Table 1 The nine investigated samples of *Piper* species with leaves collections and growing areas which are collected sites.

Plants	Collected sites
Piper betle 1*	Muang Khon Kaen District, Khon Kaen Province in northeastern Thailand
P. betle 2**	Muang Khon Kaen District, Khon Kaen Province in northeastern Thailand
P. betloides	Doi Suthep-Pui National Park, Chiang Mai Province in northern Thailand
P. crocatum	Garden and Development Department, Queen Sirikit Botanic Garden, Chiang Mai Province in northern Thailand
P. maculaphyllum	Punyaban Waterfall, Lum Nam Kraburi National Park, Ranong Province in southern Thailand
P. rubroglandulosum 1	Khao Phanom Bencha National Park, Krabi Province in southern Thailand
P. rubroglandulosum 2#	Khao Phanom Bencha National Park, Krabi Province in southern Thailand
P. semiimmersum	Sri Pungnga National Park, Pungnga Province in southern Thailand
P. submultinerve 1	Garden and Development Department, Queen Sirikit Botanic Garden, Chiang Mai Province in northern Thailand
P. submultinerve 2	Beside 105 road, Mae Salid Sub-District, Ban Tak District, Tak Province in northern Thailand
P. submultinerve 3	Garden and Development Department, Queen Sirikit Botanic Garden, Chiang Mai Province in northern Thailand
P. submultinerve 4	Beside 105 road, Mae Salid Sub-District, Ban Tak District, Tak Province in northern Thailand
P. tricolor 1***	Muang Khon Kaen District, Khon Kaen Province in northeastern Thailand
P. tricolor 2	Garden and Development Department, Queen Sirikit Botanic Garden, Chiang Mai Province in northern Thailand
P. yinkiangense #	Khao Sok National Park, Surat Thani Province in southern Thailand

* Purchased from a market, indicating that it grows in cultivated conditions

** Grows under natural conditions

*** Transferred from forest to grow in house area under natural conditions

Grows around office areas under natural conditions

Table 2 The amount of essential oils from the leaves of the examined *Piper* species

***Piper* species**	**Date**	**Weight/kg**	**Essential oil value (mL)**	**Essential oil ratio (mL/kg)**
Piper betle 1*	29/11/2012	1.00	1.840	1.84
	9/7/2013	0.92	0.770	0.84
	9/7/2013	1.00	0.790	0.79
	26/7/2013	0.94	1.050	1.12
	5/8/2013	1.00	2.150	2.15
	5/8/2013	1.00	2.730	2.73
P. betle 2**	29/11/2012	1.00	0.950	0.95
P. betloides	4/2/57	0.82	0.078	0.10
P. crocatum	5/2/2014	0.66	0.020	0.03
P. maculaphyllum	5/8/2013	0.50	0.025	0.05
P. rubroglandulosum 1	1/4/2014	0.47	0.220	0.47
P. rubroglandulosum 2#	1/4/2014	0.33	0.240	0.72
P. semiimersum	5/8/2013	0.60	0.080	0.13
P. submultinerve 1	7/2/2014	1.00	0.115	0.12
P. submultinerve 2	7/2/2014	0.76	0.302	0.40
P. submultinerve 3	7/2/2014	0.36	0.010	0.03
P. submultinerve 4	7/2/2014	0.94	0.032	0.03
P. tricolor 1***	12/11/2013	0.78	0.590	0.76
P. tricolor 2	4/2/2014	0.98	0.030	0.03
P. yinkiangense#	1/4/2014	0.65	0.40	0.62

8 **Table 3** Preliminary phytochemicals identified in essential oil from the leaves of the examined *Piper* species

Compound	Retention time	Formula	Molecular weight	Relative content														
				Piper betle 1	*P. betle* 2	*P. betloides*	*P. crocatum*	*P. maculaphyllum*	*P. rubrogландulosum* 1	*P. rubrogландulosum* 2	*P. semiimmersum*	*P. submultinerve* 1	*P. submultinerve* 2	*P. submultinerve* 3	*P. submultinerve* 4	*P. tricolor* 1	*P. tricolor* 2	*P. yinkiangense*
Eucalyptol	5.143	$C_{10}H_{18}O$	154	-	0.654	-	-	-	-	-	-	-	-	-	-	-	-	-
trans-β-Ocimene	5.195-5.477	$C_{10}H_{16}$	136	-	-	-	-	-	0.597	0.750	-	-	-	-	-	-	0.688	-
δ-3-Carene																		
α-Ocimene																		
cis-Ocimene																		
cis-β-Ocimene																		
γ-Terpinene																		
Tricyclene																		
α-Pinene																		
trans-Sabinene hydrate	6.072	$C_{10}H_{18}O$	154	-	-	-	0.717	-	-	-	-	-	-	-	-	-	-	-
β-Terpineol	7.243-7.710	$C_{10}H_{18}O$	154	-	-	-	25.025	-	-	-	-	-	-	-	-	-	0.701	-
L-Linalool	6.406-6.683	$C_{10}H_{18}O$	154	-	-	13.629	26.590	-	0.160	-	-	-	-	5.434	-	-	7.112	1.594
α-Terpineol	7.462-7.912	$C_{10}H_{18}O$	154	-	0.494	10.111	14.218	0.636	-	-	-	-	-	-	-	2.276	2.243	-
Linalyl propionate		$C_{13}H_{22}O_2$	210															
Borneol	7.479	$C_{10}H_{18}O$	154	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.240
4-Terpineol	7.554-7.733	$C_{10}H_{18}O$	154	-	-	4.705	-	-	-	-	-	-	-	-	-	-	46.560	0.381
n-Decanal	7.612	$C_{10}H_{20}O$	156	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1.208
2-Cyclohexen-1-ol, 1-methyl-4-(1-methylethyl)-, trans-	7.658	$C_{10}H_{18}O$	154	-	3.762	-	-	-	-	-	-	-	-	-	-	-	-	-
cis-Piperitol	8.056	$C_{10}H_{18}O$	154	-	-	-	-	-	-	-	-	-	-	-	-	-	0.508	-
Geraniol	8.166-8.950	$C_{10}H_{18}O$	154	-	-	1.204	7.777	-	-	-	-	-	-	-	-	-	-	-
Chavicol	8.489-8.546	$C_9H_{10}O$	134	0.716	0.617	1.110	-	-	-	-	-	-	-	4.035	-	0.729	-	-
δ-Elemene	9.429-9.539	$C_{15}H_{24}$	204	-	-	-	-	-	0.149	-	-	1.135	-	-	-	-	-	1.337
α-Terpinene																		
δ-2-Carene																		
δ-4-Carene																		
Chavicol acetate	9.550-9.677	$C_{11}H_{12}O_2$	176	6.843	1.637	-	-	-	-	-	-	-	-	-	-	-	-	0.293
α-Cubebene	9.596-9.706	$C_{15}H_{24}$	204	-	-	-	-	1.755	-	-	-	1.379	-	-	-	-	-	0.295
Cadina-1,4-diene																		
Eugenol	9.873-11.950	$C_{10}H_{12}O_2$	164	7.847	53.559	-	-	-	-	-	-	-	-	4.797	2.730	49.942	-	-
Chavibetol																		
3-Allylguaiacol																		
Isoeugenol																		
2-Methoxy-6-(2-propenyl)phenol																		
Isochavibetol																		
2-methoxy-5-[(E)-prop-1-enyl]phenol																		
Phenol,2-methoxy-3-(2-propen-1-yl)2-Methoxy-6-(2-propenyl)phenol																		
3-Allyl-6-methoxy phenyl acetate																		
Cyclosativene	9.960	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.367
α-Copaene	10.017-13.548	$C_{15}H_{24}$	204	-	-	-	-	8.522	0.136	0.213	-	2.135	-	-	0.704	-	0.651	1.648
Geranyl acetate	10.093	$C_{12}H_{20}O_2$	196	-	-	0.910	-	-	-	-	-	-	-	-	-	-	-	-
β-Elemene	10.179-11.477	$C_{15}H_{24}$	204	1.118	-	1.012	-	1.820	1.269	1.110	-	5.195	6.424	3.337	14.384	-	1.234	2.030
8-Isopropenyl-1, 5-dimethyl-1, 5-cyclo decadiene																		
O-Methyl eugenol	10.289	$C_{11}H_{14}O_2$	178	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.397
α-Grujunene	10.571-11.685	$C_{15}H_{24}$	204	-	-	-	-	9.439	-	-	-	4.097	-	-	-	-	-	-
trans-Caryophyllene	10.646-10.802	$C_{15}H_{24}$	204	2.473	-	3.617	0.651	11.505	4.083	4.870	9.318	11.656	39.422	7.175	26.283	-	1.831	21.142
trans-β-Caryophyllene																		
γ-caryophyllene																		
Bicyclo[5.2.0]nonane,																		

4-ethenyl-4,8,8-tri methyl-2-methylene-																		
Germacrene D	10.871-11.887	$C_{15}H_{24}$	204	6.714	-	5.312	0.869	12.528	1.115	2.168	7.362	36.317	1.145	-	3.953	1.174	4.769	8.592
β-Cubebene																		
(-)-Sinularene																		
trans-β-Farnesene	10.917	$C_{15}H_{24}$	204	-	-	-	-	-	-	0.208	-	-	-	-	-	-	-	-
Aromadendrene	11.010	$C_{15}H_{24}$	204	-	-	-	-	0.842	-	-	-	-	-	-	-	-	-	-
α-Caryophyllene	11.114-11.240	$C_{15}H_{24}$	204	0.775	-	1.679	-	4.987	4.282	3.062	-	2.849	-	6.490	25.063	-	0.760	16.136
cis, cis, cis-1,1,4,8-Tetra methyl-4,7,10-cycloun decatriene																		
Calarene	11.287	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.838
Valencene																		
γ-Cadinene	11.408-11.422	$C_{15}H_{24}$	204	2.652	1.633	-	-	1.858	-	-	-	-	-	-	5.822	0.761	-	-
α-Morphine																		
α-Cadinene																		
α-Amorphene																		
4,5-Dimethyl-11-Methylenetricyclo[7.2. 1.0 (4.9)]dodecane																		
α-Selinene	11.414-11.627	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	-	1.180	-	-	-	0.820	10.749
β-Selinene	11.269-11.673	$C_{15}H_{24}$	204	-	-	10.319	-	-	-	-	-	-	36.62	2.429	7.540	-	-	-
(+)-Ledene	11.677	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	3.281	-	-	-	-	-	-
Butylated hydroxytoluene	11.713-11.765	$C_{15}H_{24}O$	220	-	-	23.912	13.521	27.542	-	-	29.474	-	9.743	7.849	7.060	1.169	-	-
Bicyclogermacrene	11.714-11.737	$C_{15}H_{24}$	204	2.748	-	-	-	-	-	-	-	5.742	-	-	-	-	14.482	-
1,5,5-Trimethyl-6-methylene-cyclohexene		$C_{10}H_{16}$	136															
δ-Cadinene	11.840-13.323	$C_{15}H_{24}$	204	-	-	1.078	-	1.043	-	-	-	3.456	1.145	0.975	-	-	-	1.133
δ-Amorphene	11.956	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	-	-	-	-	-	1.918	-
Isoeugenol acetate	11.973	$C_{12}H_{14}O_3$	206	29.739	-	-	-	1.833	-	-	-	-	-	-	-	-	-	-
Eugenol acetate																		
Calamenene	12.031	$C_{15}H_{22}$	202	-	-	-	-	-	-	-	-	0.608	-	-	-	-	-	-
α-Ionene		$C_{13}H_{18}$	174															
(-)-α-Panasinsen	12.037	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	-	-	-	-	-	1.114	-
trans-γ-Bisabolene	12.048	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	1.911	-	-	-	-	-	-	-
Elemicin	12.112	$C_{12}H_{16}O_3$	208	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.477
Isoelemicine																		
cis-Asarone																		
Nerolidol	12.308-12.417	$C_{15}H_{26}O$	222	-	-	1.368	-	-	-	-	-	5.462	2.105	2.591	1.694	-	2.488	0.651
Farnesol																		
Hedycaryol	12.348	$C_{15}H_{26}O$	222	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Elemol																		
Sesquisabinene hydrate	12.377	$C_{15}H_{26}O$	222	-	-	-	1.797	-	-	-	-	-	-	-	-	-	-	-
Germacrene B	12.533	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	1.803	-	-	-	-	-	-
γ-Elemene																		
Spathulenol	12.637	$C_{15}H_{24}O$	220	-	-	-	-	-	0.248	0.409	-	-	-	-	-	-	-	-
Caryophyllene oxide	12.723-12.844	$C_{15}H_{24}O$	220	-	-	-	-	-	0.272	0.540	-	-	1.038	-	0.924	-	-	1.804
β-Spathulenol	12.746-13.386	$C_{15}H_{24}O$	220	-	-	1.756	-	2.487	-	-	-	0.708	-	-	-	-	0.699	-
β-Bisabolene	12.827	$C_{15}H_{24}$	204	-	-	-	5.077	-	-	-	-	-	-	-	-	-	-	-
Globulol	12.837-12.879	$C_{15}H_{26}O$	222	-	-	2.286	-	3.717	-	-	-	2.154	-	-	-	-	2.204	-
Viridiflorol	12.971-13.825	$C_{15}H_{26}O$	222	-	-	1.655	-	2.786	-	-	-	0.576	-	1.081	-	-	2.144	-
Ledol		$C_{15}H_{26}O$	222															
(-)-Allospathulenol	13.127	$C_{15}H_{24}O$	220	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4-Allyl-1,2-diacetoxybenzene	13.213-13.329	$C_{13}H_{14}O_4$	234	30.163	13.559	-	-	1.036	60.018	60.089	51.935	0.930	-	31.115	-	30.066	-	21.262
Isospathulenol	13.381	$C_{15}H_{24}O$	220	-	-	1.004	-	-	-	-	-	-	-	-	-	-	-	-
α-Cadinol	13.401-13.669	$C_{15}H_{26}O$	222	-	1.657	5.431	-	1.836	-	-	-	5.697	-	2.675	-	6.712	2.105	3.028
Copaene	13.438	$C_{15}H_{24}$	204	-	-	-	-	-	-	0.212	-	-	-	-	-	-	-	-
Bicyclo[4.4.0]dec-1-ene, 2-isopropyl-5-methyl-9-methylene-	13.473	$C_{15}H_{24}$	204	-	2.149	-	-	-	-	-	-	-	-	-	-	-	-	-
(+)-δ-Cadinene		$C_{15}H_{24}$	204															
5-epi-neointermedeol	13.611-13.744	$C_{15}H_{26}O$	222	-	-	1.997	-	-	-	-	-	-	-	9.176	-	-	-	0.461
(+)-Epi-bicyclo sesquiphellandrene	13.704-13.71	$C_{15}H_{24}$	204	-	-	-	-	-	-	-	-	-	0.696	-	1.633	-	-	-
Benzoic acid, phenylmethyl ester	14.904	$C_{14}H_{12}O_2$	212	-	0.855	-	-	-	-	-	-	-	-	-	-	-	-	-
Oleamide	22.740-22.970	$C_{18}H_{35}NO$	281	-	-	0.905	1.815	-	1.079	0.801	-	-	-	1.491	-	-	-	0.899
Unknown				8.212	19.425	5.000	1.943	3.829	26.593	25.568	-	4.821	0.482	9.351	2.211	7.171	4.969	3.039
Total				100	100	100	100	100	100	100	100	100	100	100	100	100	100	100

Table 4 The summary of substances, both in type and quantity, compared to the amounts of volatile oils

Compounds	Contents (%)	Species	Amount of essential oil (mL/kg)
L-Linalool	26.590	*P. crocatum*	0.03
L-Linalool	13.629	*P. betloides*	0.10
β-Terpineol	25.025	*P. crocatum*	0.03
4-Terpineol	46.560	*P. tricolor* 2	0.03
α-Terpineol	10.111	*P. betloides*	0.10
α-Terpineol	14.218	*P. crocatum*	0.03
Eugenol/Isoeugenol	49.942	*P. tricolor* 1	0.76
Eugenol/Isoeugenol	53.559	*P. betle* 2	0.95
β-Elemene	14.384	*P. submultinerve* 4	0.03
trans-Caryophyllene	21.142	*P. yinkiangense*	0.62
trans-Caryophyllene	11.656	*P. submultinerve* 1	0.12
trans-Caryophyllene	11.505	*P. maculaphyllum*	0.05
trans-Caryophyllene	26.283	*P. submultinerve* 4	0.03
Caryophyllene	39.422	*P. submultinerve* 2	0.40
α-Caryophyllene	16.136	*P. yinkiangense*	0.62
α-Caryophyllene	25.063	*P. submultinerve* 4	0.03
β-Selinene	10.319	*P. betloides*	0.10
β-Selinene	36.62	*P. submultinerve* 2	0.40
Germacrene D	12.528	*P. maculaphyllum*	0.05
Germacrene D	36.317	*P. submultinerve* 1	0.12
α-Selinene	10.749	*P. yinkiangense*	0.62
Bicyclogermacrene	14.482	*P. tricolor* 2	0.03

Butylated hydroxytoluene	13.521	*P. crocatum*	0.03
Butylated hydroxytoluene	23.912	*P. betloides*	0.10
Butylated hydroxytoluene	27.542	*P. maculaphyllum*	0.05
Butylated hydroxytoluene	29.474	*P. semiimersum*	0.13
Eugenol acetate/Isoeugenol acetate	29.739	*P. betle* 1	2.15-2.73
4-Allyl-1,2-diacetoxybenzene	21.262	*P. yinkiangense*	0.62
4-Allyl-1,2-diacetoxybenzene	13.559	*P. betle* 2	0.95
4-Allyl-1,2-diacetoxybenzene	31.115	*P. submultinerve* 3	0.03
4-Allyl-1,2-diacetoxybenzene	30.163	*P. betle* 1	2.15-2.73
4-Allyl-1,2-diacetoxybenzene	30.066	*P. tricolor* 1	0.76
4-Allyl-1,2-diacetoxybenzene	60.018	*P. rubroglandulosum* 1	0.47
4-Allyl-1,2-diacetoxybenzene	60.089	*P. rubroglandulosum* 2	0.72
4-Allyl-1,2-diacetoxybenzene	51.935	*P. semiimersum*	0.13

Article 5: Submitted

Chaveerach, A., Sanubol, A., Tanee, T., and Liehr, T. and Sudmoon, R.* Efficient DNA barcode regions for classifying *Piper* species (Piperaceae). Submitted to Journal of Systematics and Evolution. (ISI impact factor 1.488).

Efficient DNA barcode regions for classifying *Piper* species (Piperaceae)

Arunrat Chaveerach[1,2], Arisa Sanubol[1], Pansa Monkheang[1], Neeranuch Yimpongsawat[1], Tawatchai Tanee[2,3] and Runglawan Sudmoon[1,2*]

[1]Department of Biology, Faculty of Science, Khon Kaen University, Khon Kaen 40002, Thailand

[2]Genetics and Environmental Toxicology (GET) Research Group, Khon Kaen University, Thailand

[3]Faculty of Environment and Resource Studies, Mahasarakham University, Mahasarakham 44150, Thailand

*Corresponding author: rsudmoon@yahoo.com

Abstract

As of the *Piper* species are used for spices, in traditional and processed forms of medicines, in cosmetic compounds, in cultural activities and insecticides, barcode construction using *mat*K, *rbc*L and *psb*A-*trn*H spacer regions have been done for serving plant parts, young plants and modified forms identification. Thirty-seven *Piper* species were collected, the three barcode regions were amplified, sequenced, aligned for genetic distance receiving. At intraspecific levels, the genetic distances are most effective for a *Piper* species identification starting from same sequence or no difference in each species to very low distance values. Only one economic and planted species, *P. betle* posted the highest values at 0.386 of *mat*K region, this may be caused from it is an economic and planted species, so is supported growth factors from human affected on its genetic distance. The genetic distances at interspecific level are also most effective for different species identification by *mat*K region ranged from 0.002 between 27 pair species to the highest of 0.486 excepted for eight pair species as *P. kraense* and *P. dominantinervium*, *P. magnibaccum* and *P. kraense*, *P. phuwuaense* and *P. dominantinervium*, *P. phuwuaense* and *P. kraense*, *P. pilobracteatum* and *P. dominantinervium*, *P. pilobracteatum* and *P. kraense*, *P. pilobracteatum* and *P. phuwuaense*, and *P. sylvestre* and *P. polysyphonum* posted genetic distance at 0.000 which were identified by each of the other two regions without of combination.

Keywords: barcode, *Piper* species, *mat*K gene, *rbc*L gene, *psb*A-*trn*H spacer.

Introduction

Plants in the genus *Piper* have been used since prehistoric times for a variety of human activities. They are used as spices, in traditional and processed forms of medicines, in cosmetic compounds, in cultural activities and as insecticides (Chaveerach *et al*., 2006; Scott *et al*., 2008; Fan *et al*., 2011). *Piper betle*, the betel plant, is one of the most important and well-known species of the genus. It contains important chemical substances, such as chavicol, cineol and eugenol, used in essential oils, medicines and insecticides (Yusoff *et al*., 2005; Misra *et al*., 2009). Eugenol has been reported as having anti-oxidant and anti-inflammatory properties (Misra *et al*., 2009). Although the betel plant is of great economic importance, it is challenging to cultivate. The main problem is foot and leaf rot, which caused by the fungus *Phytophthora parasitica* Dast (Silayoi *et al*., 1985; Banka and Teo, 2000). In addition, the plant is subject to leaf spot, caused by bacteria (Banka and Teo, 2000). Investigations of the genus *Piper* in Thailand (Chaveerach *et al*., 2008, 2009) have found that among the 43 *Pip*er species, some produce a betel-like scent. Of these, all are wild species and hardy, producing numerous branches and leaves. They are tolerant and resistant to disease. Some produce a stronger scent than betel. Therefore, these species might be equally or more economically beneficial than the betel plant. The assured advantage is that there are more choices of plants for the use (Sanubol et al., 2014). Medicinal plants have been used in natural and modified forms. The modified forms such as dried sliced plant part, powder and capsules, are hard to be recognized by physical features. Therefore, the reliable identification methods for these plant forms should be provided. DNA barcoding is the most reliable and applicable method for this aspect. It is developed since 2003 (Hebert et al., 2003). It principal uses short DNA sequences from appropriate genome regions for identification of organisms. The regions such as COI, and 16s rDNA regions have been successfully used for most animals for examples, Hebert et al. (2004) used the mitochondrially encoded cytochrome c oxidase I (MT-CO1) to discriminate between bird species. Zhang and Hanner (2012) used sequences of MT-CO1, 16S RNA, MT-CYB, and RNA 18S in 242 species of fish in 11 *Epinephelus* species.
For plants, however, it is more challenge. Currently, several researchers groups had seeking for suitable regions. There are researches suggested some successful regions for some plant groups, such as *mat*K gene (Siripiyasing et al., 2012; Tanee et al., 2012), *rbc*L gene (Tanee et al., 2012; Kwanda et al., 2013), *psb*A-*trn*H spacer region (Chaveerach et al., 2011).

Up to date the standard barcode of choice for most investigated plants are three plastid including *mat*K, *rbc*L genes, and *psb*A-*trn*H spacer, and one nuclear (ITS) regions proved by many researches of CBOL Plant Working Group, 2009; Chaveerach et al., 2011;

Hollingsworth et al., 2011; Monkheang et al., 2011. With the important of *Piper* species usages mentioned becoming economic plants worldwide using parts of plant from trunk, leaves, fruits or young plants, modified forms such as powder, slices etc. of many species. Therefore, these usage forms should have specific marker to prove a species for put the right plant for the right aims that is barcode construction for each species.

The research aims to barcode construction for *Piper* species in Thailand using *mat*K, *rbc*L and *psb*A-*trn*H spacer region as if they are important medicinal plants, have been fully explored and identified (Chaveerach et al., 2008); therefore their references barcode should be available for serving plant parts, young plants and modified forms.

Materials and Methods

1. Plant materials

Species of *Piper* recently reported in Thailand (Chaveerach et al., 2006, 2007, 2008; Sudmoon et al., 2011) have been collected and identified. Leaf samples were kept on ice and transferred to the laboratory then stored at -20°C.

2. DNA extraction

Whole genomic DNA was extracted by using Plant Genomic DNA Extraction Kit (RBC Bioscience) following the kit protocols.

3. Amplification of barcode fragments

Polymerase chain reactions were performed with primer pairs (5'-3') ATCCATCTGGAAATCTTAGTTC and GTTCTAGCACAAGAAAGTCG for *mat*K gene, GTCACCACAAACAGAGACTAAAGC and GTAAAATCAAGTCCACCRCG for *rbc*L gene, and TTATGCATGAACGTAATGCTC and CGCGCATGGTGGATTCACAATCC for *psb*A-*trn*H spacer region (http://www.kew.org/barcoding/update.html). The reaction mixture (30 µl) consists of 1×GoTaq Green Master Mix (Promega), 0.5 µM primers, and 30 ng DNA template. The amplification profile includes pre-denaturation at 94°C for 1 min; 35 cycles of denaturation at 94°C for 30 s, annealing at 52°C (for *mat*K) or 55°C (for *rbc*L gene and *psb*A-*trn*H spacer region) for 30 s, and extension at 72°C for 1 min; final extension at 72°C for 5 min. The amplification products were subjected to 2% agarose gel electrophoresis.

4. DNA sequencing and sequences analyses

The amplified specific fragments were sent for sequencing at the DNA Sequencing Unit, Faculty of Medicine, Ramathibodi Hospital, Bangkok, Thailand. The sequences were then analyzed for accuracy by Blast tools (http://blast.ncbi.nlm.nih.gov/Blast.cgi). All completed accurate sequences were aligned in each region for determining genetic diversity

values meaning nucleotide variations by MEGA6 (Tamura et al., 2013). The sequences were submitted to the GenBank database and the corresponding accession numbers are taken.

Results

Thirty-seven *Piper* species were collected for barcoding construction. Since to most of them are wild species, so, there were difficult to collect in sufficient sampled individuals to study reaching to different amount individuals of each barcoding region constructions. There are four satisfied individuals species only, *P. nigrum*, *P. betle*, *P. sarmentosum*, and *P. retrofractum* which are economic plants and easy to collect.

The amplification of barcode banding was not successfully amplified in two species including *P. montium* and *P. rubroglandulosum* (♀) with *mat*K region. When all sequences of all species studied with *mat*K, *rbc*L and *psb*A-*trn*H spacer were submitted to GenBank, the corresponding accession numbers, 119 sequence accessions were provided in the Table 1.

From three barcoding regions, *mat*K, *rbc*L and *psb*A-*trn*H spacer, genetic distances in intraspecific levels of each region are following: the lowest value, 0.000 in *P. dominantinervium*, *P. hongkongense*, *P. kraense* and *P. longum* to the highest 0.386 in *P. betle* of the *mat*K region; *P. dominantinervium*, *P. hongkongense*, *P. longum*, *P. pedicellatum*, *P. pilobracteatum*, *P. polysyphonum*, *P. sarmentosum*, *P. sylvestre* and *P. wallichii* to the highest value 0.166 in *P. betle* of the *rbc*L region; 0.000 in *P. dominantinervium*, *P. khasianum*, *P. kraense*, *P. longum*, *P. montium*, *P. mutabile*, *P. nigrum*, *P. pilobracteatum*, *P. polysyphonum* and *P. sarmentosum* to the highest value 0.117 in *P. boehmeriifolium* of the *psb*A-*trn*H spacer region.

The genetic distances in interspecific levels of each region are following: the lowest values, 0.000 in the pairs species *P. kraense* and *P. dominantinervium*, *P. magnibaccum* and *P. kraense*, *P. phuwuaense* and *P. dominantinervium* , *P. phuwuaense* and *P. kraense*, *P. pilobracteatum* and *P. dominantinervium*, *P. pilobracteatum* and *P. kraense*, *P. pilobracteatum* and *P. phuwuaense* and *P. sylvestr* and *P. polysyphonum* to the highest value 0.486 between *P. ribesioides* and *P. pilobracteatum* of the *mat*K region; 0.000 in pairs between *P. dominantinervium* and *P. caninum*, *P. kraense* and *P. boehmeriifolium*, *P. maculaphyllum* and *P. khasianum*, *P. magnibaccum* and *P. khasianum*, *P. magnibaccum* and *P. caninum*, *P. magnibaccum* and *P. dominantinervium*, *P. montium* and *P. khasianum*, *P. montium* and *P. magnibaccum*, *P. mutabile* and *P. caninum*, *P. mutabile* and *P. dominantinervium*, *P. mutabile* and *P. magnibaccum*, *P. nigrum* and *P. caninum*, *P. nigrum* and *dominantinervium*, *P. nigrum* and *P. magnibaccum*, *P. nigrum* and *P. mutabile, P.*

pedicellatum and *P. khasianum*, *P. pedicellatum* and *P. magnibaccum*, *P. pedicellatum* and *P. montium*, *P. pedicellatum* and *P. pendulispicum*, *P. pendulispicum* and *P. caninum*, *P. pendulispicum* and *P. dominantinervium*, *P. pendulispicum* and *P. magnibaccum*, *P. pendulispicum* and *P. mutabile*, *P. pendulispicum* and *P. nigrum*, *P. phuwuaense* and *P. caninum*, *P. phuwuaense* and *P. dominantinervium*, *P. phuwuaense* and *P. magnibaccum, P. phuwuaense* and *P. mutabile*, *P. phuwuaense* and *P. nigrum*, *P. phuwuaense* and *P. pedicellatum, P. pilobracteatum* and *P. caninum*, *P. pilobracteatum* and *P. mutabile*, *P. polysyphonum* and *P. khasianum*, *P. polysyphonum* and *P. magnibaccum*, *P. polysyphonum* and *P. montium, P. sarmentosum* and *P. longum*, *P. sylvestre* and *P. khasianum*, *P. sylvestre* and *P. magnibaccum*, *P. sylvestre* and *P. montium*, *P. thomsonii* and *P. nigrum*, *P. pilobracteatum* and *P. phuwuaense*, *P. polysyphonum* and *P. pendulispicum*, *P. polysyphonum* and *P. pedicellatum*, *P. sylvestre* and *P. pendulispicum*, *P. sylvestre* and *P. pedicellatum*, *P. sylvestre* and *P. polysyphonum*, *P. wallichii* and *P. umbellatum*, *P. protrusum* and *P. phuwuaense*, and *P. protrusum* and *P. pilobracteatum* to the highest value 0.213 in the pair *P. betle* and *P. argyritis* of the *rbc*L region; 0.000 in the pairs of *P. montium* and *P. magnibaccum*, *P. pilobracteatum* and *P. caninum*, *P. polysyphonum* and *P. pedicellatum*, *P. ribesioides* and *P. pedicellatum*, *P. sarmentosum* and *P. longum*, *P. sylvestre* and *P. pedicellatum*, *P. wallichii* and *P. khasianum*, *P. wallichii* and *P. pedicellatum*, *P. protrusum* and *P. magnibaccum*, *P. sylvestre* and *P. polysyphonum*, *P. sylvestre* and *P. ribesioides*, *P. wallichii* and *P. polysyphonum*, *P. wallichii* and *ribesioides*, *P. wallichii* and *P. sylvestre*, and *P. yinkiangense* and *P. betle* to the highest value 0.228 between *P. semiimmersum* and *P. umbellatum* of the *trn*H spacer region.

The genetic distance of the *mat*K region in the Table 2 is the representative sample.

Table 1 GenBank accession numbers of DNA barcoding from three regions of *Piper* species.

Scientific name	GenBank accession number		
	*mat*K	*psb*A-*trn*H spacer	*rbc*L
Piper argyritis	KM073990	JX442927, KM055176	JX291978, KM055126
P. betle (♀)	GU372747, KM098143	GQ891996, JQ248053	JQ248074
P. betle (♂)	KM098144	JQ248050	JQ248071
P. betloides	KM098135	JQ248051	JQ248072
P. boehmeriifolium	KM073991, KM073992	KM055177, KM055178	KM055127, KM055128
P. caninum	KM073993, KM073994	KM055179, KM055180	KM055129, KM055130
P. colubrinum	GU372751, KM073995	GQ892000	KM055131
P. crocatum	KM098136	JQ248047	JQ248068
P. dominantinervium	KM073996, KM073997	KM055181, KM055182	KM055132, KM055133
P. hongkongense	KM073998, KM073999	KM055183, KM055184	KM055134, KM055135
P. khasianum	KM074000, KM074001	KM055185, KM055186	KM055136, KM055137
P. kraense	KM074002, KM074003	KM055187, KM055188	KM055138, KM055139
P. longum	KM074004, KM074005	KM055189, KM055190	KM055140, KM055141
P. maculaphyllum	KM074006, KM098137	JQ248046, KM055191	JQ248067, KM055142
P. magnibaccum	KM074007, KM074008	KM055192, KM055193	KM055143, KM055144
P. montium	n/a	KM055194, KM055195	KM055145, KM055146
P. mutabile	KM074035	KM055196, KM055197	KM055147, KM055148
P. nigrum	KM074009, KM074010	GQ891994, KM055198, KM055199	KM055149, KM055150
P. pedicellatum var. *eglandulatum*	KM074011, KM074012	KM055200, KM055201	KM055151, KM055152
P. pendulispicum (♀)	KM074013, GU372748	KM055202, GQ891997	KM055153, JX291979
P. phuwuaense	KM074014, KM074015	KM055203, KM055204	KM055154, KM055155
P. pilobracteatum	KM074016, KM074017, KM074018, KM074019	KM055205, KM055206, KM055207, KM055208	KM055156, KM055157, KM055158, KM055159
P. polysyphonum	KM074020, KM074021	KM055209, KM055210	KM055160, KM055161
P. protrusum	KM074032, KM074033	GU980900, KM055223	KM055172, KM055173
P. retrofractum	GU372749, KM074034	GQ891998, KM055224	KM055175
P. ribesioides	GU372750, KM074022	GQ891999, KM055211	KM055162
P. rubroglandulosum (♀)	n/a	JX442926	JX291977
P. rubroglandulosum (♂)	KM098138	JX442925	JX291976
P. sarmentosum	GU372746, KM074023, KM074024	KM055212, KM055213	KM055163, KM055164
P. semiimmersum	KM098139	JQ248045	JQ248066
P. submultinerve	KM098140	JQ248048	JQ248069
P. sylvaticum	KM074025, KM074026	KM055214, KM055215	KM055174
P. sylvestre	KM074027, KM074028	KM055216, KM055217	KM055165, KM055166
P. thomsonii var. *trichostigma*	KM074029	KM055218	KM055167
P. tricolor	KM098141	JQ248049	JQ248070
P. umbellatum	EU669471*, GQ429067*	KM055219, KM055220	KM055168, KM055169
P. wallichii	KM074030, KM074031	KM055221, KM055222	KM055170, KM055171
P. yinkiangense	KM098142	JQ248052	JQ248073

Note: n/a was not amplified, * is the accessions from other publications

Table 2 Genetic distance values of the *mat*K region efficient for Piper identification by the lowest, but one in 0.002 and the highest values

	P. argyritis	*P. betle*	*P. betle*	*P. betle*	*P. betloides*	*P. boehmeriifolium*	*P. boehmeriifolium*	*P. caninum*	*P. caninum*	*P. colubrinum*	*P. colubrinum*	*P. crocatum*	*P. dominantinervium*	*P. dominantinervium*	*P. hongkongense*	*P. hongkongense*	*P. khasianum*	*P. khasianum*	*P. kraense*	*P. kraense*	*P. longum*	*P. longum*	*P. maculaphyllum*	*P. maculaphyllum*	*P. magnibaccum*	*P. magnibaccum*	*P. nigrum*	*P. nigrum*	*P. pedicellatum*	*P. pedicellatum*	*P. pendulispicum*
P. argyritis	0.000																														
P. betle	0.323	0.000																													
P. betle	0.076	0.362	0.000																												
P. betle	0.126	0.386	0.106	0.000																											
P. betloides	0.249	0.423	0.262	0.260	0.000																										
P. boehmeriifolium	0.004	0.323	0.074	0.124	0.252	0.000																									
P. boehmeriifolium	0.011	0.325	0.074	0.126	0.258	0.009	0.000																								
P. caninum	0.013	0.328	0.080	0.132	0.249	0.009	0.017	0.000																							
P. caninum	0.013	0.328	0.080	0.132	0.249	0.009	0.017	0.000	0.000																						
P. colubrinum	0.020	0.332	0.087	0.134	0.267	0.017	0.022	0.026	0.026	0.000																					
P. colubrinum	0.089	0.375	0.143	0.195	0.310	0.085	0.093	0.093	0.093	0.072	0.000																				
P. crocatum	0.054	0.358	0.106	0.145	0.267	0.052	0.056	0.061	0.061	0.065	0.130	0.000																			
P. dominantinervium	0.004	0.323	0.072	0.121	0.252	0.000	0.007	0.011	0.011	0.015	0.087	0.050	0.000																		
P. dominantinervium	0.004	0.323	0.072	0.121	0.252	0.000	0.007	0.011	0.011	0.015	0.087	0.050	0.000	0.000																	
P. hongkongense	0.013	0.321	0.080	0.130	0.260	0.011	0.011	0.020	0.020	0.024	0.095	0.059	0.009	0.009	0.000																
P. hongkongense	0.013	0.321	0.080	0.130	0.260	0.011	0.011	0.020	0.020	0.024	0.095	0.059	0.009	0.009	0.000	0.000															
P. khasianum	0.007	0.325	0.076	0.126	0.249	0.000	0.011	0.011	0.011	0.020	0.087	0.054	0.004	0.004	0.013	0.013	0.000														
P. khasianum	0.007	0.325	0.074	0.124	0.249	0.004	0.009	0.013	0.013	0.017	0.089	0.052	0.002	0.002	0.011	0.011	0.002	0.000													
P. kraense	0.004	0.323	0.072	0.121	0.252	0.000	0.007	0.011	0.011	0.015	0.087	0.050	0.000	0.000	0.009	0.009	0.004	0.000	0.000												
P. kraense	0.004	0.323	0.072	0.121	0.252	0.000	0.007	0.011	0.011	0.015	0.087	0.050	0.000	0.000	0.009	0.009	0.004	0.000	0.000	0.000											
P. longum	0.013	0.325	0.080	0.130	0.258	0.011	0.015	0.020	0.020	0.024	0.091	0.054	0.009	0.009	0.017	0.017	0.013	0.011	0.009	0.009	0.000										
P. longum	0.013	0.325	0.080	0.130	0.258	0.011	0.015	0.020	0.020	0.024	0.091	0.054	0.009	0.009	0.017	0.017	0.013	0.011	0.009	0.009	0.000	0.000									
P. maculaphyllum	0.065	0.369	0.130	0.171	0.282	0.065	0.072	0.074	0.074	0.080	0.141	0.111	0.065	0.065	0.074	0.074	0.063	0.063	0.065	0.065	0.072	0.072	0.000								
P. maculaphyllum	0.054	0.341	0.072	0.113	0.249	0.052	0.054	0.061	0.061	0.065	0.130	0.085	0.050	0.050	0.059	0.059	0.054	0.052	0.050	0.050	0.054	0.054	0.111	0.000							
P. magnibaccum	0.007	0.325	0.074	0.124	0.249	0.004	0.009	0.013	0.013	0.017	0.089	0.052	0.002	0.002	0.011	0.011	0.002	0.000	0.002	0.002	0.011	0.011	0.063	0.052	0.000						
P. magnibaccum	0.009	0.323	0.076	0.124	0.256	0.007	0.011	0.015	0.015	0.015	0.087	0.054	0.004	0.004	0.013	0.013	0.009	0.007	0.004	0.004	0.013	0.013	0.069	0.054	0.007	0.000					
P. nigrum	0.015	0.334	0.087	0.130	0.262	0.017	0.022	0.026	0.026	0.030	0.102	0.061	0.015	0.015	0.024	0.024	0.020	0.017	0.015	0.015	0.022	0.022	0.072	0.063	0.017	0.020	0.000				
P. nigrum	0.009	0.325	0.080	0.121	0.249	0.011	0.015	0.020	0.020	0.024	0.095	0.059	0.009	0.009	0.017	0.017	0.013	0.011	0.009	0.009	0.017	0.017	0.072	0.054	0.011	0.013	0.020	0.000			
P. pedicellatum	0.011	0.328	0.080	0.126	0.252	0.007	0.015	0.015	0.015	0.024	0.091	0.054	0.009	0.009	0.017	0.017	0.009	0.011	0.009	0.009	0.013	0.013	0.067	0.046	0.011	0.013	0.022	0.013	0.000		
P. pedicellatum	0.011	0.325	0.074	0.124	0.258	0.009	0.004	0.017	0.017	0.022	0.093	0.056	0.007	0.007	0.011	0.011	0.011	0.009	0.007	0.007	0.015	0.015	0.072	0.054	0.009	0.007	0.022	0.015	0.015	0.000	
P. pendulispicum	0.004	0.325	0.076	0.126	0.252	0.007	0.011	0.015	0.015	0.020	0.091	0.050	0.004	0.004	0.013	0.013	0.009	0.007	0.004	0.004	0.009	0.009	0.067	0.050	0.007	0.009	0.013	0.009	0.009	0.011	0.000

Discussion

Even though, the most *Piper* species are wild species, 43 species in Thailand, but they are most popularly used in many functional aspects, for instance, as spices, medicines, and insecticides (Chaveerach et al., 2008; Chaveerach et al., 2006; Scott et al., 2008; Fan et al., 2011). Only four species as *P. betle*, *P. retrofractum*, *P. nigrum* and *P. sarmentosum* are economic and planted species, all of them are also used in several aspects mentioned. The one economic species as betel plant, *P. betle*, is a well-known and important species that contains important chemical substances, including essential oils and substances, such as chavicol, cineol, and eugenol which can be used for medicinal and insecticidal purposes (Chaveerach et al., 2006; Yusoff et al., 2005; Misra et al., 2009). Based on their usages, several forms as traditional in part of plants, and prepared forms as powder, capsule and others, their DNA marker as barcode should be constructed for using right species in the right aims for human well-being for example in industrial of medicinal, cosmetics and house-hold products. With these form usages reaching to unidentified species using morphological characters, DNA barcode have been served and overcome the problems. In the case of flowering plants in Thailand, *trn*H-*psb*A spacer region was suggested to be efficient DNA barcode marker in *Senna* species (Monkheang et al., 2011), *Smilax* and *Cissus* species (Kritpetcharat et al., 2011), additional with other regions as *rbc*L in parasitic plants including *Scurrula*, *Dendrophthoe*, *Helixanthera*, *Macrosolen*, *Viscum* species (Kwanda et al., 2013), *mat*k studied on somes medicinal sakhan, *Piper*, Piperaceae (Sudmoon et al., 2012).

Here for the barcode of thirty-seven *Piper* species with the three regions, the genetic distance values follow the hypothesis of the barcode, in principle by Dr. Paul D.N. Hebert, a population geneticist at the University of Guelph in Ontario (Hebert et al., 2003) that results in significant variance in sequences between species and a comparatively small variance within species. At intraspecific levels, the genetic distances of all three regions are most effective for a *Piper* species identification starting from same sequence or no difference in each species to very low distance values. Only one economic and planted species, *P. betle* posted the highest values at 0.386 of *mat*K region, this may be caused from it is an economic and planted species, so is supported growth factors from human affected on its genetic distance. The genetic distances at interspecific level are also most effective for different species identification by *mat*K region showing by 27 pair species starting from 0.002 to the highest 0.486 as shown in the Table 2 small amount, eight unidentified pair species as showing genetic distance of 0.000 (Table 3). Therefore, the eight pair species can be identified by the other two regions as shown in the Table 2. That is following to the guidance

of Newmaster et al. (2007) proposed to use *mat*K and *trn*H-*psb*A spacer to identify plants in Myristicaceae and Sudmoon et al. (2012) without of regions combination following of Hollingsworth et al. (2009) recommended *rbc*L+*mat*K as the core DNA barcode regions for land plants.

Table 3 Genetic distance values in interspecific level for identification of some *Piper* species based *mat*K, rbcL and trnH-psbA spacer sequences.

Pairs of species	*mat*K region	*rbc*L region	*trn*H-*psb*A spacer region
P. kraense and *P. dominantinervium*	0.000	0.005-0.008	0.111-0.117
P. magnibaccum and *P. kraense*	0.000	0.008	0.1110-0.123
P. phuwuaense and *P. dominantinervium*	0.000	0.000-0.003	0.021-0.026
P. phuwuaense and *P. kraense*	0.000	0.005-0.008	0.021-0.129
P. pilobracteatum and *P. dominantinervium*	0.000	0.003	0.021
P. pilobracteatum and *P. kraense*	0.000	0.003	0.010-0.123
P. pilobracteatum and *P. phuwuaense*	0.000	0.003	0.016-0.021
P. sylvestre and *P. polysyphonum*	0.000	0.000	0.000-0.010

Acknowledgments

The authors are thankful for the financial support provided by the Thailand Research Fund through the Research Career Development Grant (Grant No. RSA5580054).

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ลำดับนิวคลีโอไทด์เครื่องหมายดีเอ็นเอแบบบาร์โค้ด

Nucleotide ▾ Piper Thailand matK

Display Settings: Summary, 100 per page, Sorted by Accession

Results: 56

1. **Piper** argyrites voucher A. Chaveerach 11 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073990.1 GI: 691193333

2. **Piper** boehmeriifolium voucher A. Chaveerach 2.1 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073991.1 GI: 691193335

3. **Piper** boehmeriifolium voucher A. Chaveerach 2.2 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073992.1 GI: 691193337

4. **Piper** caninum voucher A. Chaveerach 79.1 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073993.1 GI: 691193339

5. **Piper** caninum voucher A. Chaveerach 79.2 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073994.1 GI: 691193341

6. **Piper** colubrinum voucher A. Chaveerach 19 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073995.1 GI: 691193343

7. **Piper** dominantinervium voucher A. Chaveerach 43.1 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073996.1 GI: 691193345

8. **Piper** dominantinervium voucher A. Chaveerach 43.2 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073997.1 GI: 691193347

9. **Piper** hongkongense voucher A. Chaveerach 68.1 maturase K (**matK**) gene, partial cds; chloroplast
   796 bp linear DNA
   Accession: KM073998.1 GI: 691193349

10. **Piper** hongkongense voucher A. Chaveerach 68.2 maturase K (**matK**) gene, partial cds; chloroplast
    796 bp linear DNA
    Accession: KM073999.1 GI: 691193351

Piper khasianum voucher A. Chaveerach 149.1 maturase K (**matK**) gene, partial cds; chloroplast

11. 796 bp linear DNA
Accession: KM074000.1 GI: 691193353

☐ **Piper** khasianum voucher A. Chaveerach 149.2 maturase K (**matK**) gene, partial cds; chloroplast
12. 796 bp linear DNA
Accession: KM074001.1 GI: 691193355

☐ **Piper** kraense voucher A. Chaveerach 134.1 maturase K (**matK**) gene, partial cds; chloroplast
13. 796 bp linear DNA
Accession: KM074002.1 GI: 691193357

☐ **Piper** kraense voucher A. Chaveerach 134.2 maturase K (**matK**) gene, partial cds; chloroplast
14. 796 bp linear DNA
Accession: KM074003.1 GI: 691193359

☐ **Piper** longum voucher A. Chaveerach 3.1 maturase K (**matK**) gene, partial cds; chloroplast
15. 796 bp linear DNA
Accession: KM074004.1 GI: 691193361

☐ **Piper** longum voucher A. Chaveerach 3.2 maturase K (**matK**) gene, partial cds; chloroplast
16. 796 bp linear DNA
Accession: KM074005.1 GI: 691193363

☐ **Piper** argyrites voucher A. Chaveerach 126 maturase K (**matK**) gene, partial cds; chloroplast
17. 796 bp linear DNA
Accession: KM074006.1 GI: 691193365

☐ **Piper** magnibaccum voucher A. Chaveerach 5.1 maturase K (**matK**) gene, partial cds; chloroplast
18. 796 bp linear DNA
Accession: KM074007.1 GI: 691193367

☐ **Piper** magnibaccum voucher A. Chaveerach 5.2 maturase K (**matK**) gene, partial cds; chloroplast
19. 796 bp linear DNA
Accession: KM074008.1 GI: 691193369

☐ **Piper** nigrum voucher A. Chaveerach 17.1 maturase K (**matK**) gene, partial cds; chloroplast
20. 796 bp linear DNA
Accession: KM074009.1 GI: 691193371

☐ **Piper** nigrum voucher A. Chaveerach 17.2 maturase K (**matK**) gene, partial cds; chloroplast
21. 796 bp linear DNA
Accession: KM074010.1 GI: 691193373

☐ **Piper** pedicellatum var. eglandulatum voucher A. Chaveerach 181.1 maturase K (**matK**) gene, partial
22. cds; chloroplast
796 bp linear DNA
Accession: KM074011.1 GI: 691193375

☐ **Piper** pedicellatum var. eglandulatum voucher A. Chaveerach 181.2 maturase K (**matK**) gene, partial
23. cds; chloroplast

796 bp linear DNA
Accession: KM074012.1 GI: 691193377

24. **Piper** pendulispicum voucher A. Chaveerach 82 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074013.1 GI: 691193379

25. **Piper** phuwuaense voucher A. Chaveerach 46.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074014.1 GI: 691193381

26. **Piper** phuwuaense voucher A. Chaveerach 46.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074015.1 GI: 691193383

27. **Piper** pilobracteatum voucher A. Chaveerach 41.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074016.1 GI: 691193385

28. **Piper** pilobracteatum voucher A. Chaveerach 41.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074017.1 GI: 691193387

29. **Piper** pilobracteatum voucher A. Chaveerach 41.3 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074018.1 GI: 691193389

30. **Piper** pilobracteatum voucher A. Chaveerach 41.4 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074019.1 GI: 691193391

31. **Piper** polysyphonum voucher A. Chaveerach 94.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074020.1 GI: 691193393

32. **Piper** polysyphonum voucher A. Chaveerach 94.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074021.1 GI: 691193395

33. **Piper** ribesioides voucher A. Chaveerach 1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074022.1 GI: 691193397

34. **Piper** sarmentosum voucher A. Chaveerach 18.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074023.1 GI: 691193399

35. **Piper** sarmentosum voucher A. Chaveerach 18.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074024.1 GI: 691193401

36. **Piper** sylvaticum voucher A. Chaveerach 4.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074025.1 GI: 691193403

37. **Piper** sylvaticum voucher A. Chaveerach 4.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074026.1 GI: 691193405

38. **Piper** sylvestre voucher A. Chaveerach 8.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074027.1 GI: 691193407

39. **Piper** sylvestre voucher A. Chaveerach 8.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074028.1 GI: 691193409

40. **Piper** thomsonii var. trichostigma voucher A. Chaveerach 229 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074029.1 GI: 691193411

41. **Piper** wallichii voucher A. Chaveerach 91.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074030.1 GI: 691193413

42. **Piper** wallichii voucher A. Chaveerach 91.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074031.1 GI: 691193415

43. **Piper** protrusum voucher A. Chaveerach 100.1 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074032.1 GI: 691193417

44. **Piper** protrusum voucher A. Chaveerach 100.2 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074033.1 GI: 691193419

45. **Piper** retrofractum voucher A. Chaveerach 9 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074034.1 GI: 691193421

46. **Piper** mutabile voucher A. Chaveerach 52 maturase K (**matK**) gene, partial cds; chloroplast
796 bp linear DNA
Accession: KM074035.1 GI: 691193423

47. **Piper** betloides voucher A. Chaveerach 47 maturase K (**matK**) gene, partial cds; chloroplast
723 bp linear DNA
Accession: KM098135.1 GI: 697065591

Piper crocatum voucher A. Chaveerach 12 maturase K (**matK**) gene, partial cds; chloroplast

48. 589 bp linear DNA
Accession: KM098136.1 GI: 697057998

Piper argyrites voucher A. Chaveerach 126 maturase K (**matK**) gene, partial cds; chloroplast
49. 566 bp linear DNA
Accession: KM098137.1 GI: 697057999

Piper betle voucher A. Chaveerach 314 maturase K (**matK**) gene, partial cds; chloroplast
50. 553 bp linear DNA
Accession: KM098138.1 GI: 697058001

Piper semi-immersum voucher A. Chaveerach 115 maturase K (**matK**) gene, partial cds; chloroplast
51. 758 bp linear DNA
Accession: KM098139.1 GI: 697065596

Piper submultinerve voucher A. Chaveerach 223 maturase K (**matK**) gene, partial cds; chloroplast
52. 773 bp linear DNA
Accession: KM098140.1 GI: 697065598

Piper tricolor voucher A. Chaveerach 64 maturase K (**matK**) gene, partial cds; chloroplast
53. 773 bp linear DNA
Accession: KM098141.1 GI: 697065600

Piper yinkiangense voucher A. Chaveerach 133 maturase K (**matK**) gene, partial cds; chloroplast
54. 773 bp linear DNA
Accession: KM098142.1 GI: 697065602

Piper betle voucher A. Chaveerach 16 maturase K (**matK**) gene, partial cds; chloroplast
55. 773 bp linear DNA
Accession: KM098143.1 GI: 697065604

Piper betle voucher A. Chaveerach 341 maturase K (**matK**) gene, partial cds; chloroplast
56. 763 bp linear DNA
Accession: KM098144.1 GI: 697065606

Nucleotide ▾ Piper Thailand rbcL

Display Settings: Summary, 100 per page, Sorted by Accession

Results: 63

1. **Piper** semi-immersum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
   517 bp linear DNA
   Accession: JQ248066.1 GI: 383385907

2. UNVERIFIED: **Piper** argyrites ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit-like (**rbcL**) gene, partial sequence; chloroplast
   536 bp linear DNA
   Accession: JQ248067.1 GI: 383385909

3. **Piper** crocatum ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
   521 bp linear DNA
   Accession: JQ248068.1 GI: 383385910

4. **Piper** submultinerve ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
   516 bp linear DNA
   Accession: JQ248069.1 GI: 383385912

5. **Piper** tricolor ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
   529 bp linear DNA
   Accession: JQ248070.1 GI: 383385914

6. UNVERIFIED: **Piper** betle ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit-like (**rbcL**) gene, partial sequence; chloroplast
   549 bp linear DNA
   Accession: JQ248071.1 GI: 383385916

7. **Piper** betloides ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
   533 bp linear DNA
   Accession: JQ248072.1 GI: 383385917

8. **Piper** yinkiangense ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
   510 bp linear DNA
   Accession: JQ248073.1 GI: 383385919

9. **Piper** betle ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
   509 bp linear DNA

Accession: JQ248074.1 GI: 383385921

10. **Piper** betle voucher A. Chaveerach 319 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
526 bp linear DNA
Accession: JX291976.1 GI: 404435959

11. **Piper** betle voucher A. Chaveerach 340 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
427 bp linear DNA
Accession: JX291977.1 GI: 404435961

12. **Piper** argyrites voucher A. Chaveerach 11 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
420 bp linear DNA
Accession: JX291978.1 GI: 404435963

13. **Piper** pendulispicum voucher A. Chaveerach 673 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
499 bp linear DNA
Accession: JX291979.1 GI: 404435965

14. **Piper** argyrites voucher A. Chaveerach 11 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055126.1 GI: 685848467

15. **Piper** boehmeriifolium voucher A. Chaveerach 2.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
556 bp linear DNA
Accession: KM055127.1 GI: 685848469

16. **Piper** boehmeriifolium voucher A. Chaveerach 2.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055128.1 GI: 685848471

17. **Piper** caninum voucher A. Chaveerach 79.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
553 bp linear DNA
Accession: KM055129.1 GI: 685848473

18. **Piper** caninum voucher A. Chaveerach 79.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055130.1 GI: 685848475

19. **Piper** colubrinum voucher A. Chaveerach 19 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
553 bp linear DNA
Accession: KM055131.1 GI: 685848477

20. **Piper** dominantinervium voucher A. Chaveerach 43.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055132.1 GI: 685848479

21. **Piper** dominantinervium voucher A. Chaveerach 43.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055133.1 GI: 685848481

22. **Piper** hongkongense voucher A. Chaveerach 68.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055134.1 GI: 685848483

23. **Piper** hongkongense voucher A. Chaveerach 68.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055135.1 GI: 685848485

24. **Piper** khasianum voucher A. Chaveerach 149.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
553 bp linear DNA
Accession: KM055136.1 GI: 685848487

25. **Piper** khasianum voucher A. Chaveerach 149.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055137.1 GI: 685848489

26. **Piper** kraense voucher A. Chaveerach 134.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
553 bp linear DNA
Accession: KM055138.1 GI: 685848491

27. **Piper** kraense voucher A. Chaveerach 134.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055139.1 GI: 685848493

28. **Piper** longum voucher A. Chaveerach 3.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055140.1 GI: 685848495

29. **Piper** longum voucher A. Chaveerach 3.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055141.1 GI: 685848497

30. **Piper** argyrites voucher A. Chaveerach 126 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
546 bp linear DNA
Accession: KM055142.1 GI: 685848499

31. **Piper** magnibaccum voucher A. Chaveerach 5.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055143.1 GI: 685848501

32. **Piper** magnibaccum voucher A. Chaveerach 5.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055144.1 GI: 685848503

33. **Piper** montium voucher A. Chaveerach 7.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055145.1 GI: 685848505

34. **Piper** montium voucher A. Chaveerach 7.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
556 bp linear DNA
Accession: KM055146.1 GI: 685848507

35. **Piper** mutabile voucher A. Chaveerach 52.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
556 bp linear DNA
Accession: KM055147.1 GI: 685848509

36. **Piper** mutabile voucher A. Chaveerach 52.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055148.1 GI: 685848511

37. **Piper** nigrum voucher A. Chaveerach 17.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055149.1 GI: 685848513

38. **Piper** nigrum voucher A. Chaveerach 17.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
542 bp linear DNA
Accession: KM055150.1 GI: 685848515

39. **Piper** pedicellatum var. eglandulatum voucher A. Chaveerach 181.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055151.1 GI: 685848517

40. **Piper** pedicellatum var. eglandulatum voucher A. Chaveerach 181.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055152.1 GI: 685848519

41. **Piper** pendulispicum voucher A. Chaveerach 82 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055153.1 GI: 685848521

42. **Piper** phuwuaense voucher A. Chaveerach 46.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055154.1 GI: 685848523

43. **Piper** phuwuaense voucher A. Chaveerach 46.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
542 bp linear DNA
Accession: KM055155.1 GI: 685848525

44. **Piper** pilobracteatum voucher A. Chaveerach 41.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055156.1 GI: 685848527

45. **Piper** pilobracteatum voucher A. Chaveerach 41.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
552 bp linear DNA
Accession: KM055157.1 GI: 685848529

46. **Piper** pilobracteatum voucher A. Chaveerach 41.3 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
525 bp linear DNA
Accession: KM055158.1 GI: 685848531

47. **Piper** pilobracteatum voucher A. Chaveerach 41.4 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
536 bp linear DNA
Accession: KM055159.1 GI: 685848533

48. **Piper** polysyphonum voucher A. Chaveerach 94.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055160.1 GI: 685848535

49. **Piper** polysyphonum voucher A. Chaveerach 94.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
543 bp linear DNA
Accession: KM055161.1 GI: 685848537

50. **Piper** ribesioides voucher A. Chaveerach 1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055162.1 GI: 685848539

51. **Piper** sarmentosum voucher A. Chaveerach 18.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
551 bp linear DNA
Accession: KM055163.1 GI: 685848541

52. **Piper** sarmentosum voucher A. Chaveerach 18.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055164.1 GI: 685848543

53. **Piper** sylvestre voucher A. Chaveerach 8.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055165.1 GI: 685848545

54. **Piper** sylvestre voucher A. Chaveerach 8.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
540 bp linear DNA
Accession: KM055166.1 GI: 685848547

55. **Piper** thomsonii var. trichostigma voucher A. Chaveerach 229 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
542 bp linear DNA
Accession: KM055167.1 GI: 685848549

56. **Piper** umbellatum voucher A. Chaveerach 14.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055168.1 GI: 685848551

57. **Piper** umbellatum voucher A. Chaveerach 14.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
553 bp linear DNA
Accession: KM055169.1 GI: 685848553

58. **Piper** wallichii voucher A. Chaveerach 91.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
556 bp linear DNA
Accession: KM055170.1 GI: 685848555

59. **Piper** wallichii voucher A. Chaveerach 91.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
521 bp linear DNA
Accession: KM055171.1 GI: 685848557

60. **Piper** protrusum voucher A. Chaveerach 100.1 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
554 bp linear DNA
Accession: KM055172.1 GI: 685848559

61. **Piper** protrusum voucher A. Chaveerach 100.2 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
524 bp linear DNA
Accession: KM055173.1 GI: 685848561

62. **Piper** sylvaticum voucher A. Chaveerach 4 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
524 bp linear DNA
Accession: KM055174.1 GI: 685848563

63. **Piper** retrofractum voucher A. Chaveerach 9 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (**rbcL**) gene, partial cds; chloroplast
550 bp linear DNA
Accession: KM055175.1 GI: 685848565

Nucleotide ▾ Piper Thailand psbA

Display Settings: Summary, 100 per page, Sorted by Accession

Results: 71

1. **Piper** nigrum **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   285 bp linear DNA
   Accession: GQ891994.1 GI: 261279725

2. **Piper** sarmentosum **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   280 bp linear DNA
   Accession: GQ891995.1 GI: 261279727

3. **Piper** betle **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   258 bp linear DNA
   Accession: GQ891996.1 GI: 261279729

4. **Piper** pendulispicum **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   277 bp linear DNA
   Accession: GQ891997.1 GI: 261279731

5. **Piper** retrofractum **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   298 bp linear DNA
   Accession: GQ891998.1 GI: 261279733

6. **Piper** ribesioides **PsbA**-like (**psbA**) gene, partial sequence; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   315 bp linear DNA
   Accession: GQ891999.1 GI: 261279735

7. **Piper** colubrinum **PsbA**-like (**psbA**) gene, partial sequence; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   264 bp linear DNA
   Accession: GQ892000.1 GI: 261279736

8. **Piper** sp. Pi-B **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   324 bp linear DNA
   Accession: GQ892001.1 GI: 261279737

9. **Piper** protrusum **PsbA**-like (**psbA**) gene, partial sequence; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
   265 bp linear DNA

Accession: GU980900.1 GI: 300872239

10. **Piper** semi-immersum voucher A. Chaveerach 115 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
265 bp linear DNA
Accession: JQ248045.1 GI: 378756952

11. **Piper** argyrites voucher A. Chaveerach 126 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
253 bp linear DNA
Accession: JQ248046.1 GI: 378756954

12. **Piper** crocatum voucher A. Chaveerach 12 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
277 bp linear DNA
Accession: JQ248047.1 GI: 378756956

13. **Piper** submultinerve voucher A. Chaveerach 223 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
255 bp linear DNA
Accession: JQ248048.1 GI: 378756958

14. **Piper** tricolor voucher A. Chaveerach 64 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
283 bp linear DNA
Accession: JQ248049.1 GI: 378756960

15. **Piper** betle voucher A. Chaveerach 314 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
254 bp linear DNA
Accession: JQ248050.1 GI: 378756962

16. **Piper** betloides voucher A. Chaveerach 171 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
264 bp linear DNA
Accession: JQ248051.1 GI: 378756964

17. **Piper** yinkiangense voucher A. Chaveerach 133 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
264 bp linear DNA
Accession: JQ248052.1 GI: 378756966

18. **Piper** betle voucher A. Chaveerach 16 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
280 bp linear DNA
Accession: JQ248053.1 GI: 378756968

19. **Piper** betle voucher A. Chaveerach 319 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
252 bp linear DNA
Accession: JX442925.1 GI: 407750880

20. **Piper** betle voucher A. Chaveerach 340 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
256 bp linear DNA
Accession: JX442926.1 GI: 407750882

21. **Piper** argyrites voucher A. Chaveerach 11 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
256 bp linear DNA
Accession: JX442927.1 GI: 407750884

22. **Piper** pendulispicum voucher A. Chaveerach 673 **PsbA** (**psbA**) gene, partial cds; **psbA**-trnH intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast
255 bp linear DNA
Accession: JX442928.1 GI: 407750886

23. **Piper** argyrites voucher A. Chaveerach 11 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
287 bp linear DNA
Accession: KM055176.1 GI: 685848567

24. **Piper** boehmeriifolium voucher A. Chaveerach 2.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
294 bp linear DNA
Accession: KM055177.1 GI: 685848569

25. **Piper** boehmeriifolium voucher A. Chaveerach 2.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
289 bp linear DNA
Accession: KM055178.1 GI: 685848571

26. **Piper** caninum voucher A. Chaveerach 79.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
292 bp linear DNA
Accession: KM055179.1 GI: 685848573

27. **Piper** caninum voucher A. Chaveerach 79.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
291 bp linear DNA
Accession: KM055180.1 GI: 685848575

28. **Piper** dominantinervium voucher A. Chaveerach 43.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
303 bp linear DNA
Accession: KM055181.1 GI: 685848577

29. **Piper** dominantinervium voucher A. Chaveerach 43.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
293 bp linear DNA
Accession: KM055182.1 GI: 685848579

30. **Piper** hongkongense voucher A. Chaveerach 68.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
288 bp linear DNA
Accession: KM055183.1 GI: 685848581

31. **Piper** hongkongense voucher A. Chaveerach 68.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
300 bp linear DNA
Accession: KM055184.1 GI: 685848583

32. **Piper** khasianum voucher A. Chaveerach 149.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055185.1 GI: 685848585

33. **Piper** khasianum voucher A. Chaveerach 149.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055186.1 GI: 685848587

34. **Piper** kraense voucher A. Chaveerach 134.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
289 bp linear DNA
Accession: KM055187.1 GI: 685848589

35. **Piper** kraense voucher A. Chaveerach 134.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055188.1 GI: 685848591

36. **Piper** longum voucher A. Chaveerach 3.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
301 bp linear DNA
Accession: KM055189.1 GI: 685848593

37. **Piper** longum voucher A. Chaveerach 3.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
290 bp linear DNA
Accession: KM055190.1 GI: 685848595

38. **Piper** argyrites voucher A. Chaveerach 126 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
293 bp linear DNA
Accession: KM055191.1 GI: 685848597

39. **Piper** magnibaccum voucher A. Chaveerach 5.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
285 bp linear DNA
Accession: KM055192.1 GI: 685848599

40. **Piper** magnibaccum voucher A. Chaveerach 5.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
293 bp linear DNA
Accession: KM055193.1 GI: 685848601

41. **Piper** montium voucher A. Chaveerach 7.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
285 bp linear DNA
Accession: KM055194.1 GI: 685848603

42. **Piper** montium voucher A. Chaveerach 7.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
281 bp linear DNA
Accession: KM055195.1 GI: 685848605

43. **Piper** mutabile voucher A. Chaveerach 52.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055196.1 GI: 685848607

44. **Piper** mutabile voucher A. Chaveerach 52.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
307 bp linear DNA
Accession: KM055197.1 GI: 685848609

45. **Piper** nigrum voucher A. Chaveerach 17.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
282 bp linear DNA
Accession: KM055198.1 GI: 685848611

46. **Piper** nigrum voucher A. Chaveerach 17.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
299 bp linear DNA
Accession: KM055199.1 GI: 685848613

47. **Piper** pedicellatum var. eglandulatum voucher A. Chaveerach 181.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
298 bp linear DNA
Accession: KM055200.1 GI: 685848615

48. **Piper** pedicellatum var. eglandulatum voucher A. Chaveerach 181.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
299 bp linear DNA
Accession: KM055201.1 GI: 685848617

49. **Piper** pendulispicum voucher A. Chaveerach 82 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
283 bp linear DNA
Accession: KM055202.1 GI: 685848619

50. **Piper** phuwuaense voucher A. Chaveerach 46.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055203.1 GI: 685848621

51. **Piper** phuwuaense voucher A. Chaveerach 46.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
306 bp linear DNA
Accession: KM055204.1 GI: 685848623

52. **Piper** pilobracteatum voucher A. Chaveerach 41.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
302 bp linear DNA
Accession: KM055205.1 GI: 685848625

53. **Piper** pilobracteatum voucher A. Chaveerach 41.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
302 bp linear DNA
Accession: KM055206.1 GI: 685848627

54. **Piper** pilobracteatum voucher A. Chaveerach 41.3 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
299 bp linear DNA
Accession: KM055207.1 GI: 685848629

55. **Piper** pilobracteatum voucher A. Chaveerach 41.4 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
286 bp linear DNA
Accession: KM055208.1 GI: 685848631

56. **Piper** polysyphonum voucher A. Chaveerach 94.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
302 bp linear DNA
Accession: KM055209.1 GI: 685848633

57. **Piper** polysyphonum voucher A. Chaveerach 94.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055210.1 GI: 685848635

58. **Piper** ribesioides voucher A. Chaveerach 1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
291 bp linear DNA
Accession: KM055211.1 GI: 685848637

59. **Piper** sarmentosum voucher A. Chaveerach 18.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
301 bp linear DNA
Accession: KM055212.1 GI: 685848639

60. **Piper** sarmentosum voucher A. Chaveerach 18.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
302 bp linear DNA
Accession: KM055213.1 GI: 685848641

61. **Piper** sylvaticum voucher A. Chaveerach 4.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
301 bp linear DNA
Accession: KM055214.1 GI: 685848643

62. **Piper** sylvaticum voucher A. Chaveerach 4.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055215.1 GI: 685848645

63. **Piper** sylvestre voucher A. Chaveerach 8.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
297 bp linear DNA
Accession: KM055216.1 GI: 685848647

64. **Piper** sylvestre voucher A. Chaveerach 8.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
309 bp linear DNA
Accession: KM055217.1 GI: 685848649

65. **Piper** thomsonii var. trichostigma voucher A. Chaveerach 299 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
291 bp linear DNA
Accession: KM055218.1 GI: 685848651

66. **Piper** umbellatum voucher A. Chaveerach 14.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
283 bp linear DNA
Accession: KM055219.1 GI: 685848653

67. **Piper** umbellatum voucher A. Chaveerach 14.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
290 bp linear DNA
Accession: KM055220.1 GI: 685848655

68. **Piper** wallichii voucher A. Chaveerach 91.1 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
292 bp linear DNA
Accession: KM055221.1 GI: 685848657

69. **Piper** wallichii voucher A. Chaveerach 91.2 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
300 bp linear DNA
Accession: KM055222.1 GI: 685848659

70. **Piper** protrusum voucher A. Chaveerach 100 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
294 bp linear DNA
Accession: KM055223.1 GI: 685848661

71. **Piper** retrofractum voucher A. Chaveerach 9 **PsbA** (**psbA**) gene, partial cds; and **psbA**-trnH intergenic spacer, partial sequence; chloroplast
293 bp linear DNA
Accession: KM055224.1 GI: 685848663

กิจกรรมการนำผลจากโครงการไปใช้ประโยชน์

ได้นำผลการวิจัยและผลิตภัณฑ์ที่ได้ไปเผยแพร่ในงานต่างๆ

สัปดาห์วิทยาศาสตร์ คณะวิทยาศาสตร์ มหาวิทยาลัยขอนแก่น

ประจำปี 2556-2557

โครงการประกวดการพัฒนาภูมิปัญญาสู่นวัตกรรม จัดโดยกรมทรัพย์สินทางปัญญา กระทรวงพาณิชย์ ร่วมกับ สำนักงานพัฒนาเศรษกิจจากฐานชีวภาพ และ มหาวิทยาลัยขอนแก่น ณ โรงแรมเจริญธานี ขอนแก่น

23 ธันวาคม 2557

International Conference on "Research for Social Devotion" In Commemoration of the 50th Anniversary of Khon Kaen University, Thailand

22-23 January 2015