

Table S1 Microsatellite information used in the study of *Ae. albopictus*.

Locus	GenBank accession number	Primer sequence (5'-3')	Fluorescent dyes	Size range (bp)	References
AealbB51	DQ366023	F:TCCACGTGGTATAACTCTGA R: GTAGTTGTCCTAAACATCG	NED	141	[43]
AealbB52	DQ366024	F:GGGTCTAGAAGTAATAGCGATG R: GCATTCTTGCTCTGTTGC	FAM	173	[43]
AealbF3	DQ366027	F:CTCGTGAGTACGTCGCTGA R: AGGGAAACAAGGACTTCATCA	VIC	247	[43]
AealbD2	DQ366021	F:GAATCCCACACAGCGCTTT R: GGTGCGCTTGACACCTTGAAT	VIC	238	[43]
Alb-di-4	KF146971	F:TGGCGACCTTATACCCGC R: CAACTCGTTCTGACCGCTG	FAM	166-200/179	[41]
Alb-di-6	KF146972	F:TCTTCATCTACGCTGTGCTC R: GACGCCAATCCGACAAAGTC	PET	268-290/255	[41]
Alb-tri-3	KF146973	F:AGATGTGTCGCAATGCTTC R: GATTGGTGATGTTGAGGCC	NED	123-153/117	[41]
Alb-tri-18	KF146975	F:ACACAATTGCCGTGAGCTC R: CGTCTAATAGCTCCGGTCCC	VIC	250-280	[41]
Alb-tri-20	KF146976	F:GTGCCGTTGATCATCTGTC R: TCCAGCACCGTGAGTAATCC	FAM	165-201	[41]
Alb-tri-25	KF146978	F:CCAACCAACAACCCAGAAC R: TACGATGCGCAACCATCATC	PET	257-278	[41]
Alb-tri-41	KF146980	F:GATCGATTGGGAGCTCTG R: GAACCTTCTCGCTTGGCT	NED	134-155	[41]
Alb-tri-45	KF146982	F:TTTCAGCTGGTATTGGC R: TGATGTTGATGATGACTACGA	NED	120-150	[41]
Alb-tri-46	KF146983	F:TTCACAAACATACGGATCGC R: GGTCCGGTGTAAACGCCCTCC	FAM	158-192	[41]
Aealbmic8	KP859598	F: TTGTTGTTGGTGTGTTTG R: CGGGTTCCAATGATGACGA	PET	453-468	[42]
Aealbmic21	KP859611	F: CCCTACAGCCCTGATTGAGA R: CGAGTTGGGATGTTGATTG	VIC	212-232	[42]
Aealbmic23	KP859613	F: AACGGAGCGGAGTCGATTAT R: CTACTACCCGCTGCCTTCTG	PET	331-354	[42]

Table S2 Haplotype distribution and GenBank accession number of *Ae. albopictus* used in this study

Locality name	CO1	ND5
Wonju (2017)	MW526509-MW526526	MW526720-MW526737
Wonju (2020)	MW526527-MW526544	MW526738-MW526755
Yeoncheon	MW526545-MW526549	MW526756-MW526760
Yangsan	MW526550-MW526561	MW526761-MW526772
Anyang (2020)	MW526562-MW526565	MW526773-MW526776
Anyang (2018)	MW526566-MW526569	MW526777-MW526780
Chuncheon	MW526570-MW526576	MW526781-MW526787
Cheongyang	MW526577-MW526578	MW526788-MW526789
Daejeon	MW526579-MW526586	MW526790-MW526797
Gwacheon	MW526587-MW526593	MW526798-MW526804
Geoje	MW526594-MW526598	MW526805-MW526809
Gwangju	MW526599-MW526600	MW526810-MW526811
Gyeongju	MW526601-MW526602	MW526812-MW526813
Jeung-do	MW526603-MW526607	MW526814-MW526818
Jeonju	MW526608-MW526635	MW526819-MW526846
Sokcho	MW526636-MW526648	MW526847-MW526859
Seoul	MW526649-MW526651	MW526860-MW526862
Yeoju	MW526652-MW526654	MW526863-MW526865
Yeouido	MW526655-MW526656	MW526866-MW526867
Tokyo, Japan,	MW526657-MW526691	MW526868-MW526902
Vientiane, Laos,	MW526692-MW526719	MW526903-MW526930

Abbreviations: WJ-I= Wonju (2017), WJ-II= Wonju (2020), YC= Yeoncheon, YS= Yangsan, AY-I= Anyang (2018), AY-II= Anyang (2020), CC= Chuncheon, CY= Cheongyang, DJ= Daejeon, GC= Gwacheon, GJ= Geoje, GW= Gwangju, GY= Gyeongju, JD= Jeungdo, JJ= Jeonju, SC= Sokcho, SE= Seoul, YJ= Yeoju, YE= Yeouido, TJ= Tokyo, Japan, VL= Vientiane, Laos

Table S3 Pairwise differentiation (F_{ST}) for concatenated sequences of the mitochondrial DNA among populations of *Ae. albopictus*.

Locality name	Locality ID	WJ-I	WJ-II	YC	YS	AY-I	AY-II	CC	CY	DJ	GC	GJ	GW	GY	JD	JJ	SC	SE	YJ	YE	TJ	VL
Wonju (2017)	WJ-I	-																				
Wonju (2020)	WJ-II	-	0.009																			
Yeoncheon	YC	-	-	-																		
Yangsan	YS	0.051	0.103	0.022	-																	
Anyang (2018)	AY-I	0.005	0.045	0.063	0.031	-																
Anyang (2020)	AY-II	0.288	0.375	0.159	0.216	0.083	-															
Chuncheon	CC	-	0.013	0.066	0.000	0.068	0.152	0.252	-													
Cheongyang	CY	-	-	0.000	-	-	-	-	0.000	-												
Daejeon	DJ	0.000	-	0.000	0.085	0.186	0.288	0.000	0.000	-												
Gwacheon	GC	0.027	0.027	-	0.071	-	0.183	0.000	-	0.020	-											
Geoje	GJ	0.854	0.915	0.932	0.805	0.880	0.719	0.945	0.893	0.950	0.876	-										
Gwangju	GW	-	-	0.000	-	-	-	-	0.000	0.000	0.000	-										
Gyeongju	GY	0.266	0.330	0.191	0.263	0.160	-	-	-	-	-	0.313	-									
Jeung-do	JD	0.159	0.246	0.167	0.140	0.098	0.146	0.247	-0.111	0.279	0.133	0.826	-0.111	0.157	-	-						
Jeonju	JJ	0.080	0.009	-	0.210	0.181	0.530	-	-	-	0.097	0.954	-	0.737	0.405	-						
Sokcho	SC	-	-	0.108	-	0.072	0.049	0.329	-	0.072	0.332	0.061	-	0.332	-	-						
Seoul	SE	0.008	0.028	0.096	-	0.023	0.014	0.019	0.300	-	0.055	0.328	0.042	-	0.023	0.915	-0.38	0.544	0.232	0.018	-	
Yeoju	YJ	-	0.024	0.117	0.189	0.023	0.014	0.019	0.300	-	0.200	-	0.342	0.017	0.868	-	0.152	0.077	0.311	0.121	-	
Yeouido	YE	-	0.140	0.195	-	0.000	-	0.070	0.091	-	0.004	0.000	0.000	-	0.910	0.000	0.250	0.032	-	0.198	0.191	-
Yeouido	YE	-	-	0.266	0.330	0.191	0.263	0.160	-	0.000	0.000	0.000	-	0.893	0.000	0.000	-0.111	-	0.332	0.328	0.200	-
JAPAN, Tokyo	TJ	0.633	0.680	0.662	0.617	0.649	0.600	0.677	0.622	0.684	0.648	0.847	0.622	0.498	0.560	0.733	0.675	0.649	0.641	0.622	-	
LAOS, Vientiane	VL	0.695	0.729	0.688	0.668	0.672	0.665	0.704	0.646	0.711	0.682	0.810	0.646	0.551	0.631	0.778	0.717	0.666	0.665	0.646	0.583	-

Abbreviations: WJ-I= Wonju (2017), WJ-II= Wonju (2020), YC= Yeoncheon, YS= Yangsan, AY-I= Anyang (2018), AY-II= Anyang (2020), CC= Chuncheon, CY= Cheongyang, DJ= Daejeon, GC= Gwacheon, GJ= Geoje, GW= Gwangju, GY= Gyeongju, JD= Jeungdo, JJ= Jeonju, SC= Sokcho, SE= Seoul, YJ= Yeoju, YE= Yeouido, TJ= Tokyo, Japan, VL= Vientiane, Laos

Table S4 Analysis of Molecular Variance (AMOVA) by dividing Korea into A: north-south, B: east-west, C: five provincial units with concatenated sequences of mitochondrial DNA.

A: north-south

Source of variation	df	Sum of squares	Variance components	Percentage of variation (%)	F-index*
Among groups	1	1.384	-0.02047	-4.99	-0.04993
Among populations within groups	17	26.325	0.18474	45.07	0.42923
Within populations	129	31.689	0.24565	59.93	0.40074
Total	147	59.399	0.40992		

NB: North-South: North; WJ-I, WJ-II, YC, AY-I, AY-II, CC, GC, SC, SE, YJ, South; YS, CY, DJ, GJ, GW, GY, JD, JJ, YE

B: east-west

Source of variation	df	Sum of squares	Variance components	Variation (%)	F-index*
Among groups	1	1.406	-0.01871	-4.55	-0.04554

Among populations within groups	17	26.304	0.18390	44.76	0.42812
Within populations	129	31.689	0.24565	59.79	0.40207
Total	147	59.399	0.41084		

East-West: East direction, seven localities; WJ-I, WJ-II, CC, SC, GY, YS, GJ), West direction twelve localities, CY, YJ, SE, YC, JJ, JD, DJ, GC, YE, GW, AY-I, AY-II)

C: five provincial units

Source of variation	df	Sum of squares	Variance components	Variation (%)	F-index*
Among groups	4	6.977	-0.02325	-5.6	-0.05602
Among populations within groups	14	20.733	0.19262	46.41	0.43950
Within populations	129	31.689	0.24565	59.19	0.40810
Total	147	59.399	0.41052		

df, degrees of freedom. *Significant values ($P < 0.05$) are with boldface after Bonferroni correction

Provincial units: Gangwon-do; WJ-I, WJ-II, CC, SC, Gyeonggi-do; AY-I, AY-II, YJ, YC, GC, SE, Gyeongsang-do; GJ, GY, YS, Jeolla-do; JD, JJ, YE, Chungcheong-do; DJ, CY

Table S5 Microsatellite genetic diversity in the 19 populations of *Ae. albopictus*.

Locus	Population																			
	TJ	AY-I	DJ	GJ	JD	CC	JJ	WJ-I	WJ-II	YC	YS	YE	YJ	SE	GC	GY	CY	SC	VL	
N	12	4	8	5	5	9	12	9	12	6	6	2	3	3	7	2	2	12	12	
Alb-tri-3																				
<i>N_a</i>	4	2	2	-	-	-	-	-	4	-	-	3	2	-	4	3	3	4	2	
<i>A_R</i>	7	4	1	-	-	-	-	-	5	-	-	5	3	-	5	4	5	5	4	
<i>H_e</i>	0.417	0.500	0.00	-	-	-	-	-	0.58	-	-	1.00	0.33	-	0.857	1.000	1.00	0.583	0.083	
<i>H_E</i>	0.373	0.429	0.23	-	-	-	-	-	0.66	-	-	0.83	0.33	-	0.648	0.833	0.83	0.543	0.083	
<i>F_{IS}</i>	-0.122	-0.200	1.00	-	-	-	-	-	0.12	-	-	0.00	-	-	-0.358	-0.333	-	-0.077	0.000	
HW E r	-	-	*	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
	1.789	1.786	1.45	1.000	1.00	1.000	1.000	1.000	2.44	1.000	1.000	3.00	1.66	1.000	2.447	3.000	3.00	2.097	1.167	
Alb-tri-45																				
<i>N_a</i>	4	4	4	4	4	3	5	5	6	2	4	2	2	3	3	3	-	4	7	
<i>A_R</i>	12	8	10	7	4	10	4	5	3	12	2	2	11	11	6	-	6	11		
<i>H_e</i>	0.000	0.500	0.25	0.400	0.00	0.000	0.083	0.111	0.08	0.000	0.00	0.00	0.333	0.000	0.500	-	0.083	0.417		
<i>H_E</i>	0.667	0.786	0.44	0.644	0.80	0.523	0.801	0.712	0.80	0.303	0.727	0.66	0.53	0.733	0.484	0.833	-	0.591	0.823	
<i>F_{IS}</i>	1.000	0.400	0.45	0.407	1.00	1.000	0.900	0.852	0.90	1.000	1.000	1.00	1.00	0.600	1.000	0.500	-	0.864	0.505	
HW E r	*	-	-	-	*	*	*	*	*	-	*	-	*	-	*	-	*	-	*	
	2.435	2.857	1.94	2.462	2.92	2.073	2.938	2.664	2.98	1.576	2.697	2.00	1.93	2.600	2.010	3.000	1.00	2.235	3.079	
Alb-tri-41																				
<i>N_a</i>	7	4	3	2	3	5	4	5	2	4	-	-	3	5	3	3	2	3	5	
<i>A_R</i>	22	16	14	1	15	20	16	21	2	14	-	-	8	19	16	15	3	18		
<i>H_e</i>	0.250	0.250	0.12	0.000	0.20	0.333	0.000	0.333	0.00	0.167	-	-	0.333	0.143	0.500	0.50	0.167	0.000		
<i>H_E</i>	0.812	0.750	0.49	0.533	0.37	0.621	0.652	0.765	0.50	0.742	-	-	0.600	0.780	0.833	0.50	0.420	0.754		
<i>F_{IS}</i>	0.701	0.700	0.75	1.000	0.50	0.478	1.000	0.579	1.00	0.792	-	-	0.500	0.829	0.500	0.00	0.614	1.000		
HW E r	*	-	-	-	*	*	*	*	*	-	-	-	-	-	*	-	*	*	*	
	3.012	2.771	5	1.97	1.924	1.80	2.426	2.405	2.850	1.88	2.697	1.000	1.00	2.333	2.897	3.000	2.00	1.854	2.785	
AealBm2																				
<i>N_a</i>	3	2	4	-	2	2	3	5	3	2	3	2	2	2	2	-	-	4		
<i>A_R</i>	7	5	6	-	1	1	5	9	9	7	12	5	5	6	5	-	-	13		
<i>H_e</i>	0.083	0.500	0.12	-	0.00	0.000	0.083	0.222	0.25	0.333	0.833	0.50	0.33	0.000	0.143	-	-	0.250		
<i>H_E</i>	0.236	0.429	0.52	-	0.35	0.366	0.236	0.556	0.23	0.485	0.621	0.50	0.33	0.533	0.143	-	-	0.431		
<i>F_{IS}</i>	0.656	-0.200	0.77	-	1.00	1.000	0.656	0.614	-	0.333	-0.389	0.00	0.00	1.000	0.000	-	-	0.431		
HW E r	*	-	-	-	*	*	*	*	-	-	-	-	-	-	-	-	*	*	*	
	1.478	1.786	2.14	1.000	1.66	1.673	1.478	2.250	1.47	1.857	2.232	2.00	1.66	1.933	1.286	1.000	1.00	1.914		
AealB52																				
<i>N_a</i>	-	-	2	3	2	4	4	4	-	3	3	3	-	-	2	2	-	-	2	
<i>A_R</i>	-	-	10	10	10	9	9	9	-	10	9	3	-	-	1	1	-	-	1	
<i>H_e</i>	-	-	0.00	0.200	0.20	0.222	0.000	0.000	-	0.167	0.167	0.50	-	-	0.000	0.000	-	-	0.000	
<i>H_E</i>	-	-	0.23	0.600	0.20	0.595	0.435	0.732	-	0.318	0.439	0.83	-	-	0.264	0.667	-	-	0.160	
<i>F_{IS}</i>	-	-	1.00	0.692	0.00	0.640	1.000	1.000	-	0.500	0.643	0.50	-	-	1.000	1.000	-	-	1.000	
HW E r	*	-	*	-	*	*	*	*	-	*	-	*	-	-	*	-	*	-	*	
	1.000	1.000	1.45	2.229	1.40	2.289	1.933	2.682	1.00	1.667	1.909	3.00	1.00	1.000	1.505	2.000	1.00	1.000	1.312	
Alb-tri-20																				
<i>N_a</i>	5	5	3	2	5	5	2	6	3	2	3	4	3	2	2	2	-	5	2	
<i>A_R</i>	7	8	6	6	8	9	11	8	7	4	4	6	4	4	4	3	-	6	1	
<i>H_e</i>	0.750	0.250	0.12	0.200	0.20	0.111	0.250	0.000	0.50	0.333	0.000	1.00	0.66	0.333	0.571	1.000	-	0.500	0.000	
<i>H_E</i>	0.656	0.893	0.65	0.200	0.82	0.778	0.598	0.471	0.54	0.667	0.545	0.83	0.86	0.733	0.440	0.667	-	0.819	0.464	
<i>F_{IS}</i>	-0.151	0.750	0.82	0.000	0.77	0.864	0.593	1.000	0.08	0.524	1.000	-	0.27	0.600	-0.333	-1.000	-	0.400	1.000	
HW E r	*	-	*	-	*	*	*	*	-	-	-	-	-	-	-	*	*	*	*	
	2.427	3.357	2.38	1.400	3.06	2.865	2.360	1.833	2.20	2.404	1.939	3.00	3.20	2.600	1.789	2.000	1.00	3.027	1.822	
Alb-tri-46																				
<i>N_a</i>	8	5	4	3	5	2	5	4	6	3	3	2	2	4	5	5	2	3	4	4
<i>A_R</i>	14	13	6	9	7	1	13	10	10	14	10	9	11	8	8	13	8	10	4	
<i>H_e</i>	0.333	0.500	0.00	0.000	0.20	0.000	0.083	0.111	0.16	0.000	0.500	0.50	0.33	0.667	0.714	0.000	1.00	0.083	0.000	
<i>H_E</i>	0.870	0.893	0.70	0.711	0.86	0.523	0.721	0.634	0.81	0.667	0.682	0.50	0.86	0.933	0.758	0.667	0.83	0.641	0.623	
<i>F_{IS}</i>	0.627	0.478	1.00	1.000	0.78	1.000	0.889	0.833	0.80	1.000	0.286	0.00	0.66	0.333	0.063	1.000	-	0.875	1.000	

HW E r	*	-	*	-	*	*	*	*	*	*	*	*	-	-	-	-	*	*		
	3.295	3.357	2.59	2.524	3.23	1.908	2.667	2.371	3.02	2.404	2.461	2.00	3.20	3.600	2.797	2.000	3.00	2.392	2.380	
Alb-di-4	<i>N_s</i>	3	2	3	3	3	6	4	3	3	-	-	2	3	3	3	5	2		
	<i>A_R</i>	4	2	6	10	2	9	9	10	2	9	-	-	1	10	11	11	10	5	
	<i>H_o</i>	0.000	0.000	0.00	0.000	0.00	0.000	0.000	0.222	0.08	0.000	-	-	0.00	0.000	0.571	1.000	0.50	0.083	
	<i>H_E</i>	0.565	0.429	0.66	0.711	0.62	0.627	0.812	0.549	0.35	0.667	-	-	0.53	0.800	0.615	0.833	0.83	0.692	
	<i>F_{IS}</i>	1.000	1.000	1.00	1.000	1.00	1.000	0.610	0.77	1.000	-	-	1.00	1.000	0.077	-0.333	0.50	0.884		
	<i>HW E r</i>	2.121	1.786	2.41	2.524	2.32	2.323	3.020	2.211	1.71	2.404	1.000	1.00	1.93	2.800	2.281	3.000	3.00	2.551	
AcalbfD2	<i>N_s</i>	2	-	4	3	2	5	6	3	6	3	5	-	3	2	4	2	3	9	7
	<i>A_R</i>	1	-	11	11	1	11	13	4	8	4	6	--	7	1	4	3	5	9	12
	<i>H_o</i>	0.000	-	0.37	0.200	0.00	0.444	0.417	0.333	0.25	0.667	0.333	-	0.00	0.000	0.143	0.500	0.50	0.500	
	<i>H_E</i>	0.159	-	0.59	0.600	0.53	0.614	0.732	0.464	0.75	0.667	0.833	-	0.80	0.533	0.736	0.500	0.83	0.801	
	<i>F_{IS}</i>	1.000	-	0.38	0.692	1.00	0.289	0.442	0.294	0.68	0.900	0.623	-	1.00	1.000	0.818	0.000	0.50	0.386	
	<i>HW E r</i>	1.312	1.000	2.29	2.229	1.92	2.392	2.726	1.958	2.78	2.404	3.089	1.00	2.80	1.933	2.676	2.000	3.00	3.032	2.764
AcalbfF3	<i>N_s</i>	9	-	3	4	-	3	4	6	7	2	2	-	2	-	3	-	2	3	5
	<i>A_R</i>	14	-	3	13	-	10	5	6	10	4	1	-	1	-	2	-	2	2	8
	<i>H_o</i>	0.417	-	0.00	0.200	-	0.000	0.000	0.111	0.16	0.000	0.000	-	0.00	-	0.000	0.000	0.00	0.083	
	<i>H_E</i>	0.616	-	0.63	0.778	-	0.392	0.623	0.817	0.76	0.303	0.545	-	0.53	-	0.703	-	0.66	0.420	
	<i>F_{IS}</i>	0.333	-	1.00	0.765	-	1.000	1.000	0.871	0.78	1.000	1.000	-	1.00	-	1.000	-	1.00	0.864	
	<i>HW E r</i>	2.466	1.000	2.29	2.829	1.00	1.810	2.380	3.034	2.82	1.576	1.939	1.00	1.93	1.000	2.510	1.000	2.00	1.854	
Alb-tri-18	<i>N_s</i>	6	5	5	-	4	5	5	3	4	2	2	3	2	2	5	-	3	5	11
	<i>A_R</i>	13	15	18	-	21	28	10	20	16	18	14	2	6	17	-	14	13	28	
	<i>H_o</i>	0.083	0.500	0.12	-	0.20	0.333	0.167	0.000	0.00	0.000	0.000	1.00	0.33	0.333	0.143	-	0.50	0.000	0.167
	<i>H_E</i>	0.750	0.786	0.77	-	0.77	0.621	0.703	0.601	0.68	0.303	0.545	0.83	0.33	0.333	0.802	-	0.83	0.826	0.920
	<i>F_{IS}</i>	0.893	0.400	0.84	-	0.76	0.478	0.771	1.000	1.00	1.000	1.000	-	0.33	0.000	0.833	-	0.50	1.000	0.825
	<i>HW E r</i>	2.811	2.986	2.84	1.000	2.82	2.426	2.586	2.221	2.52	1.576	1.939	3.00	1.66	1.667	2.961	1.000	3.00	3.056	3.545
Acalbmie2	<i>N_s</i>	3	2	2	2	-	3	3	3	3	3	3	-	2	2	-	4	2	3	2
I	<i>A_R</i>	2	2	5	4	-	3	4	4	4	6	-	2	3	-	4	3	5	2	
	<i>H_o</i>	0.000	0.000	0.00	0.000	-	0.000	0.000	0.000	0.00	0.000	-	0.00	0.00	-	0.143	0.000	0.50	0.000	
	<i>H_E</i>	0.565	0.429	0.23	0.533	-	0.523	0.652	0.627	0.42	0.667	-	0.66	0.53	-	0.780	0.667	0.83	0.464	
	<i>F_{IS}</i>	1.000	1.000	1.00	1.000	-	1.000	1.000	1.000	1.00	1.000	-	1.00	1.00	-	0.829	1.000	0.50	1.000	
	<i>HW E r</i>	2.121	1.786	1.45	1.924	1.00	2.073	2.356	2.323	1.85	2.404	1.000	2.00	1.93	1.000	2.840	2.000	3.00	1.822	
Alb-di-6	<i>N_s</i>	7	4	4	2	3	6	5	3	6	-	2	2	3	4	3	2	2	7	6
	<i>A_R</i>	15	5	11	3	8	10	13	4	8	-	8	6	5	6	6	5	6	15	16
	<i>H_o</i>	0.417	0.001	0.12	0.000	0.40	0.000	0.083	0.000	0.16	-	0.000	0.00	0.33	0.333	0.143	0.000	0.00	0.167	
	<i>H_E</i>	0.725	0.857	0.72	0.533	0.711	0.837	0.678	0.523	0.71	-	0.545	0.66	0.73	0.867	0.539	0.667	0.66	0.844	
	<i>F_{IS}</i>	0.436	1.000	0.83	1.000	0.46	1.000	0.882	1.000	0.77	-	1.000	1.00	0.60	0.667	0.750	1.000	1.00	0.810	
	<i>HW E r</i>	2.746	3.143	2.63	1.924	2.52	3.132	2.519	2.073	2.66	1.000	1.939	2.00	2.60	3.200	2.071	2.000	2.00	3.181	
Alb-tri-25	<i>N_s</i>	5	2	4	3	4	6	4	8	7	-	2	2	2	2	3	2	-	7	7
	<i>A_R</i>	12	1	16	16	5	12	15	12	-	14	3	1	1	3	-	16	14	-	
	<i>H_o</i>	0.083	0.000	0.00	0.000	0.00	0.333	0.167	0.333	0.25	-	0.167	0.00	0.00	0.000	0.000	-	0.333	0.000	
	<i>H_E</i>	0.714	0.571	0.76	0.622	0.80	0.732	0.609	0.817	0.79	-	0.167	0.66	0.53	0.533	0.484	0.667	-	0.783	
	<i>F_{IS}</i>	0.888	1.000	1.00	1.000	1.00	0.560	0.735	0.607	0.69	-	0.000	1.00	1.00	1.000	1.000	-	0.585	1.000	
	<i>HW E r</i>	2.612	1.971	2.79	2.329	2.92	2.768	2.315	3.081	3.00	1.000	1.333	2.00	1.93	1.933	2.010	2.000	1.00	2.934	
Acalbmie8	<i>N_s</i>	7	4	4	2	2	2	7	4	7	-	2	2	-	3	4	2	3	7	7
	<i>A_R</i>	13	12	6	1	4	8	16	14	9	-	6	1	-	7	7	2	6	17	
	<i>H_o</i>	0.083	0.250	0.00	0.000	0.00	0.000	0.167	0.000	0.33	-	0.000	0.00	-	0.000	0.000	0.50	0.500	0.000	
	<i>H_E</i>	0.764	0.750	0.76	0.533	0.53	0.471	0.884	0.732	0.81	-	0.485	0.66	-	0.800	0.659	0.667	0.83	0.768	
	<i>F_{IS}</i>	0.895	0.700	1.00	1.000	1.00	1.000	0.818	1.000	0.60	-	1.000	1.00	-	1.000	1.000	0.50	0.359	1.000	
	<i>HW E r</i>	2.890	2.771	2.79	1.924	1.92	1.833	3.343	2.682	3.02	1.000	1.857	2.00	1.00	2.800	2.501	2.000	3.00	2.866	
AcalB51	<i>N_s</i>	5	-	8	5	-	8	10	9	2	5	6	2	2	2	4	4	3	6	7
	<i>A_R</i>	10	-	15	11	-	19	15	15	1	15	15	6	1	8	9	9	8	12	
	<i>H_o</i>	0.250	-	0.62	1.000	-	0.222	0.750	1.000	0.00	0.500	0.500	0.50	0.00	0.000	0.143	1.000	1.00	0.250	
	<i>H_E</i>	0.312	-	0.90	0.844	-	0.797	0.913	0.876	0.29	0.667	0.864	0.50	0.53	0.667	0.736	1.000	0.83	0.754	
	<i>F_{IS}</i>	0.205	-	0.32	-0.212	-	0.733	0.185	-0.152	1.00	0.268	0.444	0.00	1.00	1.000	0.818	0.000	-	0.678	
	<i>HW E r</i>	1.667	1.000	3.43	3.133	1.00	3.036	3.507	3.326	1.54	2.566	3.253	2.00	1.93	2.000	2.676	4.000	3.00	2.782	2.866
Total	<i>N_s</i>	4.938	2.812	3.68	2.562	2.68	3.938	4.812	4.312	4.56	2.438	2.500	2.00	2.18	2.375	2.188	2.188	4.56	5.188	
	<i>A_R</i>	10.20	7.583	9.00	7.846	7.41	10.26	10.73	10.20	7.20	8.667	9.583	5.16	3.53	6.333	7.250	6.077	7.63	8.643	10.43
	<i>H_o</i>	0.211	0.271	0.118	0.170	0.117	0.133	0.150	0.185	0.18	0.208	0.41	0.18	0.194	0.232	0.423	0.5	0.232	0.146	
	<i>H_E</i>	0.549	0.500	0.58	0.490	0.46	0.564	0.628	0.617	0.57	0.403	0.438	0.458	0.504	0.598	0.53	0.585	0.609		
	<i>F_{IS}</i>	0.650	0.630	0.81	0.743	0.82	0.789	0.784	0.731	0.70	0.685	0.664	0.48	0.73	0.759	0.631	0.522	0.38	0.663	
	<i>HW E r</i>	2.261	2.147	2.30	2.022	2.03	2.252	2.471	2.410	2.30	1.846	1.912	2.00	1.96	2.087	2.329	2.188	2.18	2.355	
	<i>N_p</i>	0.812	0.687	0.62	0.187	0.25	0.625	1.062	0.562	0.37	0.437	0.062	0.12	0	0.187	0.062	0.062	0	0.562	

N, Number of individuals; *N_a*, Number of alleles; *A_r*, Allelic range; *H_o*, observed heterozygosity; *H_e*, Expected heterozygosity; *r*, Allele richness; *F_{is}*, Inbreeding Coefficient; *N_p*, Number of private alleles HWE, Hardy-Weinberg equilibrium; *Significance of deviation from Hardy-Weinberg equilibrium at *P* < 0.001 for loci in HWE after Bonferroni correction

Abbreviations: WJ-I= Wonju (2017), WJ-II= Wonju (2020), YC= Yeoncheon, YS= Yangsan, AY-I= Anyang (2018), AY-II= Anyang (2020), CC= Chuncheon, CY= Cheongyang, DJ= Daejeon, GC= Gwacheon, GJ= Geoje, GW= Gwangju, GY= Gyeongju, JD= Jeungdo, JJ= Jeonju, SC= Sokcho, SE= Seoul, YJ= Yeoju, YE= Yeosu, TJ= Tokyo, Japan, VL= Vientiane, Laos

Table S6 Pairwise F_{ST} estimates and pairwise R_{ST} estimates for *Ae. albopictus* populations.

	TJ	AY-I	DJ	GJ	JD	CC	JJ	WJ-I	WJ-II	YC	YS	YE	YJ	SE	GC	GY	CY	SC	VL
TJ	-	0.146	0.167	0.292	0.122	0.202	0.154	0.181	0.190	0.359	0.275	0.282	0.247	0.187	0.157	0.192	0.244	0.156	0.199
AY-I	0.153	-	0.200	0.360	0.158	0.238	0.179	0.263	0.265	0.438	0.355	0.381	0.300	0.207	0.210	0.222	0.304	0.187	0.242
DJ	0.539	0.457	-	0.230	0.201	0.175	0.175	0.210	0.211	0.287	0.258	0.288	0.267	0.194	0.210	0.235	0.241	0.222	0.182
GJ	0.678	0.616	0.185	-	0.351	0.278	0.279	0.264	0.241	0.399	0.305	0.256	0.248	0.336	0.248	0.299	0.276	0.268	0.268
JD	0.045	0.07	0.489	0.643	-	0.227	0.177	0.244	0.229	0.432	0.331	0.366	0.262	0.181	0.217	0.249	0.316	0.338	0.268
CC	0.511	0.501	0.367	0.480	0.440	-	0.155	0.208	0.238	0.306	0.277	0.318	0.259	0.135	0.205	0.195	0.254	0.222	0.195
YJ	0.248	0.249	0.442	0.567	0.183	0.324	0.127	0.220	0.210	0.258	0.252	0.213	0.162	0.149	0.154	0.184	0.221	0.170	
WJ-I	0.322	0.414	0.406	0.541	0.274	0.390	0.096	0.229	0.351	0.287	0.252	0.274	0.199	0.195	0.236	0.200	0.204		
WJ-II	0.142	0.291	0.619	0.760	0.145	0.616	0.344	0.380	0.322	0.284	0.160	0.176	0.174	0.145	0.208	0.161	0.144	0.212	
YC	0.401	0.287	0.184	0.386	0.365	0.290	0.320	0.361	0.531	-	0.331	0.409	0.313	0.356	0.286	0.388	0.384	0.322	0.313
YS	0.435	0.302	0.172	0.254	0.329	0.372	0.376	0.393	0.512	0.077	-	0.282	0.312	0.303	0.235	0.357	0.309	0.265	0.268
YE	0.329	0.125	0.200	0.416	0.292	0.418	0.345	0.320	0.418	0.180	0.089	-	0.280	0.317	0.202	0.286	0.302	0.208	0.263
YI	0.198	-0.028	0.434	0.607	0.197	0.446	0.288	0.363	0.349	0.255	0.244	0.159	-	0.162	0.122	0.269	0.191	0.116	0.238
SE	0.324	0.341	0.372	0.516	0.259	0.362	0.223	0.299	0.483	0.202	0.111	0.336	0.334	-	0.173	0.206	0.238	0.168	0.214
GC	0.278	0.218	0.429	0.528	0.157	0.379	0.241	0.331	0.326	0.274	0.212	0.187	0.101	-0.040	-	0.117	0.027	0.092	0.176
GY	0.241	0.286	0.345	0.513	0.293	0.306	0.046	0.155	0.480	0.175	0.263	0.265	0.253	0.120	0.081	-	0.172	0.155	0.210
CY	0.543	0.420	0.310	0.355	0.474	0.453	0.464	0.446	0.614	0.309	0.100	0.137	0.440	0.256	0.200	0.376	-	0.144	0.207
SC	0.220	0.312	0.585	0.705	0.080	0.521	0.271	0.349	0.180	0.480	0.427	0.394	0.275	0.259	0.142	0.372	0.478	-	0.170
VL	0.433	0.478	0.455	0.593	0.460	0.357	0.196	0.350	0.574	0.349	0.458	0.485	0.440	0.431	0.383	0.139	0.581	0.527	-

Population pairwise FSTs: Distance method: Sum of squared size difference (R_{ST}) (lower diagonal), F_{ST} (upper diagonal)

Abbreviations: WJ-I= Wonju (2017), WJ-II= Wonju (2020), YC= Yeoncheon, YS= Yangsan, AY-I= Anyang (2018), AY-II= Anyang (2020), CC= Chuncheon, CY= Cheongyang, DJ= Daejeon, GC= Gwacheon, GJ= Geoje, GW= Gwangju, GY= Gyeongju, JD= Jeungdo, JJ= Jeonju, SC= Sokcho, SE= Seoul, YJ= Yeouji, YE= Yeosu, TJ= Tokyo, Japan, VL= Vientiane, Laos

Table S7 Bottleneck test for *Ae.albopictus*.

Population	M-ratio	WILCOXON TEST		
		I.A.M	T.P.M	S.M.M
TJ	0.5367	0.0005	0.0012	0.0024
AY-I	0.4955	0.0007	0.0034	0.0034
DJ	0.4416	0.1748	0.3203	0.5772
GJ	0.4354	0.0322	0.3750	0.6250
JD	0.5526	0.0005	0.0010	0.0024
CC	0.4853	0.0137	0.1055	0.3223
JJ	0.4543	0.0061	0.0342	0.1763
WJ-I	0.4804	0.0161	0.1016	0.2402
WJ-II	0.6648	0.0002	0.0002	0.0002
YC	0.3577	0.0012	0.0012	0.0081
YS	0.3623	0.0031	0.0031	0.0398
YE	0.4847	0.0840	0.0840	0.0840
YJ	0.6673	0.0012	0.0012	0.0012
SE	0.4793	0.0068	0.0122	0.0122
GC	0.5414	0.0024	0.0034	0.0342
GY	0.4614	0.0273	0.0273	0.0273
CY	0.3769	0.0137	0.0137	0.0137
SC	0.6088	0.0024	0.0034	0.0342
VL	0.5569	0.0479	0.0942	0.5879

IAM: infinite alleles model; SMM: stepwise mutation model; TPM: two phase model

Values in bold indicate a bottleneck (M-ratio ≤ 0.68 ; two-tailed Wilcoxon test $P < 0.05$).

Abbreviations: WJ-I= Wonju (2017), WJ-II= Wonju (2020), YC= Yeoncheon, YS= Yangsan, AY-I= Anyang (2018), AY-II= Anyang (2020), CC= Chuncheon, CY= Cheongyang, DJ= Daejeon, GC= Gwacheon, GJ= Geoje, GW= Gwangju, GY= Gyeongju, JD= Jeungdo, JJ= Jeonju, SC= Sokcho, SE= Seoul, YJ= Yeouji, YE= Yeosu, TJ= Tokyo, Japan, VL= Vientiane, Laos

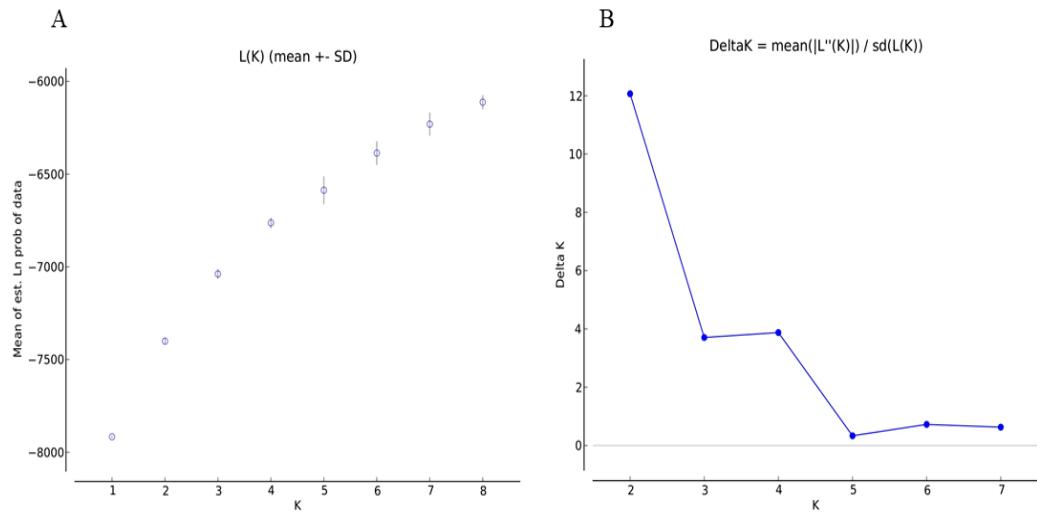


Figure S1 Estimation of the optimal number of *Aedes albopictus* populations performed using STRUCTURE software. **A** The plot of mean posterior probability ($\ln P(D)$) was based on ten repeats per cluster, K -value. **B** Optimal K -value according to maximum delta K (ΔK)

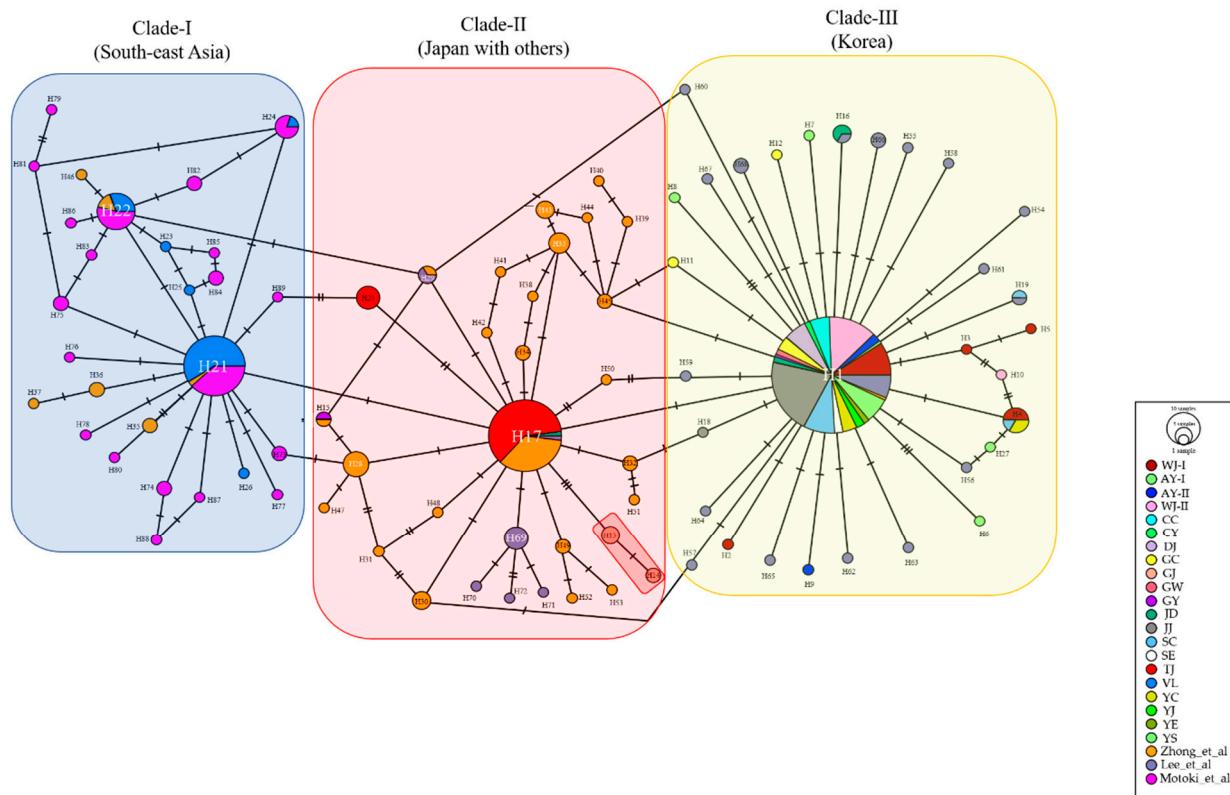


Figure S2 Minimum spanning network based on the combined NCBI-acquired *COI* sequences and *COI* sequences from this study. It can be seen that the clades clearly distinguish between Korean and South-East Asian countries. The clade is divided into three, and some Korean populations are shared in Clade-II. The table below

shows Korean populations belonging to Clade-II in bold. (Abbreviations: WJ-I= Wonju (2017), WJ-II= Wonju (2020), YC= Yeoncheon, YS= Yangsan, AY-I= Anyang (2018), AY-II= Anyang (2020), CC= Chuncheon, CY= Cheongyang, DJ= Daejeon, GC= Gwacheon, GJ= Geoje, GW= Gwangju, GY= Gyeongju, JD= Jeungdo, JJ= Jeonju, SC= Sokcho, SE= Seoul, YJ= Yeoju, YE= Yeosu, TJ= Tokyo, Japan, VL= Vientiane, Laos).

Clades	Haplotype	No. of individuals	Haplotype distribution: Reference/region/regional code (number of populations)
Clade-I	H21	34	Laos; VL (20) Zhong_et_al; Los Angeles County 2001 (1) Motoki_et_al; Laos (13)
	H22	13	Laos; VL (4) Zhong_et_al; Los Angeles County 2001 (2) Motoki_et_al; Laos (7)
	H23	1	Laos; VL (1)
	H24	4	Laos; VL (1) Motoki_et_al; Laos (4)
	H25	1	Laos; VL (1)
	H26	1	Laos; VL (1)
	H35	2	Zhong_et_al; Singapore (2)
	H36	2	Zhong_et_al; Singapore (2)
	H37	1	Zhong_et_al; Singapore (1)
	H73	2	Motoki_et_al; Laos (2)
	H74	2	Motoki_et_al; Laos (2)
	H75	2	Motoki_et_al; Laos (2)
	H76	1	Motoki_et_al; Laos (1)
	H77	1	Motoki_et_al; Laos (1)
	H78	1	Motoki_et_al; Laos (1)
	H79	1	Motoki_et_al; Laos (1)
	H80	1	Motoki_et_al; Laos (1)
	H81	1	Motoki_et_al; Laos (1)
	H82	2	Motoki_et_al; Laos (2)
	H83	1	Motoki_et_al; Laos (1)
	H84	2	Motoki_et_al; Laos (2)
	H85	1	Motoki_et_al; Laos (1)
	H86	1	Motoki_et_al; Laos (1)
	H87	1	Motoki_et_al; Laos (1)
	H88	1	Motoki_et_al; Laos (1)
	H89	1	Motoki_et_al; Laos (1)
Clade-II	H13	3	Korea; GJ (3)
	H14	2	Korea; GJ (2)
	H15	2	Korea; GY (1)
			Zhong_et_al; China (1)
	H17	49	Korea; JD (1) Japan; TJ (30) Zhong_et_al; contains mainly China (1) Lee_et_al; Korea (1)
	H20	5	Japan; TJ (5)
	H28	6	Zhong_et_al; contains mainly Los Angeles County 2001 (6)
	H29	3	Zhong_et_al; China (1) Lee_et_al; Korea (2)
	H30	3	Zhong_et_al; China (1), Taiwan (2)
	H31	1	Zhong_et_al; China (1)
	H32	2	Zhong_et_al; China (1), Taiwan (1)
	H33	4	Zhong_et_al; China (1), Italy (2), New Jersey (1)
	H34	2	Zhong_et_al; contains mainly Singapore (2)
	H38	1	Zhong_et_al; Singapore (1)
	H39	1	Zhong_et_al; Singapore (1)
	H40	1	Zhong_et_al; Singapore (1)
	H41	1	Zhong_et_al; Italy (1)

	H42	1	Zhong_et_al; contains mainly Texas (1)
	H43	3	Zhong_et_al; Italy (1), New Jersey (2)
	H44	1	Zhong_et_al; Italy (1)
	H45	2	Zhong_et_al; Italy (1), New Jersey (1)
	H46	1	Zhong_et_al; Los Angeles County 2001 (1)
	H47	1	Zhong_et_al; Los Angeles County 2011 (1)
	H48	1	Zhong_et_al; Texas (1)
	H49	2	Zhong_et_al; Hawai'i (2)
	H50	1	Zhong_et_al; Hawai'i (1)
	H51	1	Zhong_et_al; Hawai'i (1)
	H52	1	Zhong_et_al; Hawai'i (1)
	H53	1	Zhong_et_al; Hawai'i (1)
	H69	5	Lee_et_al; Korea (5)
	H70	1	Lee_et_al; Korea (1)
	H71	1	Lee_et_al; Korea (1)
	H72	1	Lee_et_al; Korea (1)
Clade-III	H1	129	Korea; WJ-I (12), WJ-II (17), AY-I (1), AY-II (3), CC (7), CY (2), DJ (8), GC (5), GW (2), GY (1), JD (2), JJ (22) SC (11), SE (3), YC (5), YJ (3), YE (2), YS (9) Zhong_et_al; Japan (1) Lee_et_al; Korea (8)
	H2	1	Korea; WJ-I (1)
	H3	1	Korea; WJ-I (1)
	H4	6	Korea; WJ-I (3), SC (1), YS (2)
	H5	1	Korea; WJ-I (1)
	H6	1	Korea; AY-I (1)
	H7	1	Korea; AY-I (1)
	H8	1	Korea; AY-I (1)
	H9	1	Korea; AY-II (1)
	H10	1	Korea; WJ-II (1)
	H11	1	Korea; GC (1)
	H12	1	Korea; GC (1)
	H16	3	Korea; JD (1) Lee_et_al; Korea (1),
	H18	1	Korea; JJ (1)
	H19	2	Korea; SC (1) Lee_et_al; Korea (1)
	H27	1	Korea; YS (1)
	H54	1	Lee_et_al; Korea (1)
	H55	1	Lee_et_al; Korea (1)
	H56	1	Lee_et_al; Korea (1)
	H57	1	Lee_et_al; Korea (1)
	H58	1	Lee_et_al; Korea (1)
	H59	1	Lee_et_al; Korea (1)
	H60	1	Lee_et_al; Korea (1)
	H61	1	Lee_et_al; Korea (1)
	H62	1	Lee_et_al; Korea (1)
	H63	1	Lee_et_al; Korea (1)
	H64	1	Lee_et_al; Korea (1)
	H65	1	Lee_et_al; Korea (1)
	H66	2	Lee_et_al; Korea (2)
	H67	1	Lee_et_al; Korea (1)
	H68	2	Lee_et_al; Korea (2)

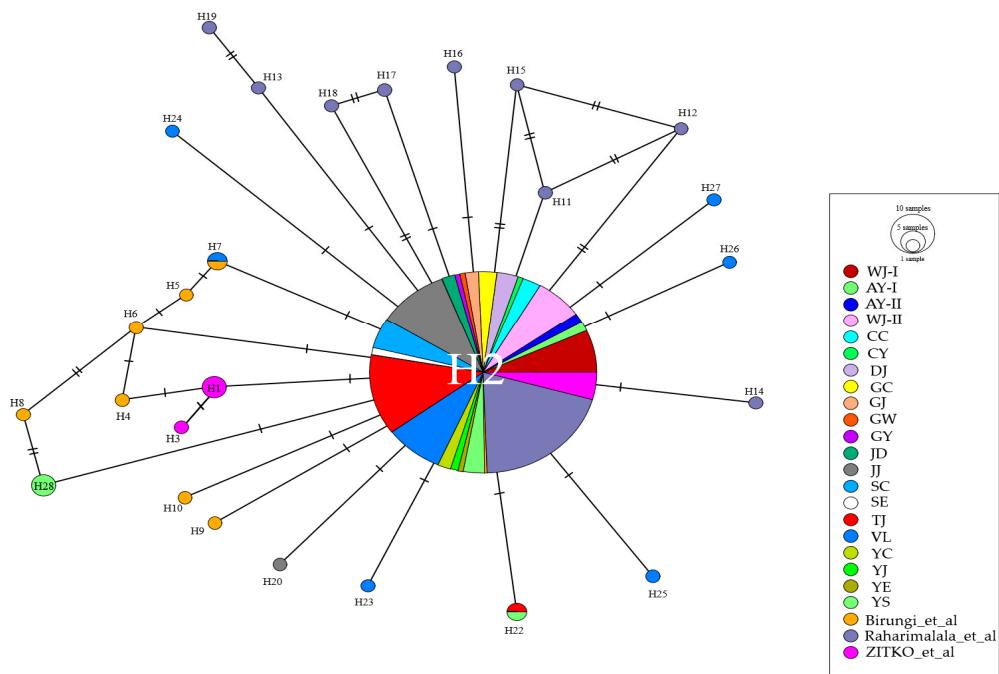


Figure S3 Minimum spanning network based on the combined NCBI-acquired *ND5* sequences and *ND5* sequences from this study. The *ND5* haplotype results shared haplotypes overall without the clear distinction from each studied country (Laos, Japan, and Korea). The table below shows the haplotype distributing to the different localities (Abbreviations: WJ-I= Wonju (2017), WJ-II= Wonju (2020), YC= Yeoncheon, YS= Yangsan, AY-I= Anyang (2018), AY-II= Anyang (2020), CC= Chuncheon, CY= Cheongyang, DJ= Daejeon, GC= Gwacheon, GJ= Geoje, GW= Gwangju, GY= Gyeongju, JD= Jeungdo, JJ= Jeonju, SC= Sokcho, SE= Seoul, YJ= Yeoju, YE= Yeosu, TJ= Tokyo, Japan, VL= Vientiane, Laos).

Haplotype	No. of individuals	Haplotype distribution: Reference/region/regional code (number of populations)
H1	3	ŽITKO_et_al; Brazil (2) Birungi_et_al; Brazil (1)
H2	262	Korea; WJ-I (18), WJ-II (18), AY-I (4), AY-II (4), CC (7), CY (2), DJ (8), GC (7), GJ (5), GW (2), GY (2), JD (5), JJ (27) SC (13), SE (2), YC (5), YJ (3), YE (2), YS (8) ŽITKO_et_al; Viet Nam (2), USA (1), Cambodia (1), Madagascar (1), France (2), Hawai’I (1), Reunion (2) Birungi_et_al; USA (1) Raharimalala_et_al; Reunion (1), Madagascar (52)
H3	1	ŽITKO_et_al;
H4	1	Birungi_et_al;
H5	1	Birungi_et_al;
H6	1	Birungi_et_al;
H7	1	Birungi_et_al;
H8	1	Birungi_et_al;
H9	1	Birungi_et_al;
H10	1	Birungi_et_al;
H11	1	Raharimalala_et_al;
H12	1	Raharimalala_et_al;
H13	1	Raharimalala_et_al;
H14	1	Raharimalala_et_al;
H15	1	Raharimalala_et_al;
H16	1	Raharimalala_et_al;
H17	1	Raharimalala_et_al;
H18	1	Raharimalala_et_al;
H19	1	Raharimalala_et_al;

H20	1	Korea; JJ (1)
H21	1	Korea; SE (1)
H22	2	Korea; YS (1)
		Japan; TJ (1)
H23	1	Laos; VL (1)
H24	1	Laos; VL (1)
H25	1	Laos; VL (1)
H26	1	Laos; VL (1)
H27	1	Laos; VL (1)
H28	1	Korea; YS (3)
