

## Supplementary data:

**Table 1.** Collection localities of *C. mystaceus* in Thailand.

Pop.	Code	N	Province	District	Region
1	BRk	9	Buri Ram	Krasang	Northeast
2	CPm	5	Chaiyaphum	Mueang	Northeast
3	KKk	5	Khon Kaen	Kranuan	Northeast
4	KKm	5	Khon Kaen	Mueang	Northeast
5	KKu	4	Khon Kaen	Ubolratana	Northeast
6	KSh	3	Kalasin	Huai Mek	Northeast
7	LEn	1	Loei	Nong Hin	Northeast
8	MHk	2	Mukdahan	Khamcha-I	Northeast
9	MHn	8	Mukdahan	Nong Sung	Northeast
10	MSk	2	Maha Sarakham	Kantharawichai	Northeast
11	Msm	5	Maha Sarakham	Mueang	Northeast
12	MSn	11	Maha Sarakham	Na Dun	Northeast
13	NBm	6	Nong Bua Lam Phu	Mueang	Northeast
14	NKt	4	Nong Khai	Tha Bo	Northeast
15	NPm	4	Nakhon Phanom	Mueang	Northeast
16	NPn	10	Nakhon Phanom	Na Wa	Northeast
17	NRk	2	Nakhon Ratchasima	Khon Buri	Northeast
18	NRp	5	Nakhon Ratchasima	Prathai	Northeast
19	NRw	2	Nakhon Ratchasima	Wang Nam Khiao	Northeast
20	REm	8	Roi Et	Mueang	Northeast
21	SIp	5	Si Sa Ket	Phrai Bueng	Northeast
22	SKk	6	Sakon Nakhon	Kut Bak	Northeast
23	SKp	12	Sakon Nakhon	Phon Na Kaeo	Northeast
24	SKw	2	Sakon Nakhon	Waritchaphum	Northeast
25	UBk	17	Ubon Ratchathani	Khemarat	Northeast
26	UDn	8	Udon Thani	Nong Han	Northeast
27	YTp	9	Yasothon	Pa Tio	Northeast
28	KBn	2	Kanchanaburi	Nong Prue	West
29	CNb	4	Chon Buri	Ban Bueng	East

30	CTm	1	Chai Nat	Mueang	Central
31	PTk	11	Pathum Thani	Khlong Luang	Central
32	SBk	5	Saraburi	Kaeng Khoi	Central
33	CMd	2	Chiang Mai	Doi Saket	North
34	CMf	1	Chiang Mai	Fang	North
35	CMm	2	Chiang Mai	Mueang	North
36	CRc	7	Chiang Rai	Chiang Saen	North
37	CRk	11	Chiang Rai	Chiang Khong	North
38	CRm	3	Chiang Rai	Mueang	North
39	CRw	10	Chiang Rai	Wiang Pa Pao	North
40	LPm	6	Lampang	Mueang	North
41	PYm	3	Pha Yao	Mueang	North
42	UTm	8	Uttaradit	Mueang	North

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**Table 2.** Summary statistics of molecular variation and neutrality analysis in 42 populations/localities of *C. mystaceus* in Thailand.

Code	N	S	H	Uh	Hd	Nd
BRk	9	1	2	2	0.389 ± 0.164	0.0006 ± 0.0002
CPm	5	6	4	3	0.900 ± 0.161	0.0055 ± 0.0014
KKk	5	4	2	0	0.600 ± 0.175	0.0039 ± 0.0011
KKm	5	4	3	2	0.800 ± 0.164	0.0032 ± 0.0009
KKu	4	7	3	3	0.833 ± 0.222	0.0062 ± 0.0017
KSh	3	0	1	0	0.000 ± 0.000	0.0000 ± 0.0000
LEn	1	NA	1	0	NA	NA
MHk	2	5	2	0	1.000 ± 0.500	0.0082 ± 0.0041
MHn	8	0	1	0	0.000 ± 0.000	0.0000 ± 0.0000
MSk	2	1	2	2	1.000 ± 0.500	0.0016 ± 0.0008
MSm	5	0	1	0	0.000 ± 0.000	0.0000 ± 0.0000
MSn	11	8	2	2	0.182 ± 0.144	0.0024 ± 0.0019
NBm	6	5	3	3	0.800 ± 0.122	0.0044 ± 0.0009
NKt	4	0	1	1	0.000 ± 0.000	0.0000 ± 0.0000
NPm	4	2	2	2	0.500 ± 0.265	0.0016 ± 0.0008
NPn	10	0	1	0	0.000 ± 0.000	0.0000 ± 0.0000
NRk	2	1	2	2	1.000 ± 0.500	0.0016 ± 0.0008
NRp	5	14	3	2	0.667 ± 0.160	0.0123 ± 0.0026
NRw	2	1	2	1	1.000 ± 0.500	0.0016 ± 0.0008
REm	8	10	2	2	0.250 ± 0.180	0.0041 ± 0.0029
SIp	5	11	3	2	0.800 ± 0.164	0.0088 ± 0.0024
SKk	6	1	2	0	0.533 ± 0.029	0.0009 ± 0.0007
SKp	12	1	2	2	0.167 ± 0.134	0.0003 ± 0.0002
SKw	2	6	2	2	1.000 ± 0.500	0.0098 ± 0.0049
UBk	17	8	3	2	0.544 ± 0.111	0.0031 ± 0.0014
UDn	8	6	4	3	0.821 ± 0.101	0.0048 ± 0.0008
YTp	9	1	2	1	0.222 ± 0.166	0.0004 ± 0.0003
KBn	2	4	2	2	1.000 ± 0.500	0.0065 ± 0.0032
CNb	4	3	3	3	0.833 ± 0.049	0.0027 ± 0.0009
CTm	1	NA	1	1	NA	NA

PTk	11	0	1	1	0.000 ± 0.000	0.0000 ± 0.0000
SBk	5	6	3	2	0.800 ± 0.164	0.0042 ± 0.0019
CMd	2	13	2	2	1.000 ± 0.500	0.0212 ± 0.0106
CMf	1	NA	1	1	NA	NA
CMm	2	16	2	1	1.000 ± 0.500	0.0261 ± 0.0131
CRc	7	0	1	0	0.000 ± 0.000	0.0000 ± 0.0000
CRk	11	2	3	3	0.473 ± 0.162	0.0010 ± 0.0004
CRm	3	0	1	0	0.000 ± 0.000	0.0000 ± 0.0000
CRw	10	1	2	1	0.467 ± 0.132	0.0008 ± 0.0002
LPm	6	18	5	4	0.933 ± 0.014	0.0167 ± 0.0032
PYm	3	4	3	2	1.000 ± 0.272	0.0043 ± 0.0016
UTm	8	0	1	1	0.000 ± 0.000	0.0000 ± 0.0000
<b>Total</b>	<b>238</b>	<b>96</b>	<b>75</b>	<b>63</b>	<b>0.975 ± 0.003</b>	<b>0.0150 ± 0.0026</b>

N, number of specimens; S, segregation sites; H, number of observed haplotypes; Uh, unique haplotype; Hd, haplotype diversity; Nd, nucleotide diversity; NA, not analysed.

**Table 3.** Genetic differentiation ( $\phi_{ST}$ ) (lower triangle) and  $P$  value (upper triangle) among *C. mystaceus* populations/localities from Thailand by *COI* sequence.

Localities	BRk	CPm	KKk	KKm	KKu	MHn	MSm	MSn	NBm	NKt	NPm	NPn	NRp	REm	Slp	SKk	SKp	UBk	UDn	YTp	CNb	PTk	SBk	CRc	CRk	CRw	LPm	UTm	
BRk		**	***	***	***	***	***	***	*	***	***	***	***	***	***	***	***	***	***	***	**	***	***	***	***	***	***	***	
CPm	0.405					***	***	***	*	**	*	***	*	***	***	***	***	***	***	***		***	***	***	***	***	***	***	
KKk	0.529	0.250			*	***	***	***	***	***	**	*	***	***	*	***	***	***	***	***	*	***	**	***	***	***	*	***	
KKm	0.447	0.150	0.167			***	***	***	*	***	*	*	***	***	***	***	***	***	***	***		***	*	***	***	***	*	***	
KKu	0.453	0.131	0.293	0.184		***	**	***		**		***	*	**		*	***	**	*	**		**		***	***	***	*	***	
MHn	0.794	0.642	0.768	0.685	0.719		***	***	***	***	***	***	***	***	***	***	***	***	***	***		**	***	**	***	***	***	***	***
MSm	0.752	0.550	0.700	0.600	0.630	1.000		***	***	***	***	***	***	**	**	***	***	***	***	***	**	***	*	***	***	***	***	***	***
MSn	0.723	0.564	0.677	0.603	0.622	0.894	0.874		***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
NBm	0.433	0.152	0.294	0.200	0.185	0.650	0.568	0.579		**	***	***	***	***	*	*	**	***	**	***		***	*	***	***	***	***	*	***
NKt	0.732	0.504	0.666	0.558	0.583	1.000	1.000	0.865	0.529		*	***	***	***	**	*	***	***	***	***	***	***	*	***	***	***	***	***	***
NPm	0.574	0.283	0.445	0.337	0.333	0.839	0.781	0.729	0.328	0.750		***	*	***	*	***	***	***	***	***	***	***	**	***	***	***	***	*	***
NPn	0.815	0.684	0.643	0.497	0.757	1.000	1.000	0.905	0.688	1.000	0.863		***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
NRp	0.484	0.227	0.363	0.273	0.265	0.686	0.474	0.618	0.270	0.585	0.400	0.719		***	*	***	***	***	***	***	*	***	***	***	***	***	***	*	***
REm	0.677	0.481	0.609	0.525	0.540	0.875	0.845	0.789	0.504	0.831	0.664	0.889	0.552		***	***	***	***	***	***	***	***	***	***	***	***	***	***	***
Slp	0.447	0.114	0.300	0.200	0.184	0.685	0.600	0.603	0.200	0.558	0.337	0.723	0.273	0.525		**	***	***	***	***	***	***	*	***	***	***	***	*	***
SKk	0.550	0.294	0.294	0.341	0.338	0.770	0.709	0.687	0.333	0.680	0.481	0.798	0.396	0.626	0.342		***	***	**	***	*	***	***	***	***	***	***	***	**
SKp	0.736	0.586	0.695	0.623	0.643	0.900	0.881	0.826	0.599	0.873	0.745	0.909	0.636	0.799	0.624	0.703		***	***	***	***	***	***	***	***	***	***	***	***
UBk	0.518	0.331	0.438	0.368	0.366	0.652	0.612	0.609	0.361	0.595	0.468	0.673	0.409	0.566	0.368	0.460	0.621		***	***	***	***	***	***	***	***	***	***	***
UDn	0.402	0.143	0.274	0.188	0.174	0.589	0.515	0.534	0.189	0.481	0.304	0.625	0.253	0.464	0.188	0.311	0.553	0.342		***	*	***	***	***	***	***	**	***	
YTp	0.694	0.513	0.635	0.554	0.571	0.000	0.856	0.800	0.532	0.844	0.689	0.895	0.577	0.765	0.555	0.649	0.809	0.582	0.490		***	***	***	***	***	***	***	***	***
CNb	0.453	0.131	0.293	0.184	0.166	0.719	0.630	0.623	0.185	0.583	0.333	0.758	0.265	0.540	0.184	0.339	0.644	0.366	0.174	0.571		***	***	***	***	***	***	***	***
PTk	0.824	0.701	0.811	0.734	0.773	1.000	1.000	0.909	0.703	1.000	0.873	1.000	0.733	0.895	0.739	0.809	0.913	0.682	0.641	0.900	0.773		***	***	***	***	***	***	***
SBk	0.447	0.150	0.300	0.200	0.184	0.685	0.600	0.603	0.200	0.558	0.337	0.723	0.273	0.525	0.200	0.342	0.624	0.368	0.188	0.555	0.184	0.739		***	***	***	*	***	
CRc	0.782	0.616	0.750	0.661	0.695	1.000	1.000	0.888	0.627	1.000	0.824	1.000	0.667	0.866	0.661	0.753	0.894	0.640	0.568	0.874	0.695	1.000	0.661		***	***	***	***	***
CRk	0.566	0.362	0.481	0.403	0.404	0.731	0.686	0.673	0.393	0.665	0.518	0.754	0.444	0.625	0.403	0.503	0.686	0.487	0.368	0.643	0.405	0.764	0.403	0.718		***	***	***	***
CRw	0.570	0.362	0.483	0.403	0.404	0.743	0.696	0.681	0.393	0.676	0.522	0.767	0.445	0.632	0.403	0.506	0.694	0.488	0.367	0.650	0.405	0.777	0.403	0.730	0.530		***	***	***
LPm	0.372	0.083	0.224	0.130	0.111	0.588	0.499	0.522	0.133	0.456	0.254	0.630	0.205	0.442	0.130	0.267	0.544	0.308	0.126	0.472	0.111	0.647	0.130	0.562	0.335	0.333		***	***
UTm	0.794	0.642	0.768	0.685	0.719	1.000	1.000	0.894	0.650	1.000	0.839	1.000	0.686	0.875	0.685	0.770	0.700	0.652	0.589	0.882	0.719	1.000	0.685	1.000	0.731	0.743	0.588		***

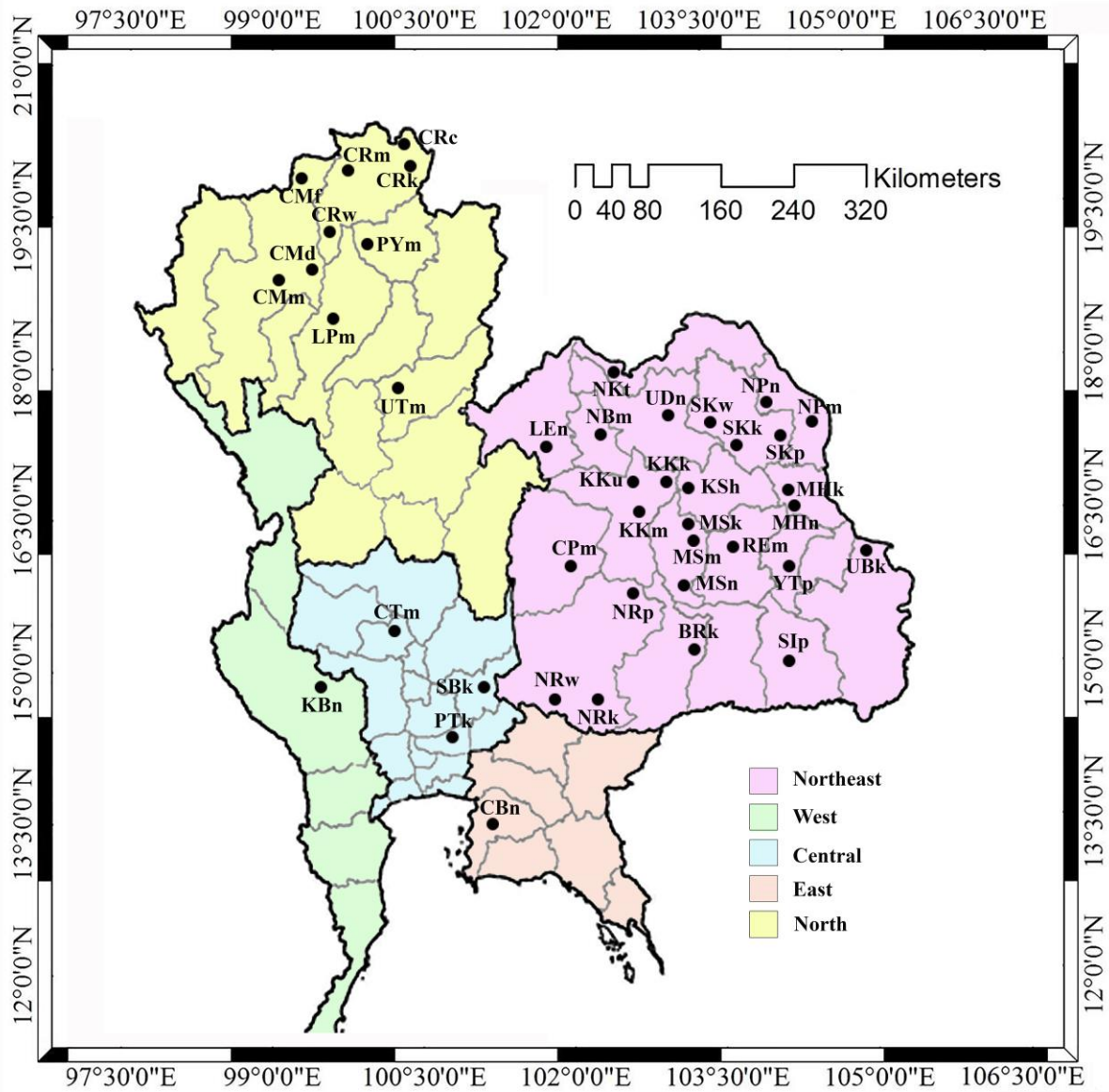
\*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ .

**Table 4.** Analysis of molecular variance (AMOVA) of *C. mystaceus* classified into different groups defined by different lineages and/or sampling localities.

Hypothesized structure	$F_{ST}$	$F_{SC}$	$F_{CT}$	AG			APWG			WP		
				Ss	Vc	Pv	Ss	Vc	Pv	Ss	Vc	Pv
<b>All lineages</b>												
2 groups [lineage I and lineage II]	0.587***	0.578***	0.019*	3.394	0.009	1.96	71.570	0.285	56.80	40.553	0.207	41.25
2 groups [north and northeast]	0.583***	0.574***	0.020	3.203	0.010	2.07	63.570	0.282	56.27	37.203	0.209	41.66
4 groups [north, east, west, central, northeast]	0.587***	0.578***	0.020	8.346	0.010	2.02	66.617	0.284	56.68	40.553	0.207	41.30
35 groups [35 different provinces]#	0.583***	0.544***	0.086	71.19	0.043	8.62	2.295	0.246	49.68	40.553	0.207	41.70
<b>Within lineage I</b>												
18 groups [18 different provinces]#	0.554***	0.551***	0.007	36.032	0.003	0.67	14.235	0.270	54.77	31.256	0.220	44.56
3 groups [central, east, northeast]#	0.557***	0.548***	0.019	8.944	0.009	1.91	41.323	0.267	53.76	31.256	0.220	44.33
<b>Within lineage II</b>												
7 groups [7 different provinces]#	0.65***	0.635***	0.043	11.905	0.021	4.35	7.875	0.299	60.73	9.297	0.172	34.92
3 groups [central, west, north]#	0.680***	0.624***	0.148	5.673	0.079	14.82	14.107	0.287	53.23	9.297	0.172	31.95

# Only the populations contained at least two specimens were included, \*  $P < 0.05$ , \*\*  $P < 0.001$ ,  $P < 0.0001$

AG, among groups; APWG, among populations within groups; WP, within populations; Ss, sum of squares; Vc, variance components; Pv, percentage of variation.



**Figure 1.** Map of sampling localities of *C. mystaceus* in Thailand.