

**Table S8** Results of the hierarchical AMOVA for the crested ibis

Grouping tested	MHC			Microsatellite		
	% var	F	P	% var	F	P
<b>Group1</b>						
<b>(Wild, YX, LGT, DQ) (BJ) (SD, HN)</b>						
Among groups [ $F_{CT}$ ]	7.29	0.073	0.010	5.10	0.051	0.009
Among populations within groups [ $F_{SC}$ ]	0.87	0.009	0.075	1.52	0.016	0.000
Among individuals within populations [ $F_{ST}$ ]	91.84	0.082	0.000	93.38	0.066	0.000
<b>Group2</b>						
<b>(Wild, LGT, DQ) (YX) (BJ) (SD, HN)</b>						
Among groups [ $F_{CT}$ ]	7.81	0.078	0.005	3.98	0.040	0.029
Among populations within groups [ $F_{SC}$ ]	-0.65	-0.007	0.813	1.67	0.017	0.000
Among individuals within populations [ $F_{ST}$ ]	92.84	0.072	0.000	94.36	0.056	0.000
<b>Group3</b>						
<b>(Wild) (YX) (LGT, DQ) (BJ) (SD, HN)</b>						
Among groups [ $F_{CT}$ ]	7.13	0.071	0.040	3.78	0.038	0.105
Among populations within groups [ $F_{SC}$ ]	-0.19	-0.002	0.529	1.77	0.018	0.000
Among individuals within populations [ $F_{ST}$ ]	93.06	0.069	0.000	94.45	0.056	0.000
<b>Group4</b>						
<b>(Wild, YX) (LGT, DQ) (BJ) (SD, HN)</b>						
Among groups [ $F_{CT}$ ]	7.22	0.072	0.019	4.25	0.043	0.010
Among populations within groups [ $F_{SC}$ ]	-0.37	-0.004	0.680	1.40	0.015	0.001
Among individuals within populations [ $F_{ST}$ ]	92.95	0.071	0.000	94.35	0.057	0.000
<b>Group5</b>						
<b>(Wild, YX) (LGT, DQ) (BJ, SD, HN)</b>						
Among groups [ $F_{CT}$ ]	2.92	0.029	0.120	1.15	0.011	0.227
Among populations within groups [ $F_{SC}$ ]	3.92	0.040	0.000	4.27	0.043	0.000
Among individuals within populations [ $F_{ST}$ ]	93.16	0.068	0.000	94.58	0.054	0.000
<b>Group6</b>						
<b>(Wild, YX) (LGT, DQ) (BJ, HN) (SD)</b>						
Among groups [ $F_{CT}$ ]	1.22	0.012	0.374	0.54	0.005	0.431
Among populations within groups [ $F_{SC}$ ]	5.20	0.053	0.000	4.74	0.048	0.000

Among individuals within populations [ $F_{ST}$ ]	93.59	0.064	0.000	94.73	0.053	0.000
<b>Group7</b>						
<b>(Wild, YX, SD) (LGT, DQ) (BJ) (HN)</b>						
Among groups [ $F_{CT}$ ]	6.72	0.067	0.026	3.74	0.037	0.048
Among populations within groups [ $F_{SC}$ ]	0.18	0.002	0.396	1.83	0.019	0.000
Among individuals within populations [ $F_{ST}$ ]	93.10	0.069	0.000	94.43	0.056	0.000
<b>Group8</b>						
<b>(Wild, YX, LGT, DQ) (BJ, SD, HN)</b>						
Among groups [ $F_{CT}$ ]	3.94	0.039	0.083	2.63	0.026	0.057
Among populations within groups [ $F_{SC}$ ]	3.72	0.039	0.000	3.53	0.036	0.000
Among individuals within populations [ $F_{ST}$ ]	92.34	0.077	0.000	93.83	0.062	0.000
<b>Group9</b>						
<b>(Wild, YX, LGT, DQ) (BJ, HN) (SD)</b>						
Among groups [ $F_{CT}$ ]	2.35	0.227	0.024	2.12	0.021	0.153
Among populations within groups [ $F_{SC}$ ]	4.59	0.000	0.047	3.74	0.038	0.000
Among individuals within populations [ $F_{ST}$ ]	93.06	0.000	0.069	94.14	0.059	0.000
<b>Group10</b>						
<b>(Wild, YX, BJ) (LGT, DQ) (HN, SD)</b>						
Among groups [ $F_{CT}$ ]	2.93	0.029	0.115	2.85	0.028	0.057
Among populations within groups [ $F_{SC}$ ]	3.80	0.039	0.000	2.83	0.029	0.000
Among individuals within populations [ $F_{ST}$ ]	93.28	0.067	0.000	94.32	0.057	0.000
<b>Group11</b>						
<b>(Wild, YX, BJ) (LGT, DQ, SD) (HN)</b>						
Among groups [ $F_{CT}$ ]	0.81	0.008	0.312	2.54	0.025	0.086
Among populations within groups [ $F_{SC}$ ]	5.56	0.056	0.000	3.10	0.032	0.000
Among individuals within populations [ $F_{ST}$ ]	93.63	0.064	0.000	94.36	0.056	0.000
<b>Group12</b>						
<b>(Wild) (YX, LGT, DQ) (BJ) (SD, HN)</b>						
Among groups [ $F_{CT}$ ]	6.44	0.064	0.030	4.72	0.047	0.010
Among populations within groups [ $F_{SC}$ ]	1.29	0.013	0.024	1.65	0.047	0.000
Among individuals within populations [ $F_{ST}$ ]	92.27	0.077	0.000	93.64	0.064	0.000
<b>Group13</b>						

<b>(Wild) (YX, LGT, DQ) (BJ, SD, HN)</b>						
Among groups [ $F_{CT}$ ]	3.02	0.030	0.169	2.18	0.022	0.131
Among populations within groups [ $F_{SC}$ ]	4.21	0.043	0.000	3.75	0.038	0.000
Among individuals within populations [ $F_{ST}$ ]	92.77	0.072	0.000	94.07	0.059	0.000
<b>Group14</b>						
<b>(Wild) (YX, LGT, DQ, BJ) (SD, HN)</b>						
Among groups [ $F_{CT}$ ]	-0.25	-0.002	0.456	3.59	0.036	0.047
Among populations within groups [ $F_{SC}$ ]	6.39	0.064	0.000	2.99	0.031	0.000
Among individuals within populations [ $F_{ST}$ ]	93.86	0.061	0.000	93.42	0.066	0.000
<b>Group15</b>						
<b>(Wild, YX, LGT, DQ, BJ) (SD, HN)</b>						
Among groups [ $F_{CT}$ ]	-0.73	0.007	0.295	4.09	0.041	0.046
Among populations within groups [ $F_{SC}$ ]	5.80	0.058	0.000	2.84	0.030	0.000
Among individuals within populations [ $F_{ST}$ ]	93.47	0.065	0.000	93.07	0.069	0.000
<b>Group16</b>						
<b>(Wild) (YX, LGT, DQ, SD) (BJ, HN)</b>						
Among groups [ $F_{CT}$ ]	1.56	0.016	0.298	1.78	0.018	0.189
Among populations within groups [ $F_{SC}$ ]	5.20	0.053	0.000	4.05	0.041	0.000
Among individuals within populations [ $F_{ST}$ ]	93.23	0.068	0.000	94.17	0.058	0.000
<b>Group17</b>						
<b>(Wild) (YX, SD) (LGT, DQ) (BJ, HN)</b>						
Among groups [ $F_{CT}$ ]	1.43	0.014	0.314	0.10	0.001	0.534
Among populations within groups [ $F_{SC}$ ]	5.03	0.051	0.000	5.11	0.051	0.000
Among individuals within populations [ $F_{ST}$ ]	93.54	0.065	0.000	94.79	0.052	0.000

Different groupings were tested to identify those which explain a greater percentage of variation (% var) among groups ( $F_{CT}$ ) than within groups ( $F_{SC}$ ).  $F_{CT}$  is the correlation of random haplotypes/alleles within a group of populations relative to that of random pairs of haplotypes/alleles drawn from the whole population.  $F_{SC}$  is the correlation of the molecular diversity of random haplotypes/alleles within populations relative to that of random pairs of haplotypes/alleles drawn from the region.  $F_{ST}$  is the correlation of random haplotypes/alleles within populations relative to that of random pairs of haplotypes/alleles drawn from the populations. For MHC and microsatellite, group 2 and group 1 (highlighted) respectively show the highest  $F_{CT}$  values with the most significant  $P$  values.