

Table S1. Populations of Lyle's flying fox (*Pteropus lylei*) at roosting sites in Thailand. All sequences were deposited in the DNA Data Bank of Japan (DDBJ).

No.	Roosting site code	Province of roosting site	Mitochondrial D-loop GenBank accession number	Cytochrome <i>b</i> GenBank accession number	Sex
1	PL1_1	Wat Khanontai, Ayutthaya	LC579448	LC580006	female
2	PL1_2	Wat Khanontai, Ayutthaya	LC579449	LC580007	male
3	PL1_3	Wat Khanontai, Ayutthaya	LC579450	LC580008	-
4	PL1_4	Wat Khanontai, Ayutthaya	LC579451	LC580009	male
5	PL1_5	Wat Khanontai, Ayutthaya	LC579452	LC580010	male
6	PL1_6	Wat Khanontai, Ayutthaya	LC579453	LC580011	male
7	PL1_7	Wat Khanontai, Ayutthaya	LC579454	LC580012	male
8	PL1_8	Wat Khanontai, Ayutthaya	LC579455	LC580013	female
9	PL1_9	Wat Khanontai, Ayutthaya	LC579456	LC580014	male
10	PL1_10	Wat Khanontai, Ayutthaya	LC579457	LC580015	male
11	PL2_1	Wat Thasung, Ayutthaya	LC579458	LC580016	-
12	PL2_2	Wat Thasung, Ayutthaya	LC579459	LC580017	male
13	PL2_3	Wat Thasung, Ayutthaya	LC579460	LC580018	male
14	PL2_4	Wat Thasung, Ayutthaya	LC579461	LC580019	male
15	PL2_5	Wat Thasung, Ayutthaya	LC579462	LC580020	female
16	PL2_6	Wat Thasung, Ayutthaya	LC579463	LC580021	male
17	PL2_7	Wat Thasung, Ayutthaya	LC579464	LC580022	male
18	PL2_8	Wat Thasung, Ayutthaya	LC579465	LC580023	female
19	PL2_9	Wat Thasung, Ayutthaya	LC579466	LC580024	female
20	PL2_10	Wat Thasung, Ayutthaya	LC579467	LC580025	female
21	PL3_1	Wat Chantraram, Angthong	LC579468	LC580026	female
22	PL3_2	Wat Chantraram, Angthong	LC579469	LC580027	male
23	PL3_3	Wat Chantraram, Angthong	LC579470	LC580028	female
24	PL3_4	Wat Chantraram, Angthong	LC579471	LC580029	male
25	PL3_5	Wat Chantraram, Angthong	LC579472	LC580030	male
26	PL3_6	Wat Chantraram, Angthong	LC579473	LC580031	female
27	PL3_7	Wat Chantraram, Angthong	LC579474	LC580032	female
28	PL3_8	Wat Chantraram, Angthong	LC579475	LC580033	male
29	PL3_9	Wat Chantraram, Angthong	LC579476	LC580034	female
30	PL3_10	Wat Chantraram, Angthong	LC579477	LC580035	female
31	PL4_1	Wat Tanen, Ayutthaya	LC579478	LC580036	male
32	PL4_2	Wat Tanen, Ayutthaya	LC579479	LC580037	female
33	PL4_3	Wat Tanen, Ayutthaya	LC579480	LC580038	male
34	PL4_4	Wat Tanen, Ayutthaya	LC579481	LC580039	male
35	PL4_5	Wat Tanen, Ayutthaya	LC579482	LC580040	-
36	PL4_6	Wat Tanen, Ayutthaya	LC579483	LC580041	male
37	PL4_7	Wat Tanen, Ayutthaya	LC579484	LC580042	-
38	PL4_8	Wat Tanen, Ayutthaya	LC579485	LC580043	male
39	PL4_9	Wat Tanen, Ayutthaya	LC579486	LC580044	male
40	PL4_10	Wat Tanen, Ayutthaya	LC579487	LC580045	male
41	PL5_1	Wat Mongkoteeparam, Saraburi	LC579488	LC580046	male
42	PL5_2	Wat Mongkoteeparam, Saraburi	LC579489	LC580047	female
43	PL5_3	Wat Mongkoteeparam, Saraburi	LC579490	LC580048	female
44	PL5_4	Wat Mongkoteeparam, Saraburi	LC579491	LC580049	male

No.	Roosting site code	Province of roosting site	Mitochondrial D-loop GenBank accession number	Cytochrome <i>b</i> GenBank accession number	Sex
45	PL5_5	Wat Mongkonteeparam, Saraburi	LC579492	LC580050	male
46	PL5_6	Wat Mongkonteeparam, Saraburi	LC579493	LC580051	male
47	PL5_7	Wat Mongkonteeparam, Saraburi	LC579494	LC580052	female
48	PL5_8	Wat Mongkonteeparam, Saraburi	LC579495	LC580053	female
49	PL5_9	Wat Mongkonteeparam, Saraburi	LC579496	LC580054	male
50	PL5_10	Wa Mongkonteeparam, Saraburi	LC579497	LC580055	male
51	PL6_1	Wat Thewabut, Prachinburi	LC579498	LC580056	female
52	PL6_2	Wat Thewabut, Prachinburi	LC579499	LC580057	male
53	PL6_3	Wat Thewabut, Prachinburi	LC579500	LC580058	male
54	PL6_4	Wat Thewabut, Prachinburi	LC579501	LC580059	male
55	PL6_5	Wat Thewabut, Prachinburi	LC579502	LC580060	female
56	PL6_6	Wat Thewabut, Prachinburi	LC579503	LC580061	female
57	PL6_7	Wat Thewabut, Prachinburi	LC579504	LC580062	female
58	PL6_8	Wat Thewabut, Prachinburi	LC579505	LC580063	male
59	PL6_9	Wat Thewabut, Prachinburi	LC579506	LC580064	female
60	PL6_10	Wat Thewabut, Prachinburi	LC579507	LC580065	female
61	PL7_1	Wat Bangkrabao, Prachinburi	LC579508	LC580066	female
62	PL7_2	Wat Bangkrabao, Prachinburi	LC579509	LC580067	female
63	PL7_3	Wat Bangkrabao, Prachinburi	LC579510	LC580068	male
64	PL7_4	Wat Bangkrabao, Prachinburi	LC579511	LC580069	female
65	PL7_5	Wat Bangkrabao, Prachinburi	LC579512	LC580070	male
66	PL7_7	Wat Bangkrabao, Prachinburi	LC579513	LC580071	male
67	PL7_8	Wat Bangkrabao, Prachinburi	LC579514	LC580072	male
68	PL7_9	Wat Bangkrabao, Prachinburi	LC579515	LC580073	male
69	PL7_10	Wat Bangkrabao, Prachinburi	LC579516	LC580074	female
70	PL8_1	Education Center, Chonburi	LC579517	LC580075	female
71	PL8_2	Education Center, Chonburi	LC579518	LC580076	male
72	PL8_3	Education Center, Chonburi	LC579519	LC580077	male
73	PL8_4	Education Center, Chonburi	LC579520	LC580078	female
74	PL8_5	Education Center, Chonburi	LC579521	LC580079	male
75	PL8_6	Education Center, Chonburi	LC579522	LC580080	female
76	PL8_7	Education Center, Chonburi	LC579523	LC580081	female
77	PL8_8	Education Center, Chonburi	LC579524	LC580082	male
78	PL8_9	Education Center, Chonburi	LC579525	LC580083	female
79	PL8_10	Education Center, Chonburi	LC579526	LC580084	female
80	PL9_2	Wat Luangphrommawat, Chonburi	LC579527	LC580085	female
81	PL9_3	Wat Luangphrommawat, Chonburi	LC579528	LC580086	female
82	PL9_4	Wat Luangphrommawat, Chonburi	LC579529	LC580087	female
83	PL9_5	Wat Luangphrommawat, Chonburi	LC579530	LC580088	female
84	PL9_7	Wat Luangphrommawat, Chonburi	LC579531	LC580089	male

No.	Roosting site code	Province of roosting site	Mitochondrial D-loop GenBank accession number	Cytochrome <i>b</i> GenBank accession number	Sex
85	PL9_8	Wat Luangphrommawat, Chonburi	LC579532	LC580090	male
86	PL9_9	Wat Luangphrommawat, Chonburi	LC579533	LC580091	male
87	PL9_10	Wat Luangphrommawat, Chonburi	LC579534	LC580092	female
88	PL10_1	Wat Phobangkla, Chachoengsao	LC579535	LC580093	male
89	PL10_2	Wat Phobangkla, Chachoengsao	LC579536	LC580094	male
90	PL10_3	Wat Phobangkla, Chachoengsao	LC579537	LC580095	female
91	PL10_4	Wat Phobangkla, Chachoengsao	LC579538	LC580096	male
92	PL10_5	Wat Phobangkla, Chachoengsao	LC579539	LC580097	male
93	PL10_6	Wat Phobangkla, Chachoengsao	LC579540	LC580098	female
94	PL10_7	Wat Phobangkla, Chachoengsao	LC579541	LC580099	male

Table S2. Genetic differentiation between the ten colonies of Lyle's flying fox (*Pteropus lylei*) for the D-loop sequence. Genetic differentiation coefficient (G_{ST}), Wright's F -statistics for subpopulations within the total population (F_{ST}), Φ_{ST} , gene flow (N_m) from sequence data and haplotype data, average number of nucleotide substitutions per site between populations (D_{xy}), net nucleotide substitutions per site between populations (D_a), and Mantel test results.

Colony 1	Colony 2	G_{ST}	Φ_{ST}	F_{ST}	D_{xy}	D_a	N_m	Presence of IBD ¹
AY1	AY2	-0.038	0.022	-0.076	0.008	-0.001	∞^2	NO
AY1	AT1	-0.045	0.018	-0.087	0.007	-0.001	∞	NO
AY1	AY3	-0.010	0.053	-0.036	0.012	0.000	∞	NO
AY1	SB1	-0.024	0.033	-0.043	0.009	0.000	∞	NO
AY1	PBR1	0.004	0.067	0.000	0.007	0.000	∞	NO
AY1	PBR2	-0.025	0.042	-0.032	0.011	0.000	∞	NO
AY1	CH1	-0.036	0.028	-0.045	0.010	-0.001	∞	NO
AY1	CH2	-0.021	0.038	-0.032	0.013	-0.001	∞	NO
AY1	CHS2	-0.034	0.043	-0.062	0.010	-0.001	∞	NO
AY2	AT1	-0.031	0.054	-0.026	0.009	0.000	∞	NO
AY2	AY3	-0.020	0.071	-0.004	0.014	0.000	∞	NO
AY2	SB1	-0.026	0.038	-0.030	0.011	0.000	∞	NO
AY2	PBR1	-0.007	0.034	-0.038	0.008	0.000	∞	NO
AY2	PBR2	-0.030	0.047	-0.062	0.012	0.000	∞	NO
AY2	CH1	-0.023	0.044	-0.014	0.011	0.000	415.000	NO
AY2	CH2	-0.030	0.049	0.001	0.015	0.000	∞	NO
AY2	CHS2	-0.030	0.044	-0.026	0.011	-0.001	∞	NO
AT1	AY3	-0.025	0.029	-0.039	0.012	-0.001	∞	NO
AT1	SB1	-0.025	0.052	-0.065	0.011	0.000	∞	NO
AT1	PBR1	0.031	0.117	-0.017	0.009	0.001	6.250	NO
AT1	PBR2	-0.024	0.047	-0.074	0.012	0.000	∞	NO
AT1	CH1	-0.037	0.034	-0.039	0.011	0.000	∞	NO
AT1	CH2	-0.018	0.043	-0.043	0.014	-0.001	∞	NO
AT1	CHS2	-0.028	0.049	-0.007	0.011	0.000	∞	NO
AY3	SB1	-0.014	0.068	0.001	0.015	0.000	337	NO
AY3	PBR1	0.033	0.114	0.072	0.013	0.002	6.432	NO
AY3	PBR2	-0.037	0.026	-0.078	0.015	-0.001	∞	NO
AY3	CH1	-0.009	0.040	-0.050	0.015	0.000	∞	NO
AY3	CH2	-0.021	0.037	-0.038	0.018	-0.001	∞	NO
AY3	CHS2	-0.027	0.023	-0.106	0.014	-0.001	∞	NO
SB1	PBR1	0.027	0.072	0.004	0.010	0.000	103.750	NO
SB1	PBR2	-0.022	0.047	-0.019	0.013	0.000	∞	NO
SB1	CH1	-0.016	0.043	-0.008	0.013	0.000	∞	NO
SB1	CH2	-0.036	0.036	-0.047	0.016	-0.001	∞	NO
SB1	CHS2	-0.018	0.048	-0.036	0.013	0.000	∞	NO
PBR1	PBR2	0.022	0.091	0.069*	0.011	0.001	6.649	NO
PBR1	CH1	0.052	0.093	0.090	0.011	0.001	5.000	NO
PBR1	CH2	0.000	0.082	0.018	0.014	0.000	26.763	NO
PBR1	CHS2	0.020	0.082	0.034	0.010	0.000	13.989	NO
PBR2	CH1	-0.025	0.022	-0.089	0.013	-0.001	∞	NO
PBR2	CH2	-0.028	0.024	-0.066	0.016	-0.001	∞	NO
PBR2	CHS2	-0.047	0.011	-0.129	0.013	-0.002	∞	NO
CH1	CH2	-0.007	0.011	-0.067	0.015	-0.002	∞	NO
CH1	CHS2	-0.041	0.020	-0.105	0.012	-0.001	∞	NO
CH2	CHS2	-0.007	0.027	-0.084	0.016	-0.001	∞	NO

Significant differentiation values * $p < 0.05$

¹ Presence of IBD = NO represents/indicates a non-significant correlation between genetic distance and geographic distance.

² ∞ = Presence of high gene flow.

Table S3. Genetic differentiation between the ten colonies of Lyle's flying fox (*Pteropus lylei*) for the Cytochrome *b* sequence. Genetic differentiation coefficient (G_{ST}), Wright's F -statistics for subpopulations within the total population (F_{ST}), Φ_{ST} , gene flow (N_m) from sequence data and haplotype data, average number of nucleotide substitutions per site between populations (D_{xy}), net nucleotide substitutions per site between populations (D_a), and Mantel test results.

Colony 1	Colony 2	G_{ST}	Φ_{ST}	F_{ST}	D_{xy}	D_a	N_m	Presence of IBD ¹
AY1	AY2	-0.003	0.065	0.024	0.007	0.000	18.023	NO
AY1	AT1	-0.015	0.013	-0.084	0.007	-0.001	∞^2	NO
AY1	AY3	-0.014	0.035	-0.035	0.006	0.000	∞	NO
AY1	SB1	0.005	0.111	0.112	0.007	0.001	3.877	NO
AY1	PBR1	0.021	0.119	0.125	0.008	0.001	3.437	NO
AY1	PBR2	-0.019	0.024	-0.066	0.006	0.000	∞	NO
AY1	CH1	0.001	0.025	-0.058	0.007	0.000	∞	NO
AY1	CH2	-0.025	0.015	-0.093	0.006	-0.001	∞	NO
AY1	CHS2	0.012	0.030	-0.073	0.007	-0.001	∞	NO
AY2	AT1	0.007	0.067	0.028	0.008	0.000	14.688	NO
AY2	AY3	0.034	0.149	0.177*	0.008	0.001	2.364	NO
AY2	SB1	0.001	0.028	-0.051	0.007	0.000	∞	NO
AY2	PBR1	0.017	0.030	-0.045	0.007	0.000	∞	NO
AY2	PBR2	0.011	0.056	0.002	0.007	0.000	278.000	NO
AY2	CH1	0.013	0.069	0.032	0.008	0.000	18.468	NO
AY2	CH2	0.039	0.075	0.033	0.008	0.000	14.340	NO
AY2	CHS2	-0.013	0.057	-0.013	0.008	0.000	∞	NO
AT1	AY3	0.002	0.041	-0.024	0.006	0.000	∞	NO
AT1	SB1	0.020	0.108	0.106	0.008	0.001	3.815	NO
AT1	PBR1	0.004	0.111	0.112	0.008	0.001	3.622	NO
AT1	PBR2	-0.007	0.028	-0.057	0.007	0.000	∞	NO
AT1	CH1	-0.005	0.029	-0.048	0.007	0.000	∞	NO
AT1	CH2	0.003	0.024	-0.073	0.007	0.000	∞	NO
AT1	CHS2	-0.015	0.031	-0.070	0.007	-0.001	∞	NO
AY3	SB1	0.033	0.211	0.276*	0.008	0.002	1.371	NO
AY3	PBR1	0.054	0.216	0.283*	0.008	0.002	1.287	NO
AY3	PBR2	-0.007	0.054	-0.005	0.006	0.000	∞	NO
AY3	CH1	0.013	0.043	-0.021	0.007	0.000	∞	NO
AY3	CH2	-0.027	0.028	-0.069	0.006	0.000	∞	NO
AY3	CHS2	0.030	0.049	-0.038	0.006	0.000	∞	NO
SB1	PBR1	0.009	0.035	-0.037	0.006	0.000	∞	NO
SB1	PBR2	-0.008	0.083	0.054	0.007	0.000	8.827	NO
SB1	CH1	0.047	0.107	0.104	0.008	0.001	4.587	NO
SB1	CH2	0.038	0.114	0.105	0.007	0.001	4.219	NO
SB1	CHS2	0.033	0.110	0.087	0.008	0.001	4.717	NO
PBR1	PBR2	0.017	0.102	0.088	0.007	0.001	5.112	NO
PBR1	CH1	0.047	0.130	0.144	0.009	0.001	3.224	NO
PBR1	CH2	0.045	0.127	0.129	0.008	0.001	3.375	NO
PBR1	CHS2	0.003	0.099	0.067	0.008	0.001	6.262	NO
PBR2	CH1	0.016	0.023	-0.066	0.007	0.000	∞	NO
PBR2	CH2	-0.016	0.013	-0.106	0.006	-0.001	∞	NO
PBR2	CHS2	0.010	0.023	-0.095*	0.007	-0.001	∞	NO
CH1	CH2	0.015	0.014	-0.093	0.007	-0.001	∞	NO
CH1	CHS2	-0.009	0.027	-0.077	0.008	-0.001	∞	NO
CH2	CHS2	0.031	0.023	-0.104	0.007	-0.001	∞	NO

Significant differentiation values * $p < 0.05$

¹ Presence of IBD = NO represents/indicates a non-significant correlation between genetic distance and geographic distance.

² ∞ = Presence of high gene flow.

Table S4. Bayesian estimates of mutation-scaled effective population sizes (Θ) and asymmetric migration rates (M) among *Pteropus lylei* for the mt D-loop and *Cytb* sequence. Credibility intervals are reported at 95% for each derived migration rate parameter N_{em} , reflecting the effective number of migrants per generation.

Parameter	2.5%	25%	Mode	75%	97.5%
Θ_1^1	0.022	0.040	0.047	0.049	0.051
Θ_2^2	0.000	0.000	0.001	0.002	0.002
Θ_3^3	0.005	0.009	0.011	0.014	0.031
Θ_4^4	0.011	0.034	0.045	0.048	0.049
Θ_5^5	0.000	0.000	0.002	0.003	0.008
Θ_6^6	0.000	0.000	0.003	0.005	0.011
Θ_7^7	0.000	0.000	0.002	0.004	0.005
Θ_8^8	0.019	0.033	0.042	0.045	0.049
Θ_9^9	0.000	0.000	0.002	0.005	0.005
Θ_{10}^{10}	0.001	0.002	0.003	0.005	0.021
$M_{1>2}$	0.0	72	116.3	180	332
$M_{1>3}$	18.7	80.7	106.3	180	309.3
$M_{1>4}$	0.0	46.7	84.3	106.7	329.3
$M_{1>5}$	152.7	228.7	300.3	339.3	492
$M_{1>6}$	184	346	458.3	481.3	488.7
$M_{1>7}$	0.0	24	57	124.7	298.7
$M_{1>8}$	220	416	478.3	496.7	506.7
$M_{1>9}$	14	57.3	144.3	197.3	400
$M_{1>10}$	76	100.7	187	274.7	488.7
$M_{2>1}$	194	309.3	379.7	470.7	492.7
$M_{2>3}$	0.0	13.3	36.3	90.7	236
$M_{2>4}$	202.7	321.3	411	492	504
$M_{2>5}$	265.3	359.3	479	493.3	503.3
$M_{2>6}$	0.0	0.0	10.3	56	144
$M_{2>7}$	0.0	0.0	0.3	60	165.3
$M_{2>8}$	0.0	265.3	361	407.3	510.7
$M_{2>9}$	38.7	159.3	239	321.3	426
$M_{2>10}$	152	380	415.7	480	498.7
$M_{3>1}$	216	345.3	368.3	409.3	504
$M_{3>2}$	70	126.7	170.3	232.7	421.3
$M_{3>4}$	20	26	59.7	162.7	178
$M_{3>5}$	82.7	328.7	476.3	496.7	498.7
$M_{3>6}$	229.3	402	431	484.7	501.3
$M_{3>7}$	264	361.3	438.3	484	497.3
$M_{3>8}$	142	279.3	316.3	377.3	491.3
$M_{3>9}$	168.7	281.3	364.3	421.3	491.3
$M_{3>10}$	0.0	0.0	22.3	84	389.3
$M_{4>1}$	0.0	8.7	79.7	200	296.7
$M_{4>2}$	0.0	21.3	51.7	140	230
$M_{4>3}$	0.0	11.3	25.7	43.3	342
$M_{4>5}$	177.3	402.7	447.7	484	500.7
$M_{4>6}$	0.0	0.0	91	172	340.7
$M_{4>7}$	0.0	4.7	13.7	24	306.7
$M_{4>8}$	202.7	396.7	443	490	507.3
$M_{4>9}$	0.0	0.0	0.3	35.3	362
$M_{4>10}$	0.0	0.0	12.3	24.7	251.3
$M_{5>1}$	17.3	130	205	235	410.7
$M_{5>2}$	0.0	0.0	0.3	68.7	342.7
$M_{5>3}$	38.7	82.7	140.3	194.7	439.3
$M_{5>4}$	292	325.3	368.3	446.7	479.3
$M_{5>6}$	0.0	0.0	0.3	146	248.7

Parameter	2.5%	25%	Mode	75%	97.5%
M5->7	178.7	354.7	393.7	484.7	504
M5->8	60	126.7	203.7	282	486
M5->9	85.3	132	231	261.3	460.7
M5->10	298	442	472.3	482.7	506.7
M6->1	200.7	371.3	475.7	491.3	498.7
M6->2	0.0	0.0	18.3	62.7	424
M6->3	38	270.7	298.3	334.7	363.3
M6->4	152	377.3	421.7	481.3	497.3
M6->5	0.0	0.0	19.7	120	271.3
M6->7	0.0	0.0	0.3	50	299.3
M6->8	0.0	0.0	0.3	91.3	314.7
M6->9	20	183.3	207.7	300	482
M6->10	80	156	219.7	308	499.3
M7->1	259.3	368	414.3	451.3	503.3
M7->2	264.7	440.7	477	490.7	508.7
M7->3	3.3	10	37	113.3	173.3
M7->4	0.0	8.0	71	138	453.3
M7->5	0.0	0.0	0.3	67.3	421.3
M7->6	190.7	386.7	420.3	490	498
M7->8	7.3	40	119.7	184	348.7
M7->9	40.7	178.7	209.7	288.7	408.7
M7->10	9.3	104.7	186.3	244	486
M8->1	212.7	358	440.3	480	498.7
M8->2	177.3	252	295.7	340.7	489.3
M8->3	0.0	22.7	36.3	86	273.3
M8->4	78	173.3	215.7	282.7	493.3
M8->5	180.7	221.3	385	431.3	359.3
M8->6	0.0	0.0	0.3	60	165.3
M8->7	0.0	0.0	0.3	46	217.3
M8->9	249.3	435.3	475.7	494	505.3
M8->10	0.0	0.0	0.3	145.3	334
M9->1	186	356	400.3	473.3	501.3
M9->2	0.0	0.0	0.3	42	228.7
M9->3	102.7	256	307.7	384	468.7
M9->4	0.0	0.0	19	76	498.7
M9->5	88.7	190.7	265.7	314.7	477.3
M9->6	140.7	337.3	393.7	480.7	495.3
M9->7	0.0	0.7	33.7	144.7	394
M9->8	79.3	328	413	480.7	496.7
M9->10	108.7	361.3	399	462.7	500
M10->1	69.3	176.7	241	310.7	494
M10->2	0.0	0.0	0.3	42	228.7
M10->3	199.3	295.3	341.7	408	490.7
M10->4	293.3	429.3	476.3	496.7	510
M10->5	138	264.7	327.7	412.7	499.3
M10->6	0.0	29.3	43	79.3	199.3
M10->7	270.7	350.7	397	484	487.3
M10->8	180	261.3	323	347.3	495.3
M10->9	53.3	370	403	486.7	496

1= Wat Khanontai, Ayutthaya (AY1); 2= Wat Thasung, Ayutthaya (AY2); 3= Wat Chantraram, Anghthong (AT1)
4= Wat Tanen, Ayutthaya (AY3); 5= Wat Mongkonteeparam, Saraburi (SB1); 6= Wat Thewabut, Prachinburi (PBR1); 7= Wat Bangkrabao, Prachinburi (PBR2); 8= Education Center, Chonburi (CH1); 9= Wat Luangphrommawat, Chonburi (CH2); 10= Wat Phobangkla, Chachoengsao (CHS2)