Taxonomic Reconsideration and Phylogeographic Implication for *Nertera yamashitae* (Rubiaceae)

Goro Kokubugata^{1,*}, Koh Nakamura², Yumiko Hirayama¹, Ching-I Peng² and Masatsugu Yokota³

¹Department of Botany, National Museum of Nature and Science, Tsukuba, Ibaraki, 305–0005 Japan ²Biodiversity Research Center, Academia Sinica, Nangang, Taipei 115, Taiwan ³Laboratory of Ecology and Systematics, Faculty of Science, University of the Ryukyus, Nishihara, Okinawa, 903–0213 Japan * E-mail: gkokubu@kahaku.go.jp

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Abstract Anatomical and morphological characters and phylogenetic position of *Nertera ya-mashitae* were investigated with those of related species in the family Rubiaceae. In the anatomy and morphology, disk morphology and number of ovules in an ovary locule of *N. yamashitae* differed from those of other *Nertera* species, and were more similar to those of *Ophiorrhiza* species. In the sequence similarity search of ITS in nrDNA, and *atpB-rbcL* and *trnK/matK* in cpDNA, *N. yamashitae* showed the highest similarity to *Ophiorrhiza* species. In the MP phylogenetic analyses based on nrITS, *atpB-rbcL*, and *trnK/matK*, *N. yamashitae* was outside of a clade of the genus *Nertera* in tribe Anthospermeae, while it was included in a clade of the genus *Ophiorrhiza* in tribe Ophiorrhiza as a new combination; and in phylogeography, implies that it could be a relict species lineage in Amami Island of the Ryukyu Archipelago.

Key words: dwarfism, Nertera, Ophiorrhiza, Rubiaceae, Ryukyus.

Introduction

The genus Nertera Banks et Sol. ex Gaertn. is composed of ca. 16 (or six in a strict sense) species found in Malesia, Oceania and Americas; and is classified in tribe Anthospermeae (subfamily Rubioideae), being well supported by morphological and molecular data (Bremekamp, 1966; Bremer and Manen, 2000; Bremer, 2009). Although Heads (1996) included Nertera species in the genus Coprosma, disagreeing with most taxonomic treatments, he still recognized it as a taxon at section level, namely sect. Nertera. As the first species of the genus Nertera discovered in Japan, Nertera yamashitae T. Yamazaki (Fig. 1) studied herein was described based on a type specimen collected from Amami Island in the Ryukyu Archipelago (Yamazaki, 1998), because it has small leaves, four stamens, and a fourlobed corolla, showing the generic-representative morphologies for Nertera (e.g. Lo, 1999; Liu and Yang, 1998). This species has been thought to be an insular endemic species of Amami Island, and only three populations have been found in two river systems in this island (Hotta, 2004). Therefore, it is treated as critically endangered by the Japanese Ministry of the Environment (2007). After Yamazaki's description (1998), although a few studies on cytology (Kokubugata et al., 1998) and conservation biology (Hotta, 2004) have been carried out, further taxonomical reconsideration based on anatomical, morphological, and molecular data has never been applied to this species.

Dwarfism, a phenomenon in which body size is strongly reduced, is well-known in alpine



Fig. 1. Nertera yamashitae. (A) Habit (photographed by H. Yamashita); (B) flower in plants (GK11029) cultivated in Tsukuba Botanical Garden, National Museum of Nature and Science. Bar=5 mm.

ecosystems (e.g. Körner, 1999). In the Ryukyus, some leaf dwarfisms are known at elevations over 1,000 m on Yakushima Island in the northern Ryukyus, and phylogenetic and their evolutionary biology has been examined in these plants (e.g. Yokoyama et al., 2003; Shinohara and Murakami, 2006; Tsukaya et al., 2007). Also, certain dwarf leaf species are known at altitudes of less than 100 m on Amami Island, such as N. yamashitae studied herein, Lysimachia liukiuensis Hatus. (Myrsinaceae), Oxalis exilis A. Cunn. (Oxalidaceae), Rubus amamianus Hatus. et Ohwi (Rosaceae), and Sphenomeris minutula Sa. Kurata (Lindsaeaceae) (Hatusima, 1975). In contrast with leaf dwarfism at high elevation on Yakushima Island, however, few phylogenetic studies have examined for the dwarf leaf species at low altitude on Amami Island without Lysimachia liukiuensis (Kokubugata et al., 2010).

In the present study, we investigated the floral anatomy and morphology of *N. yamashitae*; and its phylogenetic position among related species of subfamily Rubioideae based on three molecular loci to reconsider the taxonomic status, and to discuss the dwarfism of this species.

Materials and Methods

Plant materials

Plants of *Nertera yamashitae* were collected from two localities in two river systems in Amami Island (Table 1). Also, plants of *N. granadense* (Mutis ex L.f.) Druce following a strict taxonomic treatment of Liu and Yang (1998) in four Asian countries, and two *Ophiorrhiza* species in two Asian countries were collected and used in the present molecular phylogenetic analyses (Table 1). Voucher specimens were deposited in the herbarium of the National Museum of Nature and Science (TNS).

DNA extraction, polymerase chain reaction, and sequencing

Fresh leaves were harvested from the plants cultivated in a greenhouse of the Tsukuba Botanical Garden for DNA extraction, which was conducted using the DNeasy Plant Mini Kit (Qiagen, Valencia, CA) following the manufacturer's protocols. Total DNA samples isolated were deposited in the Molecular Biodiversity Research Center of the National Museum of Nature and Science.

GenBank accession numbers					
Snariae	T anality	Vouchard		Accession no. ^b	
60100dc	LOCATILY		ITS (type)	atpB-rbcL (type)	trnK/matK (type)
Nertera yamashitae T. Yamaz.	JAPAN, Ryukyus: Naze, Amami Is., Kagoshima	GK9854	AB559526 (A)	AB559538 (a)	AB559550(I)
	JAPAN, Ryukyus: Sumiyo, Amami Is., Kagoshima	GK11029	AB559527 (A)	AB559539 (a)	AB559551(I)
N. granadense (Mutis ex L.f.) Druce	TAIWAN: Nanao, Ilan	GK11028	AB559529 (B)	AB559540 (b)	
	TAIWAN: Taoyuan, Kaohsiung	GK8824	AB559528 (B)	AB559541 (c)	
	TAIWAN: Taoyuan, Kaohsiung	GK10821	AB559530 (C)	AB559542 (d)	
	PHILIPPINES: Bontoc, Mountain Province, Luzon	GK8301	AB559531 (D)	AB559543 (e)	
	PHILIPPINES: Trinidad, Benguet, Luzon Is.	GK8254	AB559532 (E)	AB559544 (f)	
	PHILIPPINES: Banaue, Ifuga, Luzon Is.	GK9647	AB559533 (E)	AB559545 (g)	
	MALAYSIA, Borneo: Kinabaru, Sabah	GK7903	AB559534 (F)	AB559546 (h)	
	INDONESIA, West Java: Cibodas, Cianjur	GK8559	AB559535 (G)	AB559547 (i)	
<i>Ophiorrhiza longiflora</i> Blume	INDONESIA, West Java: Cibodas, Cianjur	GK8503	AB559536	AB559548	AB559552
Ophiorrhiza sp.	THAILAND: Ang Kang, Chiang Mai	GK12391	AB559537	AB559549	AB559553

Table 1. Plant materials of Nertera and Ophiorrhiza investigated in the present study, and their localities, voucher numbers, and ITS, atpB-rbcL and trnK/matK

In the present study, ITS1, 5.8S rDNA and ITS2 with part of the 18S rDNA (ITS) of nuclear ribosomal DNA (nrDNA), the intergenic spacer of *atpB* and *rbcL* genes (*atpB-rbcL*), the maturaseK gene and adjacent trnK introns (trnK/matK) of cpDNA were selected for the molecular phylogenetic analyses. In the polymerase chain reaction (PCR), we amplified ITS using the primer set AB101 and AB102 (Douzery et al., 1999), atpB-rbcL using atpB2F and rbcL2R (Nakamura et al., 2006), trnK/matK using trnK-3914(D)F (Johnson and Soltis, 1994) and psbA5'R (M. Nepokroeff, University of South Dakota, personal communication). The PCR amplifications were performed using Takara Ex Taq (Takara, Tokyo) with Ampdirect Plus (Shimadzu, Kyoto) on an iCycler (BioRad, Hercules, CA). The PCR profile comprised 35 cycles of 30 s at 94°C, 30 s at 55°C, and 1 min at 72°C for ITS, and 35 cycles of 30s at 94°C, 30s at 55°C, and 3 min at 72°C for atpB-rbcL and trnK/matK. After purification of PCR products using ExoSAP-IT (USB Corp., Cleveland, OH), direct sequencing was performed using the BigDye Terminator Cycle Sequencing Kit ver. 3 (ABI PRISM; Applied Biosystems, Foster City, CA), with the PCR primers AB101 and AB102, and two additional primers ITS2 and ITS3 (White et al., 1990) for the ITS; the PCR primers atpB2F and rbcL2R for atpB-rbcL; and the PCR primers trnK-3914 (D) and psbA5'R and additional primers of matK-300F (Yamashita and Tamura, 2000), trnK2621R (Liston and Kadereit, 1995), matK-AF, matK-8R (Ooi et al., 1995), and matK-AR (Kazempour Osaloo et al., 1999) for matK/trnK. Automated sequencing was performed on a 3130xl Genetic Analyzer (Applied Biosystems). The sets of sequence data were assembled using ATGC ver. 4.01 (GENETYX Co., Tokyo). Sequence data of ITS, atpB-rbcL, and trnK/matK were deposited in the DDBJ/ EMBL/GenBank international DNA database under the accession numbers shown in Table 1.

^a GK: G. Kokubugata (TNS). ^b Sequences investigated here and registered in the DDBJ/EMBL/GenBank database; letters in parentheses indicate the locus type.

Sequence similarity searches and taxon sampling in DNA database

Sequence similarity searches in the ITS, *atpB–rbcL*, and *matK/trnK* regions of *N. ya-mashitae* were conducted with the program Basic Local Alignment Search Tool (BLAST) ver. 2.2.18 (Altschul *et al.*, 1997) in the DDBJ/EMBL/GenBank database (http://blast.ddbj.nig. ac.jp/top-j.html) on 23 February 2010. Following the BLAST results, we selected tribe members that showed high similarity to *N. yamashitae* in the examined three regions, and their sequence data deposited in the DNA database were added to the present phylogenetic analyses under the accession numbers shown in Table 2.

Phylogenetic analysis

DNA sequences were aligned using the program ClustalX 1.8 (Thompson et al., 1994) and then manually adjusted. Phylogenetic analyses were conducted based on a maximum parsimony (MP) criterion using PAUP* version 4.0b10 (Swofford, 2002). First, to verify the phylogenetic position of N. yamashitae at the tribe level, MP phylogenetic analyses based on ITS and *atpB-rbcL* were independently conducted with members of tribes Anthospermeae including Nertera species, Ophiorrhizeae including Ophiorrhiza, and Urophylleae, which is thought to be a sister group of tribe Ophiorrhizeae (Rydin et al., 2009a, 2009b). Second, to elucidate the phylogenetic position of N. vamashitae among phylogenetically closely related species, MP phylogenetic analysis was conducted based on combined data of ITS, atpB-rbcL, and trnK/matK. The combinability of the two cpDNA regions was assessed using the incongruence length difference (ILD) test (Farris et al., 1994), with the partition homogeneity test implemented in PAUP* version 4.0b10 (Swofford, 2002). Indels were treated as missing data. Characters were treated as unordered, and character transformations were weighted equally. The branch collapse option was set to collapse at a minimum length of zero. A heuristic parsimony search was performed with 200 replicates of random additions

of sequences, with the ACCTRAN character optimization, tree bisection-reconnection (TBR) branch swapping, MULTREES, and STEEPEST DESCENT options on. Statistical support for each clade was assessed by bootstrap analysis (Felsenstein, 1985). One thousand replicates of heuristic searches, with the TBR branch swapping and MULTREES options off, were performed to calculate bootstrap values. Strict consensus trees of the output tree files from PAUP were generated by TREEVIEW (Page, 1996).

Floral anatomical and morphological observations in Nertera yamashitae

Corolla morphology of *N. yamashitae* was observed based on living plants and herbarium specimens (GK 9854 and 11029 in TNS). Number of ovules was counted on a mature flower (GK 11029) fixed in FAA solution after cultivation in the Tsukuba Botanical Garden of National Museum of Nature and Science. The ovary was torn using a pair of tweezers, the number of ovules counted, and their position observed and photographed under a light microscope.

Results

Sequence similarity searches of ITS, atpB–rbcL, and matK/trnK

In two plants of Nertera yamashitae collected from two different river systems on Amami Island, no intraspecific sequence variation was detected in the three sequences of ITS, *atpB-rbcL*, and *trnK/matK*. The results of the sequence similarity searches using BLAST are summarized in Table 3. The BLAST analyses indicated that ITS (684 bp) of N. yamashitae had highest similarity to 18 accessions of six Ophiorrhiza species in Japan and Taiwan. An accession of N. dichondrifolia Hook. f. (DQ501279; Wright et al., 2006) was 91st in the BLAST list. The atpB-rbcL (1149 bp) of N. yamashitae had the highest similarity to 17 accessions of six Ophiorrhiza species in Japan and Taiwan. An accession for *atpB-rbcL* of Nertera sp. (DQ131755; J. F. Manen, unpubl. data) was 78th in the BLAST list. The *trnK/matK*

Tribo ^a	Chanize	Vouchar		Accession no. ^b	
2011			ITS (type)	atpB-rbcL (type)	trnK/matK (type)
Anthospermeae	Anthospermum herbaceum L.f. Nertera granadensis (Mutis ex L.f.) Druce	Bremer 3039(UPS) —	EU145355 ¹ AF257927 ⁴	AJ234028 ¹ —	
Ophiorrhizeae	Normandia neocaledonica Hook.f. Lerchea bracteata Valeton	Munzinger 532(MO) Axelius 343(S)	$ m AF257930^{4}$ EU145374 ¹	A.1233.997 ²	
	Neurocalyx championii Benth. ex Thwaites	Thor 601(S)	EU145376 ¹		
	Neurocalyx zeylanicus Hook. Onbiowebiza almowi Merr	B & Bremer 937(S) Vialdean & Doulean 232(AAID)	EU145375 ¹ EU145378 ¹	AJ233995 ²	
	Ophiorrhiza eunen mon. Ophiorrhiza mungos L.	Bremer 2201(UPS)	EU145377 ¹		
	Ophiorrhiza amamiana (Hatus.) Koh Nakam.,	NK061455(RYU)	AB269875 ⁵ (H)	$AB269877^{5}(j)$	AB270601 ⁵ (II)
	Denda, Kameshima et Yokota	NKT0126(RYU)	AB269875 ⁵ (H)	$AB269877^{3}(j)$	AB270601 ⁵ (II)
		NK 061456(RY U) NK T0128(RV11)	AB269875 ⁵ (H) AB269875 ⁵ (H)	AB2698775(j) AB2698775(j)	AB270601 ⁵ (II) AB270601 ⁵ (II)
		NKT0129(RYU)	$AB269875^{5}(H)$	$AB269878^{5}(k)$	$AB270601^{5}(II)$
		NK061458(RYU)	$AB269875^{5}(H)$	$AB269878^{5}(k)$	$AB270601^{5}(II)$
		NKT0127(RYU)	AB269876 ⁵ (I)	$AB269877^{5}(j)$	$AB270601^{5}(II)$
	Onbiombiza ianonioa Bl	NKU0145/(KYU) NKT01015(DVTI)	$AB2098/0^{-}(I)$	AB2098///U)	AB2/0001-(11) AB2/77/55/111)
	Opinion mizu Jupomica Di.	NKT0104(RYI)	$AB269874^{5}(K)$	$AB247238^{5}(1)$	$AB247121^{5}(IV)$
		NKT0107(RYU)	AB269874 ⁵ (K)	AB247238 ⁵ (1)	$AB247245^{5}(III)$
		NKT0111(RYU)	$AB269874^{5}(K)$	$AB257115^{5}(m)$	$AB257122^{5}(V)$
		NK061419(RYU)	AB269874 ⁵ (K)	AB257115 ⁵ (m)	AB257122 ⁵ (V)
		NK050501(RYU)	$AB269874^{5}(K)$	$AB257115^{5}(m)$	$AB257122^{5}(V)$
		NKT0113(RYU)	$AB269874^{5}(K)$	$AB257115^{5}(m)$	$AB257122^{5}(V)$
		NK050790(RYU)	AB269874°(K)	$AB257115^{5}(m)$	AB257122°(V)
		NKT0118(RYU)	AB269874 ⁵ (K)	$AB247239^{5}(n)$	$AB247246^{\circ}(VI)$
		NKT0120(RYU)	$AB269874^{\circ}(K)$	$AB247239^{\circ}(n)$	AB247246 ² (VI)
		NKT0119(RYU)	AB269874 ⁻ (K)	AB247239 ² (n)	AB247247 ⁵ (VII)
		NKT0121(RYU)	$AB247258^{3}(L)$	$AB247239^{2}(n)$	$AB247246^{\circ}(VI)$
		NKIUI22(KYU)	AB24/258 (L)	AB24/239'(n)	AB24/246'(VI)
		NKT0123(RYU)	$AB269874^{2}(K)$	$AB247240^{\circ}(0)$	AB247248 ⁵ (VII)
		NK 10124(RY U) CV 2080/TNS)	$AB2698/4^{\circ}(K)$	AB247241°(p)	AB247246°(VI) AD247250 ⁵ (IV)
		NK GOOT(RYTT)	$AB247260^{5}(N)$	$AB247238^{5}(1)$	$AB247240^{5}(X)$
	<i>Ophiorrhiza hayatana</i> Masam.	NKC001(RYU)	AB247336 ⁵ (0)	AB247243 ⁵ (q)	AB247252 ⁵ (XI)
		NKC002(RYU) NKC004(RYU)	AB247339 ⁵ (P) AB247339 ⁵ (P)	AB247243 ⁵ (q) AB247243 ⁵ (a)	AB247253 ⁵ (XII) AB247253 ⁵ (XII)

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Ophiorrhizeae <i>Oph</i>	sanada	AUNCIE			
			ITS (type)	atpB-rbcL (type)	trnK/matK (type)
Oph	<i>Ophiorrhiza hayatana</i> Masam.	NKC003(RYU)	AB247337 ⁵ (Q)	AB247243 ⁵ (q)	AB247254 ⁵ (XIII)
Oph		NKC005(RYU)	$AB247338^{5}(R)$	$AB247243^{5}(q)$	AB247255 ⁵ (XIV)
	Ophiorrhiza kuroiwae Ohwi	NKT0141(RYU)	$AB247341^{5}(S)$	$AB247244^{5}(r)$	AB247256 ⁵ (XV)
		NKT0142(RYU)	$AB247342^{5}(T)$	$AB247244^{5}(r)$	AB247256 ⁵ (XV)
Oph	Ophiorrhiza michelloides (Masam.) H.S. Lo	NKW001(RYU)	AB247340 ⁵ (U)	$AB247242^{5}(s)$	AB247251 ⁵ (XVI)
Oph	Ophiorrhiza pumila Champ. ex. Benth.	NKH001(RYU)	$AB247273^{5}(V)$	AB247147 ⁵ (t)	AB247150 ⁵ (XVII)
1		NKH002(RYU)	$AB247273^{5}(V)$	$AB247147^{5}(t)$	AB247150 ⁵ (XVII)
		NKT0137(RYU)	$AB247274^{5}(W)$	$AB247147^{5}(t)$	AB247150 ⁵ (XVII)
		GK3979(TNS)	$AB247272^{5}(X)$	$AB247147^{5}(t)$	AB247150 ⁵ (XVII)
Spir	Spiradiclis bifida Kurz	J.B.H. 55(S)	EU145379 ¹		
Xan	Xanthophytum borneense (Valeton) Axelius	Axelius 316(S)	EU145381 ¹	EU145567 ¹	
Xan	Xanthophytum capitellatum Ridl.	Ridsdale 2473(L)	$EU145380^{1}$	$AJ233996^{2}$	
Urophylleae Amp	Amphidasya ambigua (Standl.) Standl.	Clark & Watt 736(UPS)	EU145383 ¹	EU145337 ¹	
Mas	Maschalocorymbus corymbosus (Blume) Bremek.	Ridsdale 2471(L)	$EU145384^{1}$		
Pau	Pauridiantha paucinervis (Hiern) Bremek.	Lantz 123(UPS)	EU145385 ¹	$AJ233998^{2}$	
Pau	Pauridiantha symplocoides (S. Moore) Bremek.	Bremer 2090(UPS)	EU145386 ¹	EU145338 ¹	
Pra	Praravinia suberosa (Merr.) Bremek.		EU145387 ¹		
Pra	Pravinaria leucocarpa Bremek. Beaman	Beaman 7950(S)	EU145388 ¹	$AJ234001^{2}$	
Uro	Urophyllum arboreum (Reinw. ex Blume) Korth.	Boeea 7887(S)		DQ131793 ³	
Uro	Urophyllum ellipticum (Wight) Thwaites	Lundqvist 11085(UPS)	EU145389 ¹	$AJ234002^{2}$	
^a Taxonomic treatment follows Bremer a ^b Sequences in the DDBJ/EMBL/GenB ² DDBJ/EMBL/GenB	^a Taxonomic treatment follows Bremer and Manen (2000). ^b Sequences in the DDBJ/EMBL/GenBark database; letters in parentheses indicate the types of three loci; references are as follows: ¹ Rydin <i>et al.</i> (2009a, 2009b);	and Manen (2000). and database: letters in parentheses indicate the types of three loci; references are as follows: ¹ Rydi	se loci; references are s	is follows: ¹ Rydin <i>e</i>	t al. (2009a, 2009b);

Table 2. (Continued)

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Species	Locality	Locus ^a	Accession no. ^b	Score (bits)	Identities
ITS					
Ophiorrhiza amamiana	JAPAN (Okinawa Is.)	ITS(I)	AB269876	1144	659/684 (96%)
Ophiorrhiza amamiana	JAPAN (Amami, Tokunoshima, & Okinawa Isls. in the Ryukyus)	ITS(H)	AB269875	1136	658/684 (96%)
Ophiorrhiza japonica	TAIWAN	ITS(N)	AB247260	1128	657/684 (96%)
Ophiorrhiza japonica	JAPAN (Shikoku, Kyushu & Amami, Tokunoshima, Okinawa, Ishigaki & Iriomote Isls. in the Ryukyus)	ITS(K)	AB269874	1120	656/684 (95%)
Ophiorrhiza japonica	TAIWAN	ITS(M)	AB247259	1112	655/684 (95%)
atpB–rbcL					
Ophiorrhiza japonica	JAPAN (Tokunoshima & Okinawa Isls.)	<i>atpB–rbcL</i> (m)	AB257115	1132	597/608 (98%)
Ophiorrhiza hayatana	TAIWAN	atpB-rbcL(q)	AB247243	1132	597/608 (98%)
Ophiorrhiza michelloides	TAIWAN	<i>atpB–rbcL</i> (s)	AB247242	1132	597/608 (98%)
Ophiorrhiza japonica	JAPAN (Iriomote Is.); Taiwan	<i>atpB–rbcL</i> (p, l)	AB247241, AB247238	1132	597/608 (98%)
Ophiorrhiza amamiana	JAPAN (Amami, Tokunoshima, & Okinawa Isls. in the Ryukyus)	atpB-rbcL(j)	AB269877	1124	596/608 (98%)
matK/trnK					
Ophiorrhiza michelloides	TAIWAN	matK/trnK(XVI)	AB247251	4220	2276/2335
Ophiorrhiza japonica	JAPAN (Ishigaki & Iriomote Isls. in the Ryukyus)	matK/trnK(VI)	AB247246	4209	2274/2334 (97%)
Ophiorrhiza hayatana	TAIWAN	matK/trnK (XIII, XIV)	AB247254, AB247255	4205	2274/2335 (97%)
Ophiorrhiza japonica	JAPAN (Iriomote Is. in the Ryukyus)	(<i>null</i> , <i>nu v</i>) <i>matK/trnK</i> (VII)	AB247248	4201	2273/2334 (97%)
Ophiorrhiza hayatana	TAIWAN	matK/trnK(XI)	AB247252	4197	2273/2335 (97%)

Table 3. The top five accessions with high similarity to the sequences of *Nertera yamashitae* using BLAST and their localities

^a Letters in parentheses indicate locus type in Table 2.

^b Sequences in the DDBJ/EMBL/GenBank database.

locus (2328 bp) of *N. yamashitae* had highest similarity to 19 accessions of six *Ophiorrhiza* species in Japan and Taiwan. No accession for *trnK/matK* of *Nertera* species was found in the DDBJ/EMBL/GenBank database.

Phylogenetic position of Nertera yamashitae *at the tribe level*

In the MP analyses at tribe level based on the

ITS sequence (Fig. 2), 233 of the 313 variable characters were parsimony-informative, and 305 equally most parsimonious trees of 726 steps were obtained, with a consistency index (CI)= 0.65, a retention index (RI)=0.87, and a rescaled consistency index (RC)=0.56. In the MP analyses at tribe level based on the *atpB*-*rbcL* sequences (Fig. 3), 110 of the 228 variable characters were parsimony-informative, and 216 equal-

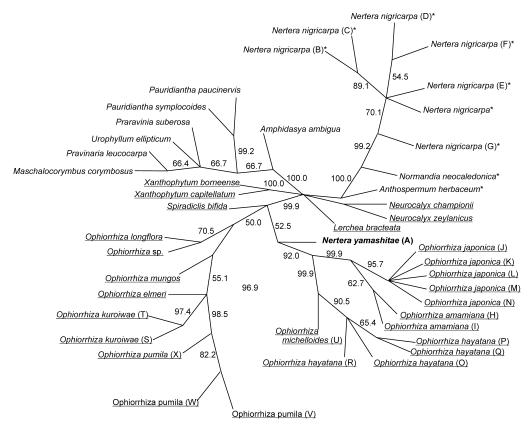


Fig. 2. Unrooted maximum parsimony, strict consensus tree to detect phylogenetic position of *Nertera yamashitae* in tribes Anthospermeae, Ophiorrhizeae, and Urophylleae based on the ITS locus. Species with underlines and asterisks are members of tribes Ophiorrhizeae and Anthospermeae, respectively (Bremer and Manen, 2000). Numerals above branches indicate bootstrap percentages (≥50%). Letters in parentheses indicate loci types in *N. yamashitae*, other *Nertera* species, and *Ophiorrhiza* species (Tables 1 and 2).

ly most parsimonious trees of 288 steps were obtained (CI=0.89, RI=0.95, and RC=0.85). Both of the unrooted strict consensus trees based on the ITS and *atpB-rbcL* loci indicated that N. yamashitae was not positioned in a clade with other Nertera species nor in a clade of Anthospermeae (Figs. 2 and 3). On the other hand, N. yamashitae was included in a clade with Ophiorrhiza species and Spiradiclis bifida (tribe Ophiorrhizeae) based on analysis of the ITS sequence (BP=99.9%; Fig. 2). Based on the *atpB-rbcL* sequence (Fig. 3), a clade consisting of N. yamashitae and Ophiorrhiza species had high bootstrap support (97.2%). In both of the unrooted strict consensus trees, N. yamashitae included in a subclade with four Ophiorrhiza species of O. amamiana

(Hatus.) Koh Nakam., Denda, Kameshima et Yokota, *O. japonica* Bl., *O. hayatana* Masam. and *O. michelloides* (Masam.) H.S. Lo.

Phylogenetic relationship of Nertera yamashitae to the other Ophiorrhiza species

To analyze the phylogenetic relationship within the subclade consisting of *N. yamashitae* and four *Ophiorrhiza* species (Figs. 2 and 3), the MP analysis was conducted based on the full set of ITS, *atpB–rbcL*, and *matK/trnK* loci with other four *Ophiorrhiza* species, namely *O. kuroiwae* Ohwi, *O. pumila* Champ. ex Benth., *O. longiflora* Blume and an unknown *Ophiorrhiza* species as an outgroup following the two independent analyses based on ITS (Fig. 2) and *atpB–rbcL*

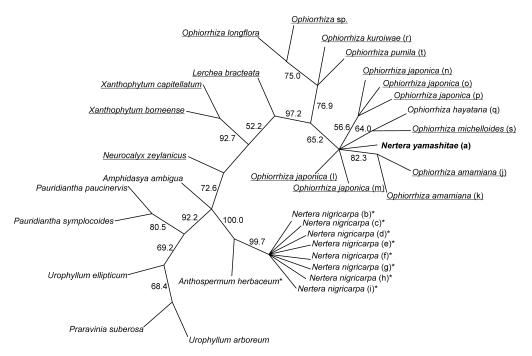


Fig. 3. Unrooted maximum parsimony, strict consensus tree to detect phylogenetic position of *Nertera yamashitae* in tribes Anthospermeae, Ophiorrhizeae, and Urophylleae based on the *atpB–rbcL* locus. Detail explanation given in Fig. 2.

(Fig. 3) loci. In the MP analysis, 124 of 188 variable characters were parsimony-informative, and six most parsimonious trees of 239 steps were obtained, with CI=0.86, RI=0.94, and RC=0.81 (Fig. 4).

The MP analysis (Fig. 4) indicated that *N. yamashitae* was connected to a basal position of a subclade consisting of *O. amamiana*, *O. japonica*, *O. hayatana*, and *O. michelloides* with high probability (BP=99.4%). Another dwarf leaf species of *O. michelloides* in Taiwan was not sister to *N. yamashitae*.

Floral anatomy and morphology of Nertera yamashitae

Flowers of *N. yamashitae* had a four-lobed and whitish corolla, a style with stigma bilobed at the top (Fig. 1) and four stamens (not shown). The ovary of *N. yamashitae* was inferior, bilocular, and had ca. 25 ovules in a locule, and the disk on the ovary was thick (Fig. 5).

Discussion

Taxonomic reconsideration of Nertera yamashitae

Following previous taxonomic studies, the genera Nertera and Ophiorrhiza commonly have a two-celled ovary, but the former has a single ovule in a locule, while the latter has many ovules in a locule (e.g. Verdcourt, 1958; Liu and Yang, 1998; Bremer and Manen, 2000). Furthermore, the former genus has an annular disk and a style with stigma bilobed at the base, or no disk (Puff, 1986), a four-lobed corolla, and four stamens; while the latter genus has a thick disk (Fukuoka, 1979), a style with stigma bilobed at the top, a five- or six-lobed corolla, and five or six stamens (Chen and Zhu, unpubl. data). Although N. yamashitae was similar to other Nertera species in the numbers of corolla lobes and stamens, it was similar to Ophiorrhiza species in the number of ovules, the morphologies of disk and stigma. Out of these anatomical and morpho-

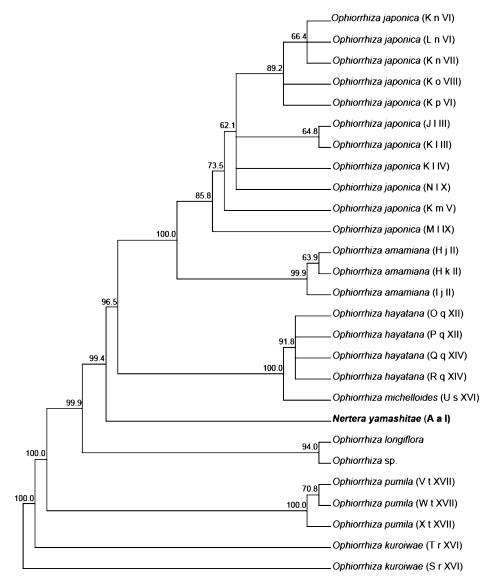


Fig. 4. Rooted maximum parsimony, strict consensus tree to detect phylogenetic position of *Nertera yamashitae* within the genus *Ophiorrhiza* based on the full dataset of ITS, *atpB−rbcL*, and *trnK/matK* loci. Numerals above branches indicate bootstrap percentages (≥50%). Letters in parentheses indicate the types of three loci in *N. yamashitae* and *Ophiorrhiza* species (Tables 1 and 2).

logical characters, the number of ovules in an ovary locule was thought to be an important character for delimitations at the tribes (Bremer and Manen, 2000) and generic level (e.g. Hooker, 1873; Bremekamp, 1966) in the family Rubiaceae. In terms of anatomy and morphology, *N. yamashitae* should not be treated as a species of the genus *Nertera*.

Previous phylogenetic studies at tribal or generic levels in the family Rubiaceae commonly verified that tribe Anthospermeae including *Nertera* spp., and tribe Ophiorrhizeae including *Ophiorrhiza* spp., branched at a basal position in a clade of subfamily Rubioideae and that they were obviously not sister groups (Bremer and Manen, 2000; Bremer, 2009; Rydin *et al.*, 2009a, 2009b).

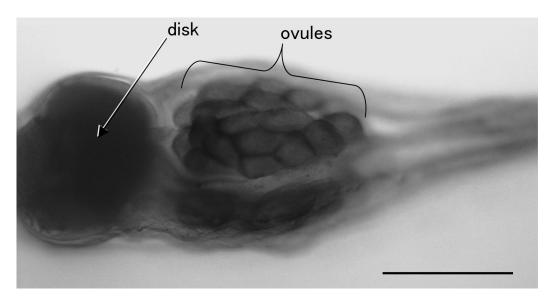


Fig. 5. Anatomical and morphological observations of the disk and ovules in Nertera yamashitae. Bar=500 µm.

The present molecular analyses reveal that *N*. *yamashitae* is apparently included in the *Ophior-rhiza* clade in tribe Ophiorrhizeae but is distantly related to the *Nertera* clade in tribe Anthospermeae.

For taxonomy based on the anatomical, morphological and molecular results, we propose to treat *N. yamashitae* as a species of the genus *Ophiorrhiza*.

Ophiorrhiza yamashitae (T. Yamaz.) Kokubugata, Koh Nakam. et Yokota, **comb. nov.** Basionym: *Nertera yamashitae* T. Yamazaki, J. Jpn. Bot. 73: 89–91, Figs. 1 and 2, 1998.

Fruit morphology is also a very valuable character to delineate the genera *Nertera* and *Ophiorrhiza*; the former has succulent (drupe) and the latter has dry (dehiscent) fruits (e.g. Liu and Yang 1998; Chen and Zhu, unpubl. data). However, no fruit of *O. yamashitae* has been observed in wild in spite of long-term efforts to find it (Yamazaki, 1998; Hotta, 2004), and thus this species is assumed to have lost ability to reproduce by means of intrapopulation crossing (Hotta, 2004). Artificial hand-pollination between plants from different populations in cultivation could be useful to investigate the fruit morphology of *O. yamashitae*.

Phylogeography of Ophiorrhiza yamashitae

In the present phylogenetic trees based on ITS, atpB-rbcL, and trnK/matK (Fig. 4) O. yamashitae, being an insular-endemic to Amami Island of the Ryukyus, was connected to a basal position of a clade consisting of four Ophiorrhiza species, namely O. amamiana being endemic to the central Ryukyus (Nakamura et al., 2007); O. japonica widely distributing in China, Japan, Taiwan, and Vietnam (Yamazaki, 1993); and O. hayatana and O. michelloides being endemic to Taiwan (Liu and Yang, 1998; Nakamura et al., 2006). Of four Ophiorrhiza species, O. amamiana and O. japonica presently occur on Amami Island (Hatusima and Amano, 1994). However, our phylogenetic analyses suggest that O. yamashitae is not derived from O. amamiana nor O. japonica. These results imply that the ancestral species of O. yamashitae has been extinct, and O. yamashitae could survived as a relict species lineage in Amami Island.

Previously, some species lineages assumed to be relicts are reported in the central part of the Ryukyu Archipelago, including Amami Group and Okinawa Group for terrestrial plants (Hatusima, 1975; Hotta, 2004), amphibians and reptiles (Hikida et al., 1989; Ota, 1998). Hikida and Ota (1997) suggested that these relict species lineages of amphibians and reptiles migrated to the central Ryukyus when the area was connected to surrounding landmasses by a landbridge via the northern and southern Ryukyus. After partial submergence of the landbridge during the Pliocene, the lineages were isolated in the central Ryukyus and have been extinct in other areas of this archipelago (Hikida and Ota, 1997). There is a possibility that O. yamashitae might have a similar phylogeographic background to the relict species lineages of the terrestrial amphibians and reptiles in the central part of the Ryukyu Archipelago.

Parallel evolution and ecological aspects of dwarf leaf species

In the *Ophiorrhiza* species in Japan and Taiwan, *O. michelloides* being endemic to Taiwan was regarded as a dwarf leaf species (Masamune, 1932; Liu and Yang, 1998; Nakamura *et al.*, 2006). Although *O. yamashitae* and *O. michelloides* commonly have dwarf leaves, they are distantly related in the present phylogenetic analyses. The results suggest that leaf dwarfism events have occurred independently in *O. yamashitae* and *O. michelloides*.

In habit environments, O. yamashitae is found along streams at low elevation on Amami Island (Yamazaki, 1998), while O. michelloides is found at altitudes above 1,000 m in the Central Mountain Range of Taiwan (Liu and Yang, 1998). However, they commonly occur on oligotrophic rocky slopes (data not shown). In evolutionally aspect of leaf dwarfism, Sugimoto (1957) suggested that oligotrophic environment is one of possible factors to lead to leaf dwarfism. We can hypothesize that leaf dwarfisms might be an adaptation to survive in oligotrophic environments on the rocky slopes as a common phenomenon between O. yamashitae and O. michelloides, but parallel events in Amami Island and Taiwan. Further studies including soil physicochemical investigations of these dwarf leaf species on Amami Island and in Taiwan are necessary to address these hypotheses.

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