23	310	235	1
		3	570	485	24	295	240	1
		4	565	484	23	288	231	1
		5	675	478	22	276	225	1
		6	680	498	24	294	246	2
		7	640	478	23	306	235	4
		8	615	482	22	315	230	4
		9	625	458	24	304	247	4
		10	590	485	23	287	239	5
		11	620	486	21	297	228	5
	Ryangang	12	600	485	22	306	234	1
		13	630	492	22	297	243	1
		14	550	478	25	295	239	1
		15	530	498	23	289	237	2
		16	575	470	22	296	237	2
		17	520	480	23	297	240	4
		18	525	475	24	300	258	4
		19	530	483	21	294	268	5
		20	520	481	22	294	249	5
		21	500	478	23	305	253	5
		Jagang	22	540	480	22	310	248
	23		530	479	21	306	268	1
	24		535	483	23	308	249	2
	25		530	485	22	294	268	2
	26		575	478	24	275	267	4
	27		580	470	23	268	264	4
	28		570	487	21	297	246	5
	29		565	473	23	316	236	5
	30		530	485	22	300	238	5
female	Hamgyong	31	1250	545	28	360	265	1

	32	1175	550	28	354	278	1
	33	1180	546	29	348	264	1
	34	1070	565	26	357	286	3
	35	1160	558	27	355	275	3
	36	1150	560	26	348	278	4
	37	1030	564	24	362	263	5
	38	1160	531	29	346	289	5
	39	1150	520	28	358	264	5
	40	1090	530	28	351	295	5
	41	970	560	27	352	291	1
	42	1040	598	26	354	267	1
	43	1110	525	25	357	286	1
	44	990	560	26	356	264	1
Ryangang	45	1040	568	28	360	294	2
	46	1065	530	29	356	305	4
	47	1100	568	27	357	267	4
	48	975	540	28	354	264	4
	49	960	562	24	360	275	5
	50	1050	542	26	348	268	1
	51	1070	530	28	342	275	1
	52	1120	549	27	348	283	1
Jagang	53	1150	558	32	342	271	1
	54	1090	565	28	358	267	5
	55	930	567	27	353	286	5
	56	1130	569	27	356	300	5

Table S4.

Hierarchical analysis of molecular variance of simple sequence repeat (SSR) markers within sites, among sites within bioregions, and within bioregions of Eurasia.

Population hierarchy ^a	df	Sum of squares	Variance ^b	Percent variation	Fixation indices	Significance
Among bioregions	2	24.931	$0.01391V_a$	0.45	$F_{CT} = 0.005$	$P = 0.23$
Among sites within bioregions	6	66.198	$0.17883V_b$	5.81	$F_{SC} = 0.058$	$P < 0.00001$
Within sites	407	1173.534	$2.88338V_c$	93.73	$F_{ST} = 0.062$	$P < 0.00001$

^a bioregion: Korean peninsula, Japan, Cenral Asia and eastern Europe.

^b V_a is $\sigma_a^2 = (F_{CT})\sigma^2$; V_b is $\sigma_b^2 = (F_{ST} - F_{CT})\sigma^2$; V_c is $\sigma_c^2 = (1 - F_{ST})\sigma^2$; $\sigma^2 = \sigma_a^2 + \sigma_b^2 + \sigma_c^2$

Table S5.

Mitochondrial COI and cyt b sequence data from Genbank.

	No	Accession number
COI	1	KM261771
	2	EF515766
	3	EF515771
	4	GQ922622
	5	GQ922623
	6	GQ922624
	7	GQ922625
	8	AB842491
	9	AB842492
	10	AB842493
	11	AB842494
	12	AB842495
	13	AB842496
	14	AB842497
	15	AB842498
	16	AB842499

17	AB843322
18	AB843323
19	AB843324
20	GU571207
21	GU571208
22	GU571687
23	GU571688
24	JF312195
25	JF792342
26	KF946551
27	KF946552
28	AY666492
29	AY666498
30	DQ433276
31	DQ433277
32	DQ433278
33	DQ433279
34	DQ432695

cyt b

1

KM261772

2

X86738

3

EU583321

Table S6.

Continental structure of COI haplotype for northern goshawk subspecies populations. Dots indicate no change from EF515766/DQ433279.

Continent	Accession number	Distribution range ^a	Locus-specific mutational change														
			192	222	228	294	310	334	375	387	393	453	456	471	564	654	657
Eurasia	EF515766	K, Ch, J, No, S, Ne	G	T	G	C	T	G	T	C	C	A	A	T	G	C	C
	KM261771	K	T
	GQ922624	Ch	T
North America	DQ433279	U, Ca	A	C	A	T	C	G	C	T	C	G	G	C	A	A	T
America	AY666492	Ca	C

^a K = Korean peninsula, Ch = China, J = Japan, No = Norway, S = Switzerland, Ne = Netherlands, U = USA, Ca = Canada.

Table S7.

Continental structure of *cyt b* haplotype for northern goshawk subspecies populations. Dots indicate no change from KM261772

Continent ^a	Accession number	Distribution range ^b	Locus-specific mutational change																										
			131	302	383	398	416	443	452	476	479	527	539	578	611	614	666	696	785	893	977	980	990	1007	1010	1034	1052	1064	1069
Eurasia	KM261772	K, J	C	T	C	C	A	T	G	G	A	C	C	C	C	C	C	T	T	G	T	C	A	T	T	T	T	C	C
	X86738	G	A	C
NA	EU583321	U	T	C	T	T	G	.	.	A	G	T	T	T	T	A	T	C	C	A	C	T	G	C	C	C	C	T	T

^a NA = North America.

^b K = Korean peninsula, J = Japan, G = Germany, U = USA.