Full Length Research Paper

# Ethnobotany and species specific molecular markers of some medicinal *sakhan* (*Piper*, Piperaceae)

# Runglawan Sudmoon<sup>1</sup>, Tawatchai Tanee<sup>2</sup>, Varima Wongpanich<sup>3</sup>, Nat Bletter<sup>4</sup> and Arunrat Chaveerach<sup>1</sup>\*

<sup>1</sup>Department of Biology, Faculty of Science, Khon Kaen University, Khon Kaen 40002, Thailand. <sup>2</sup>Faculty of Environment and Resource Studies, Mahasarakham University, Mahasarakham 44000, Thailand. <sup>3</sup>Department of Botany and Pharmacognosy, Faculty of Pharmaceutical Sciences, Khon Kaen University, Khon Kaen 40002, Thailand.

<sup>4</sup>Department of Botany, University of Hawaii at Manoa, Hawaii 96822, USA.

Accepted 22 November, 2011

Sakhan, jakhan and takhan are some of Thai common names for Piper species especially for unidentified forest species. They are widely used as vegetables, spices, decoration, traditional medicines and ceremonially. Seven of these species were collected and identified of which the sliced stems are often used as medicinal plants and spices, and are easily preserved as dried powder or slices: Piper betle L. (phlu), Piper colubrinum Link. (prik thai tua phu), Piper nigrum L. (prik thai), Piper pendulispicum C. DC. (jakhan jin), Piper retrofractum Vahl. (dee plee), Piper ribesioides Wall. (takhan lek), and Piper sarmentosum Roxb. (12:WQ: cha phlu). Stem slices and a powder of what was called sakhan were brought from pharmacies for analysis. The ethnobotany of these species was studied by literature reviews, traditional healers and interviews with locals. DNA barcoding of the main stem from all wild species and slices and powder from pharmacies was performed to provide specific markers which can be standardized for further identification of medicinal sakhan samples. The barcode marker accession numbers are GQ500612-GQ500619 for the *rpo*C1 gene, GU372746-GU372751 for matK gene, and GQ891994-GQ892001 for trnH-psbA.

Key words: DNA barcodes, ethnobotany, molecular markers, Piper, Thai medicinal sakhan.

# INTRODUCTION

Sakhan, jakhan and takhan generic names are supplemented with specific suffixes, such as sakhan daeng, jakhan jin, and takhan lek are the names for Piper species growing in the forest. Also, sakhan is the name for powders or slices of medicinal Piper species sold at drugstores. Piper species used in traditional Thai medicine for a long time include well known species such as Piper betle, Piper nigrum, Piper sarmentosum, Piper retrofractum and unidentified species just called sakhan.

*Piper* species are commonly used by Thai people as vegetables, spices, decoration, in ceremonies and as traditional medicines. There are presently forty species documented in Thailand (Chaveerach et al., 2008) and

some are commonly found cultivated in home gardens, which suggests that Thais have had a long relationship with them and are familiar with their use. *Piper* leaves contain distinctively aromatic and acrid volatile oils such as cadinene, carvacrol, caryophyllene, chavibetol, chavicol, eugenol, terpinyl and acetate (Dyer et al., 2004), piperine, piperlongumine, pyridine aikaloids, sesamin, tannins, oxalic acid and iron (De Waard and Anunciado, 1999; Teo and Banka, 2000).

Several *Piper* species have great economic and cultural importance among Thais and are used in complex spice mixtures and as medicines, stimulants, antiseptics and antioxidants (Chaveerach et al., 2006, 2008). Since *Piper* species are always used for medicinal plants, traditional healers will often take unidentified *sakhan* species as from the nearest forest. Some *Piper* species are made into powders or slices for pharmacies or used as cultivated species in Thailand as spices or

<sup>\*</sup>Corresponding author. E-mail: raccha@kku.ac.th. Tel: 66 4334-2908, 66 823095690. Fax: 66 4336-4169.

traditional medicines namely *P. betle*, *P. retrofractum* and *P. nigrum*. Therefore, the species of what is called *sakhan* will depend on geographic collection area, the seller, the traditional healer, the illness treated and the form of the final medicine (that is, only common species such as the four mentioned above are abundant enough to be turned into powder, while rarer species are usually just sold as dried slices). This leads us to assert that a better taxonomic understanding of the *Piper* genus and how common names relate to species leads to the benefit of knowing which species most effectively treats each illness.

DNA barcoding is a popular method for species identification and can be used in samples which have only a short region of reliable DNA or even highly degraded DNA found in processed food, fossil remains, and herbarium specimens. However, Taberlet et al. (2007) claimed that this approach only allows the identification to the level of families, but not genera or species in most cases. Conversely, there has been much more research of this approach in plants starting from 2003 by Hebert et al. (2003). Subsequently, there have been many studies testing standard barcoding regions in different plant taxa aiming to provide rapid, accurate and automatable species identification (Hebert and Gregory, 2005). The land plant chloroplast genome has been suitably proposed as a standard region for plant barcoding (Palmer, 1985, 1991; Downie and Palmer, 1991; Katayama and Ogihara, 1993; Downie et al., 1996; Thiede et al., 2007). There is still a lot of DNA barcoding research in progress such as Kress et al. (2005) who identified some flowering plants using certain regions and suggested that the sequences in the pair of loci, the nuclear internal transcribed spacer region and the plastid trnH-psbA intergenic spacer are potentially usable DNA regions for barcoding flowering plants.

As a standard protocol for barcoding all land plants, Chase et al. (2007) proposed to use two options of three regions each: rpoC1, matK, and trnH-psbA intergenic spacer or rpoB, matK and trnH-psbA. Newmaster et al. (2008) proposed using matK and trnH-psbA to identify plants solely in Myristicaceae. Finally, Hollingsworth et al. (2009) at the Consortium for the Barcode of Life (CBOL) plant working group, recommended *rbcL* and *matK* as the core DNA barcode for land plants. Our research aims to study ethnobotany of sakhan and make standard barcode markers for automatable identification of many species of the popular Thai medicinal plants named sakhan. Powder and slices of unknown species of Piper were also barcoded and compared against the known species in determine the species of the dried order to pharmaceutical samples.

#### MATERIALS AND METHODS

#### **Plant materials**

Fresh plant materials were collected from sites described in

Chaveerach et al. (2008). Powder and slices of *sakhan* were bought from pharmacies in Khon Kaen province, northeastern Thailand in 2008.

#### Procedures

Plant usage information was recorded from observations, market surveys, literature review and interviews with traditional healers and local people. Samples were collected and identified by morphological characters from Chaveerach et al. (2008). All collected samples from fresh plants and pharmacies were analyzed with DNA extraction, DNA barcoding amplification and DNA barcoding sequencing, as described below. DNA barcoding was done following Chase et al. (2007) suggestion of using the *rpo*C1, *trn*H-*psb*A and *mat*K regions. Standard sequence regions of seven known species were aligned and compared with stem slices and powder from pharmacy samples based on DNA barcoding sequence analysis.

#### **DNA** extraction

Genomic DNA was extracted in all collected samples using the Plant Genomic DNA Extraction Kit (RBC Bioscience). Extracted DNA was examined by subjecting it to 0.8% agarose gel electrophoresis stained with ethidium bromide and observed. The quality and quantity of DNA were determined by a gel documenting instrument. DNA samples were then diluted to a final concentration of 20 ng/µl, and these dilutions were used as DNA templates in the PCR reaction.

#### DNA barcoding amplification

Amplifications were performed for DNA barcoding development using 5'forward and reverse primers, 5′-GTGGATACACTTCTTGATAATGG-3' and TGAGAAAACATAAGTAAACGGGC-3' rpoC1 5'for gene, 5'-TAATTTACGATCAATTCATTC-3' and 5'-GTTCTAGCACAAGAAAGTCG-3' for matK gene, and GTTATGCATGAACGTAATGCTC-3' and 5'-CGCGCATGGTGGATTCACAATCC-3' for trnH-psbA (http://www.kew.org/barcoding/update.html; 28 January 2009). The reaction mixture was done in 25 µl consisting of GoTaq Green Master mix (Promega), 0.25 µM each primer, and 10 ng DNA template. The reaction mixture was incubated at 94°C for 1 min and the amplification was performed with the following thermal cycles: 35 cycles of denaturation for 30 s at 94°C, 40 s annealing at 53°C, 40 s extension at 72°C, and 5 min final extension at 72°C. Amplification products were detected by 1.2% agarose gel electrophoresis in TAE buffer and visualized using ethidium bromide staining.

#### DNA barcode sequencing

The amplified specific fragments of the studied samples were sequenced and the sequences were tested for genetic distances using MEGA software version 4 (Tamura et al., 2007). The sequences were submitted to GenBank database.

#### RESULTS

#### Morphological treatment

Collected	fresh	samples	were	identified	using
-----------	-------	---------	------	------------	-------



**Figure 1.** Collected plants, *P. betle* (A), *P. colubrinum* (B), *P. nigrum* (C), *P. pendulispicum* (D), *P. retrofractum* (E), *P. ribesioides* (F), and *P. sarmentosum* (G).

morphological characters from Chaveerach et al. (2008) for which the major distinguishing characters are stamen and stigma numbers and characters, floral bract morphology, leaf shape, and leaf venation. The collected fresh samples were identified as *P. betle* L. (*phlu*), *Piper colubrinum* Link. (*prik thai tua phu*), *P. nigrum* L. (*prik thai*), *P. pendulispicum* C. DC. (*jakhan jin*), *P. retrofractum* Vahl. (*dee plee*), *P. ribesioides* Wall. (*takhan lek*), and *P. sarmentosum* Roxb. (*cha phlu*) as shown in Figure 1. Powder and slices of *sakhan* from pharmacies in Khon Kaen province are shown in Figure 2.

# Ethnobotany treatment

The five species including *P. betle*, *P. nigrum*, *P. pendulispicum*, *P. retrofractum* and *P. sarmentosum* have long been used in traditional Thai medicine as mentioned in Chaveerach et al. (2006). The two most commonly used species are *P. colubrinum* and *P. ribesioides* and

their uses are described subsequently.

P. colubrinum is cultivated in lowland gardens usually used as a rootstock for grafting P. nigrum, which is the most important economic plant in Thailand. P. nigrum are cultivated largely in eastern Thailand especially Chanthaburi province, but bacterial sensitivity has usually caused root rot. Therefore, agriculturalists currently use P. colubrinum as the rootstocks for P. nigrum in plantations (Figure 3). P. colubrinum is locally called "prik thai tua phu" which derives from its usage as a rootstock and the fact that it has only a male flower. Prik thai is the local name of *P. nigrum* and *tua phu* means "male plant". Stems of P. ribesioides have long been used to flavor food giving its spicy, peppery taste, as well as being a traditional medicine in Thailand. For food, P. ribesioides greatly improves the flavor and smell of kaeng (a Northeastern Thai food resembling a curry), such as in Loei province (a province at the Northeast Thai border with Laos) where it is used in kaeng naw mai (curry with bamboo shoot), kaeng om (curry with many kinds of



**Figure 2.** Sliced *sakhan* (A) and powdered *sakhan* (B) bought from pharmacies in Khon Kaen province, northeastern Thailand.



**Figure 3.** *Piper colubrinum* prepared as rootstocks (A) and the grafted plants of *P. nigrum* (B).

vegetables and a kind of meat such as fish, pork or beef), among other dishes, P. ribesioides is always added with pieces of jakhan jin (P. pendulispicum; Chaveerach et al., 2006). As a traditional medicine, all parts of P. ribesioides have been used to treat many different symptoms. The root is used to treat an illness caused from asthma, secrete sweat and treat abnormalities in the body's wind element. The stem helps secrete sweat, increases appetite and supports body elements activities and treats abnormalities in the body's wind element, excess phlegm, and disability of four body elements (earth, water, wind and fire), diarrhea, and abdominal pain. The leaves treat body wind element abnormality incurred in phlegm and blood, alleviate chest congestion, and excrete phlegm. The flowers treat urticaria. The fruits treat body air element abnormality. All parts are use for countering disabilities with and support of body element activities, and to treat diarrhea, abdominal pain, flatulence, and colic.

# Molecular treatment

DNA barcoding amplifications for *rpo*C1, *mat*K, and *trn*H*psb*A showed DNA fragment sizes of about 700, 900 and 500 bp, respectively (Figure 4).

## Sequence alignment

DNA barcodes of the seven known *Piper* samples acted as standards for the powdered *sakhan* samples from pharmacies via sequence analysis and alignment (an example shown in Figure 5). The comparison of the genetic distance of the two sequences, *rpo*C1 and *trn*H*psb*A, of an unknown powder and the seven studied species are shown in Tables 1 and 2. Genetic distances between species range from 0.036 (*P. pendulispicum* and *P. betle*) to 0.205 (*P. colubrinum* and *P. sarmentosum*) in the *rpo*C1 sequence. For the *trn*H-*psb*A sequence, the distances range from 0.004 (*P. betle* and *P. nigrum*) to 0.031 (*P. colubrinum* and *P. pendulispicum*). All studied sample sequences were submitted to the GenBank database with accession numbers shown in Table 3.

# DISCUSSION

The *Piper* species sampled in the research were based on popularity of use among Thais, abundance, and ease



**Figure 4.** DNA barcode fragments of the seven fresh samples and powdered *sakhan* of the standard *rpo*C1, *mat*K, and *trn*H-*psb*A regions.

of collection for trade of powder and dried stem slices: *P. betle, P. colubrinum, P. nigrum, P. pendulispicum, P. retrofractum, P. ribesioides, and P. sarmentosum.* The other *Piper* species mentioned in Chaveerach et al. (2008) that grow in Thailand are not usually found ground or sliced because they grow mainly in evergreen forests, are rare, and are difficult to collect as these forests are protected areas and access is restricted by national law.

DNA extraction was successful for fresh samples and powdered sakhan. Powdered sakhan found in pharmacies should be made from a mixture of young and mature plant parts, but only the young plant parts yield viable DNA. While stem slices are usually made from mature plants because the plant's medicinal substances are mostly secondary metabolites and gradually accumulate as the plant ages, and therefore the more mature specimens are more powerful medicines. This meant that stems harvested for medicinal use are mature which lead to our unsuccessful DNA extraction attempts, even after trying other sakhan powders from other pharmacies. The factor should be considered before attempting DNA barcoding in other dried plants.

Chase et al. (2007) give two useful region combinations, *rpo*C1, *trn*H-*psb*A and *mat*K, and *rpo*B, *trn*H-*psb*A and *mat*K for barcoding all land plants. We

tried the first option, but were unsuccessful as the amplification of *mat*K region failed with *prik thai* and powdered *sakhan*. In our second attempt to amplify *mat*K, we were successful only with powdered *sakhan*. *Prik thai* may have base variations at the priming site caused by human activities. Since *prik thai* is a very important economic plant and widely planted in Thailand for medicine, food and spices. Human breeding of *prik thai*, fertilizers, soil, or weather may affect the genetic variation in the chloroplast DNA.

For *rpo*C1 sequence analysis, the distance values of *Piper* sp. and the other studied species are 0.113 (*Piper* sp. and *P. betle*) to 0.205 (*Piper* sp. and *P. retrofractum*) agreeing with the distance ranges of the other studied species (Table 1). The *trn*H-*psb*A distance values of *Piper* sp. and the other studied species are rather high, ranging from 0.602 (*Piper* sp. and *P. retrofractum*) to 0.614 (*Piper* sp. and *P. pendulispicum*, and *Piper* sp. and *P. colubrinum*) which are much higher values than the range found among the known species (Table 2). The sequence similarity had good enough resolution to determine fresh samples, but the dissimilarity of the powdered *sakhan* sequence from any studied sequence did not allow us to decide whether the unknown powdered *sakhan* was one of the studied species or

Piper nigrum	GCTCACAACTT-CCCTCTAGACTTGGCTG-CTGTTGAAGCTCCATCTACAAATGGA
P. sarmentosum	
P. betle	
P. pendulispicum	
P. retrofractum	ACGTAAT
P. ribesioides	GCATGGAACGTAAT
P. colubrinum	CT
Piper sp.	GCATGGTGGATTCCA.TGCTTCCACTG.CACATCCCT.AA.TCTGG.TT
P. nigrum	TAATGCTTCCTCCTTAT-GTTAATGTATAGGAGTTGTTGAAGGAGCAATACCCAATTTCTTGTTTTT
P. sarmentosum	
P. betle	
P. pendulispicum	
P. retrofractum	
P. ribesioides	
P. colubrinum	
Piper sp.	.CCTA.TAG.AA.AACTAT.CC.AA.ACGT.TTA.AAA.TGT.TGCC.GCCG.
P. niarum	-Cbbcccrtrrecccbccccbbcccccbbccccbbccccbbccccbbccccbbcccc
P. sarmentosum	
P. betle	
P. perdulienicum	
P. retrofractum	3
P. riberioidee	
P. colubrinum	
Piner en	
riper sp.	ATT.AA.S.A-AAAAA.A.TASGA
P. nigrum	${\tt TAATTTTTTTAATCGTTTAGGTATAGTATATTATTATTACTAGAA{\tt TACAGGAAACCCAGATTTAAAGGAAACCCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGATTTAAAGGAAACCCAGAAACCCAGATTTAAAGGAAACCCAGAAACCCAGATTTAAAGGAAACCCAGAAACCCAGAAACCCAGAAACCCAGAAACCCAGATTTAAAGGAAAAGGAAACCCAGAAACCCAGAAACCCAGAAACCCAGAAACCCAGAAACCCAGAAACGAAACCCAGAAACCCCAGAAACCCAGAAACCCAGAAACCCAGAAACCCAGAAACCCCAGAAACCCCAGAAACCCCAGAAACCCCAGAAACCCAGAAACCCCAGAAACCCCAGAAACCCCAGAACCCAGAACCCCAGAAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACGAAACCCCAGAACCCCCAGAACCCCAGAACCCCCAGAACCCCAGAACCCCAGAACCCCCAGAACCCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCCAGAACCCCAGAACCCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCAGAACCCCCAGAACCCCAGAACCCCAGAACACCCCAGAACACCCCAGAACACCCCAGAACACCCCAGAACCCCAGAACACACACACACACACACACACACACACACACACACCCC$
P. sarmentosum	
P. betle	
P. pendulispicum	
P. retrofractum	
P. ribesioides	G
P. colubrinum	
Piper sp.	.GG.AGC.CCTAACATAC.CCTACACA.GGG.AGC.TTATCC.TTTGT.GA.GG
P nigram	CCCCCCATCTCCCCCATCABCCCCA_CTCC
P earmentoeum	a a aracreatare
P hatla	
P pandulianicum	C
<ul> <li>pendulispicum</li> <li>pendulispicum</li> </ul>	
P. rectorraccum	CARCTCARA
P. ribestorues	C
F. COLUDITINUM	
riper sp.	CIT.AACA.CACT.GAGG.AAGTTGT.AGCATTAUGTTCATGC

Figure 5. Sequence analysis of the *trn*H-*psb*A spacer region of the seven studied samples and an unknown powdered *sakhan* (*Piper* sp.) from a pharmacy in Khon Kaen province using MEGA4.

different species. To better make this determination, we would need sequences for all *Piper* in Thailand and

perhaps worldwide. We are gradually accumulating barcodes for all the *Piper* species in Thailand, as shown

Variable	P. nigrum	P. sarmentosum	P. betle	P. pendulispicum	P. retrofractum	P. ribesioides	P. colubrinum	Piper sp.
Piper nigrum	0.000							
P. sarmentosum	0.169	0.000						
P. betle	0.108	0.187	0.000					
P. pendulispicum	0.095	0.174	0.036	0.000				
P. retrofractum	0.113	0.172	0.086	0.079	0.000			
P. ribesioides	0.099	0.176	0.086	0.072	0.113	0.000		
P. colubrinum	0.133	0.205	0.041	0.065	0.108	0.113	0.000	
<i>Piper</i> sp.	0.149	0.205	0.113	0.122	0.133	0.142	0.129	0.000

Table 1. Genetic distance (D)\* matrix of *Piper* species from sequence analysis of the *rpo*C1 region.

\*Overall D = 0.136.

Table 2. Genetic distance (D)\* matrix of *Piper* species from sequence analysis of the *trn*H-*psb*A region.

	P. nigrum	P. sarmentosum	P. betle	P. pendulispicum	P. retrofractum	P. ribesioides	P. colubrinur	n Piper sp.
Piper nigrum	0.000							
P. sarmentosum	0.008	0.000						
P. betle	0.004	0.012	0.000					
P. pendulispicum	0.008	0.016	0.012	0.000				
P. retrofractum	0.008	0.008	0.012	0.016	0.000			
P. ribesioides	0.012	0.012	0.016	0.020	0.012	0.000		
P. colubrinum	0.024	0.024	0.028	0.031	0.024	0.028	0.000	
Piper sp.	0.610	0.606	0.606	0.614	0.602	0.602	0.614	0.000

\*Overall D = 0.360

by the sequences in GenBank database. This research shows advantages and disadvantages of barcoding for *Piper* species. However, one must consider the possibility of sample adulteration when attempting species determination as it is difficult to test adulterated powder or dried slice samples.

There are four Thai traditional medicine formulas used to treat four kinds of cancer (liver, lung, breast cervical and skin cancer), and *sakhan* is important because it is an ingredient in one of these, called "the Five Spices Formula" (*Tumrub* benja kun) which comprises dee plee (P. retrofractum), cha phlu (P. sarmentosum), sakhan (Piper sp.), and other two plant species, Plumbago indica Linn. and Zingiber officinale Roscoe (Juengprasert, 2010). In addition to the Piper species used in this formula, traditional healers in different regions of Thailand may often add other unidentified plants which may or may not be the same Piper species as powder or slices. The benefits of this research is to use

species specific barcode markers to better determine the species of *Piper* for the medicinally important plants called *sakhan* in Thailand. This will lead to taking the right plant for the right disease.

## ACKNOWLEDGEMENTS

This work was granted by Office of the Higher Education Commission. R. Sudmoon was

Lob designation	Colontifio nomo	Accession number					
Lab designation	Scientific name	rpoC1	matK	trnH-psbA			
Pi-1	P. nigrum	GQ500612	-	GQ891994			
Pi-4	P. sarmentosum	GQ500613	GU372746	GQ891995			
Pi-5	P. betle	GQ500614	GU372747	GQ891996			
Pi-6	P. pendulispicum	GQ500615	GU372748	GQ891997			
Pi-7	P. retrofractum	GQ500616	GU372749	GQ891998			
Pi-14	P. ribesioides	GQ500617	GU372750	GQ891999			
Pi-15	P. colubrinum	GQ500618	GU372751	GQ892000			
Pi-B	Piper sp., unknown powder	GQ500619	-	GQ892001			

Table 3. Scientific names and GenBank accession numbers of the three barcoding regions of the Piper species studied.

supported by CHE-RES-PD scholar. Part of the research was supported by Khon Kaen University Research Fund.

#### REFERENCES

- Chaveerach A, Mokkamul P, Sudmoon R, Tanee T (2006). Ethnobotany of the genus *Piper* (Piperaceae) in Thailand. Ethnobot. Res. Appl., 4: 223-231.
- Chaveerach A, Sudmoon R, Tanee T, Mokkamul P (2008). The species diversity of the genus *Piper* from Thailand. Acta Phytotax. Geobot., 59: 105-163.
- Chase MW, Cowan RS, Hollingsworth PM, Van Den Berg C, Madriñán S, Petersen G, Seberg O, Jørgsensen T, Cameron KM, Carine M, Pedersen N, Hedderson TAJ, Conrad F, Salazar GA, Richardson JE, Hollingsworth ML, Barraclough TG, Kelly L, Wilkinson M (2007). A proposal for a standardized protocol to barcode all land plants. Taxonomy, 56: 295-299.
- De Waard PWF, Anunciado IS (1999). *Piper nigrum* L. In: De Guzman CC, Siemonsma JS (eds) Plant Resources of South-East Asia No. 13: Spices. Backhuys Publishers, Leiden, Pp.183-194.
- Downie SR, Llanas É, Katz-Downie DS (1996). Multiple independent losses of the *rpo*C1 intron in angiosperm chloroplast DNA's. Syst. Bot., 21: 135-151.
- Downie SR, Palmer JD (1991). Use of chloroplast DNA rearrangements in reconstructing plant phylogeny. In: Soltis PS, Soltis DE, Doyle JJ (eds) Molecular Systematics of Plants, Chapman and Hall, NY, pp. 14-35.
- Dyer LA, Richards J, Dodson CD (2004). Isolation, synthesis, and evolutionary ecology of *Piper* amides. In: Dyer LA, Palmer AN (eds) *Piper*: A Model Genus for Studies of Evolution, Chemical Ecology, and Trophic Interactions, Kluwer Academic Publishers, Boston, pp. 117-139.
- Hebert PDN, Cywinska A, Ball SL, De Waard JR (2003). Biological identifications through DNA barcodes. Proc. Roy. Soc. London, Ser. B, Biol. Sci., 270: 313-321.
- Hebert PDN, Gregory TR (2005). The promise of DNA barcoding for taxonomy. Syst. Biol., 54: 852-859.
- Hollingsworth PM, Forrest LL, Spouge JL, Hajibabaei M, Ratnasingham S, van der Bank M, Chase MW, Cowan RS, Erickson DL, Fazekas AJ, Graham SW, James KE, Kim KJ, Kress WJ, Schneider H, van

Alphen Stahl J, Barrett SC, van den Berg C, Bogarin D, Burgess KS, Cameron KM, Carine M, Chacón J, Clark A, Clarkson JJ, Conrad F, Devey DS, Ford CS, Hedderson TA, Hollingsworth ML, Husband BC, Kelly LJ, Kesanakurti PR, Kim JS, Kim YD, Lahaye R, Lee HL, Long DG, Madriñán S, Maurin O, Meusnier I, Newmaster SG, Park CW, Percy DM, Petersen G, Richardson JE, Salazar GA, Savolainen V, Seberg O, Wilkinson MJ, Yi DK, Little DP (2009). A DNA barcode for land plants. Proc. Natl. Acad. Sci. U.S.A., 106: 12794-12797.

- Juengprasert W (2010). Director-General of Department for Development of Thai Traditional and Alternative Medicine, Dairy News, 12 September 2010. Available from http://thebeauty24hours.com/2010/09/27/herbs-and-cancertreatment/ [accessed 8 November 2010].
- Katayama H, Ogihara Y (1993). Structural alterations of the chloroplast genome found in grasses are not common in monocots. Curr. Genet., 23: 160-165.
- Kress WJ, Wudak KJ, Zimmer EA, Weigt LA, Janzen DH (2005). Use of DNA barcodes to identify flowering plants. Proc. Natl. Acad. Sci. U.S.A., 102: 8369-8374.
- Newmaster SG, Fazekas AJ, Steeves AJ, Janovec J (2008). Testing candidate plant barcode regions in the *Myristicaceae*. Mol. Ecol. Resou., 8: 480-490.
- Palmer JD (1985). Comparative organization of chloroplast genome. Annu. Rev. Genet., 19: 325-354.
- Palmer JD (1991). Plastid chromosomes: structure and evolution. In: Bogorad L, Vasil IK (eds) The Molecular Biology of Plastids. Cell Culture and Somatic Cell Genetics of Plants, Academic Press, San Diego, 7A: 5-53.
- Taberlet P, Coissac E, Pompanon F, Gielly L, Miquel C, Valentini A, Vermat T, Corthier G, Brochmann C, Willerslev E (2007). Power and limitations of the chloroplast *trn*L (UAA) intron for plant DNA barcoding. Nucleic Acids Res., 35:el4.
- Tamura K, Dudley J, Nei M, Kumar S (2007). MEGA4-Molecular evolutionary genetics analysis (MEGA) software version 4.0. Mol. Biol. Evol., 24: 1596-1599.
- Teo SP, Banka RA (2000). *Piper betle* L. In: Van Der Vossen HAM, Wessel M (eds) Plant Resources of South-East Asia No. 16: Stimulants, Backhuys Publishers, Leiden, Pp. 135-140.
- Thiede J, Schmidt SA, Rudolph B (2007). Phylogenetic implication of chloroplast *rpo*C1 intron loss in the *Aizoaceae* (Caryophyllales). Biochem. Syst. Ecol., 35: 372-380.