

**Analyses of reticulate evolution in the apogamous species
of the *Dryopteris varia* complex (Dryopteridaceae) using
five nuclear genetic markers**

複数の核遺伝マーカーを用いたイタチシダ類（オシダ科）の
無配生殖種における網状進化の解明（英文）

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Summary

Several lineages of ferns perform apogamous reproduction, which is considered as a type of asexual reproduction. However, many apogamous species show large morphological and genetic variation. Therefore, the “hybridization cycle hypothesis” was proposed, supposing that triploid apogamous species sometimes produce diploid sperms through unequal meiosis and hybridize with haploid ovum originating from other diploid sexual species (Lin *et al.*, 1995; Yamamoto, 2012). Moreover, apogamous species may hybridize with distantly related diploid sexual species because apogamous species sometimes have even greater genetic variation than their relatives with sexual reproduction.

In Chapter 1, I revealed reticulate evolution in the apogamous *Dryopteris varia* complex using the biparentally inherited nuclear *PgiC* gene as well as the maternally inherited plastid *rbcL* gene as genetic markers. The obtained data suggested that the apogamous species hybridized with distantly related species because some species of the complex had the same nuclear *PgiC* gene as *D. caudipinna* and *D. chinensis*, which had not been included in the *D. varia* complex. These two diploid sexual species were also shown to be distantly related to the complex by phylogenetic analysis using *rbcL* (Ebihara, 2011). When the *PgiC* sequences of the diploid sexual species *D. varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna*, and *D. chinensis* are represented by A, B, C, D, and E, respectively, the genetic constitution of the apogamous species of the *D. varia* complex was suggested to be as follows: *D. bissetiana* (B + C), *D. pacifica* (α , A + C; β , A + B + C; γ , A + C + D), *D. sacrosancta* (A + C + E), and *D. kobayashii* (B + C + E).

However, the use of a single nuclear marker may not be sufficient to understand the behaviors of the genome of the parental species in apogamous species. If many crosses with sexual relatives occur, the genome constitution of several nuclear genes can differ from each other. To solve this problem, in Chapter 2, I used five single-copy nuclear markers encoding enzymes that had often been used for allozyme analyses. For each marker, five types of alleles, namely A, B, C, D, and E, were recognized in the sexual types of *Dryopteris varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna*, and *D. chinensis*, respectively. The genetic constitution of the apogamous species was consistent with those of Chapter 1, which used only one nuclear marker, the *PgiC* gene. Therefore, the results presented in Chapter 2 strongly suggest that apogamous species of the *D. varia* complex can cross only a few times or they maintain their genome constitutions even if they cross several times with diploid sexual species.

The results of Chapter 2 clearly show that the former classification of the apogamous species of the *Dryopteris varia* complex (Iwatsuki 1992) had taxonomical problems, particularly for *D. pacifica*, because three genotypes (α , β , and γ types) were recognized in this species. The α type comprises the genomes of *D. varia* (A) + *D. protobissetiana* (C), the β type comprises *D. varia* (A) + *D. saxifraga* (B) + *D. protobissetiana* (C), and the γ type comprises *D. varia* (A) + *D. protobissetiana* (C) + *D. caudipinna* (D). Therefore, in Chapter 3, the species classification of the *D. varia* complex was revised on the basis of the genome constitution of each species as elucidated in Chapter 2. Firstly, diploid sexual taxa with distinct chloroplast and nuclear genomes are treated as independent species. Then, apogamous species are recognized on the basis of differences in the combination of genomes. In other words, apogamous cytotypes with different nuclear genome constitutions are classified as independent

species. I summarized the taxonomical treatment of 11 species of the *D. varia* complex [*D. bissetiana*, *D. chichisimensis*, *D. erythrovaria* (=*D. pacifica* γ), *D. hikonensis* (=*D. pacifica* α), *D. insularis*, *D. kobayashii*, *D. protobissetiana*, *D. sacrosancta*, *D. saxifraga*, *D. subhikonensis* (=*D. pacifica* β), and *D. varia*]

It is still debatable whether fern taxonomists should use several nuclear markers because the allele constitutions of five nuclear loci were concordant in the *Dryopteris varia* complex. If apogamous ferns do not cause chromosome recombinations through unequal meiosis, there will be no problem in estimating genome constitutions and discussing the evolution of the apogamous fern complex using only one biparental nuclear marker. However, if some apogamous ferns cause chromosome recombinations through unequal meiosis, pteridologists must use several nuclear DNA markers to understand the origin and reticulate evolution of the apogamous fern complex. To resolve this issue, similar studies to this study but using several unlinked nuclear genetic markers of several phylogenetically distant apogamous complexes of ferns should be conducted.

General Introduction

The life cycle of ferns is characterized by sporogenesis and the existence of a free-living gametophyte (prothallium), which produces eggs and sperm. In most diploid ferns, motile sperm from the prothallium must swim through water to reach the eggs in the mature archegonia of a different prothallium that is growing nearby. Fertilization usually cannot occur within a gametophyte (intra-gametophytic selfing), possibly due to the existence of recessive deleterious genes (Soltis and Soltis 1990; Watano and Iwatsuki 1988). Therefore, fertilization is a highly risky process in ferns, especially under dry conditions.

However, this only applies to sexual reproduction. Apogamy or agamospory in ferns is a type of asexual reproduction. In most sexual ferns, the archesporial cell undergoes four mitotic divisions to yield 16 spore mother cells (SMCs) in each sporangium, which subsequently undergo meiosis to form 64 spores. By contrast, in most apogamous ferns, sporogenesis follows the Döpp–Manton scheme (Manton 1950), where the fourth mitosis is terminated in the early anaphase and a restitution nucleus is formed. The resultant eight SMCs possess doubled sets of chromosomes. Subsequently, the SMCs undergo meiosis (two sequential cell divisions) and produce 32 unreduced spores. Next, the gametophytes formed from the spores produce the sporophytes for the next generation without fertilization (Manton 1950). Therefore, apogamous ferns do not need water for their fertilization.

Apogamous reproduction is common in ferns. About 10% of all fern species (Lovis 1977) and approximately 13% of Japanese fern taxa are reported to exhibit apogamous reproduction (Takamiya 1996). Unlike other asexual reproductive modes,

such as vegetative reproduction via gemma or adventitious buds, apogamous reproduction involves the production of spores that can tolerate dry conditions. Therefore, apogamous reproduction is advantageous, especially for long distance dispersal and for the formation of new populations from a small number of spores, which might explain why apogamous ferns are common.

However, apogamous reproduction has a severe drawback in terms of the production of genetic variation within populations or even within species because the normal processes of meiosis (recombination) and fertilization, which contribute to the maintenance of intra-specific genetic variation in sexual reproduction, are lacking. Genetic variation is evolutionarily important. In the case of apogamous reproduction, only genetic clones of the parental individual are produced, and thus genetic variation will eventually disappear within the species. In this situation, the extinction risk is high in an apogamous species if extreme environmental changes or an infectious disease epidemic occurs.

Apogamous fern species are expected to exhibit low levels of genetic variation. Indeed, Darnaedi *et al.* (1990) reported that *Dryopteris yakusilvicola* Kurata, a triploid apogamous species of recent hybrid origin that is endemic to Yakushima Island, did not exhibit any allozyme variation in five enzymes within 56 individuals examined in this species. Comparisons of the enzyme banding patterns suggested that the genome of *D. yakusilvicola* was derived through hybridization between *D. sabaei* and either a sexual tetraploid or an agamosporous triploid of *D. sparsa*. Cytological evidence (Darnaedi *et al.* 1989) supports the idea that the sexual tetraploid cytotype of *D. sparsa* is a parent because the hybrid between diploid sexual and triploid apogamous cytotypes is expected to be tetraploid rather than triploid. This monomorphic pattern implies that *D.*

yakusilvicola originated from a single hybrid between the parental species, and that it is a neo-endemic of Yakushima Island.

However, this situation is not common. Despite the clonal nature of apogamous reproduction, many apogamous fern species exhibit high morphological variation and at least some genetic variation (Watano and Iwatsuki 1988; Suzuki and Iwatsuki 1990; Lin *et al.* 1995; Takamiya *et al.* 2001). Previous analyses of genetic variation in apogamous fern species using enzyme electrophoresis found 45, four, and 14 different clones from *D. nippensis* Koidz. (Ishikawa *et al.* 2003a), *Hymenophyllum hondoense* N. Murak. et Hatanaka (Watano and Iwatsuki 1988), and *D. bissetiana* (Baker) C. Chr. (Lin *et al.* 1995), respectively. Furthermore, genetic and cytological variations have been reported in apogamous ferns. Six different triploid and five diploid clones have been reported in *Pteris cretica* L. (Suzuki and Iwatsuki 1990), and one tetraploid and four triploid clones have been reported in *Diplazium doederleinii* (Luerss.) Makino (Takamiya *et al.* 2001). Thus, despite the clonal nature of apogamous reproduction, many apogamous fern species exhibit high genetic variation.

Several hypotheses have been proposed to explain the increased genetic variation within apogamous fern species: (1) the recurrent origin of apogamous races from sexual species (Gastony and Gottlieb 1985); (2) genetic segregation by homoeologous chromosome pairing (Klekowsky 1973; Ishikawa *et al.* 2003 a, b); and (3) hybridization with closely related sexual species (Walker 1962; Suzuki and Iwatsuki 1990). The specific details of these hypotheses are as follow.

(1) Gastony and Gottlieb (1985) proposed a hypothesis that assumes the recurrent origin of apogamous species from related sexual species, thereby leading to genetic variation within an apogamous species. Apogamous species would acquire

genetic variation from their sexual relatives if the former originated repeatedly from the latter. However, the process of sporogenesis that produces unreduced spores in apogamous ferns is extremely complicated and precise, as noted earlier. It might be unlikely that mutations generated such a complicated sporogenesis process independently several times in several apogamous species belonging to different fern families. Therefore, this hypothesis cannot explain the major factors that produced genetic variation in apogamous fern species.

(2) Klekowski (1973) first proposed that the pairing of homoeologous chromosomes could be a mechanism that generates genetic variation in apogamous ferns, although no positive evidence was provided in his study. For example, we can say that assuming that the genotype of the parental triploid apogamous sporophyte is *abc*, the genotype of its SMCs should be *aabbcc*. In the usual process of apogamous reproduction, the genotype of all offspring from such an apoprophyte would also be *abc* because only sister chromatid pairing (a-a, b-b, c-c) occurs in the SMCs. By contrast, if homoeologous chromosome pairing (*a-b*, *a-b*, *c-c*) occurs, then gametophytic progeny with *aac* and *bbc* genotypes will be produced in addition to those with the *abc* genotype. In the same manner, if homoeologous chromosome pairing (*a-c*, *a-c*, *b-b*) occurs, then progeny with *aab* and *bcc* genotypes will also be produced. Thus, genetic segregation via homoeologous chromosome pairing can generate genetic variation among clones within an apogamous fern species.

Ishikawa *et al.* (2003a) first reported positive evidence to support genetic segregation via homoeologous chromosome pairing in apogamous ferns using *Dryopteris nippensis* Koidz. as their test material. They compared the genotypes of the parent sporophyte and its progeny using the allozyme method. Among 250 progeny

gametophytes that developed from the spores of a parental sporophyte of *D. nippensis* with the *PgiC* genotype *abc*, four had genotypes that differed from that of the parent (three *aac* and one *bbc* gametophytes). Similarly, among 34 sporophyte offspring of the parent sporophyte with the *abc* genotype, one had the *bcc* genotype, whereas the other 33 had *abc*. Thus, Ishikawa *et al.* (2003a) clearly demonstrated the existence of occasional genetic segregation, possibly via homoeologous chromosome pairing in apogamous ferns.

Subsequently, Otsuki *et al.* (2012) obtained more robust data to support genetic segregation in apogamous ferns via homoeologous chromosome pairing using *Cyrtomium fortunei* J. Sm. as plant materials and nucleotide sequence information from *pgiC* as genetic markers. They examined a total of 732 progeny (250 gametophytes and 482 sporophytes) obtained from a parental sporophyte, where the *pgiC* genotype was estimated as *aab*. Their results indicated that 11 (4.4%) gametophytes and eight (1.7%) sporophytes had a genotype (*aaa*) that differed from that of the parent sporophyte. They analyzed a large number of progeny and detected sufficient numbers of segregated offspring, so they were able to demonstrate that genetic segregation occurs in apogamous *C. fortunei* at a relatively high frequency. Moreover, they showed that the segregation frequency in gametophytes is significantly higher than that in sporophytes in the next generation ($\chi^2 = 4.90$, $P = 0.027$). They hypothesized that these results might suggest that apogamous fern species harbor deleterious genes and that these genes might be expressed in greater numbers in sporophytes, with a more complex morphology than that in gametophytes.

It is now evident that genetic segregation via homoeologous chromosome pairing is an important mechanism for generating genetic variation in apogamous ferns,

but this process is not sufficient to maintain the levels of genetic diversity that have been observed in most apogamous species. If genetic segregation occurs at a high frequency in apogamous ferns, heterozygosity will be lost rapidly within individuals and eventually within species. However, a high heterozygosity was observed in them (Watano and Iwatsuki 1988; Darnaedi *et al.* 1989; Suzuki and Iwatsuki 1990; Lin *et al.* 1995; Takamiya *et al.* 2001; Yamamoto 2013); therefore, apogamous species may possess mechanisms that increase heterozygosity.

(3) Hybridization with related sexual species can explain the observed levels of heterozygosity in a species and/or even within individuals of an apogamous fern species. The ability of apogamous ferns to cross with closely related sexual species was first demonstrated by Walker (1962) in artificial crossing experiments between apogamous and sexual races of *Pteris* species. He reported that the reduced egg of the sexual diploids is fertilized by the unreduced sperm of the apogamous triploid to produce tetraploid hybrids, which can reproduce apogamously. Suzuki and Iwatsuki (1992) supported this hypothesis by showing that the wild populations of apogamous *P. cretica* L. in Japan were derived via hybridization between the apogamous parents of the species and the closely related sexual species *P. kidoi* Kurata.

However, crossing between sexual and apogamous species is still not sufficient to explain the existence of genetic variation in apogamous fern species. If an apogamous species crosses with a sexual species in the manner suggested by Walker (1962), the resultant apogamous species would become higher polyploid (tetraploid, pentaploid, hexaploid, *etc.*) because the genome of the sexual species is added to that of the apogamous species in every cross. However, most apogamous fern species are actually triploid and tetraploids or higher polyploids are extremely rare in apogamous ferns.

Thus, apogamous species should also possess mechanisms that decrease the ploidy levels (Takamiya 1996).

The unequal meiosis reported by Lin *et al.* (1992) can cause ploidy reduction in apogamous ferns. In order to elucidate the origin of its intra-specific cytological variation, they performed cytological and genetic studies using *Dryopteris pacifica* (Nakai) Tagawa, in which both diploid and triploid apogamous cytotypes have been recorded. In each sporangium, they found that triploid apogamous *D. pacifica* produced 16 SMCs, some with $n = 41\text{II} + 41\text{I}$ chromosomes, in addition to eight SMCs with $n = 123\text{II}$. In the former case, the 16 SMCs usually underwent abnormal meiosis to yield about 50 spores, some of which were regular in shape where the eight SMCs multiplied into 32 spores by normal meiosis. Furthermore, they reported that two (1.3%) of the 150 gametophytes that they examined cytologically were diploid and one (0.9%) of the 110 sporophyte offspring was diploid. They also cytologically observed unequal meiosis in the triploid apogamous sporophyte to produce diploid spores. Thus, they showed that diploid spores and diploid gametophytes could arise from the spores, while diploid apogamous sporophyte offspring are also formed occasionally from parental triploid apogamous sporophytes. However, they could not clarify whether this process truly contributes to the genetic variation observed in wild populations of apogamous ferns.

Lin *et al.* (1992, 1995) proposed the “hybridization cycle hypothesis,” which assumes that a recurrent cycle with ploidy reduction (oligoploidization) from triploid to diploid apogamous plants, and polyploidization from diploid to triploid by crossing with related sexual diploid species (from triploid apogamous to diploid apogamous, and from diploid apogamous back to triploid apogamous) might explain the existence of genetic variation within a triploid apogamous fern species (Figure GI-1). According to their

hypothesis, triploid apogamous fern species can incorporate genetic variation from related diploid sexual species without polyploidization. Some individuals (gametophytes and/or sporophytes) of the apogamous species decrease their ploidy by unequal meiosis in the first step. In the second step, the apogamous individuals with decreased ploidy hybridize with sexual species that can normally perform meiosis and produce haploid eggs.

The hybridization cycle hypothesis has not yet been verified because each step in the hypothesis has been documented separately in different groups of apogamous ferns under experimental conditions. This hypothesis can be justified only when all the steps occur together in nature. Yamamoto (2013) selected a triploid apogamous species, *Dryopteris erythrosora* (Eaton) O. Kuntze., and its closely related diploid sexual species, *D. caudipinna* Nakai, as the plant materials to determine whether all the steps assumed by the hybridization cycle hypothesis occur in anapogamous species. Yamamoto (2013) performed artificial crossing 596 times between apogamous *D. erythrosora* and sexual *D. caudipinna*, and obtained 31 hybrids that shared nuclear genetic markers of the two parental species. Among the 31 hybrids, 22 (71%) were tetraploids and the remaining nine (29%) were triploids. Thus, triploid hybrids between the triploid apogamous and diploid sexual species were clearly produced under the experimental condition.

However, Yamamoto (2013) did not discuss how many times hybridization occurred between sexual and apogamous species in nature. If apogamous fern species cross repeatedly with related sexual species, then their chromosomes would be replaced mostly by those of the sexual species. To test this possibility, the genome constitutions of apogamous species must be clarified by using several nuclear genetic markers.

This study used the *Dryopteris varia* complex (subg. *Erythrovariae*, sect. *Variae*

Fraser-Jenk., Dryopteridaceae) as plant materials. This fern group is characterized by the lowest basiscopic pinnules on the lowest pinna being markedly elongated with densely scaled petioles. Six species and one variety (*D. bissetiana* (Baker) C. Chr., *D. insularis* var. *insularis* Kodama, *D. insularis* var. *chichisimensis* (Nakai ex H. Ito) H. Ito, *D. pacifica* (Nakai) Tagawa, *D. sacrosancta* Koidz., and *D. saxifraga* H. Ito, *D. varia* (L.) Kuntze) were listed by Iwatsuki (1995). Recently, the classification of the *D. varia* complex has been subjected to revision. Serizawa (2009) recently separated *D. kobayashii* Kitag. from *D. sacrosancta* *sensu lato* on the basis of observations that the former has thinner fronds and curved sickle-shaped pinna. In addition, Hori *et al.* (2015) discovered *D. protobissetiana* Hori et N. Murakami, which is a new species of the *D. varia* complex from Yakushima Island, Japan. This species is similar to *D. bissetiana* due to its slightly bullate scales and a dark green lamina surface, but it differs in terms of its flat, serrate margins at the apex of the upper pinnae. At present, eight species and one variety are recognized as Japanese members of the *D. varia* complex.

Most species of the *Dryopteris varia* complex are triploid apogamous, such as *D. bissetiana* (Hirabayashi 1967; Nakato *et al.* 1995; Lin *et al.* 2003; Lee *et al.* 2006), *D. insularis* var. *chichisimensis* (Lin *et al.* 2003), *D. pacifica* (Hirabayashi 1970; Lin *et al.* 1992; Nakato *et al.* 1995; Lin *et al.* 2003; Lee *et al.* 2006), *D. sacrosancta* (Mitui 1965; 1968; Hirabayashi 1969; Nakato *et al.* 1995; Lin *et al.* 2003; Lee *et al.* 2006), and *D. varia* (Mitui 1966; 1968; Hirabayashi 1970; Nakato *et al.* 1995; Lin *et al.* 2003; Lee *et al.* 2006; Ebihara *et al.* 2014). Only two species are known to be diploid sexual, *i.e.*, *D. saxifraga* (Hirabayashi 1967; Mitui 1975; Lee *et al.* 2006) and *D. protobissetiana* (Hori *et al.* 2014). Ebihara *et al.* (2014) recently reported that *D. varia* also has a diploid sexual cytotype. In addition, a few species have been reported as having diploid

apogamous cytotypes in addition to triploid apogamous cytotypes, such as *D. bissetiana* (Hirabayashi 1966; Lee *et al.* 2006), *D. pacifica* (Lin *et al.* 1992; Nakato *et al.* 1995), and *D. varia* (Hirabayashi 1966, 1967, 1974). Therefore, the *D. varia* complex is useful to clarify reticulate evolution between sexual species and apogamous species via the hybridization cycle.

Large morphological variations are observed in each species of the *Dryopteris varia* complex, which cause taxonomic problems, especially for *D. pacifica*. This apogamous species exhibits large variations in the texture of the lamina (coriaceous or papyraceous), margin of the pinnae (deeply or shallowly serrated), and indusia (red or translucent) (Figure GI-2). The taxonomic problems also affect *D. sacrosancta*. Serizawa (2009) recently separated *D. kobayashii* from *D. sacrosancta sensu lato*, as mentioned above. Thus, each species of the *D. varia* complex exhibits large and continuous morphological variation, which makes it difficult to classify the members of this complex based only on their morphological characteristics. In order to clarify the classification of this complex, it is important to elucidate the genetic background and variations in each species of the complex, especially those in the apogamous species.

In this study, I carefully investigated numerous individuals of the *Dryopteris varia* complex from many localities throughout Japan and Taiwan in order to clarify the genetic constitution of each species. To clarify reticulate evolution between diploid sexual and triploid apogamous species, I analyzed the *D. varia* complex using one nuclear marker, *PgiC*, as described in Chapter 1. Subsequently, I could postulate a schematic summary of evolution in the apogamous *D. varia* complex. In Chapter 2, I present an analysis of whether the *D. varia* complex underwent recurrent reticulation or not on the basis of the genome constitutions of the members of the complex determined

using five nuclear markers. Finally, I revised the species classification for the *D. varia* complex on the basis of the genome constitution, as described in Chapter 3.

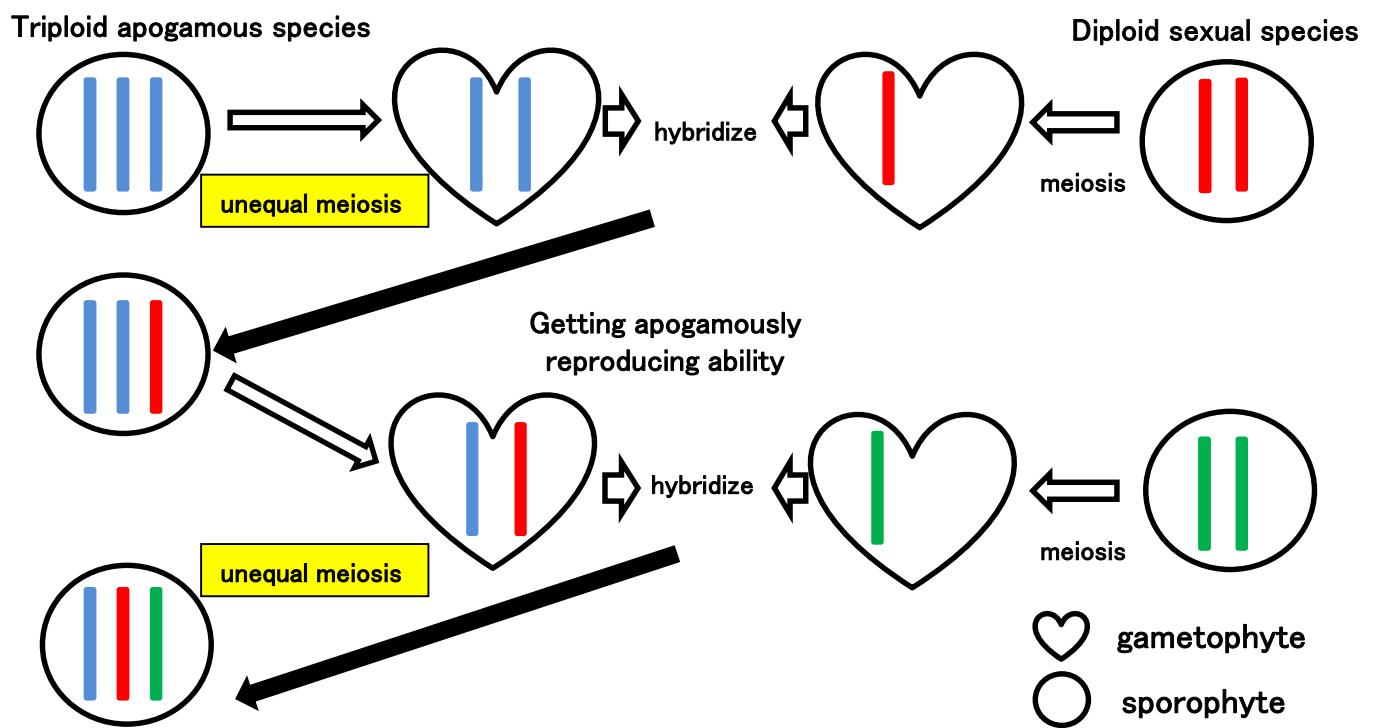


Figure GI-1. Hybridization cycle hypothesis (Lin et al. 1992, 1995).

Hybridization occurs between triploid apogamous species and diploid sexual species without polyploidization. The ‘hybridization cycle hypothesis’ assumes a recurrent cycle with ploidy reduction (oligoploidization) from triploid to diploid apogamous plants and polypliodization from diploid to triploid by crossing with related sexual diploid species. Circles indicate sporophytes and hearts indicate gametophytes. Detailed explanation is in the text (p. 10).



Coriaceous lamina

Papyraceous lamina



Pinnae deeply serrated,
Indusia translucent

Pinnae shallowly serrated,
Indusia translucent

Indusia red

Figure GI-2. Morphological variations of apogamous *Dryopteris pacifica*.

Chapter 1. Reticulate evolution in the apogamous *Dryopteris varia* complex inferred from their nuclear *PgiC* allele constitutions

1.1 Introduction

Apogamy in ferns is a type of asexual reproduction where unreduced spores are formed and the resultant gametophytes produce the sporophytes for the next generation without fertilization (Manton 1950). In apogamous ferns, all of the offspring from a sporophyte are genetically the same unless mutations occur during reproduction. Therefore, the amount of genetic variation within an apogamous species is expected to be very low unless the apogamous species has an old or recurring origin.

However, if the apogamous species has undergone reticulate evolution via hybridization between apogamous species and sexual species, then the apogamous species can acquire genetic variation from the sexual species. Yamamoto (2013) showed that apogamous *Dryopteris erythrosora* has a relatively high ability to hybridize with its closely related sexual species, *D. caudipinna*. In addition, Yamamoto (2013) showed that the two species share genetic variation, where the amount of genetic variation in apogamous *D. erythrosora* was higher when they grew together in Izu-Oshima Island. Thus, it was suggested that reticulate evolution via hybridization with sexual species can occur in apogamous fern species in nature.

The *Dryopteris varia* complex (subg. *Erythrovariae*, sect. *Variae* Fraser-Jenk.) contains many apogamous species and a few sexual species. The apogamous species in this complex exhibit large and continuous variation, and it is difficult to distinguish the members of the *D. varia* complex. In Japan, sexual cytotypes of the *D. varia* complex

are known only in *D. saxifraga* and all the other species reportedly have apogamous cytotypes (Figure 1-1). Recently, Ebihara *et al.* (2014) discovered the diploid sexual *D. varia* in Taiwan, and more recently, Hori *et al.* (2015) discovered a new diploid sexual species, *D. protobissetiana* on Yakushima Island. Therefore, this complex may be a useful material for elucidating reticulate evolution in apogamous ferns because several sexual relatives are known.

However, how these three diploid sexual species (or cytotypes) participate in forming apogamous species in the complex has not been well resolved. Genetic analyses using both biparentally inherited nuclear and maternally inherited plastid markers are necessary to elucidate the occurrence of reticulate evolution in this complex. Lee *et al.* (2013) recently attempted to elucidate reticulate evolution in species from the *Dryopteris varia* complex in Korea: *D. varia*, *D. pacifica*, *D. sacrosancta* *sensu lato*, *D. bissetiana*, and *D. saxifraga*, where they analyzed the nucleotide sequences of the nuclear *PgiC* gene as well as those of plastid *rbcL*, *trnL*–*trnF* intergenic spacer (IGS), and *atpF*–*atpH* IGS regions. They recognized 14 *PgiC* genotypes and five cpDNA haplotypes, and they concluded that gene flow has occurred between the apogamous *D. bissetiana* and sexual *D. saxifraga* in Korea because these two species shared the same genetic variation in the nuclear *PgiC*. In addition, their results strongly suggested that the apogamous triploid *D. varia* is probably of autopolyploid origin because nuclear *PgiC* haplotypes from the species formed a monophyletic group in the molecular phylogenetic tree of the complex. Their results also suggested cytoplasmic gene flow from *D. sacrosancta* to *D. chinensis* (Baker) Koidz. *Dryopteris chinensis* belongs to another subgenus of *Dryopteris* (subg. *Dryopteris*, sect. *Aemulae*), and its morphological characteristics are clearly different

from those of the *D. varia* complex. They reached this anomalous conclusion because the same plastid DNA sequences were shared by the two species, but the nuclear sequences were not shared. However, they did not clarify how the plastid DNA flowed between these two distantly related species.

The results obtained by Lee *et al.* (2013) suggest that wider taxon sampling is necessary to understand reticulate evolution in the *Dryopteris varia* complex. According to the molecular phylogenetic tree obtained for most Japanese fern species based on the *rbcL* sequences (Ebihara 2011), members of the *D. varia* complex are as closely related to diploid sexual species, *i.e.*, *D. caudipinna* (sect. *Erythrorovariae*), *D. gymnophylla* (sect. *Aemulae*), *D. koidzumiana* (sect. *Erythrorovariae*), *D. hasseltii* (sect. *Nephrocystis*), *D. polita* (sect. *Politae*), and *D. sordidipes* (sect. *Variae*), as they are to *D. chinensis* (sect. *Aemulae*). With the exception of *D. gymnophylla*, Lee *et al.* (2013) did not include these species in their study. Therefore, even wider taxon sampling than that performed by Lee *et al.* (2013), *i.e.*, not restricted to the *D. varia* complex, is needed to clarify the origin and reticulate evolution in the *D. varia* complex.

The method employed by Lee *et al.* (2013) also has some problems because they used a cloning method to separate multiple nuclear DNA sequences present within a fern sample. However, the cloning involves the risk of missing some alleles or selecting false alleles due to PCR errors. Thus, I consider that PCR-single strand conformation polymorphism (SSCP) analysis is more effective for separating nuclear DNA with different sequences in each sample. This method can separate DNA fragments with different nucleotide sequences on polyacrylamide gel according to differences in their three-dimensional folding conformation, where each fragment appears as a separate band on the gel (Ebihara *et al.* 2005; Adjie *et al.* 2007; Jaruwattanaphan *et al.* 2013).

After extracting each DNA band from the gel, the DNA obtained can then be re-amplified and subjected to direct sequencing. Even if false alleles due to PCR errors are present in the same bands, their number should be sufficiently low to not influence the results obtained by direct sequencing, thereby avoiding the problems in the cloning method.

In Chapter 1, the following two questions were addressed by using *PgiC* as the nuclear genetic marker and the plastid *rbcL* as a maternally inherited marker for indicating the maternal parent of the hybrids. (1) How did reticulate evolution occur in the *Dryopteris varia* complex? (2) Did other *Dryopteris* species that were not previously considered as members of the *D. varia* complex, such as *D. chinensis*, participate in reticulate evolution in the *D. varia* complex?

1.2. Materials and methods

Plant materials

Leaf samples were collected from 274 individuals belonging to the *Dryopteris varia* complex and its closely related species, mainly in my original field surveys throughout 19 prefectures in Japan. The reproductive mode of most individuals among the samples was estimated by counting the number of spores per sporangium (32, apogamous; 64, sexual). Four leaf samples were collected in Taiwan. Moreover, 44 living stocks of the *D. varia* complex were collected in 20 localities in Japan. In addition, a single leaf sample of the triploid apogamous *D. pacifica* ($2n = 123$), called “K111,” which has been reported to produce diploid apogamous progeny (Lin *et al.* 1992), was collected from cultivated stocks in the Koishikawa Botanical Garden of the University of Tokyo. Material from *D. shibipedis* was not available, so this species was excluded from my study. Species identification was performed on the basis of gross morphology using the keys provided in previous studies (Iwatsuki *et al.* 1995; Serizawa 2009). *Dryopteris expansa* and *D. sieboldii*, which are classified in different subgenera of the genus *Dryopteris* (Fraser-Jenkins 1986), were used as outgroups. All of the voucher specimens have been deposited in Makino Herbarium of Tokyo Metropolitan University (MAK) and/or National Museum of Nature and Science Herbarium (TNS).

Ploidy analyses

To examine the ploidy level in the plant materials, the DNA content (2C-value) of each nucleus extracted from 31 fresh pinnae samples was measured by flow cytometry using CyFlow Ploidy Analyzer PA-II (Partec, Munster, Germany) and a CyStain UV

Precise P Kit (Partec). A segment of pinnae (approximately 100 mm²) was torn into several pieces, chopped finely with a razor blade, and placed in 0.25 mL of nuclei extraction buffer from the kit. Next, 0.8 mL of staining solution from the kit was added to the chopped tissues. The crushed tissue and buffers were filtered through a 30-μm nylon mesh (Partec). The filtered samples were measured using the Ploidy Analyzer as soon as possible. Approximately 1,000–2,000 nuclei were measured for each sample. For most of the samples, the measurement was performed only once because high reproducibility was confirmed with five samples. Fresh leaf tissues from *Nicotiana tabacum* L., which has a genome size of 11.71 pg per nucleus (Narayan 1987), (approximately 25 mm²) were used as the internal standard.

Molecular analyses

For the molecular analyses, a small amount of leaf sample was dried in a small plastic bag using silica gel. Subsequently, the total DNA was extracted by using CTAB solution, according to the method described by Doyle and Doyle (1987).

In this study, *rbcL* was used as the cpDNA marker. PCR amplification of a *rbcL* fragment was performed by using the primers aF and cR, as described by Hasebe *et al.* (1994), with an annealing temperature at 50 °C. The nucleotide sequences of *rbcL* were determined by direct sequencing. Two primers, aR (Hasebe *et al.* 1994) and D. paci-bf (5'-TATCCTTGATCTATCGAAGAAGGTTC-3'), which were developed in this study, were only used to sequence the *rbcL* fragment. PCR amplification was performed by using PrimeSTAR Max DNA Polymerase (Takara, Kyoto, Japan) with a Model 9700 thermal cycler (Applied Biosystems, Foster City, CA, USA).

A *PgiC* fragment including exons 14–16 and introns 14–15 was used as the nuclear marker. The *PgiC* fragment was amplified by using the primers 14F and 16R, as described by Ishikawa *et al.* (2002), with an annealing temperature at 58 °C.

PCR-SSCP analysis

The PCR-SSCP analysis was used to determine allelic variation at the nuclear *PgiC* locus for each individual according to the method described by Jaruwattanaphan *et al.* (2013). A portion of the PCR sample (3.5 µL) was mixed with 6.5 µL of formamide dye solution (90% formamide, 0.005% bromophenol blue, and 8% glycerol) and then denatured for 3 min at 95 °C. The denatured samples were cooled on ice and 5 µL of the sample was loaded onto a 0.5× MDE gel (180 mm × 180 mm × 1 mm; Takara Bio., Shiga, Japan). The electrophoresis was performed by using gels containing 2% glycerol at 18 °C for 16 h and 350 V in 50% TBE Buffer (50 mM Tris, 41.5 mM boric acid, and 0.5 mM EDTA-Na₂), followed by silver staining. For silver staining, the gels were shaken in 250 mL of 10% acetic acid for 20 min. The gels were then shaken three times in 250 mL of distilled water for 2 min, before shaking in 250 mL of 0.1% AgNO₃ water solution (containing 250 µL of 37% formaldehyde). Next, the gels were shaken in 250 mL of distilled water for 30 s, followed by 250 mL of developing solution (250 mL distilled water, 6.25 g Na₂CO₃, 250 µL of 37% formaldehyde, and 250 µL of 2% Na₂S₂O₃) for 2–10 min until the bands are visualized, before shaking in 250 mL of stop developing solution (250 mL of distilled water, 3.65 g EDTA 2Na) for 5 min. Finally, the gels were shaken in 250 mL of medium (75 mL ethanol, 11.5 mL of 50% glycerol, and 163.5 mL of distilled water) for 30 min and then stored at 4 °C overnight.

To sequence the bands separated on the SSCP gels, the polyacrylamide gel was

dried after silver staining by sandwiching the gel between Kent paper and a cellophane sheet on an acrylic back plate at 55 °C for 3 h. To extract the DNA, a piece of the DNA band was peeled from the dried gel by using a cutter knife and triturated in 100 µL of distilled water. After removing the distilled water, the small piece of gel was incubated in 50 µL of TE buffer (10 mM Tris-HCl and 1 mM EDTA, pH 8.0) at 65 °C for 1 h. The supernatant solution was used as a template for further PCR amplification with the same primer set employed for the original PCR amplification.

The PCR products were purified by using ExoSAP-IT (USB, Ohio, USA) or Illustra ExoStar 1-Step (GE Healthcare, Wisconsin, USA) and used as templates for direct sequencing. Reaction mixtures for sequencing were prepared by using the BigDye Terminator v.3.1 Cycle Sequencing Kit (Applied Biosystems). The reaction mixtures were analyzed by using an ABI 3130 Genetic Analyzer (Applied Biosystems).

All of the plant samples were classified based on their PCR-SSCP banding patterns and the genomic constitution of each band pattern was identified by determining the nucleotide sequence of each DNA band separated on the SSCP gel.

Phylogenetic analyses

In the phylogenetic analyses, only one sequence representing each haplotype for cpDNA (*rbcL*) and each allele for the nuclear DNA (*PgiC*) were used in our data sets. The cpDNA and nuclear DNA data sets were analyzed separately by maximum parsimony (MP) analysis with MEGA version 5 (Tamura *et al.* 2011) and Bayesian Markov chain Monte Carlo (B/MCMC) analysis with MrBayes 3.2 (Ronquist *et al.* 2012). The MP tree was obtained using the subtree-pruning-regrafting algorithm (Swafford *et al.* 1996) at search level 1, where the initial trees were obtained by the

random addition of sequences (10 replicates). The bootstrap method with 10,000 replicates was employed to estimate the confidence levels of monophyletic groups. In the B/MCMC analysis, the best fitting sequence evolution model for each DNA region was selected by jModelTest 2 (Posada 2008). The *PgiC* tree was constructed with the HKY+I model and the *rbcL* tree with the SYM+I model. Indels were treated as missing characters for the *PgiC* data sets, as recommended by the MEGA and MrBayes documentations. No indels were found in the *rbcL* fragment. Four rounds of MCMC were run simultaneously and sampled every 100 generations for a total of 1 million generations. Tracer v1.5 (Rambaut and Drummond 2007) was used to examine the posterior distribution of all the parameters and their associated statistics, including the estimated sample sizes. The first 2,500 of the sample trees from each run were discarded as a burn-in period.

1.3. Results

Ploidy analyses

The DNA content of the K111 individual (triploid apogamous *Dryopteris pacifica*) was 1.87 times that of the internal standard (*Nicotiana tabacum*) according to our ploidy analyses. Given that the 2C-value of *N. tabacum* is approximately 11.71 pg per nucleus (Narayan, 1987), the DNA content of this triploid material was estimated as approximately 21.89 pg. The DNA contents of the other 22 samples (including *D. bissetiana*, *D. kobayashii*, *D. pacifica*, *D. sacrosancta*, and *D. varia*) were similar to that of K111 (20.95–27.16 pg). The DNA contents of the other eight samples (including *D. pacifica* and *D. protobissetiana*) were 14.63–17.08 pg. The DNA contents of these eight samples were approximately two-thirds of those of the 22 samples and K111. Therefore, the ploidy levels of these eight samples were estimated to be diploid and those of the other 23 samples were estimated to be triploid.

Plastid rbcL sequence variation and phylogenetic analysis results

Seven types of *rbcL* sequences (Types A–E) were found in the *Dryopteris varia* complex and its closely related species (Figure 1-2). Among the 1,205 sites, 84 (7%) were polymorphic and 35 (3%) were parsimony informative. MP and B/MCMC analyses showed that the phylogenetic trees basically had the same topology. The 50% majority-rule consensus tree obtained from the Bayesian trees with bootstrap percentages (BP) based on the MP analysis and Bayesian posterior probabilities (PP) is shown in Figure 1-2.

Nuclear PgiC sequence variation and phylogenetic trees based on them

Several different sequences of nuclear *PgiC* were detected by the SSCP analyses in most of the samples. However, the number of different sequences was never more than the assumed ploidy level of the sample. According to nucleotide sequences from DNA sequencer, no double peaks were observed for each band separated by the SSCP analyses. Thus, all the distinct sequences in the *PgiC* fragment among the samples were separated on our SSCP gel. In total, 31 different sequences were identified in the samples from the *Dryopteris varia* complex and the length of the sequences varied between 629–684 bp. The data matrix for phylogenetic analyses included 691 characters after editing, where 133 (19%) were polymorphic and 63 (9%) were parsimony informative. The 50% majority-rule consensus tree obtained from the Bayesian trees with BP based on MP analysis and Bayesian PP is shown in Figure 1-3. Five monophyletic groups (groups A, B, C, D, and E in Figure 1-3) were recognized, each of which was supported by the high BP and PP values according to Bayesian inference (Figure 1-3).

The genotype estimated for each sample is summarized in Appendix 2-1 together with according to the data obtained in Chapter 2. It should be noted that the current method cannot distinguish differences in gene dosage in polyploids; therefore, unidentified genomes are denoted by asterisks (*e.g.*, A₁C₁* indicates a genotype of either A₁A₁C₁, A₁C₁, or A₁C₁C₁, whereas A₁A₁* indicates a genotype of either A₁A₁A₁ or A₁A₁).

1.4. Discussion

Reticulogram of the Dryopteris varia complex based on the plastid rbcL and nuclear PgiC genes

The *PgiC* tree (Figure 1-3) shows that the *PgiC* sequences found in the *Dryopteris varia* complex can be grouped into five clades (A–E). Except for *D. varia*, all of the apogamous individuals in the *D. varia* complex had several different *PgiC* sequences from different clades, thereby supporting their hybrid origin. Each clade contained sequence(s) from at least one sexual diploid species (or cytotype), and thus hypothetically, the genome of its sexual progenitor had been transferred to apogamous taxa. Moreover, the information based on plastid *rbcL* (Figure 1-2) could be used to trace the maternal line of each taxon with a hybrid origin. According to the constitution of the nuclear *PgiC* and the maternally inherited plastid *rbcL* identified for each plant sample, I considered the evolutionary diversification processes in the *D. varia* complex by hybridization between the progenitor diploid sexual species and the apogamous species derived from them. Thus, the hypothetical complex reticulate relationships among the species in the *D. varia* complex are summarized in Figure 1-4 as a reticulogram. The reticulogram excludes some of the results obtained in this study, which were not directly related to the formation of the species in the *D. varia* complex.

Sexual diploid progenitors involved in reticulate evolution in the Dryopteris varia complex

To understand complex reticulate evolution, it is important to identify the diploid sexual species (or diploid sexual cytotypes when intra-specific cytotypic variation is observed) involved in the *Dryopteris varia* complex. This is because diploid sexual species or cytotypes should be progenitors of apogamous species and they can also be the sources of genetic variation in apogamous species via hybridization. In this study, I first attempted to identify the progenitor diploid sexual species of apogamous taxa in the *D. varia* complex.

Four diploid sexual species (*Dryopteris caudipinna*, *D. koidzumiana*, *D. protobissetiana*, and *D. saxifraga*) as well as the diploid sexual cytotypes of *D. chinensis* and *D. varia* were identified as the progenitor species that probably provided genomes for the *D. varia* complex. These sexual species and the sexual cytotypes of the two species only had one type of *rbcL* and nuclear *PgiC*, excluding *D. varia*. Among these six species or cytotypes, *D. caudipinna*, *D. chinensis*, and *D. koidzumiana* are not included in the *D. varia* complex. According to the classification system proposed for the genus *Dryopteris* by Fraser-Jenkins (1986), *D. caudipinna* and *D. koidzumiana* belong to sect. *Erythrovariae* of subg. *Erythrovariae*, and *D. chinensis* belongs to sect. *Aemulae* of subg. *Dryopteris*, whereas the members of the *D. varia* complex were classified in sect. *Variae* of subg. *Erythrovariae*. Furthermore, the *rbcL* sequences of these species were found to be phylogenetically distant from those of the species in the *D. varia* complex (Ebihara 2011). This demonstrates that the genomes of relatively distant species were also involved in reticulate evolution in the apogamic *D. varia* complex.

Dryopteris caudipinna and *D. koidzumiana* had similar nucleotide sequences for *rbcL* (Type D) and *PgiC* (the sequences in Clade D). Thus, these two species may

well be the same biological species. In this study, the name *D. caudipinna* is used to indicate the genome of *D. caudipinna* or *D. koidzumiana* because the former species is much more widely distributed and more common than the latter. Therefore, it is assumed that five diploid sexual species or cytotypes have participated in the evolution of the *D. varia* complex.

A diploid sexual cytotype of *Dryopteris varia* was found recently in Taiwan (Ebihara *et al.* 2014), in addition to the diploid and triploid apogamous cytotypes (Figure 1-1). A tetraploid sexual cytotype was also reported for this species by Tsai and Shieh (1975, 1985), but this report was not sufficiently reliable. Lee *et al.* (2013) suggested that the triploid apogamous *D. varia* is of autoploid origin because the sequences of *D. varia* formed a monophyletic group in both the cpDNA and *PgiC* trees. The data obtained in the present study based on wider sampling surveys in Japan and Taiwan also supported their conclusion because *D. varia* only had one type of nuclear *PgiC* sequence (Clade A). The three *rbcL* sequences (Types A) in *D. varia* were not monophyletic, but these sequences were not shared by other diploid sexual species or cytotypes. Therefore, the results of the present study also demonstrate that the apogamous triploids of *D. varia* are autoploid.

Dryopteris protobissetiana is a new diploid sexual species that I recently described from Yakushima Island, Kagoshima Prefecture, Japan (Hori *et al.* 2015). This species had nuclear *PgiC* sequences belonging to Clade C (Figure 1-3). The plastid *rbcL* sequence of *D. protobissetiana* was Type C, and it was shared by *D. bissetiana* and *D. pacifica*. The other three diploid sexual species, *i.e.*, *D. saxifraga*, *D. caudipinna*, and *D. chinensis*, had nuclear *PgiC* sequences in clades B, D, and E, respectively. Therefore, these five clades were resolved in the *PgiC* tree (Figure 1-3)

containing the sequence(s) of their respective sexual species or cytotypes.

All of the genotypes observed in the apogamous species of the *Dryopteris varia* complex, which contained several different nuclear *PgiC* sequences, can be interpreted as combinations of the genomes of the five diploid sexual species or cytotypes represented by clades A–E in the *PgiC* tree (Figure 1-3). Their genomes are denoted by the names of the clades determined in the present study. The genome constitution (*PgiC* constitution) of *D. bissetiana* was B + C (i.e., *D. saxifraga* + *D. protobissetiana*). The genome constitutions of *D. sacrosancta sensu stricto* and *D. kobayashii*, which were separated from *D. sacrosancta sensu lato* by Serizawa (2009), were A + C + E (where E is from *D. chinensis*) and B + C + E, respectively. Thus, the *PgiC* constitutions differed between the two species. These results support the taxonomical treatment of Serizawa (2009) who separated the two species. For *D. pacifica*, three types of genome constitutions were observed in this species: A + C, A + B + C, and A + C + D (where D is from *D. caudipinna*), which are designated as the α type (*PgiC* constitution: A + C), β type (A + B + C), and γ type (A + C + D), respectively. It is difficult to distinguish these types based on their morphology, but the γ type is more readily distinguishable from the others due to its larger fronds (which often reach up to 1 m in length) and papery lamina. Among the apogamous species or apogamous cytotypes in the *D. varia* complex, those containing genomes derived from progenitors outside the *D. varia* complex are as follows: *D. sacrosancta sensu stricto*, *D. kobayashii*, and *D. pacifica* (γ type). *Dryopteris sacrosancta sensu stricto* and *D. kobayashii* contained the genome of *D. chinensis*. The γ type of *D. pacifica* had the genome of *D. caudipinna*.

Possible cytoplasmic gene flow from Dryopteris sacrosancta to D. chinensis

Lee *et al.* (2013) suggested that cytoplasmic gene flow might have occurred from *Dryopteris sacrosancta sensu lato* to *D. chinensis* based on their demonstration that they shared a plastid *rbcL* sequence and that *D. sacrosancta sensu lato* did not possess the nuclear *PgiC* sequence of *D. chinensis*. However, in the present study, the nuclear *PgiC* (E) of *D. chinensis* was detected in *D. kobayashii* and *D. sacrosancta sensu stricto*, which were separated from *D. sacrosancta sensu lato* by Serizawa (2009). For *D. chinensis*, only triploid and tetraploid apogamous types have been reported from Japan and China (Figure 1-1). However, I discovered a new diploid sexual cytotype of *D. chinensis* in Japan (Hori *et al.* 2015). Therefore, it is reasonable to consider that these two species originated via hybridization between *D. chinensis* and members of the *D. varia* complex. The contradictory results obtained by Lee *et al.* (2013) and in the present study might be explained by the different methods employed for selecting nuclear sequences, where they used a cloning method to separate and select nuclear *PgiC* sequences from each sample, whereas the SSCP method was used in the present study. The latter method allowed the selection of all the nuclear DNA sequences in each sample more reliable than the cloning method.

Origins of apogamous species in the Dryopteris varia complex

Excluding *Dryopteris varia*, all the apogamous species in the complex examined in this study had hybrid origins because their nuclear *PgiC* sequences belonged to two or three clades. Some apogamous species possess sequences from three clades of *PgiC*, which were derived from three different diploid sexual species, so hybridization between two species with different genomes have likely occurred at least

twice during the genetic diversification of apogamous members of the *D. varia* complex.

(1) Apogamous species originated by hybridization between two species

Apogamous species with two *PgiC* types belonging to two different clades, *Dryopteris bissetiana* and *D. pacifica* (α type), can be considered to have originated by hybridization between two species. *Dryopteris bissetiana* (*PgiC* constitution: B + C) is a hybrid of *D. saxifraga* (B) and *D. protobissetiana* (C).

The α type of *Dryopteris pacifica* (A + C) originated by hybridization between *D. varia* (A) and *D. protobissetiana* (C). This species had two plastid *rbcL* sequences: one shared with *D. varia* and another shared with *D. protobissetiana*. Therefore, the maternal parent of *D. pacifica* (α) must be *D. varia* or *D. protobissetiana*. At least two hybridization events have likely occurred during their development.

(2) Apogamous species originated from hybrids between diploid apogamous species and diploid sexual species

In addition, the apogamous species with three *PgiC* types belonging to three different clades (*Dryopteris kobayashii*, *D. pacifica* (β , γ), and *D. sacrosancta*) can be considered to have originated by hybridization between one diploid apogamous species with a previous hybrid origin and one diploid sexual species. These apogamous species might also have developed from at least two hybridization events.

Dryopteris kobayashii (B + C + E) originated by hybridization between the diploid apogamous *D. bissetiana* (B + C) and the diploid sexual *D. chinensis* (E). This species shared one plastid sequence with *D. chinensis*. Therefore, the maternal parent of *D. kobayashii* must be *D. chinensis*. In this study, a diploid apogamous sporophyte of *D.*

bissetiana was not found. However, Lee *et al.* (2006) reported a diploid apogamous *D. bissetiana* from Korea. Even if diploid apogamous sporophytes are not found, the existence of diploid apogamous gametophytes is expected because Lin *et al.* (1992) reported that diploid apogamous spores are produced from triploid sporophytes of members of the *D. varia* complex. The diploid sexual cytotype of *D. chinensis* has not been identified in Japan and China (Kurita 1961; Hirabayashi 1966, 1974; Mitui 1968; Nakato *et al.* 1995), but I found it in Japan, as mentioned above.

Dryopteris sacrosancta sensu stricto (A + C + E) had two plastid *rbcL* sequences, which were shared with *D. varia* (A) and *D. chinensis* (E), respectively. *Dryopteris sacrosancta* individuals with the same plastid *rbcL* sequence as *D. chinensis* might have originated by hybridization between the diploid apogamous *D. pacifica* (α) (A + C) and the diploid sexual *D. chinensis* (E). In this case, *D. chinensis* must be the maternal parent. *Dryopteris sacrosancta* individuals that shared *rbcL* sequences with *D. varia* may have originated by hybridization between sexual *D. varia* (A) and one diploid apogamous strain from the *D. varia* complex (C + E). However, an apogamous strain with the *PgiC* constitution has not been discovered in the *D. varia* complex. Therefore, the latter case may suggest that the diploid apogamous *D. pacifica* (α) (A + C) could act as the maternal parent during the hybridization with *D. chinensis*.

The γ type of *Dryopteris pacifica* (A + C + D) shared two plastid *rbcL* sequences (Type A) with *D. varia*. Therefore, *D. pacifica* (γ) could have originated by hybridization between sexual *D. varia* (A) and one diploid apogamous strain from the *D. varia* complex (C + D), but again an apogamous strain with the *PgiC* constitution has not been discovered in the *D. varia* complex. Therefore, the diploid apogamous *D. pacifica* (α) (A + C), which has the *rbcL* Type A sequence, might be the maternal parent

and the diploid sexual *D. caudipinna* might be the paternal parent. This situation is similar to that in *D. sacrosancta sensu stricto*.

The β type of *Dryopteris pacifica* (A + B + C) had *rbcL* Type A and B sequences, which were shared with *D. varia* (A) and *D. saxifraga* (B), respectively. *Dryopteris pacifica* (β) individuals with the plastid *rbcL* sequence shared with *D. varia* might have originated by hybridization between the diploid apogamous *D. bissetiana* (B + C) and sexual *D. varia* (A). *Dryopteris pacifica* (β) individuals with the plastid *rbcL* sequence shared with *D. saxifraga* might have originated by hybridization between the diploid apogamous *D. pacifica* (α) (A + C) and sexual *D. saxifraga* (B).

The results of the present study suggest that diploid apogamous cytotypes can hybridize with diploid sexual cytotypes because many triploid apogamous species with three types of nuclear *PgiC* belonged to three different clades. These results may support the “hybridization cycle hypothesis” suggested by Lin *et al.* (1992, 1995), although I did not confirm whether apogamous triploid species can produce unequally reduced diploid spores. According to the results of this study, diploid apogamous individuals might be able to act as the maternal species during hybridization with sexual individuals because unknown apogamous strains are required if apogamous individuals are assumed to be only the paternal parent. However, previous studies suggested that apogamous species act only as paternal parents and not as maternal parents (Gastony and Yatskievych 1992; Grusz *et al.* 2009; Jaruwattanaphan *et al.* 2013; Suzuki and Iwatsuki 1990; Walker 1962). To address these problems, I plan to perform artificial crossing between diploid apogamous species, particularly *Dryopteris pacifica* (α), and diploid sexual species, *D. caudipinna* or *D. chinensis*.

The present study provides the most comprehensive information for reticulate

evolution in the *Dryopteris varia* complex (Figure 1-4). The results demonstrate that any apogamous cytotypes in the complex can be explained by a combination of two or three nuclear genomes from five species (*D. caudipinna*, *D. chinensis*, *D. protobissetiana*, *D. saxifraga*, and *D. varia*) with diploid sexual cytotypes. This study also showed that the genomes of relatively distant diploid sexual species (*D. caudipinna* and *D. chinensis*) were involved in reticulate evolution in the apogamic *D. varia* complex (subg. *Erythrovariae*, sect. *Variae*).

Taxon	Reproductive mode	Ploidy level	Chromosome number	Locality	Literature cited
<i>D. bissetiana</i>	apogamous	2x	'n' = 82	Japan	Hirabayashi (1966)
		3x	'n' = 123	Japan	Hirabayashi (1967), Lin et al. (2003)
		2x	2n = 123	China	Nakato et al. (1995)
		2x, 3x	2n = 82, 123	Korea	Lee et al. (2006)
	sexual	4x	n = 82	China	Weng (1989)
<i>D. insularis</i>		2x	2n = 82	Japan	Lin et al. (2003)
<i>D. insularis</i> (var. <i>chichimiensis</i>)		3x	2n = 123	Japan	Lin et al. (2003)
2x		'n' = 82, 2n = 82	Japan	Lin et al. (1992)	
<i>D. pacifica</i>	apogamous	2x	2n = 82	China	Nakato et al. (1995)
		3x	'n' = 123	Japan	Hirabayashi (1970)
		3x	'n' = 123, 2n = 123	Japan	Lin et al. (1992)
		3x	2n = 123	China	Nakato et al. (1995)
		3x	2n = 123	Japan	Lin et al. (2003)
		3x	2n = 123	Korea	Lee et al. (2006)
<i>D. protobissetiana</i>	sexual	2x	2n = 82	Japan	Hori et al. (2015)
3x	'n' = 123	Japan	Mitui (1965, 1968), Hirabayashi (1969)		
<i>D. sacrosancta</i>	apogamous	3x	2n = 123	China	Nakato et al. (1995)
		3x	2n = 123	Japan	Lin et al. (2003)
		3x	2n = 123	Korea	Lee et al. (2006)
		2x	n = 41	Japan	Hirabayashi (1967), Mitui (1975)
<i>D. saxifraga</i>	sexual	2x	2n = 82	Korea	Lee et al. (2006)
		3x	2n = 123	Korea	Lee et al. (2006)
	apogamous	2x	2n = 82	Tawian	Ebihara et al. (2014)
		2x	n = 82	Tawian	Tsai & Shieh (1975, 1985)
		2x	'n' = 82	Japan	Hirabayashi (1966, 1967, 1974)
		3x	'n' = 123	Japan	Mitui (1966, 1968), Hirabayashi (1970)
		3x	2n = 123	China	Nakato et al. (1995)
		3x	2n = 123	Japan	Lin et al. (2003)
		3x	2n = 123	Tawian	Ebihara et al. (2014)
		3x	2n = 123	Korea	Lee et al. (2006)

Figure 1-1. The reproductive mode, ploidy level, and chromosome numbers of the *Dryopteris varia* complex.

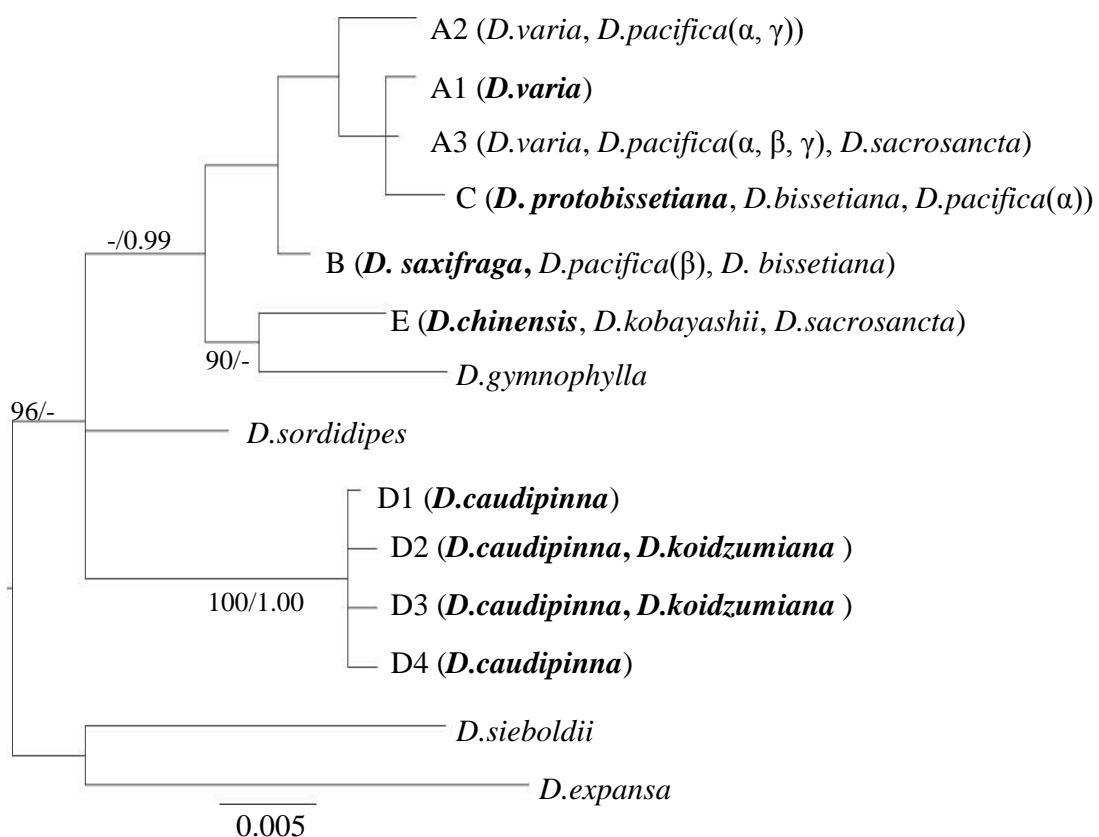


Figure 1-2. A 50% majority-rule consensus tree resulting from Bayesian Markov chain Monte Carlo (B/MCMC) analysis of chloroplast *rbcL* sequences of the *Dryopteris varia* complex.

Numbers at the branches show bootstrap percentages (BP) of maximum parsimony analysis and the posterior probability (PP) of B/MCMC analysis for strong supporting clades (BP ≥ 80 , PP ≥ 0.95). The scale bar indicates a branch length corresponding to 0.005 substitutions per site. The sexually reproducing species are indicated in bold.

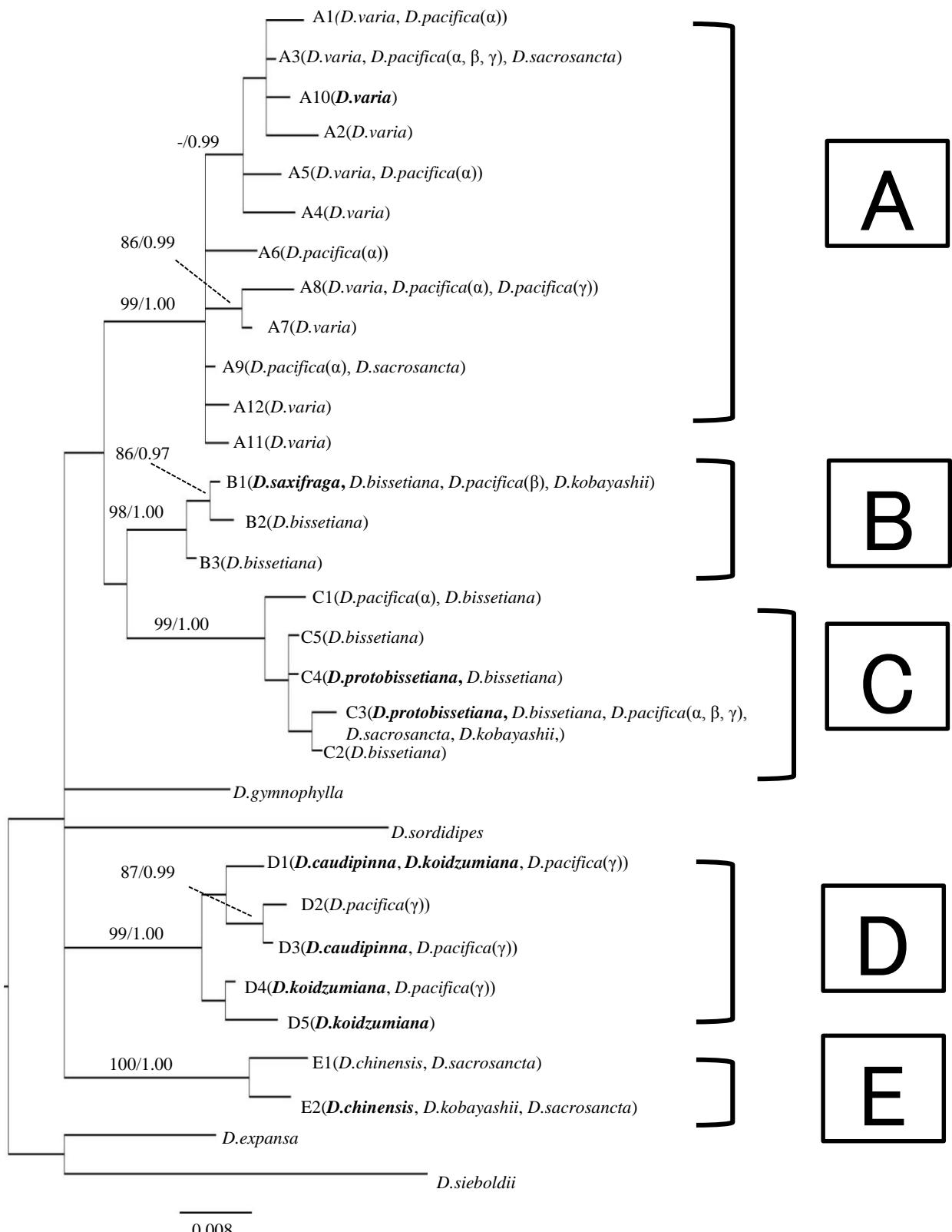


Figure 1-3. 50% majority-rule consensus tree resulting from Bayesian Markov chain Monte Carlo (B/MCMC) analysis of nuclear *PgiC* sequences of the *Dryopteris varia* complex. Numbers at the branches show bootstrap percentages (BP) of maximum parsimony analysis and the posterior probability (PP) of Bayesian analysis for strong supporting clades (BP ≥ 80, PP ≥ 0.95). The scale bar indicates a branch length corresponding to 0.008 substitutions per site. The sexually reproducing species are indicated in bold.

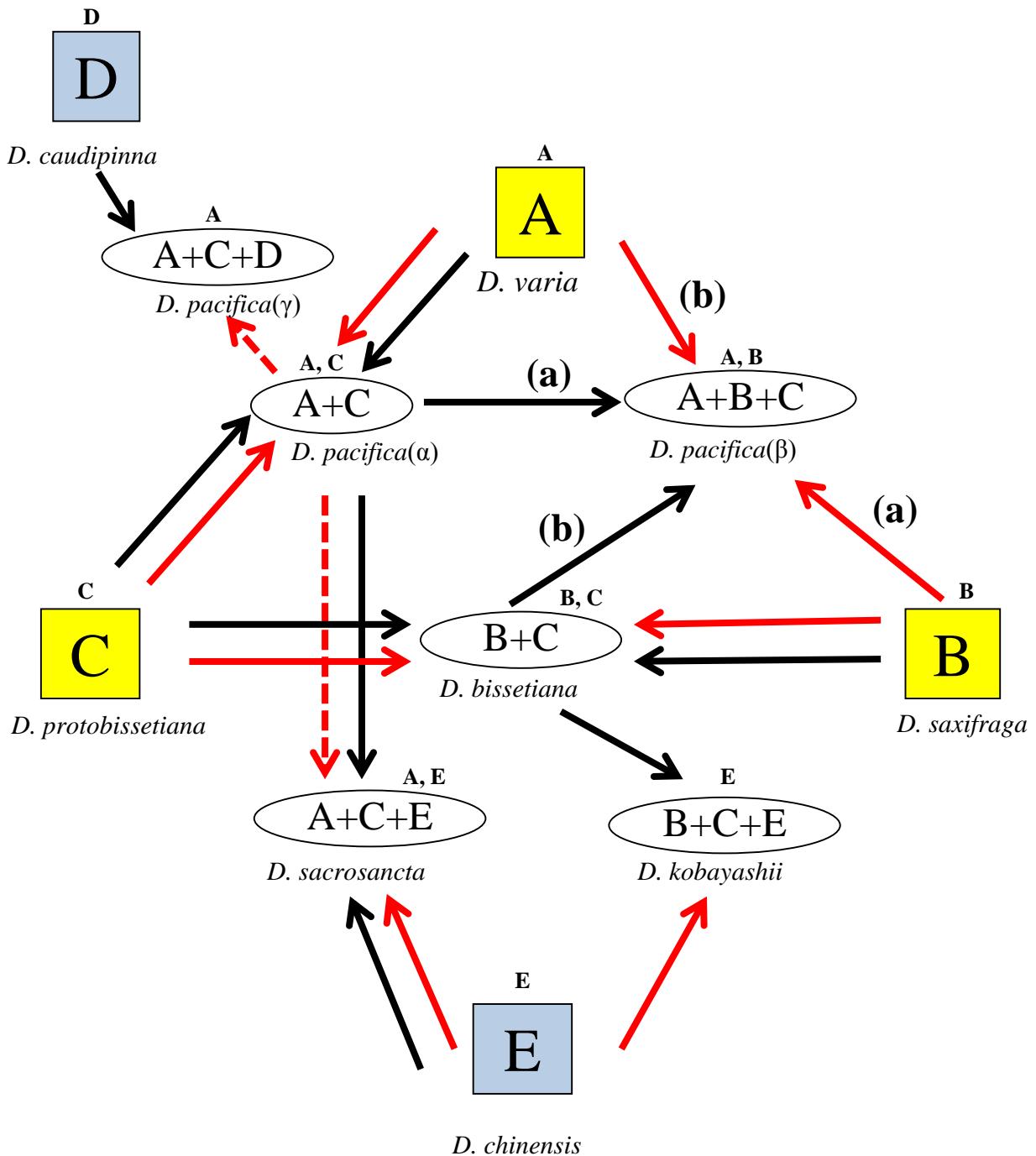


Figure 1-4. The reticulogram of the *Dryopteris varia* complex. The yellow square and the blue square indicate diploid progenitors of the *D. varia* complex and related diploid species other than the complex, respectively. The ellipses indicates apogamous species. The alphabets in squares and ellipses indicate their PgiC constitutions. Even in the case that their PgiC constitution is A+A+C or A+C+C, it is simply shown as A+C. The alphabets above the squares or ellipses indicate cpDNA genotypes. Red and black arrows indicate maternal and paternal species, respectively. Red-dashed arrows indicate apogamous maternal species. Two courses of hybridization can be supposed for related to the formation of *D. pacifica* (β) and show the courses as (a) and (b).

Chapter 2

Analyses of reticulate evolution in the apogamous species of the *Dryopteris varia* complex using five nuclear genetic markers

2.1. Introduction

In Chapter 1, the nucleotide sequences of *PgiC* from five diploid sexual species of the *Dryopteris varia* complex and the related species were identified as the following five monophyletic groups of sequences (A-E): A, *D. varia*; B, *D. saxifraga*; C, *D. protobissetiana*; D, *D. caudipinna*; and E, *D. chinensis*. It was also shown that each triploid apogamous species of the *D. varia* complex contained two or three *PgiC* sequences originated from two or three of the above diploid sexual species: *D. bissetiana*, B + C; *D. pacifica* (α), A + C; *D. pacifica* (β), A + B + C; *D. pacifica* (γ), A + C + D; *D. kobayashii*, B + C + E; *D. sacrosancta*, A + C + E. Therefore, these apogamous species may have undergone a complicated reticulate evolution among the diploid sexual species or have undergone recurrent reticulation through unequal meiosis and hybridization with sexual species (Figure 1-3).

If recurrent reticulation occurred in the apogamous species of the *Dryopteris varia* complex, they should have experienced unequal meiosis many times. Meiosis causes genetic recombination by segregation of homologous (or homoeologous, in the case of apogamous species) chromosomes and chromosomal crossing over (Muller 1932), producing offspring with various combinations of both parental and chimeric

alleles. Therefore, allele constitutions can be different among several nuclear loci located on homoeologous chromosomes that originated from different diploid sexual species and are now a single apogamous species. The base chromosome number of *Dryopteris* is $x = 41$. This means that 41 kinds of chromosomes exist and are able to behave independently.

Figure 2-1 explains how chromosome segregation and recombination occur during repeated reticulation in triploid apogamous species, although it assumes the case of $x = 3$ (three non-homologous chromosomes: square, circle, and diamond), instead of $x = 41$. Assume that the first hybridization occurs between a triploid apogamous species (Species A) with only blue chromosomes and a diploid sexual species (Species B) with only red chromosomes. Species A produces diploid apogamous gametophytes with two sets of the three blue chromosomes; whereas, Species B produces haploid sexual gametophytes with a set of the three red chromosomes. If these gametophytes succeed in fertilization, a new hybrid with two sets of blue and a set of red chromosomes is produced. This new hybrid triploid apogamous species (Species C) can produce fertile spores because the apogamous gene is dominant to the sexual gene in ferns, and a hybrid between an apogamous and a sexual species can often reproduce apogamously (Walker 1962). The allele constitution encoded on a locus in one chromosome type (either square, circle or diamond) from Species C should also correspond to the constitution of the three chromosomes; Blue–Blue–Red.

Then, a second hybridization occurs between the triploid apogamous species C and another diploid sexual species (Species D) with only green chromosomes. When Species C produces diploid apogamous gametophytes, their constitution might be

different among the three kinds of chromosomes (i.e., Square chromosome, Blue–Blue; Circle chromosome, Blue–Blue; Diamond chromosome, Blue–Red). On the other hand, Species D produces haploid sexual gametophytes with a set of green chromosomes. If these gametophytes succeed in fertilization, a new triploid apogamous species (Species E) will be produced. The constitution of Species E should be partially different among the three kinds of chromosomes: Square chromosome, Blue–Blue–Green; Circle chromosome, Blue–Blue–Green; Diamond chromosome, Blue–Red–Green.

A third hybridization occurs between the triploid apogamous species E and another diploid sexual species (Species F) that has only orange chromosomes. Species E produces diploid apogamous gametophytes. The constitution of Species E might be again different among the three kinds of chromosomes (i.e., Square chromosome, Blue–Blue; Circle chromosome, Blue–Green; Diamond chromosome, Blue–Red), whereas Species F produces haploid sexual gametophytes with a set of orange chromosomes. If these gametophytes succeed in fertilization, a new triploid apogamous species (Species G) can be produced. The constitution of Species G should be different among the three kind of chromosomes (i.e., Square chromosome, Blue–Blue–Orange; Circle chromosome, Blue–Green–Orange; Diamond chromosome, Blue–Red–Orange).

If such hybridization cycles repeat, the resultant apogamous species can display huge amounts of interclonal genetic variation. In the case of $x = 41$, chromosome constitutions can display a maximum of $3^{41} = 3.6472996e+19$ patterns in a triploid apogamous species. If this is the case, classification of apogamous species according to their genomic constitution must be hopeless. In Chapter 1, only one nuclear genetic marker, *PgiC*, was used; therefore, inconsistencies in allele constitutions among loci on

different kinds of chromosomes were not examined. Other than *PgiC* (as used in Chapter 1), the *GapCp* gene also has been used frequently as a nuclear marker for fern genetic studies. However, if the loci of the two nuclear markers (*PgiC* and *GapCp*) are linked, it is impossible to determine whether recombination of the chromosomes has occurred through the hybridization of these markers. Further evaluation of unlinked nuclear markers is necessary to solve this problem.

In Chapter 2, additional nuclear markers were developed to explore this question by analyzing a total of five nuclear genes: *PgiC*, *GapCp*, *AK1*, *Esterase*, and *G6pdh*. These loci code for enzymes that often have been used for electrophoretic analyses to estimate genetic diversity within a population or among populations of particular plant species (Schall 1980; Levin 1981; Hamrick 1982; Loveless and Hamrick 1984; Gastony and Gottlieb 1982, 1985; Haufler and Soltis 1984; Haufler 1985a-b, 1987; McCauley *et al.* 1985; Holzinger 1987; Smyth and Hamrick 1987; Soltis and Soltis 1987 a-d, 1988; Shinohara *et al.* 2010). Therefore, these nuclear genetic markers are expected to be useful for a wide-range of taxonomic and population genetic studies, including those on the reticulate evolution of apogamous ferns. Additional taxon sampling was conducted in Chapter 2 to include *Dryopteris insularis* var. *insularis* and *D. insularis* var. *chichisimensis*, which are also the members of the *D. varia* complex (Lin *et al.* 1995), because sufficient outgroup materials were not included in the Chapter 1 research.

In Chapter 2, I examine whether or not genome constitutions of the apogamous species in the *Dryopteris varia* complex are different across several nuclear gene loci, at least some of which are unlinked and coded on non-homologous chromosomes. Furthermore, several samples collected from other localities are added to cover genetic

variation within each species of the *D. varia* complex.

2.2. Materials and Methods

Plant materials

The numbers of leaf samples used in this study are as follow for the members of the *Dryopteris varia* complex: *D. varia*, 24; *D. saxifraga*, 18; *D. protobissetiana*, 10; *D. pacifica* (α), 94; *D. pacifica* (β), 13; *D. pacifica* (γ), 40; *D. sacrosancta*, 47; *D. kobayashii*, 14; and *D. bissetiana*, 56; *D. insularis* var. *insularis*, two; *D. insularis* var. *chichisimensis*, two. The *Dryopteris* species not attributed to the *D. varia* complex, but related to it include: *D. chinensis*, 10; *D. caudipinna*, five; *D. koidzumiana*, four. In addition, six samples of *D. sordidipes*, and one sample each of *D. sabaei*, *D. handeliana*, *D. hasseltii*, *D. polita*, *D. monticola*, *D. expansa*, *D. gymnophylla*, *Polystichum lepidocaulon*, *P. retroso-paleaceum*, and *Arachnioides exillis* were used as outgroups. Of these newly collected specimens, 22 samples (*D. varia*, seven; *D. saxifraga*, one; *D. protobissetiana*, one; *D. pacifica* (α), five; *D. pacifica* (γ), one; *D. sacrosancta*, one; *D. kobayashii*, one; *D. bissetiana*, two; *D. insularis* var. *insularis*, one; *D. insularis* var. *chichisimensis*, one) were also collected as living stocks. Voucher information for these samples is listed in the Appendix 2-1. All the voucher specimens have been deposited in MAK and/or TNS.

Cytological observation and estimation of reproductive mode

To observe mitotic chromosomes, root tips of the living stocks were pretreated

with 0.004-M 8-hydroxyquinoline for 7 h at approximately 15°C–18°C. After fixation overnight in ethanol and acetic acid (3:1), the root tips were hydrolyzed in 1-N HCl and 45% acetic acid (1:1) at 60°C for 10 min before being mashed in a 2% aceto–orcein solution. The chromosomes were observed under a microscope (Leica DM2500) and then photographed by using a digital camera (Leica Application Suite LAS ver. 4.4).

To estimate the reproductive mode of each sample or herbarium specimen, the spore numbers in each sporangium were counted. The sample was estimated to be sexually reproduced if the number was 64, whereas it was estimated to be apogamously reproduced if the number was 32 (Manton 1950).

Ploidy analysis

The method for ploidy analysis is described in Chapter 1.

Molecular analysis of plastid and nuclear markers

For molecular analyses, small amounts of leaf samples were dried in small plastic bags of size 20 cm × 10 cm with silica gel. Subsequently, total DNA was extracted from the dried leaves by using cetyltrimethylammonium bromide solution, according to the method of Doyle & Doyle (1987).

Plastid gene *rbcL* was used in this study as the cpDNA marker. Polymerase chain reaction (PCR) amplification of a *rbcL* fragment was performed by using the primers

aF3 (5'-ATGTCACCACAAACGGAGACTAAAGC-3') and cR3 (5'-GCGGCAGCCAATTCCGGACTCCA-3'), which were newly designed in this study. The nucleotide sequences of *rbcL* were determined by direct sequencing. For sequencing *rbcL*, aF3, aR-D (5'-CGATCTCTCCAACGCATGAATGGCTG-3'), which was also newly designed in this study, D. paci-bf (Hori *et al.* 2014, See also Chapter 1.) and cR3 primers were used.

To analyze nuclear genes, the *PgiC* fragment was amplified by using the primers 14F (5'-GTGCTTCTGGGTCTTTGAGTG-3') and 16R (5'-GTTGTCCATTAGTTCCAGGTTCCCC-3') of Ishikawa *et al.* (2002). The *GapCp* fragment was amplified by using the primers 132F (5'-GTGCTCCGGAGTTAAATGG-3') and 488R (5'-CAACATCATCTCGGTGTATCC-3') of Hori *et al.* (2016).

For developing new nuclear genetic markers, total RNA was extracted from fresh living individuals of *Dryopteris saxifraga* (diploid sexual species) by using the Spectrum Total Plant RNA Kit (Sigma-Aldrich, St. Louis, Missouri, U.S.A.). cDNA was obtained by the cDNA Synthesis Kit (Roche, Basel) and amplified by PCR. Sequencing was performed on Roche's 454 GS Junior system (Roche, Basel) and approximately 122,963 reads were obtained. The reads were assembled by using SOAPdenovo software (<http://soap.genomics.org.cn/soapdenovo.html>) and 3,925 contigs (contiguous overlapping sequences) were obtained. Homologs of the genes, which had been often used for the allozyme method, were searched for in databases of the *Arabidopsis thaliana* project (<http://pgsb.helmholtz-muenchen.de/plant/athal/>) and the 1,000 Plants project (<https://www.bioinfodata.org/Blast4OneKP/>).

Finally, PCR primers for *Adenylate kinase 1* gene (*AK1*), *Esterase/Lipase/Thioesterase family protein* gene (*Esterase*) and *Glucose-6-phosphate dehydrogenase* (*G6pdh*) gene were designed (Figure 2-2). These newly designed pairs of PCR primers were as follows:

AK4F (5'- GATGAAGCCATCAAGAAACCA-3') and AKR2 (5'- ATGGATCCAGCGACCAGTAA-3') for *AK1* (*Adenylate kinase 1*) gene;

EST-F (5'- GGCTGGAGCAGTCTCTGT-3') and EST-R (5'- GCACTAGCAGCTTCGGAAT-3') for *Esterase* gene;

G6F (5'-TTTGGTGGCTATGGAGAAGC-3') and

G6R (5'-CGAATGTTGGGTATTGGAG-3') for *G6pdh* gene.

PCR-single-strand conformation polymorphism (SSCP) analysis

PCR-SSCP analysis was performed to examine allelic variation at each nuclear marker, following the method described in Chapter 1.2. Electrophoresis was performed using MDE gel solution (Lonza) under the following conditions: 2% glycerol at 18°C for 16 h at 350 V for *AK1* and *PgiC*; 2% glycerol at 15°C for 14 h at 300 V for *G6pdh* (Figure 2-3); 2% glycerol at 15°C for 9.5 h at 300 V for *GapCp* (Figure 2-4); 5% glycerol at 15°C for 15 h at 300 V for *Esterase*.

Phylogenetic analyses

For phylogenetic analyses, only one sequence representing each allele for the nuclear gene loci (*AK1*, *Esterase*, *GapCp*, *G6pdh*, and *PgiC*) and each haplotype for cpDNA (*rbcL*) was used in the datasets. The chloroplast and nuclear DNA sequences were aligned using MUSCLE (Edgar 2004) and analyzed separately by neighbor-joining (NJ), maximum parsimony (MP), or maximum likelihood (ML) analyses by using MEGA version 6 (Tamura et al. 2013). The NJ tree was obtained with the p-distance method (Nei & Kumar 2000), and the data are expressed as the number of base differences per site. All sites with ambiguous bases were removed from each sequence pair before analysis. The MP tree was obtained by using the subtree-pruning-regrafting algorithm (Swafford et al. 1996) at search level 1, in which the initial trees were obtained by the random addition of sequences (10 replicates). In ML analysis, the best-fitting model of nucleotide substitution for each DNA region was selected by using MEGA version 6 (Tamura et al. 2013). The *AK1* tree was constructed with the Hasegawa-Kishino-Yano model (Hasegawa et al. 1985) +I, the *Esterase* tree with the Tamura 3-parameter model (Tamura 1992) + G, the *GapCp* tree with the Tamura 3-parameter model, the *G6pdh* tree with the Tamura 3-parameter model, the *PgiC* tree with the Hasegawa-Kishino-Yano + G model, and the *rbcL* tree using the Kimura 2-parameter model (Kimura 1980) + G. The percentages of trees in which the associated taxa clustered together are shown next to the branches. Initial tree(s) for the heuristic search were obtained by applying the NJ method to a matrix of pairwise distances estimated by the Maximum Composite Likelihood approach. The indels were treated as missing characters in MP and ML analyses. The bootstrap method with 1,000

replications was employed to estimate the confidence levels of monophyletic groups.

Genetic linkage of the nuclear markers

AK1 and *Esterase* loci were checked to determine any genetic linkages between the two. Gametophytes were grown for 1 month on agar plates (Yamada *et al.*, 2016) from spores collected from a single individual of the diploid sexual *Dryopteris protobissetiana* (*Hori* 917). Then, total DNAs were extracted from 46 gametophytes that had been silica gel-dried by the same method as mentioned previously for DNA extraction from the sporophyte samples. Genotypes of the *AK1* and *Esterase* genes were estimated by SSCP analysis. Finally, linkage equilibrium between these two nuclear loci was statistically examined by the chi-square test.

2.3. Results

Ploidies and reproductive modes

Diploid ($2n = 82$) sexual cytotypes were observed in *Dryopteris varia*, *D. saxifraga*; diploid apogamous cytotypes in *D. pacifica* (α), *D. insularis*, and triploid ($2n = 123$) apogamous cytotypes in *D. pacifica* (α), *D. pacifica* (γ), *D. bissetiana*, *D. sacrosancta*, *D. kobayashii*, and *D. insularis* var. *chichisimensis*.

The DNA contents of each species of the complex were estimated as follows: *Dryopteris saxifraga*, 21.12 ± 0.26 pg ($N = 7$); *D. pacifica* (α , diploid apogamous cytotype), 16.42 ± 0.14 pg ($N = 8$); *D. pacifica* (α , triploid apogamous cytotype), 23.60 ± 0.52 pg ($N = 8$); *D. pacifica* (β , triploid apogamous cytotype), 23.76 ± 1.07 pg ($N = 3$); *D. pacifica* (γ , triploid apogamous cytotype), 26.02 ± 0.60 pg ($N = 4$); *D. bissetiana*, 26.23 ± 0.36 pg ($N = 25$); *D. kobayashii* (triploid apogamous cytotype), 23.42 pg ($N = 1$); *D. sacrosancta* (triploid apogamous cytotype), 21.93 ± 0.31 pg ($N = 7$). DNA content data for diploid sexual type of *D. varia*, *D. insularis* and *D. insularis* var. *chichisimensis* were not available by ploidy analysis.

Molecular phylogenetic trees according to nucleotide sequences of the five nuclear markers

In most of the samples, several alleles were detected by SSCP analyses. In total, 28,

36, 28, 27, and 31 distinct sequences were identified in *AK1*, *Esterase*, *GapCp*, *G6pdh*, and *PgiC* loci, respectively. The length of the sequences varied from 451 to 655 bp, 357 to 594 bp, 301 to 353 bp, 276 to 322 bp, and 617 to 687 bp, respectively. The data matrix for phylogenetic analyses included 767, 674, 374, 344, and 698 characters, respectively, after editing, of which 164 (21%), 182 (27%), 123 (32%), 124 (36%), 230 (33%) were polymorphic and 117 (15%), 110 (16%), 72 (19%), 68 (19%), and 133 (19%) were parsimoniously informative, respectively. The ML trees (highest log likelihood = -2422.5814, -2552.5997, -1659.5745, -1515.4124, and -2850.2708, respectively) according to the sequences of *AK1*, *Esterase*, *GapCp*, *G6pdh*, and *PgiC* with bootstrap percentages (BPs) of NJ/MP/ML analyses are shown in Figure 2-5, 2-6, 2-7, 2-8, and 2-9, respectively.

In each of the molecular trees of the nuclear markers, the sequences from the five diploid sexual species were distinguished (A = *Dryopteris varia*, B = *D. saxifraga*, C = *D. protobissetiana*, D = *D. caudipinna* and *D. koidzumiana*, E = *D. chinensis*) as monophyletic groups except in the *Esterase* tree. As for *Esterase*, diploid sexual *D. varia* had two types of sequences (A and A'), which made different clades (Figure 2-6). However, some individuals of diploid sexual *D. varia* had both A and A' sequences (in other words, heterozygous of the two types of alleles). Therefore, A and A' sequences of *Esterase* are likely allelic.

The genotypes (combination of alleles) of each sample of the apogamous species of the complex were the same among the five nuclear loci (Table 2-2): apogamous type

of *Dryopteris varia*, A (AA or AAA); diploid apogamous *D. pacifica* (α), AC; triploid apogamous *D. pacifica* (α), AAC, ACC, or A/C (meaning either AAC or ACC); *D. pacifica* (β), ABC; *D. pacifica* (γ), ACD; *D. bissetiana*, BCC or B/C; *D. sacrosancta*, ACE; *D. kobayashii*, BCE; *D. insularis* var. *insularis* (diploid apogamous), M; *D. insularis* var. *chichisimensis*, ACM. The alleles observed in the samples of *D. insularis* and *D. saxifraga* belong to the same clades in the *GapCp* tree (Figure 2-7), but they were still able to be distinguished by the positions of indels in their *GapCp* sequences. Genotypes of triploid apogamous *D. pacifica* (α) were either AAC or ACC. However, the genotypes of each individual of *D. pacifica* (α) coincided among the five loci. In other words, when the genotype in *AK1* locus was AAC, those in the other four loci were also AAC or A/C, never ACC.

Molecular phylogenetic tree according to rbcL sequences

In the *Dryopteris varia* complex and its diploid sexual relatives, eight types of *rbcL* sequences were recognized. Among the 1,205 sites, 156 (12%) were polymorphic and 88 (7%) were parsimoniously informative. NJ, MP, and ML analyses resulted in phylogenetic trees with similar topology. The ML tree (highest log likelihood = -3118.1608) with BPs of NJ/MP/ML analyses is shown in Figure 2-10.

The haplotype of *rbcL* observed in each species or type of the complex is as follows: *Dryopteris varia* (contains diploid sexual type), A1 or A3; *D. protobissetiana* (diploid sexual species), C; *D. saxifraga* (diploid sexual species), B; *D. insularis* var.

insularis, M; *D. pacifica* α, A1 or A3; *D. pacifica* β, A3 or B; *D. pacifica* γ, A2 or A3; *D. bissetiana*, B or C; *D. insularis* var. *chichisimensis*, A1; *D. kobayashii*, E; *D. sacrosancta*, A3 or E. Each diploid sexual species of the complex had a different type of *rbcL*, except for *D. varia*; however, even *D. varia* did not share haplotypes with the other diploid sexual species. Triploid apogamous species always shared their *rbcL* haplotypes with one of the diploid sexual species of the complex or relatives.

Linkage of the nuclear markers

The sporophyte of *Dryopteris protobissetiana* (Hori 917, no. 7) had two alleles in each of the *AK1* (C1 and C6 alleles) and *Esterase* (C4 and C6 alleles) loci. In 46 gametophytes derived from this sporophyte, the p-value of the chi-square test of these two nuclear loci did not indicate marginally significant conflict ($P = 0.23$). Therefore, *AK1* and *Esterase* are independently inherited nuclear markers. The other three nuclear loci (*GapCp*, *G6pdh*, and *PgiC*) showed too little intraspecific variation within any of the diploid sexual species to test for their independence from other loci.

2.4. Discussion

Recurrent reticulations accompanying chromosomal recombination seemed to occur only a few times within the *Dryopteris varia* complex because the genotypes (allele combinations) were the same among the five nuclear loci used as genetic markers in this study. The genotypes (combination of alleles) of each sample of the apogamous species of the complex were the same among the five nuclear loci (*AK1*, *Esterase*, *GapCp*, *G6pdh*, *PgiC*): apogamous cytotype of *D. varia*, A; diploid apogamous *D. pacifica* (α), AC; triploid apogamous *D. pacifica* (α), AAC, ACC, or A/C (A/C means either AAC or ACC); *D. pacifica* (β), ABC; *D. pacifica* (γ), ACD; *D. bissetiana*, BCC or B/C; *D. sacrosancta*, ACE; *D. kobayashii*, BCE; *D. insularis* var. *insularis* (diploid apogamous), M (MM); *D. insularis* var. *chichisimensis*, ACM. Furthermore, SSCP analyses of the 46 gametophytes derived from the sporophyte of *D. protobissetiana* (Hori 917, no. 7), which had two alleles in each of *AK1* (C1 and C6 alleles) and *Esterase* (C4 and C6 alleles) loci, clearly indicated that these two loci are not linked. Therefore, the behavior of chromosomes within reticulate evolution in the *D. varia* complex described in Figure 2-1 is likely inaccurate, and occurs rather as described in Figure 2-12.

In Figure 2-12, the first hybridization occurs between the triploid apogamous Species A with three sets of three blue chromosomes, and the diploid sexual Species B with two sets of red chromosomes, producing a new triploid apogamous species, Species C. The allele constitution of Species C should be Blue–Blue–Red, and this is the same as that in Figure 2-1; however, the behavior of chromosomes in the second hybridization is different from that shown in Figure 2-1. Hybridization occurs between

Species C and another diploid sexual species, Species D, with only green chromosomes. Species C produces diploid apogamous gametophytes, but the allele constitution of the gametophytes is the same among the three kinds of chromosomes: Square, Blue–Red; Circle, Blue–Red; Diamond, Blue–Red. In other words, a set of three kinds of chromosomes from a particular diploid sexual species (i.e., Blue square, Circle, and Diamond chromosomes) always behaves together. If these gametophytes succeed in fertilization with those of species D that has only green chromosomes, a new triploid apogamous species (Species E) will result with three sets of three kinds of chromosomes (Blue, Red, and Green). At this point, the hybridization cycle cannot continue successfully. If it occurs at all, all offspring with chromosome recombinations will likely die and be removed from the gene pool.

In the previous studies, it has been considered that apogamous species can act only as the paternal, and not as the maternal parent (Walker 1962, Suzuki & Iwatsuki 1990, Gastony & Yatskievych 1992, Grusz *et al.* 2009, Jaruwattanaphan *et al.* 2013). However, as discussed in Chapter 1, this study suggests that diploid apogamous individuals might often act as the maternal parent in the hybridization with sexual individuals within the *D. varia* complex. This is because many unknown apogamous strains must be assumed if apogamous individuals can act only as the paternal parent. For example, some individuals of triploid apogamous *D. pacifica* (γ) (genome constitution: A + C + D) and *D. sacrosancta* (genome constitution: A + C + E) shared their *rbcL* haplotype with the diploid sexual *D. varia* (A). If the diploid sexual *D. varia* (A) is the maternal parent, the genome constitution of the diploid apogamous paternal parents should be C + D and C + E, respectively. However, individuals of apogamous

species with such genotypes have yet to be found in the field despite the fact that as many as 338 individuals of this complex have been genetically analyzed. Thus, this study's results suggest that diploid apogamous *D. pacifica* (α) (A + C) can be the maternal parent of *D. pacifica* (γ) and *D. sacrosancta* because plastid genes in ferns are well known as being inherited only from the maternal parent (Gastony & Yatskievych 1992). Therefore, apogamous species can also be maternal parents and involve reticulate evolution in the apogamous fern complex.

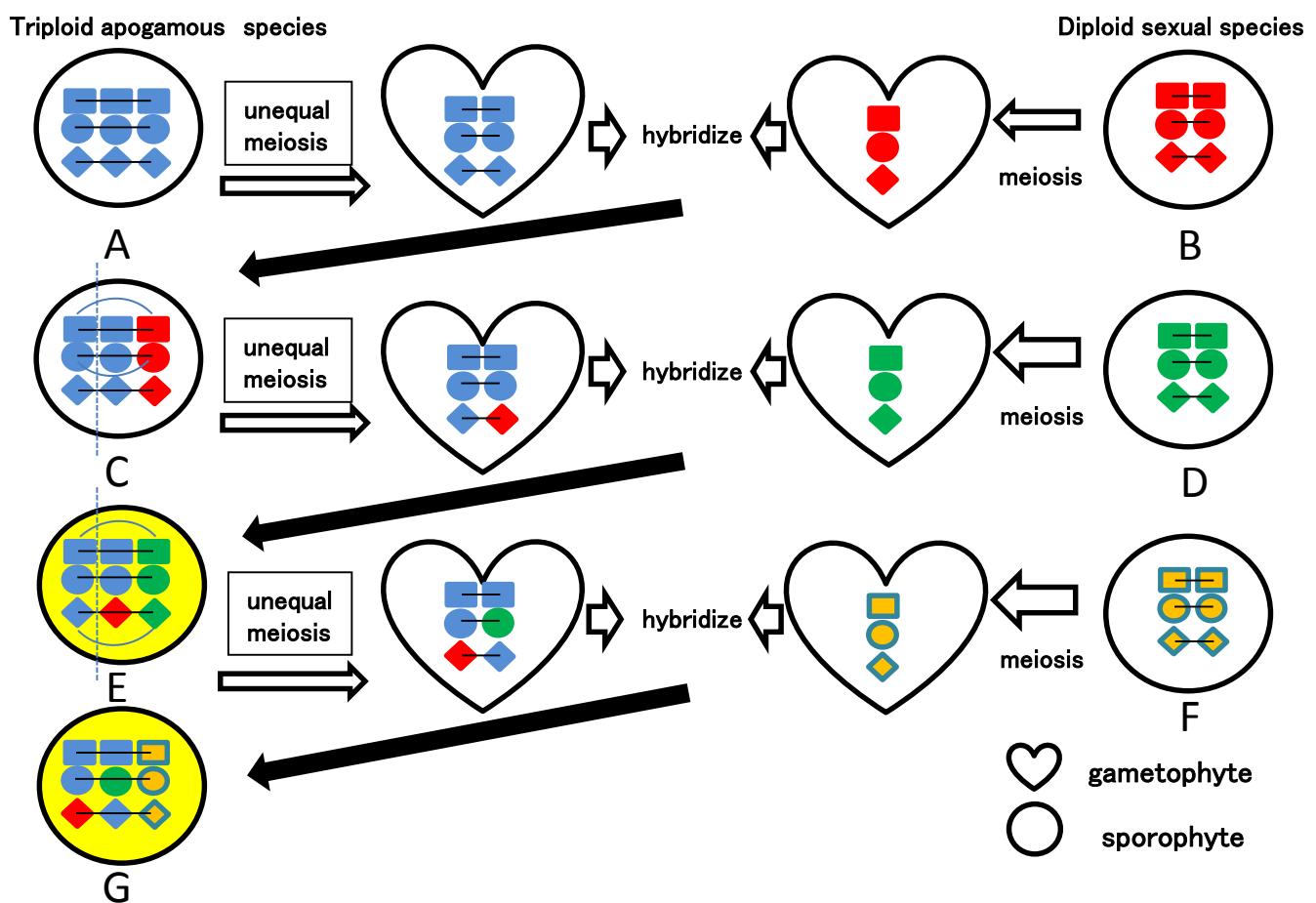


Figure 2-1. The genome constitutions of three kind of chromosomes during repeated hybridization cycles of apogamous species. Each genome consists of three kind of chromosomes (square, circle and diamond). See details in text (p. 40-42.)

Gene	PCR primers (5' - 3')		Homologs and their source plant species		
	Forward	Reverse	<i>Arabidopsis thaliana</i>	<i>Dryopteris saxifraga</i>	<i>Polystichum acrostichoides</i>
AK1 (Adenylate kinase 1) gene	AK4F (GATGAAGCCA TCAAGAAACC A)	AKR2 (ATGGATCCAG CGACCAGTAA)	AT5G63400.2	-:-	scaffold-FQGQ-2073286
Esterase (Esterase/Lipase/Thioesterase family protein) gene	EST-F (GGCTGGAGCA GTCTCTCTGT)	EST-R (GCACTAGCA GCTTCGGAA T)	AT3G50790.1	This study	scaffold-FQGQ-2010471
GapCp - short (glyceraldehyde-3-phosphate dehydrogenase) gene	132F (GTGCTTCCGG AGTTAAATGG)	488R (CAACATCATC TTCGGTGTAT CC)	-:-	-:-	-:-
G6pdh (Glucose-6-phosphate dehydrogenase) gene	G6F (TTTGGTGGCT ATGGAGAAGC)	G6R (CGAATGTTGG GGTATTGGAG)	AT5G40760.1	This study	scaffold-FQGQ-2071416

Figure 2-2. The list of nuclear markers newly developed in this study and homologs used to design these new PCR primers.

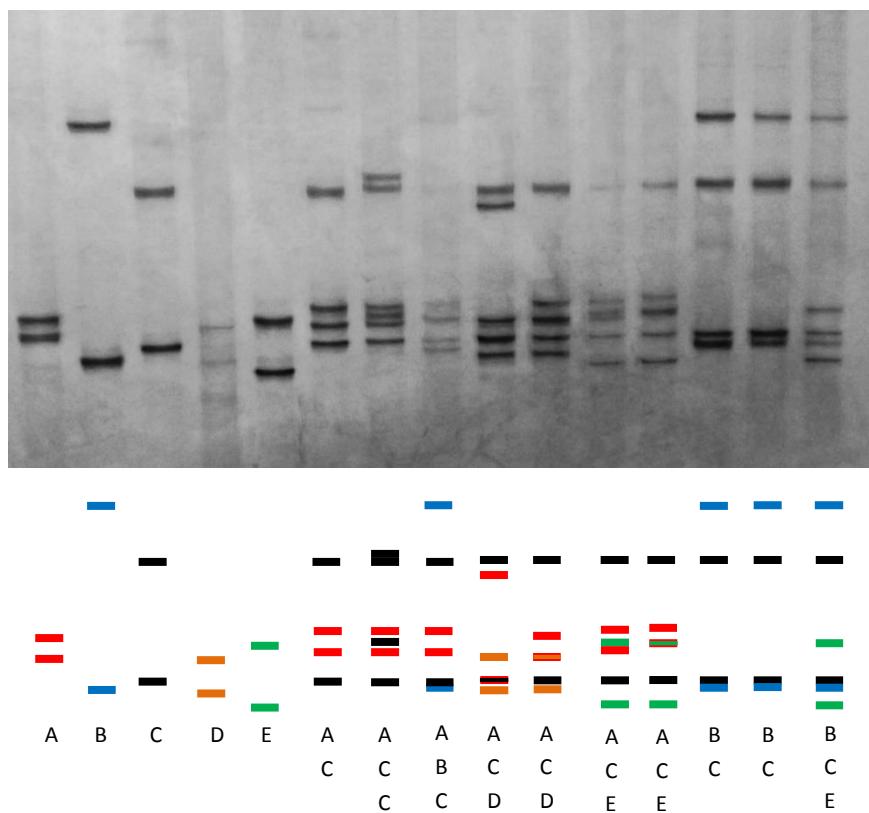


Figure 2-3. The SSCP band patterns of *G6pdh* gene. Electrophoretic band patterns on MDE gel under 2% glycerol at 15° C are shown in the above. The colored bands in below indicate the allele of red (*A*, *D. varia*), blue (*B*, *D. saxifraga*), black (*C*, *D. protobissetiana*), brown (*D*, *D. caudipinna*) and green (*E*, *D. chinensis*), each from the diploid sexual species of the *Dryopteris varia* complex.

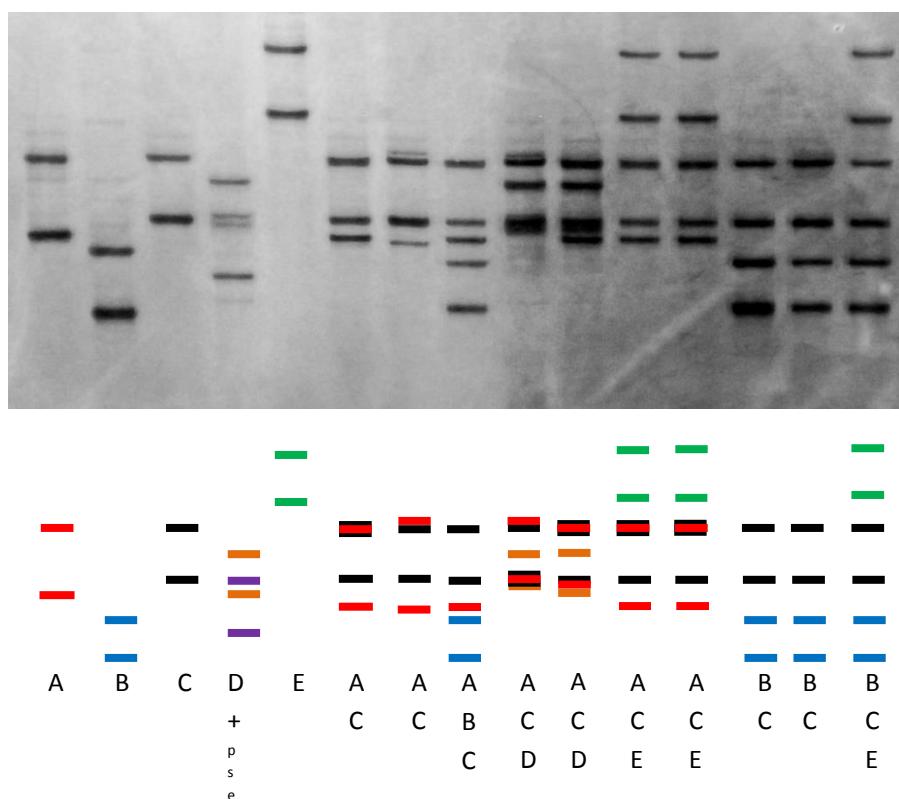


Figure 2-4. The SSCP band patterns of *GapCp* gene. Electrophoretic patterns on MDE gel solution under 2% glycerol at 15° C. The colored bands indicate the allele of red (A, *D. varia*), blue (B, *D. saxifraga*), black (C, *D. protobissetiana*), brown (D, *D. caudipinna*), green (E, *D. chinensis*) and purple (pseudo allele amplified by PCR), each from the diploid sexual species except purple ones .

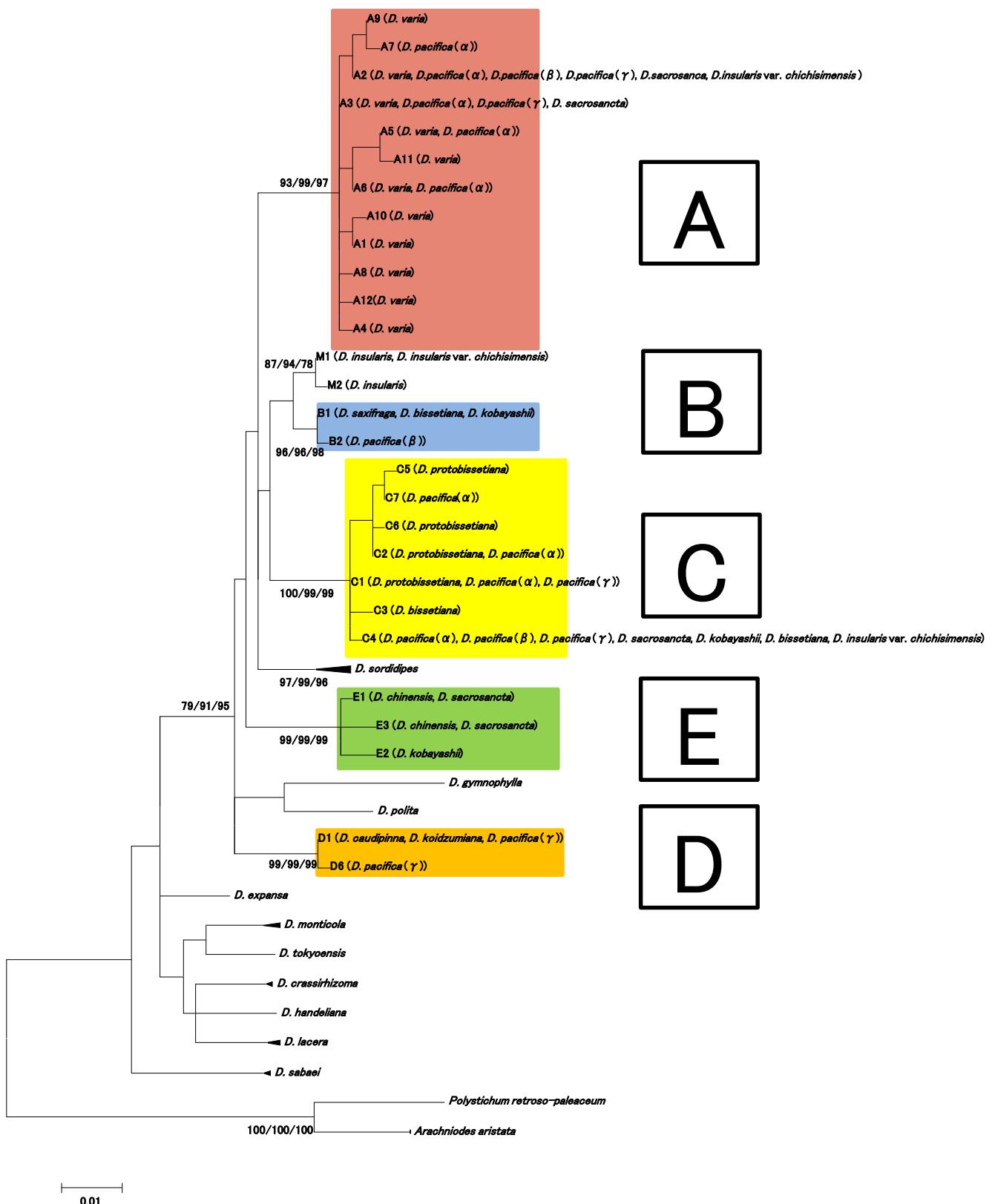


Figure 2-5. The ML tree (highest log likelihood = -2422.5814) based on the sequence variation of the nuclear gene *AK1* with BPs (>70) of NJ/MP/ML analyses on each branch. Square A, B, C, D and E indicate the clades of *Dryopteris varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna* and *D. chinensis*, respectively.

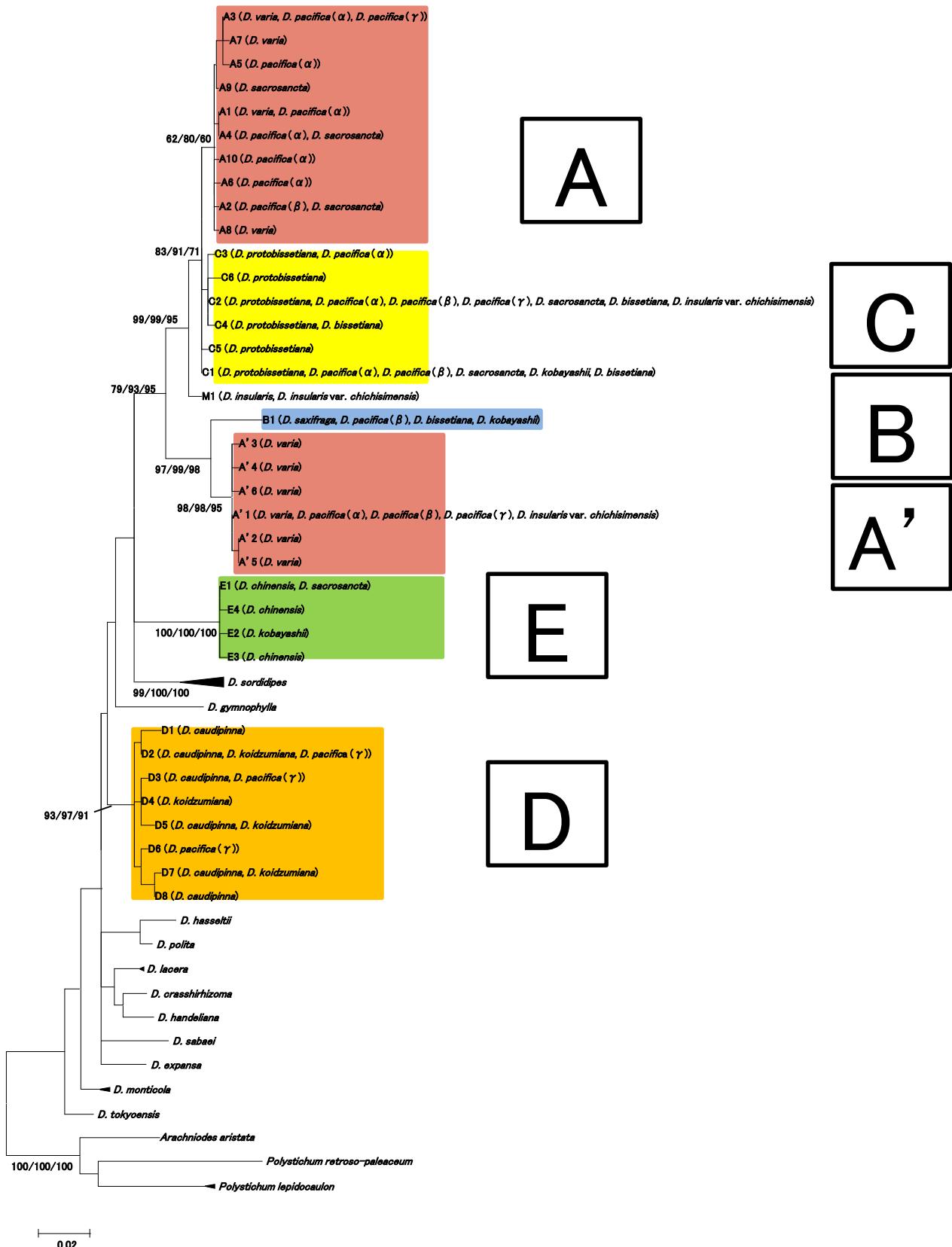


Figure 2-6. The ML tree (highest log likelihood = -2552.5997) based on the sequence variation of the nuclear gene *Esterase* with BPs (>70) of NJ/MP/ML analyses on each branch. Square A, A', B, C, D and E indicate the clades of *Dryopteris varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna* and *D. chinensis*, respectively.

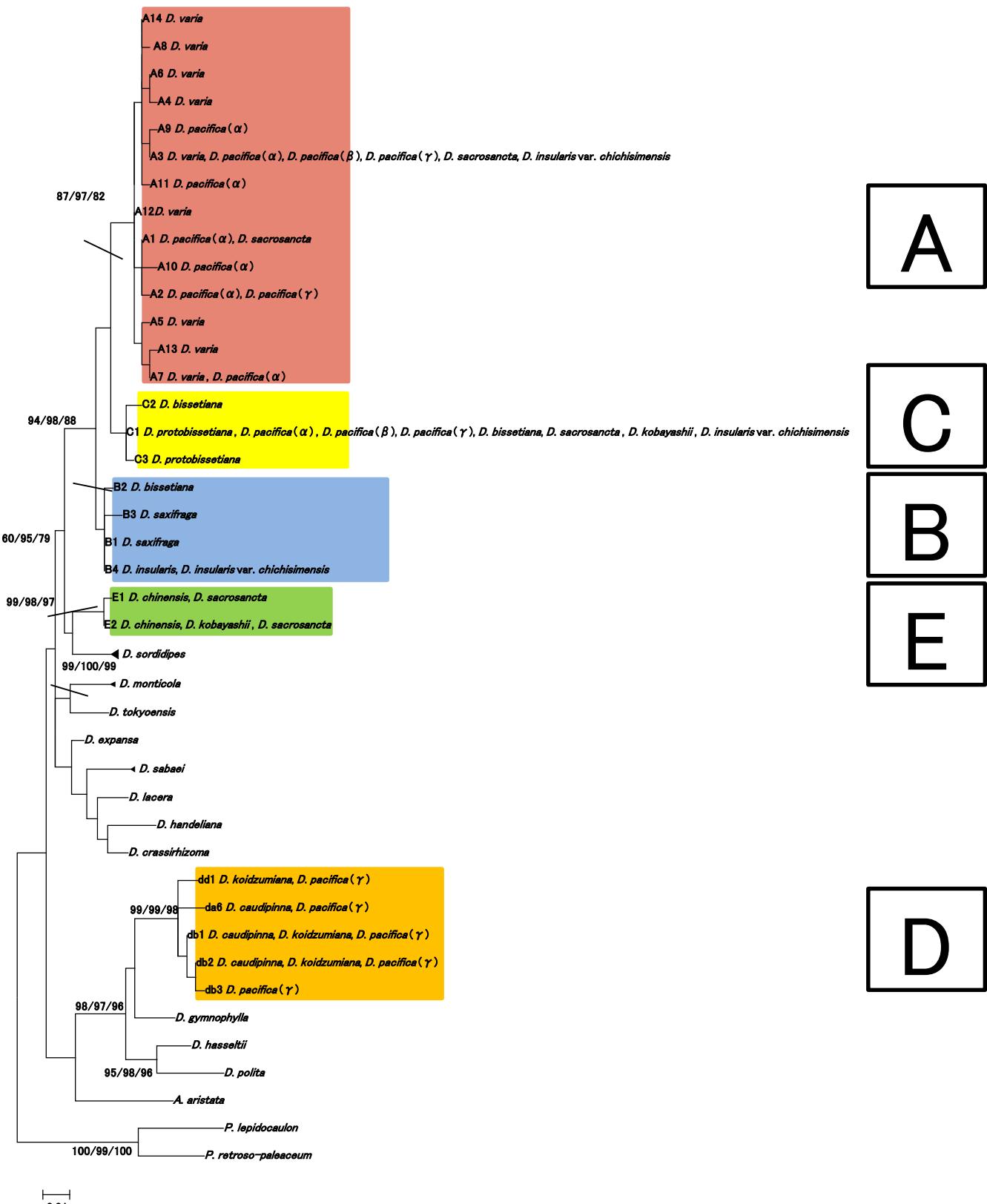


Figure 2-7. The ML tree (highest log likelihood = -1659.5745) based on the sequence variation of the nuclear gene *GapCp* with BPs (>70) of NJ/MP/ML analyses on each branch. Square A, B, C, D and E indicate the clades of *Dryopteris varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna* and *D. chinensis*, respectively.

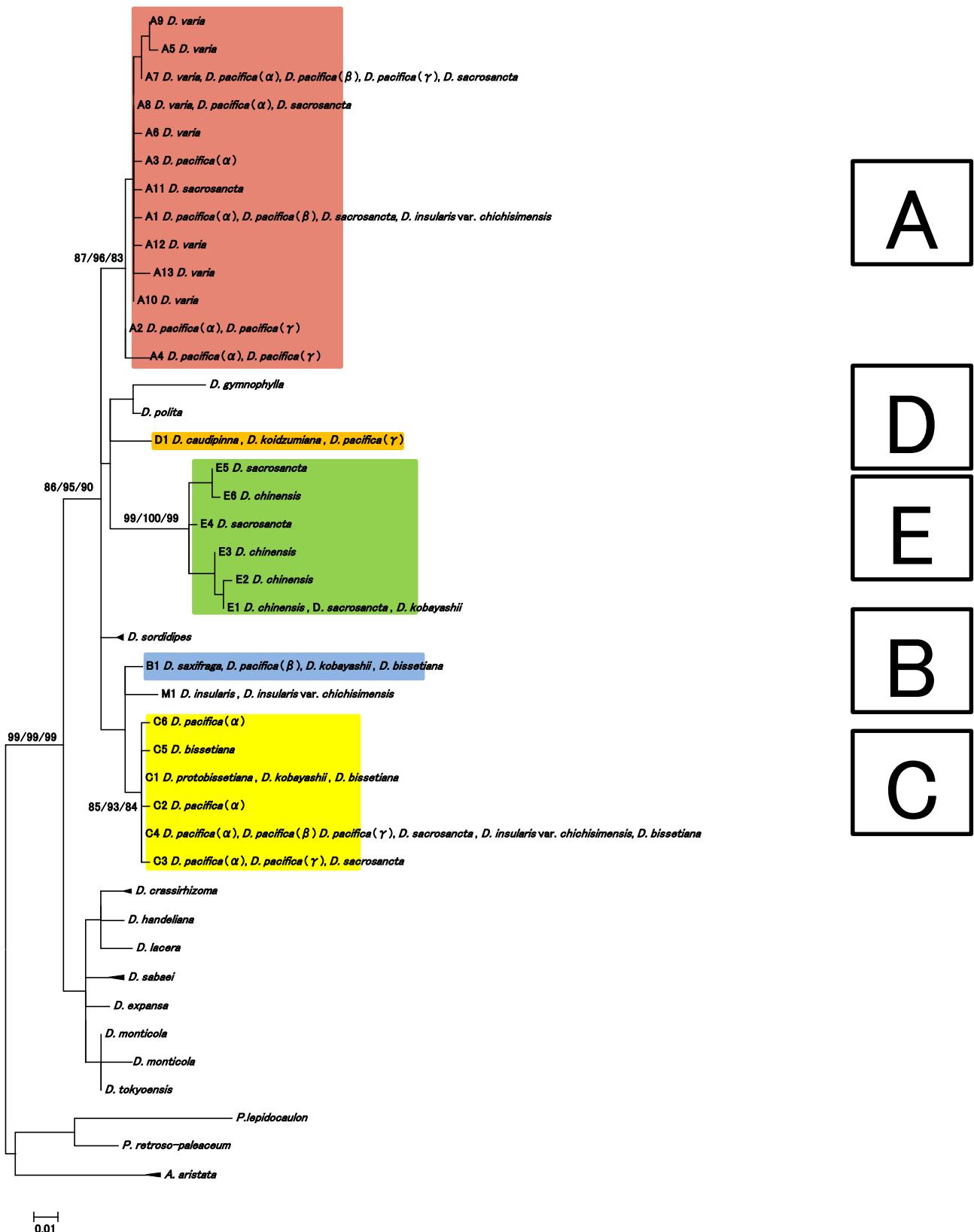


Figure 2-8. The ML tree (highest log likelihood = -1515.4124) based on the sequence variation of the nuclear gene *G6pdh* with BPs (>70) of NJ/MP/ML analyses on each branch. Square A, B, C, D and E indicate the clades of *Dryopteris varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna* and *D. chinensis*, respectively.

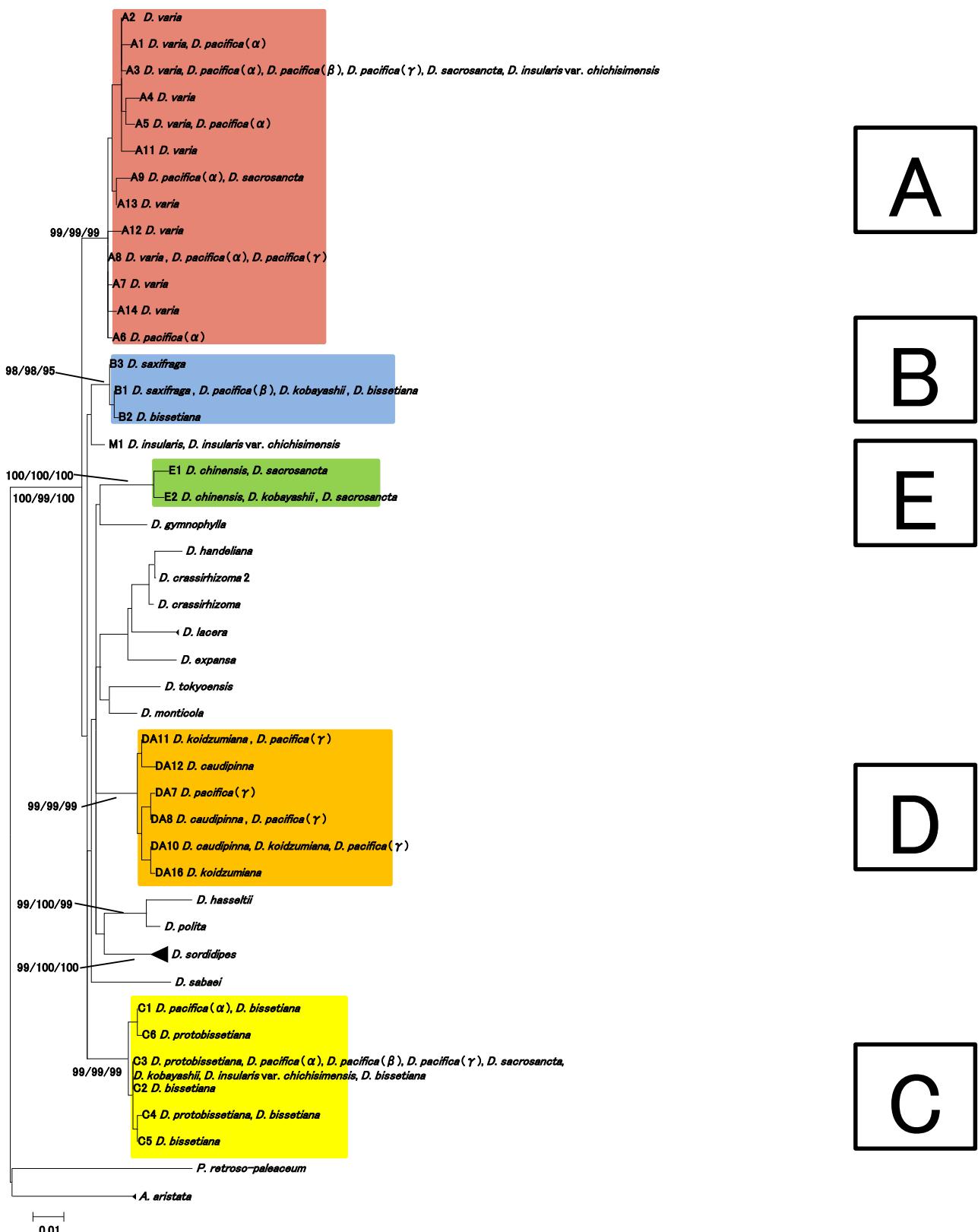


Figure 2-9. The ML tree (highest log likelihood = -2850.2708) based on the sequence variation of the nuclear gene *PgiC* with BPs (>70) of NJ/MP/ML analyses on each branch. Square A, B, C, D and E indicate the clades of *Dryopteris varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna* and *D. chinensis*, respectively.

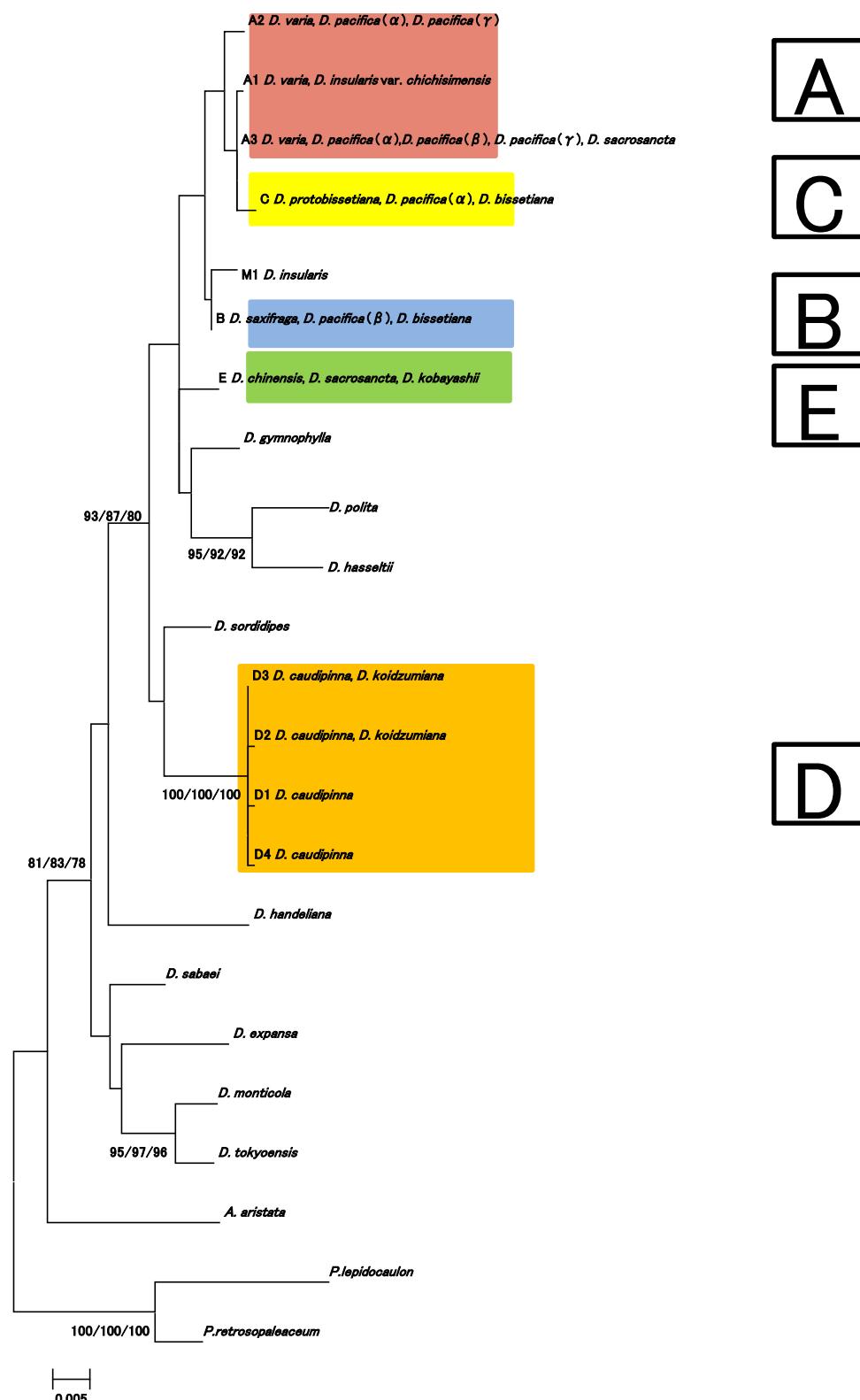


Figure 2-10. The ML tree (highest log likelihood = -3118.1608) based on the sequence variation of the nuclear gene *rbcL* with BPs (>70) of NJ/MP/ML analyses on each branch. Square A, B, C, D and E indicate the clades of *Dryopteris varia*, *D. saxifraga*, *D. protobissetiana*, *D. caudipinna* and *D. chinensis*, respectively.

	AK1			EST			GapCp			G6pdh			PgiC			N
<i>D. varia</i>	A			A			A			A			A			24
<i>D. saxifraga</i>	B			B			B			B			B			18
<i>D. protobissetiana</i>	C			C			C			C			C			10
<i>D. caudipinna</i>	D			D			D			D			D			9
<i>D. chinensis</i>	E			E			E			E			E			10
<i>D. bissetiana</i>	B	C	C	B	C	C	B	/	C	B	C	C	B	C	C	56
	B	/	C	B	/	C				B	/	C	B	/	C	
<i>D. pacifica</i> (α)	A	A	C	A	A	C	A	A	C	A	A	C	A	A	C	94
	A	C	C	A	C	C	A		C	A	C	C	A	C	C	
	A	C	A	C			A		C	A	C		A	C		
	A	/	C	A	/	C				A	/	C	A	/	C	
<i>D. pacifica</i> (β)	A	B	C	A	B	C	A	B	C	A	B	C	A	B	C	12
<i>D. pacifica</i> (γ)	A	C	D	A	C	D	A	C	D	A	C	D	A	C	D	38
<i>D. sacrosancta</i>	A	C	E	A	C	E	A	C	E	A	C	E	A	C	E	47
<i>D. kobayashii</i>	B	C	E	B	C	E	B	C	E	B	C	E	B	C	E	14

Figure 2-11. The genome constitution of each species of the *Dryopteris varia* complex estimated. Genome constitutions “AAC” or “ACC,” of apogamous triploids are shown as A/C to simplify. A, B, C, D, E indicate the allele of each diploid sexual species.

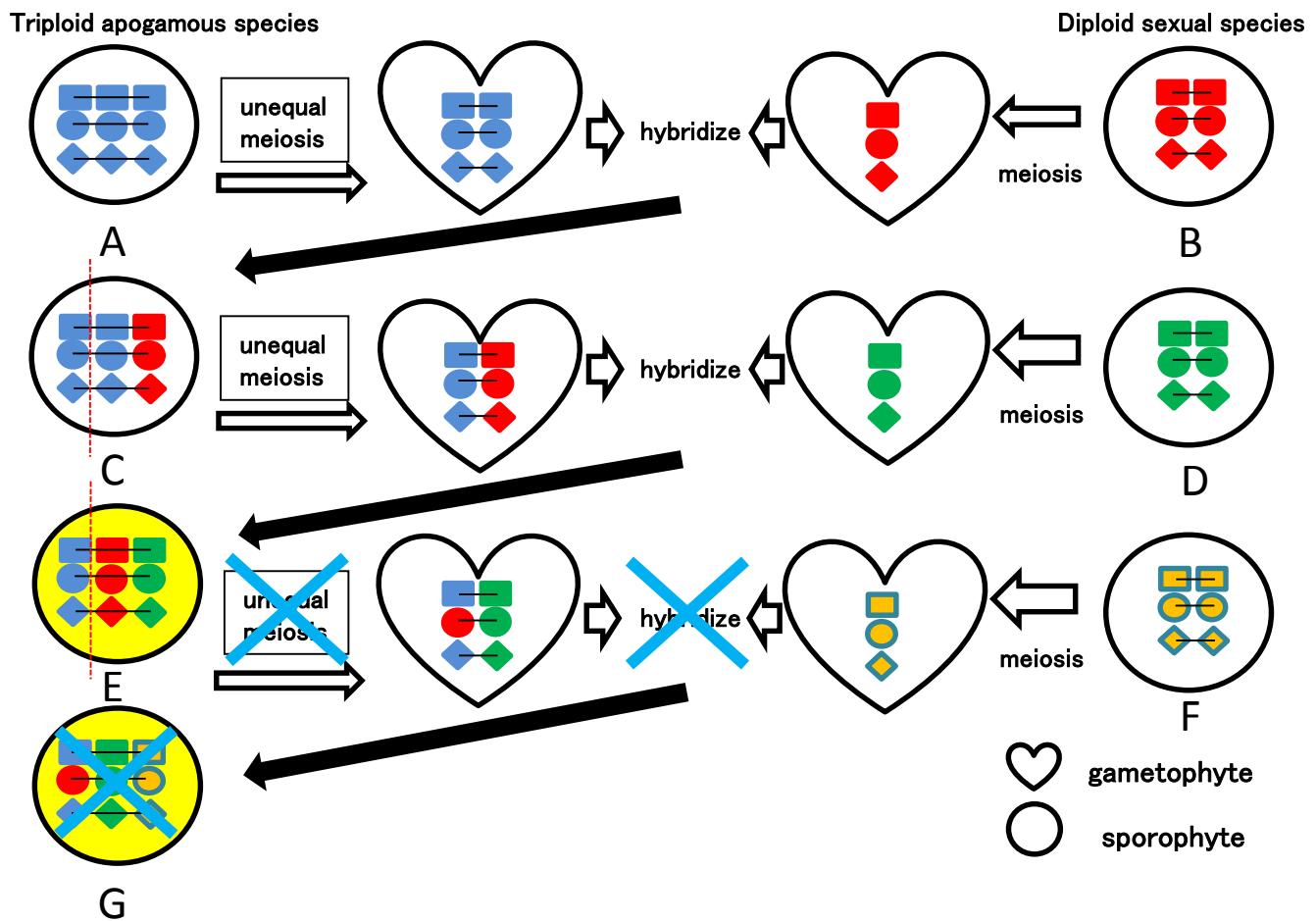


Figure 2-12. The genome constitutions of three kind of chromosomes during hybridization cycles in the case that chromosome recombinations do not occur. This figure shows the case of $x=3$. Each genome consists of three kind of chromosomes (square, circle and diamond). See details in text (p. 52-53.)

Chapter 3.

Revised classification of the species within the *Dryopteris varia* complex (Dryopteridaceae) in Japan

3.1. Introduction

The results of Chapter 2 suggested that classification of the *Dryopteris varia* complex, especially that of the apogamous species, can be revised according to the information for their genome constitutions. This is because the hybridization cycle did not seem to have repeated many times among the members of the *D. varia* complex, and genome constitution of each apogamous species was a simple combination of two or three genomes of the diploid sexual species. Although many Japanese pteridologists have considered classification of the apogamous species within the *D. varia* complex as impossible to perform (Tagawa 1959, Lin *et al.* 1995, Iwatsuki 1995), it is possible if the species are recognized according to their genomic constitutions.

Moreover, the results of Chapter 2 clearly showed that the former classification of the apogamous species of the *Dryopteris varia* complex (Iwatsuki 1992) had issues, especially for *D. pacifica*, because three genotypes (α , β , and γ types) were recognized within this species. The α type consists of the genomes of *D. varia* (A) + *D. protobissetiana* (C), the β type consists of *D. varia* (A) + *D. saxifraga* (B) + *D. protobissetiana* (C), and the γ type consists of *D. varia* (A) + *D. protobissetiana* (C) + *D. caudipinna* (D). The scientific name of *Dryopteris pacifica* (Nakai) Tagawa also needs

revision. This name was originally described as *Polystichum pacificum* by Nakai (1925) from Japan. Tagawa (1959) recombined it to *Dryopteris*. Christ (1912), however, previously had published this name from the Samoan Islands for a different species of *Dryopteris*. Christ (1912) commented that *D. pacifica* was similar to *Dryopteris dissecta*, and *D. dissecta* now belongs to *Tectaria* (Xing *et al.* 2013). Therefore, *Dryopteris pacifica* of Nakai (1925) must be an illegitimate name, and new names are required for the Japanese *D. pacifica*.

In Chapter 3, species classification of the *Dryopteris varia* complex will be revised according to the genome constitution of each species, as elucidated in Chapter 2. Firstly, diploid sexual taxa with distinct chloroplasts and nuclear genomes are treated as independent species. Next, apogamous species are recognized according to differences in the combinations of the genomes. In other words, apogamous cytotypes with different nuclear genome constitutions are classified as independent species. There were several genome constitutions for *D. pacifica* (a), ACC, AAC, AC or A/C. The same might be true also for *D. bissetiana*, BCC or BBC, although two alleles of B were not recognized because of low genetic variation in *D. saxifraga* (B). However, in this study, I have treated these genotypes as belonging to the same species because it is nearly impossible to distinguish them morphologically. Autopolyploid apogamous cytotypes were classified as the same species as the diploid sexual cytotypes sharing the same genome because there were no significant differences in morphological characteristics. I summarized the taxonomic treatment of 11 species within the *D. varia* complex (*D. bissetiana*, *D. chichisimensis*, *D. erythrovaria*, *D. hikonensis*, *D. insularis*, *D. kobayashii*, *D. protobissetiana*, *D. sacrosancta*, *D. saxifraga*, *D. subhikonensis*, and *D.*

varia.) with their reticulate relationships according to their genome constitutions in

Figure 3-1.

For this study, herbarium specimens of the *Dryopteris varia* complex deposited at MAK, MBK, PE, and TNS were examined (Appendix 3-1). The voucher specimens whose genomic constitutions had been fully elucidated were useful especially for describing their morphology and geographic distribution.

3.2. Key to the Japanese species of the *Dryopteris varia* complex (*Dryopteris* subg.

***Erythrovariae* sect. *Variae*)**

- 1a. Sori born only on upper part of lamina..... *D. insularis*
- 1b. Sori born on whole lamina..... 2
- 2a. Scales deflected..... *D. saxifraga*
- 2b. Scales ascending..... 3
- 3a. Lamina papyraceous; center of indusia often red *D. erythrovaria*
- 3b. Lamina herbaceous or coriaceous; center of indusia translucent 4
- 4a. Lamina herbaceous 5
- 4b. Lamina coriaceous 6
- 5a. Lamina narrowly triangular (width / length = 2/3–1/2); apex of pinnae curved, obtuse *D. kobayashii*
- 5b. Lamina pentagonal (width / length = 3/4–2/3); apex of pinnae straight, acute *D. sacrosancta*
- 6a. Scales on pinna rachis flat..... *D. varia*
- 6b. Scales on pinna rachis bullate..... 7
- 7a. Scales sub-sparingly covered on rachis; endemic to the Bonin Islands.....

.....	<i>D. chichisimensis</i>
7b. Scales densely covered on rachis; not distributed in the Bonin Islands.....	8
8a. Scales on upper petiole bullate.....	<i>D. protobissetiana</i>
8b. Scales on upper petiole flat.....	9
9a. Margin of apex of upper pinnae entire.....	<i>D. bissetiana</i>
9b. Margin of apex of upper pinnae deeply–shallowly serrated.....	10
10a. Margin of apex of upper pinnae deeply serrated; indusia ciliate or entire.....	<i>D. hikonensis</i>
10b. Margin of apex of upper pinnae shallowly serrated; indusia entire <i>D. subhikonensis</i>

3.3. Taxonomic Treatment

Dryopteris bissetiana (Baker) C. Chr., *Ind. Fil.* 245. 1905. Type: Japan, Miyanoshita (may be Kanagawa pref.) (J. Bisset, May 24, 1876, K) in *J. Bot, British and Foreign* 15 (180): 366. 1877 (*Nephrodium bissetianum* Baker). **Figure 3-2a.**

Polypodium setosum Thunb., *Fl. Jap.* 337. 1784

Aspidium setosum (Thunb.) Sw., in *Schrad. J. Bot.* 1800-2: 39. 1801

Dryopteris setosa (Thunb.) Akasawa, in *Bull. Kochi. Wom. Univ.* 7: 27. 1959

Dryopteris varia subsp. *setosa* (Thunb.) Sugimoto, *Keys Herb. Pl. Jap. Pterid.* 405. 1966

Nephrodium bissetianum Baker, in *J. Bot.* 1877: 366

Polystichum bissetianum (Bak.) Nakai, in *Bot. Mag. Tokyo* 45: 102. 1931

Dryopteris thunbergii Koidz., in *Bot. Mag. Tokyo* 38: 106. 1924

Dryopteris saxifragivaria Nakai in *J. Jap. Bot.* 18: 286. 1942.

Dryopteris varia var. *setosa* (Thunb.) Ohwi, in *Fl. Jap. Pterid.* 88: 1957.

Diagnosis. *Dryopteris bissetiana* (Baker) C. Chr. is an apogamous species of hybrid origin between *D. protobissetiana* and *D. saxifraga*. This species is similar to *D. protobissetiana*, *D. hikonensis*, and *D. subhikonensis*. However, *D. bissetiana* differs from these in having pinnules with entire margin, entire indusial, and gradually narrowing lamina. This species is sometimes also similar to *D. saxifraga*. Such intermediate form has been identified as *D. saxifragivaria* Nakai; however, both *D. bissetiana* and *D. saxifragivaria* are of hybrid origin between *D. protobissetiana* and *D. saxifraga*. They share the same genomes from the two parental diploid sexual species. Therefore, this study treated them as the same species, *D. bissetiana*.

Plants terrestrial, evergreen, rhizome erect, or slightly ascending; leaves cespitose; scales dense on rhizome, petiole, pinna stalks, rachises, and pinna rachises; petiole 10–40 cm long; scales lanceolate, ascending or deflected, filiform at apex; scales on basal petiole black, transpicuous; base of scales on basal petiole narrow; base of scales on upper petiole spread; base of scales on rachises and pinna rachises bullate; lamina bipinnate, occasionally tripinnate at base, narrowly triangular, gradually narrowing to apex, 20–50 cm long, 10–30 cm wide, dark green or whitish green, soft coriaceous in texture, surface shiny or dull, recurved at margin; pinnules entire at apical margin; lowest basiscopic pinnules on lowest pinna elongated but not markedly more than second one; sori round, born between the margin and the costa; indusia reniform or circular, entire at margin, transpicuous, approximately 1.5–1.8 mm in diameter; 32 spores per sporangium; chromosome number $2n = 123$, triploid apogamous.

Notes. From South Korea, Lee et al. (2006) reported diploid apogamous *Dryopteris bissetiana*. Lee & Park (2013) reported several sequences of nuclear *PgiC* from *D. bissetiana*. However, all of their sequences nested within the clade of diploid sexual *D. saxifraga* (Clade B). Their sample might not be the diploid apogamous *D. saxifraga* because its chloroplast DNA coincided with that of *D. protobissetiana*. Therefore, it seems possible that they failed to select the nuclear *PgiC* sequences belonging to *D. protobissetiana* (Clade C) from their samples of *D. bissetiana*. So, far, only the triploid apogamous cytotype has been found from *D. bissetiana* in Japan, even though as many as 25 samples have been cytologically analyzed using ploidy analysis or chromosomal observations.

Lee et al. (2006) distinguished *Dryopteris saxifragivaria* Nakai from *D. bissetiana*, which has intermediate morphological characteristics between *D. bissetiana* and *D. saxifraga*, in Korea. However, continuous morphological variations are observed between *D. bissetiana* and *D. saxifragivaria* in Japan, and it is difficult to distinguish them morphologically. I concluded that they belong to the same species (*D. bissetiana*) because they share the same genomic constitutions (the genomes from diploid sexual *D. saxifraga* and *D. protobissetiana*).

Habitat and distribution. Growth occurs both in deciduous and evergreen broad-leaved forests of Japan (Hokkaido, Honshu, Shikoku, Kyusyu), Korea, and the mainland of China. The distribution map for Japan is shown in Figure 3-2b.

Japanese name. Yama-itachishida.

Dryopteris chichisimensis Nakai ex H. Ito, in *J. Bot. Mag. Tokyo* 49: 435. 1935.

Type: Japan, the Bonin Islands, Chichijima Island, Mt. Tsutsuiyama (T. Nakai, July 4, 1932, TI) **Figure 3-3a**

Dryopteris insularis var. *chichisimensis* (Nakai ex H. Ito) H. Ito, in *Nakai et Honda, Nova Fl. Jap.* 4: 57. 1939.

Diagnosis. *Dryopteris chichisimensis* Nakai ex H. Ito is an apogamous species of hybrid origin between *D. hikonensis* and *D. insularis*. Its genome constitution consists of those from *D. varia*, *D. protobissetiana* and *D. insularis*. This species is hardly distinguished from *D. hikonensis* based only on morphological traits. Therefore, it is recommended to check nuclear DNA constitution when reporting new localities of this species. However, *D. chichishimensis* often differs from *D. hikonensis* in scales on petiole being sparser.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome and pinna rachises, sub-sparse on petiole, pinna stalks, rachises; petiole 10–40 cm long; scales lanceolate, filiform at apex; base of scales on basal petiole, upper petiole, and rachises narrow; base of scales on pinna rachises bullate; lamina bipinnate, occasionally tripinnate at base, wide triangular, gradually narrowing to apex, 10–30 cm long, 20–50 cm wide, dark green, soft

coriaceous in texture, surface shiny, flat at margin; pinnules deeply serrated at apical margin; lowest basiscopic pinnules on lowest pinna elongated markedly a little more than second one; sori round, born between the margin and the costa; indusia reniform or circular, ciliate at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 32 spores per sporangium; chromosome number $2n = 123$, triploid apogamous.

Habitat and distribution. Subtropical wet evergreen forests. Japan (the Ogasawa Islands, including the Kazan-retto Islands). The distribution map for Japan is shown in Figure 3-3b.

Japanese name. Chichijima-Itachishida.

Notes. Iwatsuki (1995) commented on the distribution of this species in Izu-Islands without indicating a voucher specimen. On the other hand, I have found the specimens of this species, newly collected, from Kita-iwoto Island in addition to Chichijima Island in MAK. Previous reports have called this species Chichijima-Benishida, as its Japanese name. However, it does not have an affinity to Benishida (the *D. erythrosora* complex), but rather to Itachishida (the *D. varia* complex). Therefore, a new Japanese name, Chichijima-Itachishida is proposed in this study.

Dryopteris erythrovaria K. Hori et N. Murak., sp. nov. TYPE: Japan, Tokyo, Inagi City, Momura, approximately 100 m altitude, on soil cliff near dry road in forests, K. Hori 2478, collected on June 18, 2016 (holotype, MAK). **Figure 3-4a**

Diagnosis. *Dryopteris erythrovaria* K. Hori et N. Murak. is an apogamous species of hybrid origin between *D. hikonensis* and *D. caudipinna*. Its genome consists of those from *D. varia*, *D. protobissetiana*, and *D. caudipinna*. This species is characterized by the combination of large papyraceous lamina and red indusia. Large papyraceous lamina is one of the characteristics of *D. caudipinna*. Red indusia are also one of the characteristics of *D. caudipinna*, though it sometimes has transpicuous indusia. The above mentioned genome constitution might be the reason why *D. erythrovaria* sometimes has transpicuous indusia, like the other members of the *D. varia* complex.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, petiole, pinna stalks, rachises, and pinna rachises; petiole 20–50 cm long; scales lanceolate, filiform at apex; scales on basal petiole black; base of scales on basal petiole narrow; base of scales on upper petiole and rachises spread; base of scales on pinna rachises bullate; lamina bipinnate to tripinnatifid, wide triangular, sub-abruptly narrowing to apex, 30–80 cm long, 20–40 cm wide, dark green or yellowish green, papyraceous in texture, surface shiny or dull, flat at margin; pinnules deeply serrated at apical margin; lowest basiscopic pinnules on lowest pinna

elongated markedly a little more than second one; sori round, born between the margin and the costa; indusia red to white in center or transpicuous, reniform or circular, almost entire or rarely ciliate at margins, approximately 1.5–1.8 mm in diameter; 32 spores per sporangium; chromosome number $2n = 123$, triploid apogamous.

Habitat and distribution. Warm temperate evergreen forests. Japan (Honshu, Shikoku, Kyusyu), Korea (Cheju-Island) and eastern parts of mainland China (Anhui, Zhejiang Provinces). The distribution map for Japan is shown in Figure 3-4b.

Japanese name. Beni-O-Itachishida.

Dryopteris hikonensis (H. Ito) Nakaike, in *New Fl. Jp.*: 841. 1992. Type: Japan, Shiga pref. (H. January 15, 1933, TI). **Figure 3-5a**

Polystichum pacificum Nakai in *Bot. Mag. Tokyo* 39: 119. 1925 (illegitimate name)

Polystichum hololepis var. *hikonensis* H. Ito in *J. Jap. Bot.* 10: 451. 1934

Dryopteris bissetiana var. *hikonensis* (H. Ito) in *Bot. Mag. Tokyo* 50: 36. 1936

Dryopteris varia subsp. *hikonensis* (H. Ito) Sugimoto, *Keys Herb. Pl. Jap. Pterid.* 281. 404. 1966

Dryopteris bissetiana var. *typica* H. Ito in *Nakai et Honda, Fl. Jap.* 4: 55. 1939.

Dryopteris fuyangensis Ching & P. S. Chiu in *Bot. Res. Academia Sinica* 2: 26–7, t. 9, f. 4. 1987

Dryopteris immixta Ching in *Fl. Tsinling.* 2: 225–226, pl. 41, f. 1–2. 1974

Dryopteris lungjingensis Ching & P. S. Chiu ["luntsingensis"] in *Bot. Res. Academia Sinica* 2: 27–28, pl. 10. 1987

Dryopteris paravaria Ching & P. S. Chiu in *Bot. Res. Academia Sinica* 2: 22–23, t. 8, f. 3. 1987

Dryopteris pudouensis Ching in Bull. in *Bull. Bot. Res. Harbin* 3(3): 11–12, f. 9. 1983

Dryopteris quadrifida Ching ex K. H. Shing & J. F. Cheng in *Jiangxi Sci.* 8(3): 49. 1990

Dryopteris shanghaiensis Ching & P. S. Chiu in *Bot. Res. Academia Sinica* 2: 24, t. 9, f. 1. 1987

Dryopteris tieanzuensis Ching & P. S. Chiu in *Bot. Res. Academia Sinica* 2:

24–25, t. 9, f. 2. 1987.

Dryopteris yushanensis Ching & P. S. Chiu in *Bot. Res. Academia Sinica* 2:

28–29, t. 10, f. 2. 1987

Diagnosis. *Dryopteris hikonensis* (H. Ito) Nakaike is an apogamous species of hybrid origin between *D. varia* and *D. protobissetiana*. This species is different from *D. varia* in having slightly bullate scales on rachises. It is also different from *D. protobissetiana* in having flat scales on petiole, and most basiscopic pinnules are not very markedly elongated.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, petiole, pinna stalks, rachises, and pinna rachises; petiole 10–40 cm long; scales lanceolate, ascending, filiform at apex; scales on basal petiole black to blackish brown; base of scales on basal petiole, upper petiole, and rachises spread; base of scales on pinna rachises bullate; lamina bipinnate, occasionally tripinnate at base, wide triangular, not very abruptly narrowing to apex, 20–50 cm long, 10–30 cm wide, dark, yellowish or whitish green, soft coriaceous in texture, surface shiny or dull, flat at margin; pinnules deeply serrated at apical margin; lowest basiscopic pinnules on lowest pinna elongated markedly a little more than second one; sori round, between the margin and the costa; indusia reniform or circular, entire to ciliate at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 32 spores per

sporangium; chromosome number $2n = 82$ (diploid apogamous) or $2n = 123$ (triploid apogamous).

Habitat and distribution. Warm temperate to subtropical evergreen forests. Japan (Honshu, Shikoku, Kyusyu, Ryukyu), Korea, and mainland of China. The distribution map for Japan is shown in Fig. 3-5b.

Japanese name. O-Itachishida.

Dryopteris insularis Kodama, *Icon. Pl. Koisik.* 2: t. 49. 1914. Type: Japan (the Bonin Islands, Tokyo pref.) (TI, Specimen number, collector, and date are not cited).

Figure 3-6a

Dryopteris insularis var. *typical* H. Ito, in *Nakai et Honda, Nova Fl. Jap.* 4: 57.

1939

Dryopteris varia var. *insularis* (Kodama) H. Ohba, in *Sci. Rep. Tohoku Univ.* (B) 36: 113. 1971.

Diagnosis. *Dryopteris insularis* Kodama is characterized by having sori borne only on upper part of lamina and glandular ciliate at margins of indusia. Its genome is different from another sexual species and apogamous species.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome and pinna rachises, not very dense on petiole, pinna stalks, and rachises; petiole 20–35 cm long; scales brown, lanceolate, ascending, filiform at apex; base of scales on basal petiole, upper petiole, and rachises narrow; scales on pinna rachises bullate; lamina bipinnate to tripinnatifid, wide triangular, gradually narrowing to apex, 35–45 cm long, 25–35 cm wide, whitish green, soft coriaceous in texture, surface shiny, flat at margin; pinnules obtuse, finely serrated at apical margin; lowest basiscopic pinnules on lowest pinna elongated but not markedly more than second one; sori round, borne on upper part of lamina and expand downwardly, soriferous pinnae more or less contracted, between margin and the costa on pinnules; indusia reniform, glandular ciliate at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 32 spores per sporangium; chromosome number $2n = 82$, diploid apogamous.

Habitat and distribution. Subtropical dry evergreen forests. Japan (Bonin Islands). The distribution map for Japan is shown in Figure 3-6b.

Japanese name. Munin-Itachishida.

Notes. In previous studies, this species has been called as Munin-Benishida. However, as is similar in the case of *Dryopteris chichisimensis*, this species does not have an affinity to Benishida (the *D. erythrosora* complex), but instead definitely belongs to the group of Itachishida (the *D. varia* complex). Thus, a new Japanese name is proposed in this study.

Dryopteris kobayashii Kitagawa, in *Rep. First Sci. Exped. Manchoukuo* 4 (2): 56–58, f. 11. 1935. Type: China, Fengtian, Hsiao-ping-tao. (M. Kobayashi, n 39. October 9, 1932, TI). **Figure 3-7a**

Diagnosis. *Dryopteris kobayashii* Kitagawa is an apogamous species of hybrid origin between *D. bissetiana* and *D. chinensis*. Its genome consists of those from *D. saxifraga*, *D. protobissetiana* and *D. chinensis*. This species is very similar in gross morphology to *D. sacrosancta*, but is distinguishable by its narrowly triangular lamina, curved pinnae with obtuse apex and always-whitish green young pinnule.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, sparse on petiole, pinna stalks, rachises, and pinna

rachises; petiole 10–40 cm long; scales lanceolate, filiform at apex; base of scales on basal petiole, upper petiole narrow; base of scales on rachises spread; base of scales on pinna rachises bullate; lamina bipinnate to tripinnatifid, narrowly triangular, gradually narrowing to apex, 20–40 cm long, 10–20 cm wide, yellowish green, herbaceous in texture, surface dull, flat at margin; pinnules entire or shallowly serrated or entire at apical margin; lowest basiscopic pinnules on lowest pinna longest but not markedly elongated more than second one; sori round, born between the margin and the costa; indusia transpicuous, reniform or circular, entire at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 32 spores per sporangium; chromosome number $2n = 123$, triploid apogamous.

Habitat and distribution. Warm temperate evergreen forests. Japan (Honshu, Shikoku, Kyushu), Korea, and northeastern part of mainland China. The distribution map for Japan is shown in Figure 3-7b.

Japanese name. Ryoto-Itachishida.

Dryopteris protobissetiana K. Hori et N. Murak., in *Acta Phytotaxa. Geobot.* (2015). Type: Japan, Kagoshima pref., Yakushima Island, Mt. Myojo, 300 m alt, K. Hori Dpaci 913 (holotype, MAK). **Figure 3-8a**

Diagnosis. *Dryopteris protobissetiana* K. Hori et N. Murak. is most similar to *D. bissetiana* (Baker) C. Chr. in having slightly bullate scales and a dark green lamina surface, but differs from it in having flat and serrated margins at apexes of upper pinnae and flat lamina margins.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, petiole, pinna stalks, rachises, and pinna rachises; petiole 10–30 cm long; base of scales on basal petiole and upper petiole spread; base of scales on rachises and pinna rachises bullate; lamina bipinnate, occasionally tripinnate at base, narrowly triangular, gradually narrowing to apex, 10–40 cm long, 10–20 cm wide, dark green, soft coriaceous in texture, surface shiny, flat at margin; pinnules finely serrated at apical margin; lowest basiscopic pinnules on lowest pinna elongated but not markedly more than second one; sori round, born between the margin and the costa or relatively nearer to the margin than to the costa; indusia reniform or circular, entire or erose at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 64 spores per sporangium; chromosome number $2n = 82$, diploid sexual.

Habitat and distribution. Warm temperate evergreen forests. Japan (southern part of Yakushima Island, Kagoshima pref., Kyushu). The distribution map for Japan is shown in Figure 3-8b.

Japanese name. Moto-Itachishida.

Dryopteris sacrosancta Koidz., in *Bot. Mag. Tokyo* 38: 108. 1924. Type: Japan, Hiroshima pref., Miyajima Island. (Faurie, November 1913, TI). **Figure 3-9a**

Polystichum sacrosanctum (Koidz.) Koidz., in *Bot. Mag. Tokyo* 43: 388. 1929

Polystichum bissetianum var. *sacrosanctum* (Koidz.) Nakai, in *Bot. Mag. Tokyo* 45: 103. 1931

Dryopteris bissetiana var. *sacrosancta* (Koidz.) H. Ito, in *Bot. Mag. Tokyo* 50: 36. 1936

Dryopteris varia subsp. *sacrosancta* (Koidz.) Sugimoto, *Keys Herb. Pl. Jap. Pterid.* 281. 405. 1966

Dryopteris bissetiana var. *tenuifrons* H. Ito, in *Bot. Mag. Tokyo* 50: 37. 1936

Dryopteris varia var. *sacrosancta* (Koidz.) Ohwi, *Fl. Jap. Pterid.* 88. 1957.

Diagnosis. *Dryopteris sacrosancta* Koidz. is an apogamous species of hybrid origin between *D. hikonensis* and *D. chinensis*. Its genome consists of those from *D. varia*, *D. protobissetiana* and *D. chinensis*. This species and *D. kobayashii* are very similar in morphology by having herbaceous yellowish green lamina. The scales of these two species are sparser than the other members of the *D. varia* complex. However, this species is distinguished from *D. kobayashii* by having widely triangular lamina,

pinnae with straightly acute apex, and sometimes reddish-brown young pinnule.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, sparse on petiole, pinna stalks, rachises, and pinna rachises; petiole 10–40 cm long; scales lanceolate, filiform at apex; scales on basal petiole black, transpicuous at margin; base of scales on basal petiole, upper petiole, rachises, and pinna rachises spread; lamina bipinnate to tripinnatifid, pentagonal, sub-abruptly narrowing to apex, 20–50 cm long, 10–30 cm wide, yellowish green, herbaceous in texture, surface weakly shiny or dull, flat at margin; pinnules finely serrated at apical margin; lowest basiscopic pinnules on lowest pinna elongated markedly a little more than second one; sori round, born between the margin and the costa; indusia transpicuous, reniform or circular, entire at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 32 spores per sporangium; chromosome number $2n = 123$, triploid apogamous.

Habitat and distribution. Warm temperate evergreen forests. Endemic to Japan (Honshu, Shikoku, Kyusyu). The distribution map is shown in Figure 3-9b.

Japanese name. Hime-Itachishida.

Dryopteris saxifraga H. Ito, in *Bot. Mag. Tokyo.* 50: 125 (1936). Type: Japan, Shizuoka pref. or Yamanashi pref., Mt. Hujisan (B. Hayata F3, TI). **Figure 3-10a**

Dryopteris varia subsp. *saxifraga* (H. Ito) Sugimoto, *Keys Herb. Pl. Jap. Pterid.* 282. 405. 1966

Dryopteris varia var. *saxifraga* (H. Ito) H. Oba, in *Sci. Rep. Tohoku Univ.* (B) 36: 111. 1971.

Diagnosis. *Dryopteris saxifraga* H. Ito is characterized by having pinnules with entire margin and oblong lamina. This species is a sexual diploid and has a distinct genome.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, petiole, pinna stalks, rachises, and pinna rachises; petiole 5–20 cm long; scales lanceolate, deflected, filiform at apex; base of scales on basal petiole spread; base of scales on upper petiole, rachises, and pinna rachises bullate; lamina bipinnate, occasionally tripinnate at base, oblong, gradually narrowing to apex, 5–30 cm long, 5–15 cm wide, whitish green, soft coriaceous in texture, surface dull, recurved at margin; pinnules obtuse, entire or sinuate at apical margin; lowest

basiscopic pinnules on lowest pinna elongated but not markedly more than second one; sori round, born between the margin and the costa; indusia reniform or circular, entire or erose at margins, transpicuous, approximately 1.5–2.0 mm in diameter; 64 spores per sporangium; chromosome number $2n = 82$, diploid sexual.

Notes. From South Korea, Lee & Park (2006) reported the triploid apogamous cytotype of *Dryopteris saxifraga*. Lee & Park (2013) reported sequences of nuclear *PgiC* from the triploid apogamous *D. saxifraga*, which made a clade with those of diploid sexual *D. saxifraga* in their *PgiC* molecular tree. However, *D. bissetiana* is sometimes similar to *D. saxifraga* in gross morphology because *D. bissetiana* is of hybrid origin between *D. saxifraga* and *D. protobissetiana*. Their plant samples were confirmed as triploid apogamous. On the other hand, so far, only the diploid sexual cytotype has been found from *D. saxifraga* in Japan. These facts suggested that triploid apogamous *D. saxifraga* in Lee & Park (2013) might be *D. bissetiana*.

Habitat and distribution. Deciduous broad-leaved forests. Japan (Hokkaido, Honshu, Shikoku, Kyusyu), Korea, and the mainland of northeastern China. The distribution map for Japan is shown in Figure 3-10b.

Japanese name. Iwa-Itachishida.

Dryopteris subhikonensis K. Hori et N. Murak., sp. nov. TYPE: Japan, Saitama, Han-nou City, Shirako, 200 m, on soil cliff near dry road in forests, K. Hori 2270, collected on July 2, 2016 (holotype, MAK). **Figure 3-11a**

Diagnosis. *Dryopteris subhikonensis* K. Hori et N. Murak. is an apogamous species of hybrid origin between *D. hikonensis* and *D. saxifraga* or between *D. bissetiana* and *D. varia*. Its genome consists of those from *D. protobissetiana*, *D. saxifrage*, and *D. varia*. This species is hardly distinguished from *D. hikonensis* based only on their morphological traits; therefore, it is recommended to check nuclear DNA constitution when reporting new localities of this species. However, *D. subhikonensis* is usually different from *D. hikonensis* in having shallowly serrated or entire pinnules, as well as entire indusia. *D. hikonensis* is commonly observed in the forests along the Pacific Ocean and Seto Inland sea, whereas *D. subhikonensis* is mainly observed in the mountains in southeastern Honshu and in the forests along the Japan sea.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, petiole, pinna stalks, rachises, and pinna rachises; petiole 10–40 cm long; scales lanceolate, filiform at apex; base of scales on basal petiole and upper petiole narrow; base of scales on rachises spread; base of scales on

pinna rachises bullate; lamina bipinnate, occasionally tripinnate at base, wide triangular, sub-abruptly narrowing to apex, 20–50 cm long, 10–30 cm wide, dark green, soft coriaceous in texture, surface weakly shiny, flat at margin; pinnules shallowly serrated or entire at apical margin; lowest basiscopic pinnules on lowest pinna elongated markedly a little more than second one; sori round, born between the margin and the costa; indusia reniform or circular, entire at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 32 spores per sporangium; triploid apogamous (ploidy level was checked by ploidy analysis, the chromosome number was not determined).

Habitat and distribution. Warm temperate evergreen forests. Japan (South eastern Honshu and southern part of Japan sea side). The distribution map for Japan is shown in Figure 3-11b.

Japanese name. Iwa-O-Itachishida.

Dryopteris varia* (L.) Kuntze **Figure 3-12a*

Fraser-Jenkins (1986) designated holotypes of *Lastrea opaca* Hook. and

Nephrodium coriaceum C. Hope as the lectotype, because the holotype of *Polypodium varium* L. was lost.

Lastrea opaca Hook., in *Hooker's J. Bot.* 9: 339 (1857).—*Aspidium opacum* (Hook.) Benth., *Fl. Hongk.*: 456 (1861). Type: Hong Kong and mainland N.W. of Hong Kong, *J. C. Bowman* (K!—lectotype)

Nephrodium coriaceum C. Hope, in *J. Bot., Lond.* 28: 328 (1890). Type: India, Kapili Hot Springs, North Cachar Hills, Assam, 1000ft, February 1890, *Gustav Mann* (K - lectotype; BM, DD, E, K, P, PE - isolectotypes).

Polypodium varium L., *Sp. Pl.* 2: 1090. 1753

Aspidium varium (Linnaeus) Sweet in *Schrad. J. Bot.* 1800–2: 35. 1801

Nephrodium varium (L.) C. Presl, *Reliq. Haenk.* 1. 36. 1825

Polystichum varium (L.) C. Presl, *Abh. Königl. Böhm. Ges. Wiss., ser. 5.* 5. 1851

Lastrea varia (L.) Moore, *Ind. Fil.* 107. 1858

Aspidium opacum (Hooker) Bentham., *Fl. Hongk.* 456. 1861

Dryopteris yabei Hayata, *Mat. Fl. Formos.* 424. 1911

Polystichum hololepis Hayata, *Ic. Pl. Formos.* 5: 332. 1915

Dryopteris matsuzoana Koidz., in *Bot. Mag. Tokyo* 39: 15. 1925

Dryopteris ogawai H. Ito in Nakai, *Ic. Pl. As. Or.* 1: 18. Pl. 9. 1935

Dryopteris yabei var. *ogawai* (H. Ito) H. Ito, in *Bot. Mag. Tokyo* 50: 128. 1935

Dryopteris yabei var. *hololepis* (Hayata) H. Ito, in *Bot. Mag. Tokyo* 50: 128. 1936

Dryopteris yabei var. *matsuzoana* (Koidz.) H. Ito, in *Bot. Mag. Tokyo* 50: 128. 1936

Dryopteris yabei form. *ogawai* (H. Ito) H. Ito, in Nakai et Honda, *Nova Fl. Jap.* 4: 59. 1939

Dryopteris yabei form. *typica* H. Ito, in Nakai et Honda in *Nova Fl. Jap.* 4: 59. 1939

Dryopteris sinobissetiana Ching & Z. Y. Liu in Bull., in *Bot. Res., Harbin* 4(4): 8–9, f. 36. 1984

Dryopteris caudifolia Ching & P. S. Chiu, in *Bot. Res. Academia Sinica* 2: 21–22, t. 8, f. 2. 1987

Dryopteris lingii Ching, in *Bot. Res. Academia Sinica* 2: 23–24, t. 8, f. 4. 1987

Dryopteris glabrescens Ching & P. S. Chiu ex K. H. Shing & J. F. Cheng, in *Jiangxi Sci.* 8(3): 48. 1990

Dryopteris pseudobissetiana Ching ex K. H. Shing & J. F. Cheng, in *Jiangxi Sci.* 8(3): 49. 1990

Diagnosis. *Dryopteris varia* (L.) Kuntze is very variable in morphology; however, it can be characterized by having abruptly narrowed lamina at apex, hard texture of lamina, and flat scales. Intraspecific cytological variation is observed in this species, but the genome constitution is different from the other members of the *D. varia* complex.

Plants terrestrial, evergreen, rhizome erect or slightly ascending, leaves cespitose; scales dense on rhizome, petiole, pinna stalks, rachises, and pinna rachises; petiole 10–40 cm long; scales lanceolate, ascending, filiform at apex; base of scales on basal petiole narrow; base of scales on upper petiole, rachises, and pinna rachises spread; lamina bipinnate, occasionally tripinnate at base, pentagonal to wide triangular, abruptly narrowing to apex, 20–40 cm long, 10–30 cm wide, dark, yellowish or whitish green, hard coriaceous in texture, surface shiny to dull, flat at margin; pinnules acute, entire, shallowly, finely or deeply serrated at apical margin; lowest basiscopic pinnules on lowest pinna elongated markedly more than second one; sori round, between the margin and the costa; indusia reniform or circular, entire to ciliate at margins, transpicuous, approximately 1.5–1.8 mm in diameter; 64 or 32 spores per sporangium; chromosome number $2n = 82$ (diploid sexual, known only from Taiwan) or 123 (triploid apogamous).

Notes. Tsai & Shieh (1975, 1985) reported the tetraploid sexual cytotype of *Dryopteris varia* from Taiwan. However, so far, tetraploid cytotype has never been found, even though Ebihara et al. (2014) and I (the present study) cytologically reexamined four and five individuals of *D. varia*, respectively, from the same localities in Taiwan, respectively. Lin et al. (1995) reported one individual of the “diploid apogamous” form from Mie pref., Japan. However, they did not indicate voucher specimen, and it is impossible to confirm the information. Hirabayashi (1966, 1967) also reported the diploid apogamous cytotype from Mie pref. and Wakayama pref., Japan. He did not indicate voucher specimen. Taxonomy of the *D. varia* complex is confused, and the plants of *D. hikonensis* might be often misidentified as *D. varia* because they are similar in gross morphology.

Habitat and distribution. Warm temperature to subtropical evergreen forests. Japan (Honshu, Shikoku, Kyushu, Ryukyu), Korea, the mainland of China, Taiwan, India, Thailand, Indochina, and the Philippines. The distribution map for Japan is shown in Figure 3-12b.

Japanese name. Nankai-Itachishida.

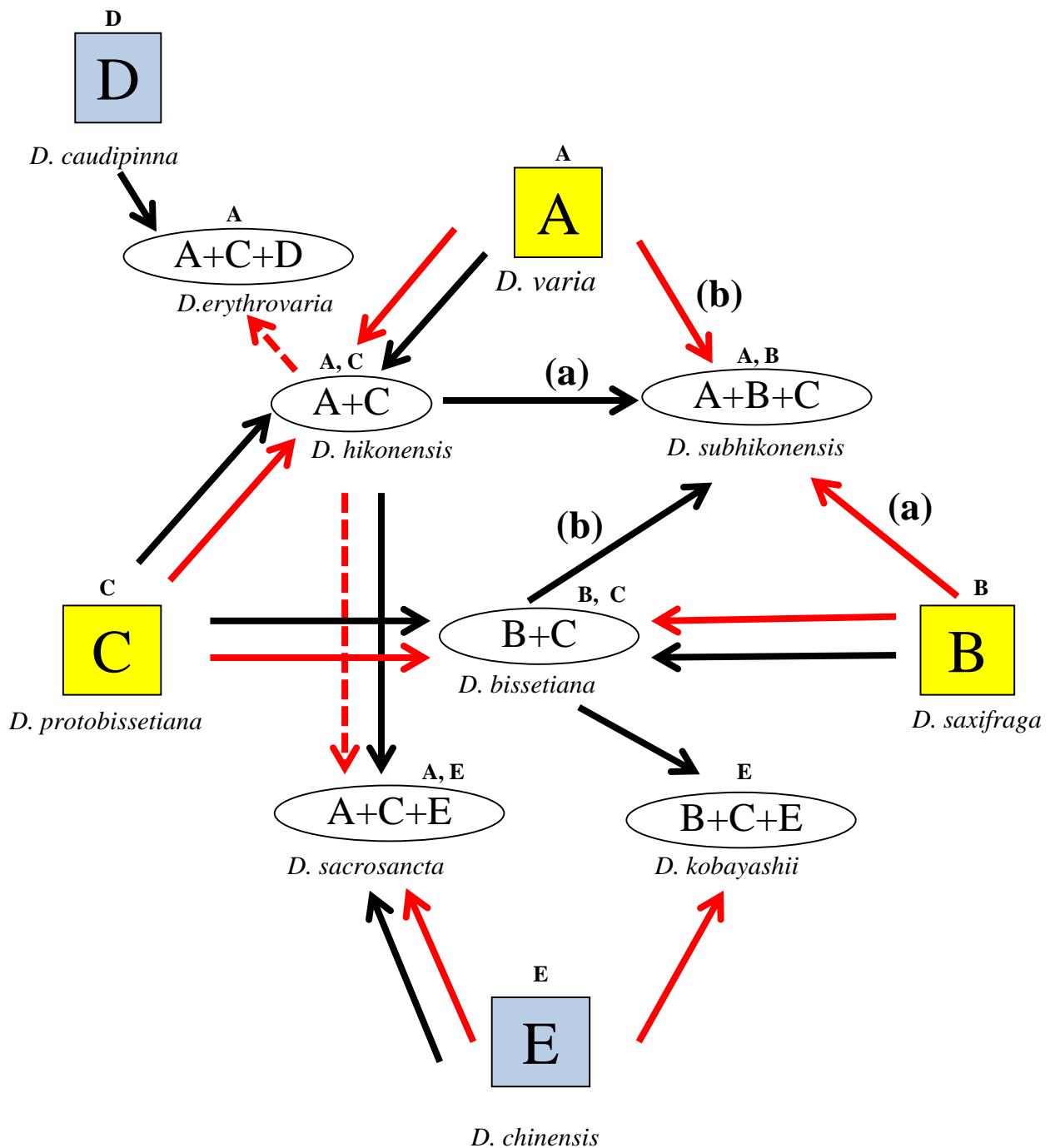


Figure 3-1. The reticulogram of the *Dryopteris varia* complex and revised scientific name of each species. This figure is the same as Figure 1-3 except that revised scientific names for the three types of *D. pacifica* (α , β , γ) are indicated as *D. hikonensis*, *D. subhikonensis* and *D. erythrovaria*, respectively.

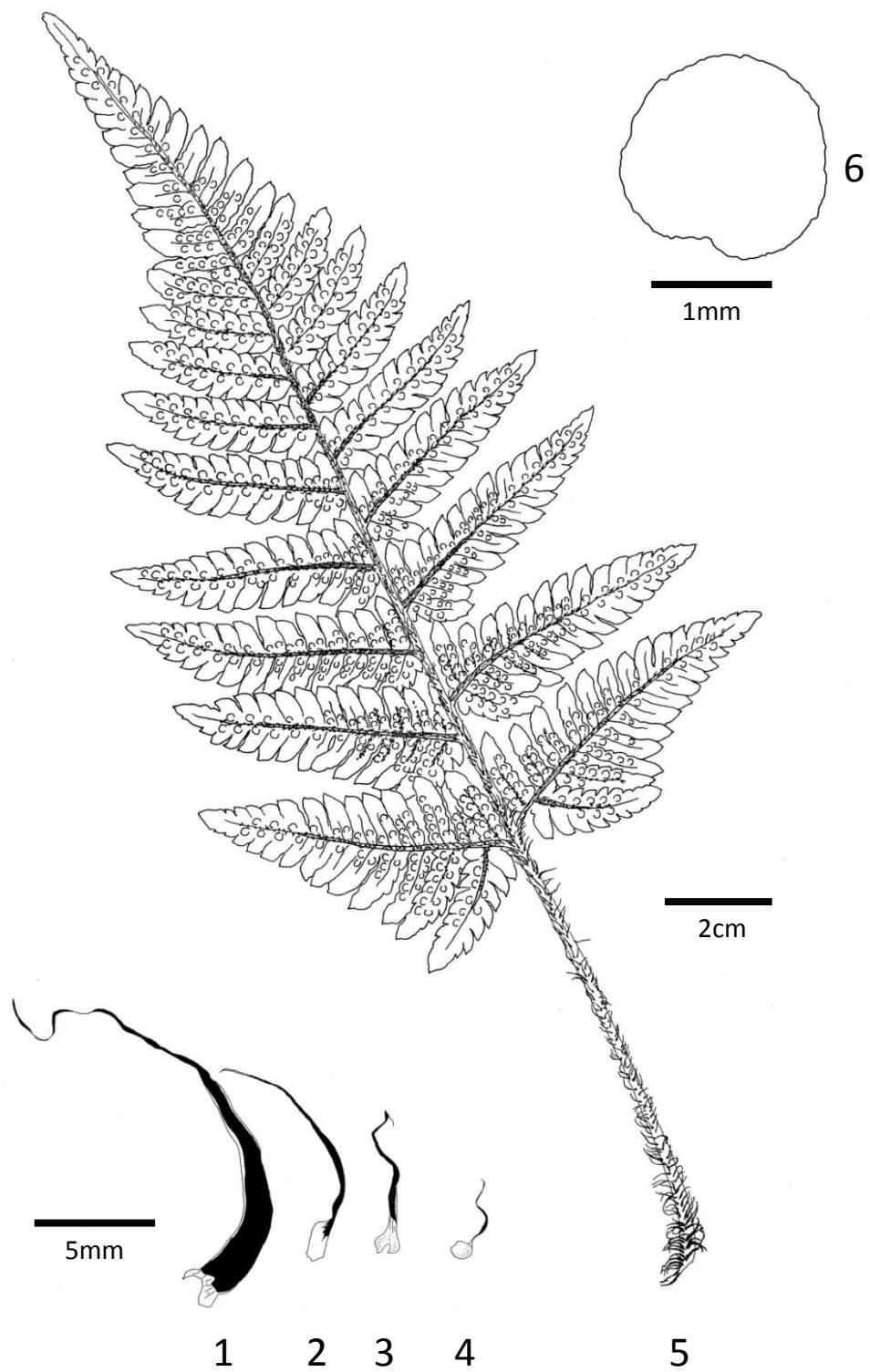


Figure 3-2a. *Dryopteris bissetiana* (Baker) C.Chr. 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from the specimen of MAK 449107).



Figure 3-2b. The distribution map of *Dryopteris bissetiana* (Baker) C.Chr. in Japan.

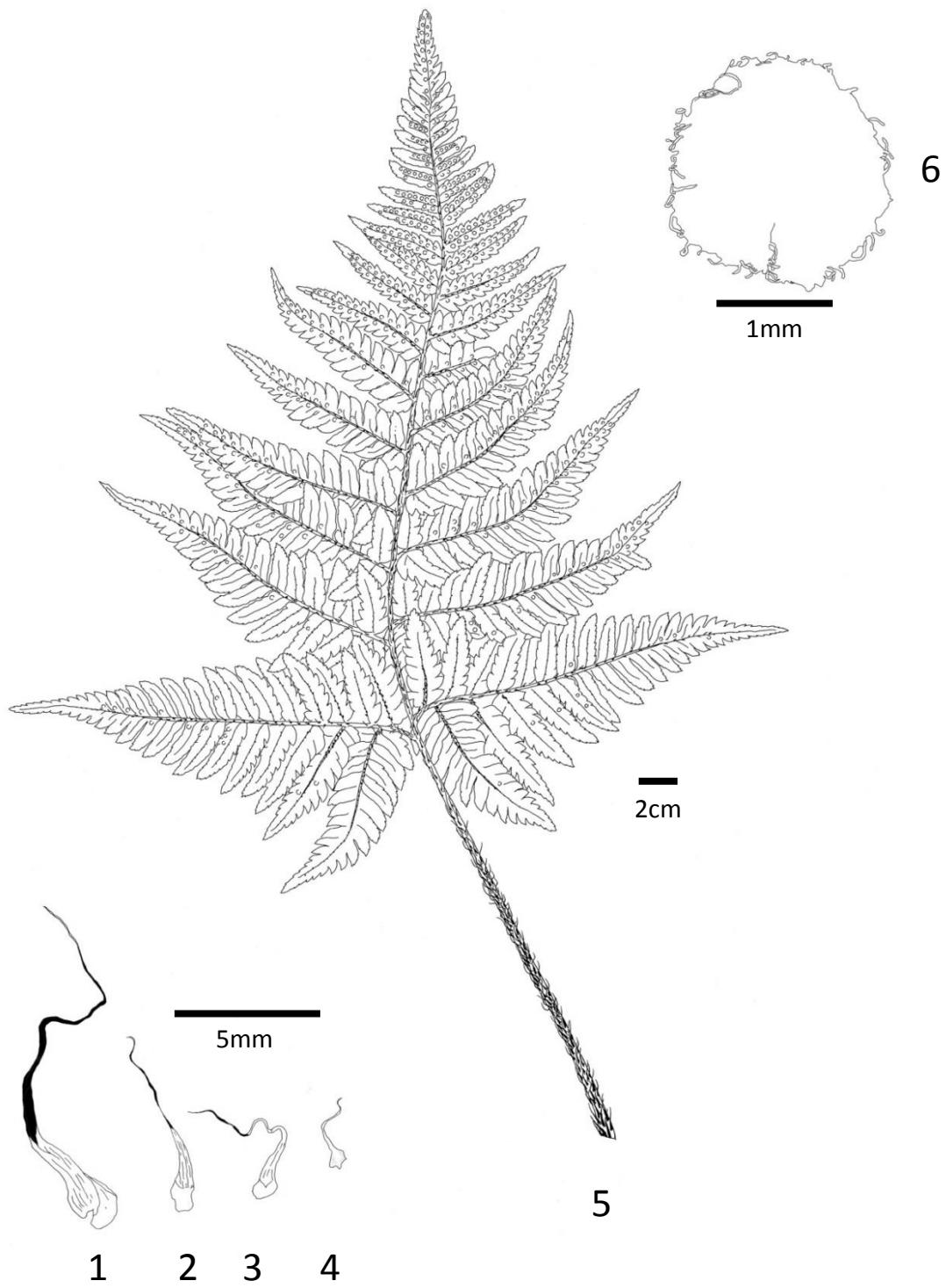


Figure 3-3a. *Dryopteris chichisimensis* Nakai ex H. Ito 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from the specimen of MAK 449110).



Figure 3-3b. The distribution map of *Dryopteris chichimensis* Nakai ex H. Ito in Japan.

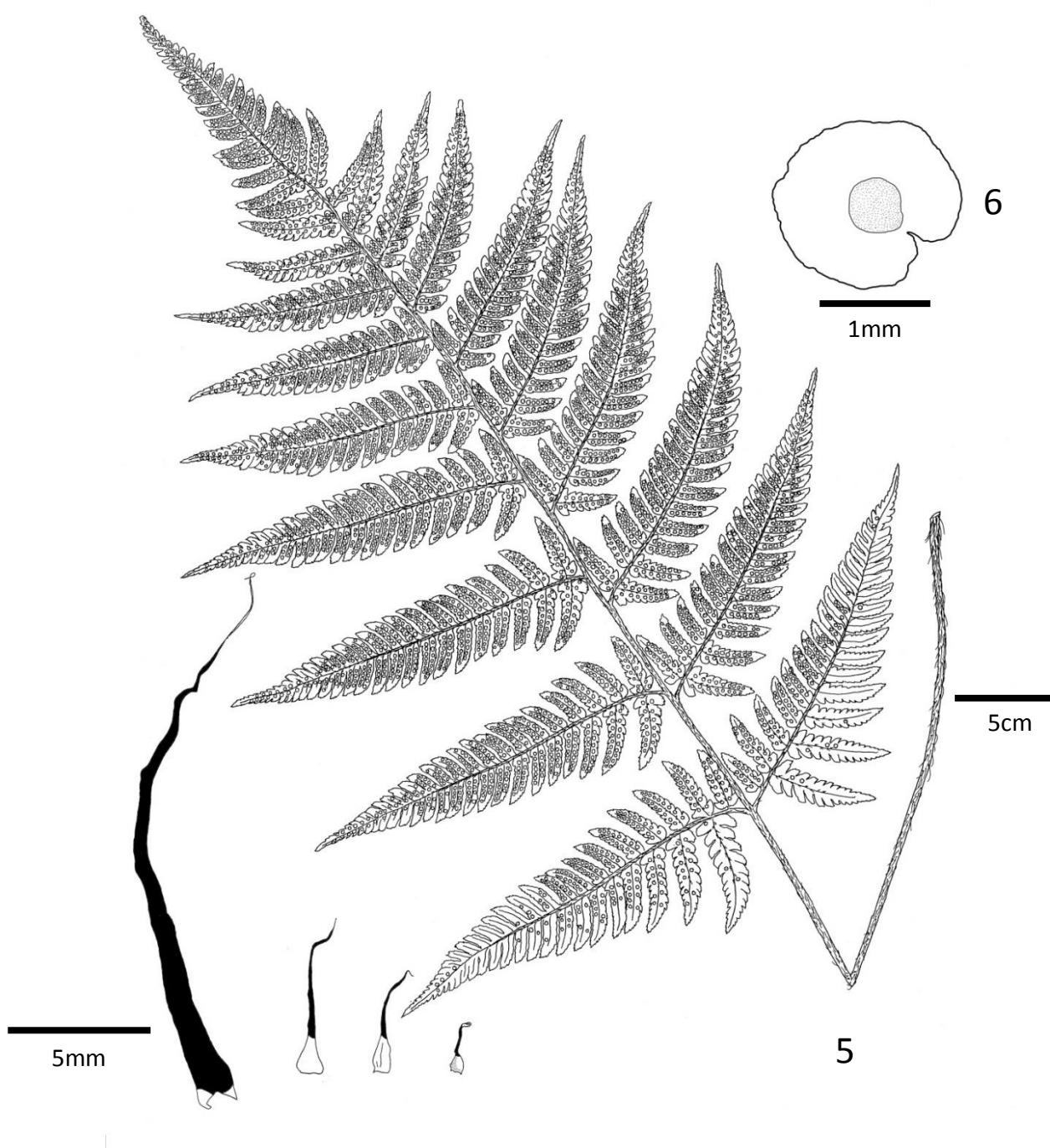


Figure 3-4a. *Dryopteris erythrovaria* K. Hori et N. Murak. 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from type specimen of MAK 449109).

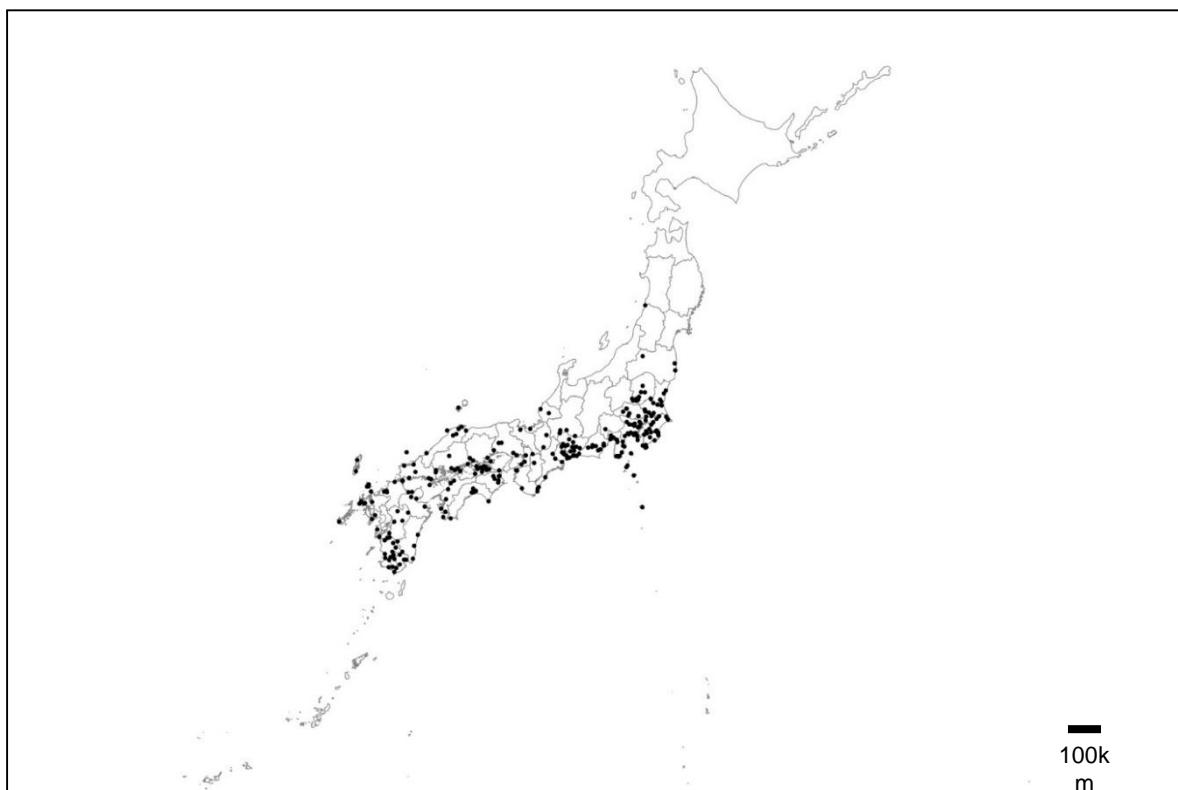


Figure 3-4b. The distribution map of *Dryopteris erythrovaria* K.Hori et N.Murak. in Japan.

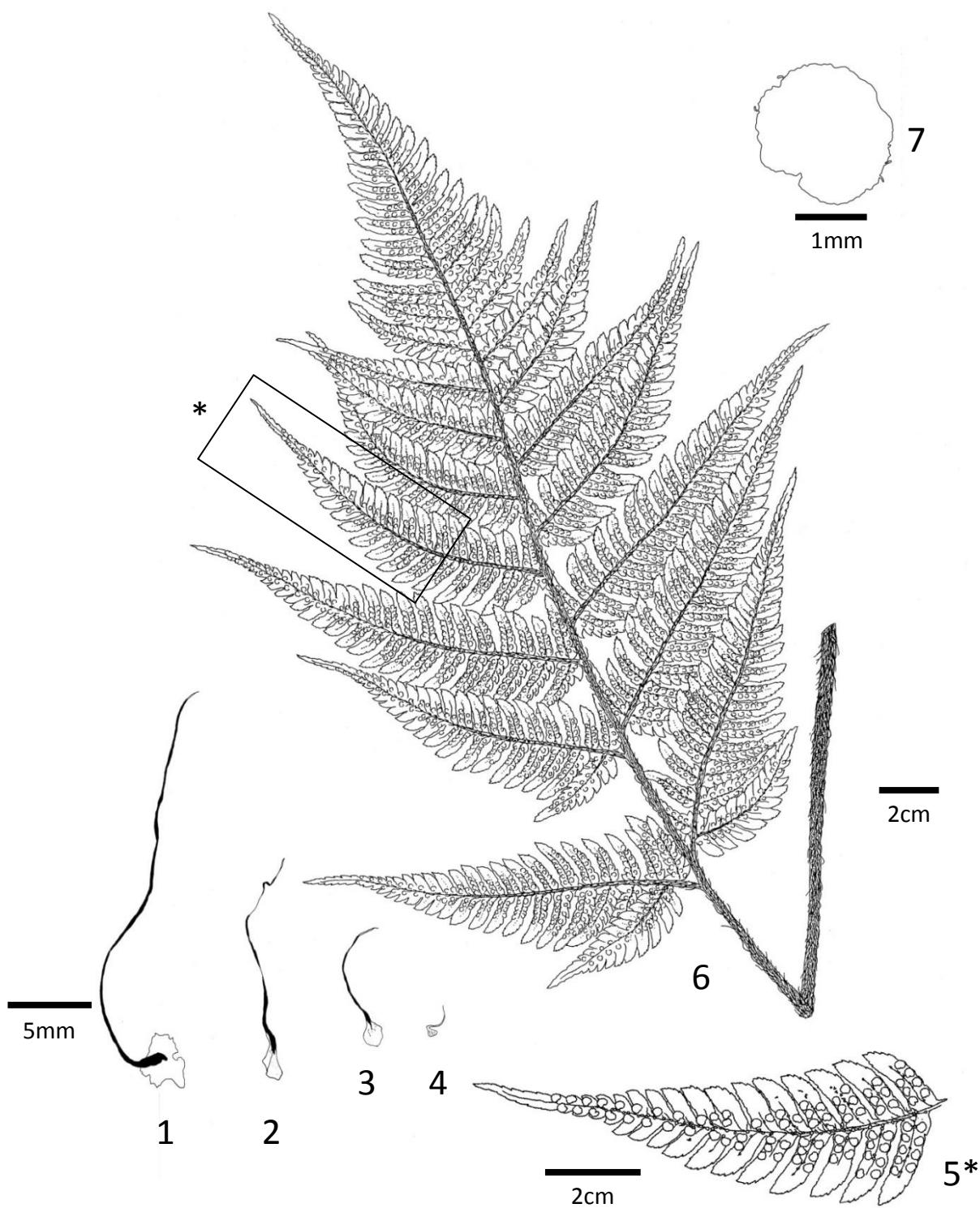


Figure 3-5a. *Dryopteris hikonensis* (H. Ito) Nakaike 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of upper pinnae. 6: abaxial surface of frond. 7: indusium. (drawn from the specimen of MAK 449113).

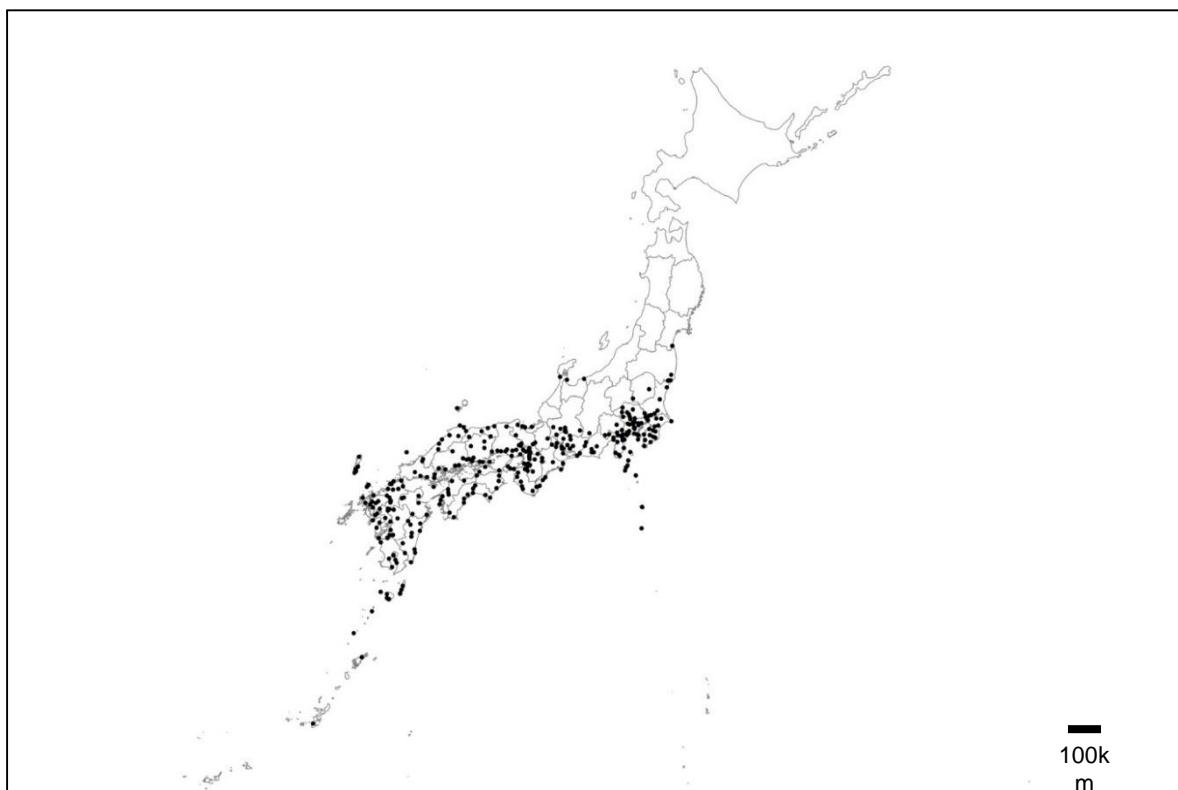


Figure 3-5b. The distribution map of *Dryopteris hikonensis* (H. Ito) Nakaike in Japan.

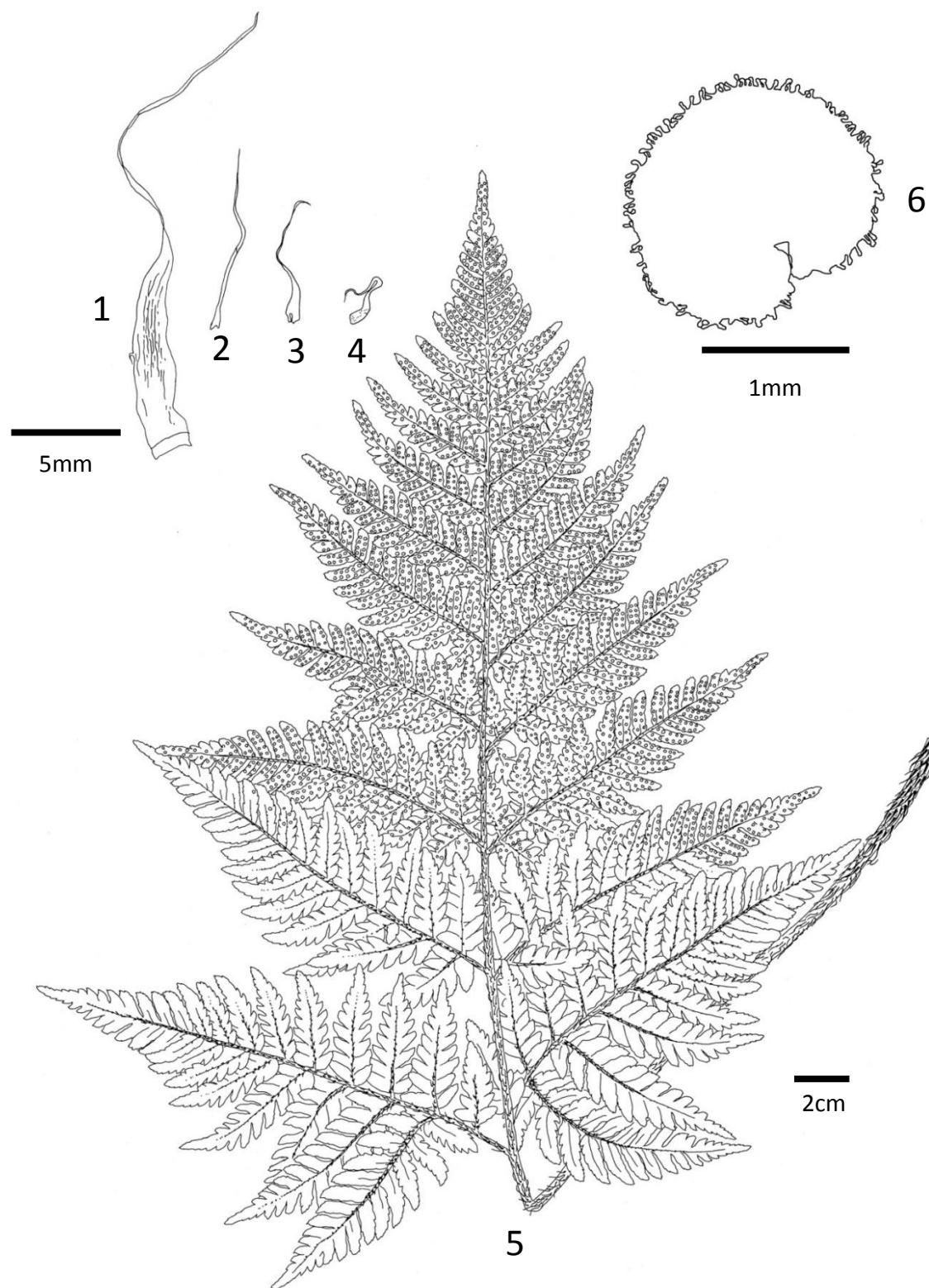


Figure 3-6a. *Dryopteris insularis* Kodama 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from the specimen of MAK 449111).



Figure 3-6b. The distribution map of *Dryopteris insularis* Kodama in Japan.

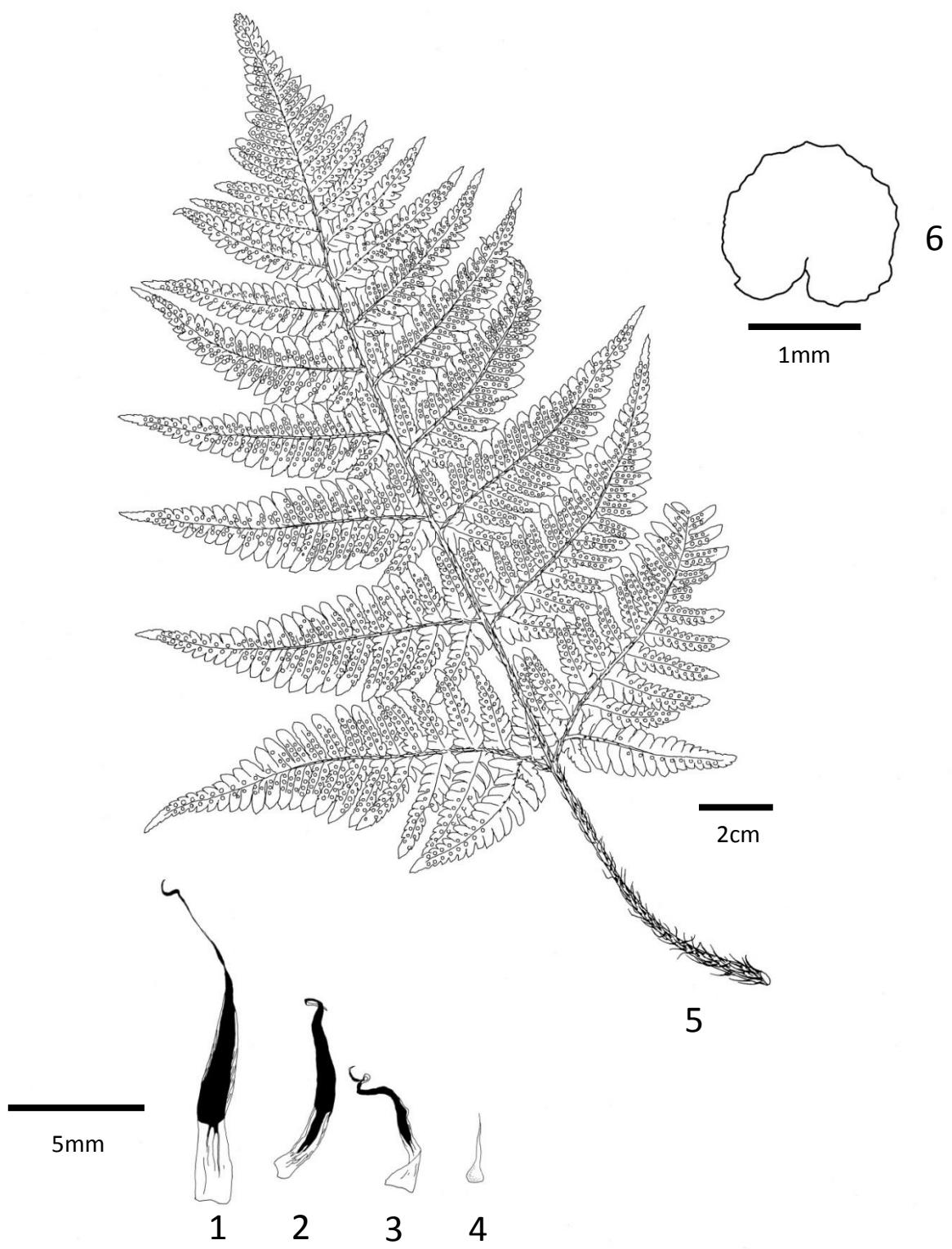


Figure 3-7a. *Dryopteris kobayashii* Kitagawa 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from the specimen of MAK 449112).



Figure 3-7b. The distribution map of *Dryopteris kobayashii* Kitagawa in Japan.

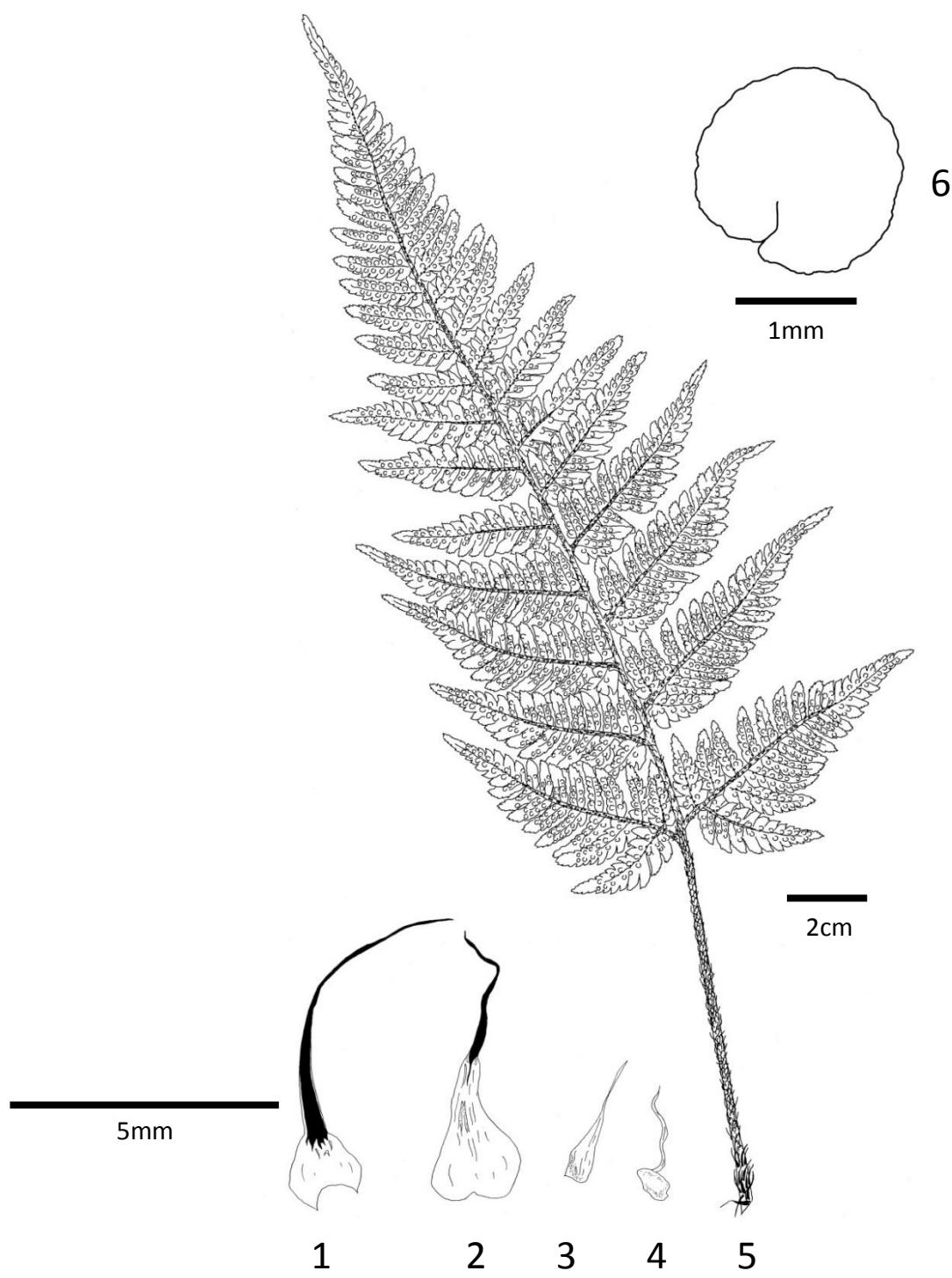


Figure 3-8a. *Dryopteris protobissetiana* K. Hori et N. Murak. 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from type specimen of MAK 449114).



Figure 3-8b. The distribution map of *Dryopteris protobissetiana* K.Hori et N.Murak. in Japan.

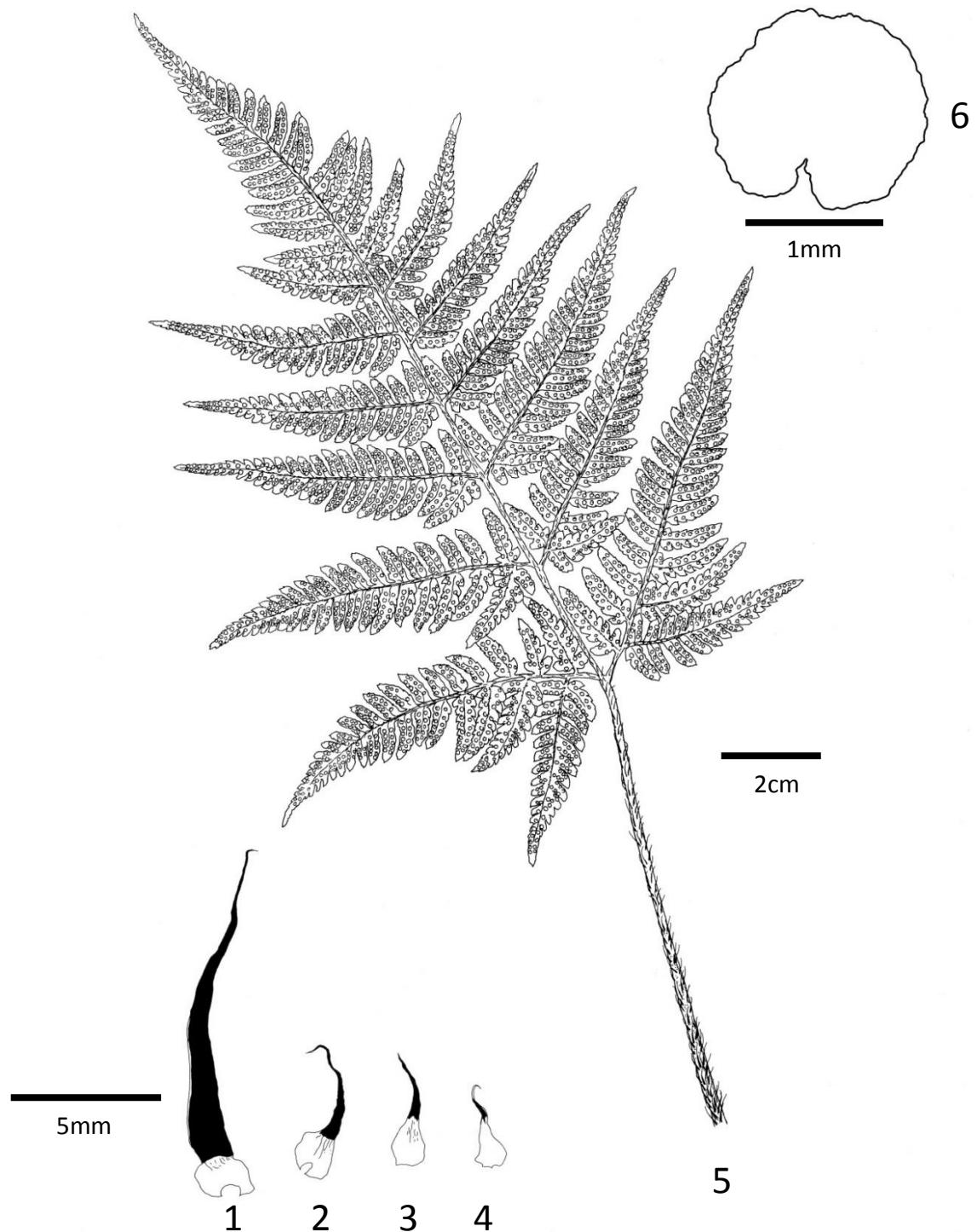


Figure 3-9a. *Dryopteris sacrosancta* Koidz. 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from the specimen of MAK 449115).

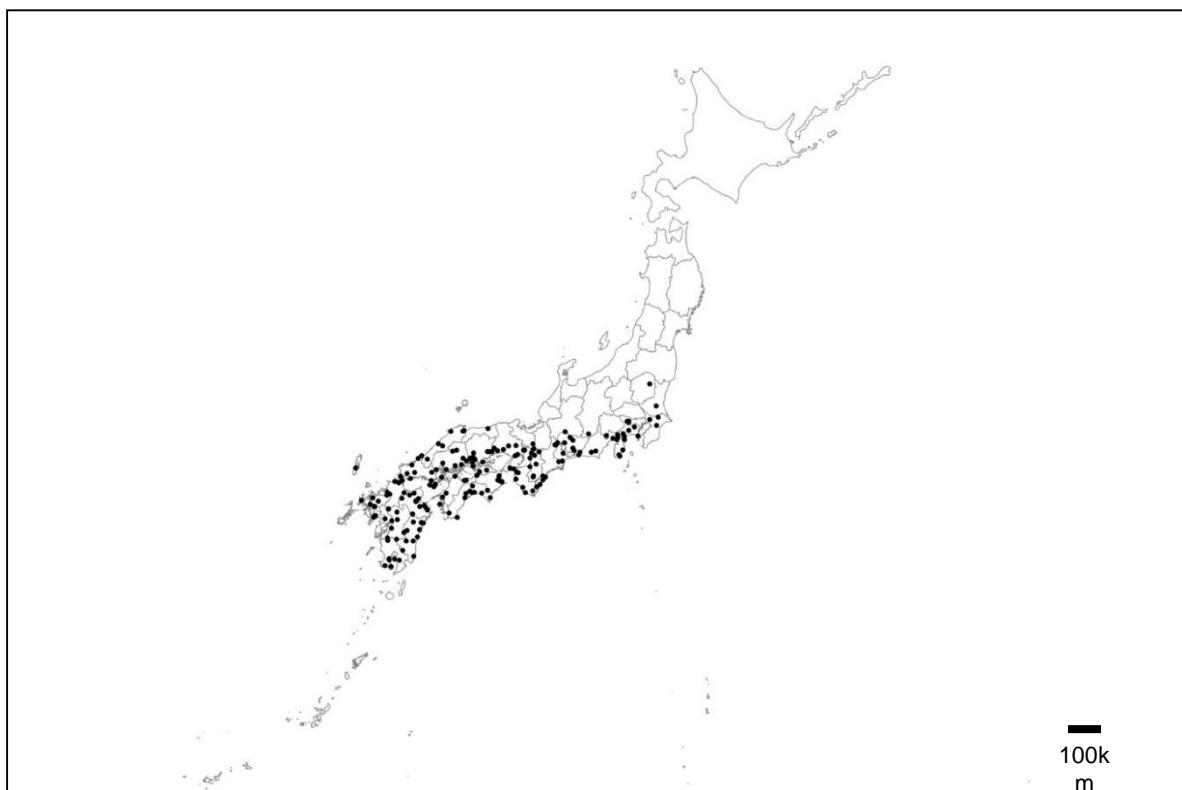


Figure 3-9b. The distribution map of *Dryopteris sacrosancta* Koidz. in Japan.

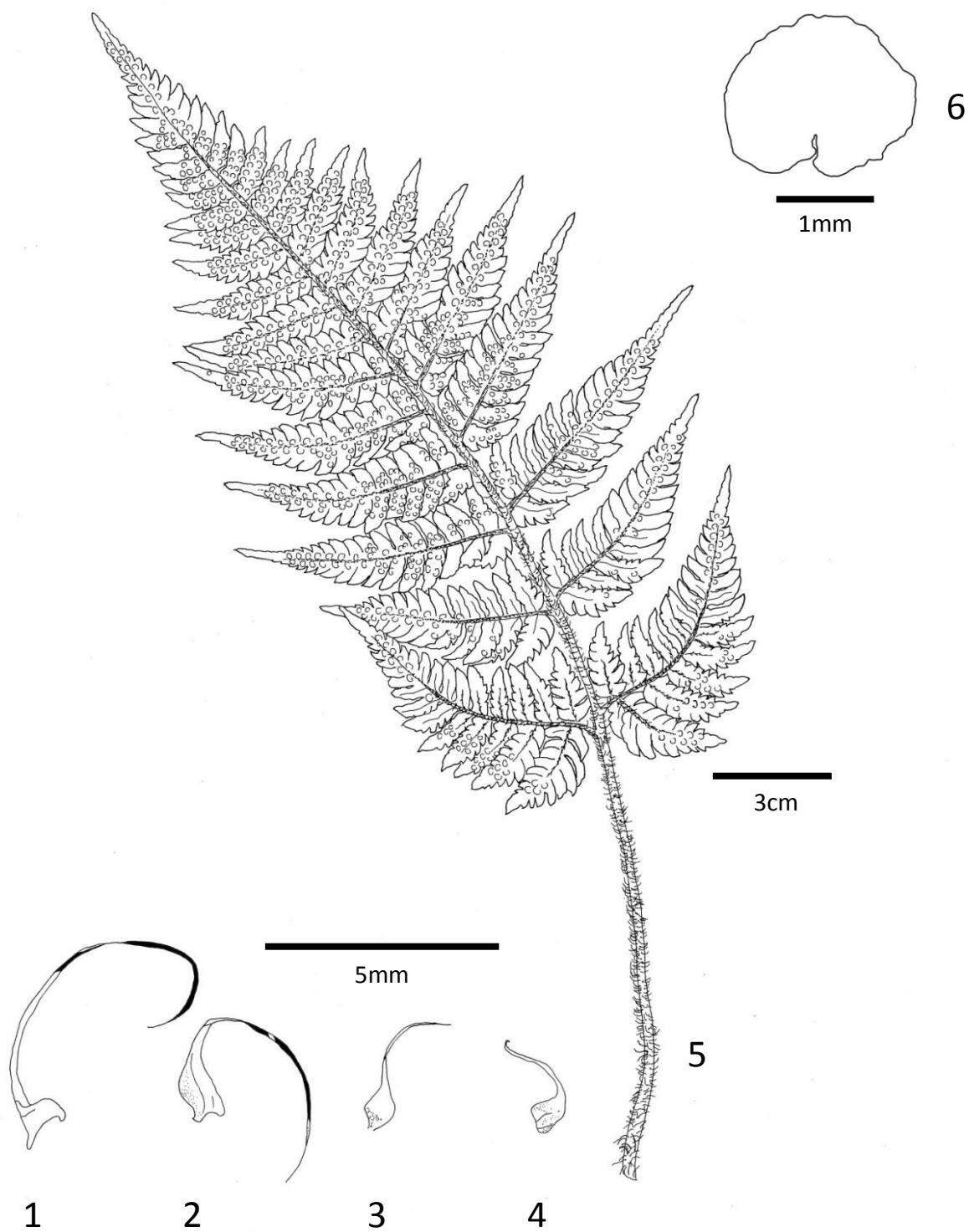


Figure 3-10a. *Dryopteris saxifraga* H. Ito 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from the specimen of MAK 44916).



Figure 3-10b. The distribution map of *Dryopteris saxifraga* H. Ito in Japan.

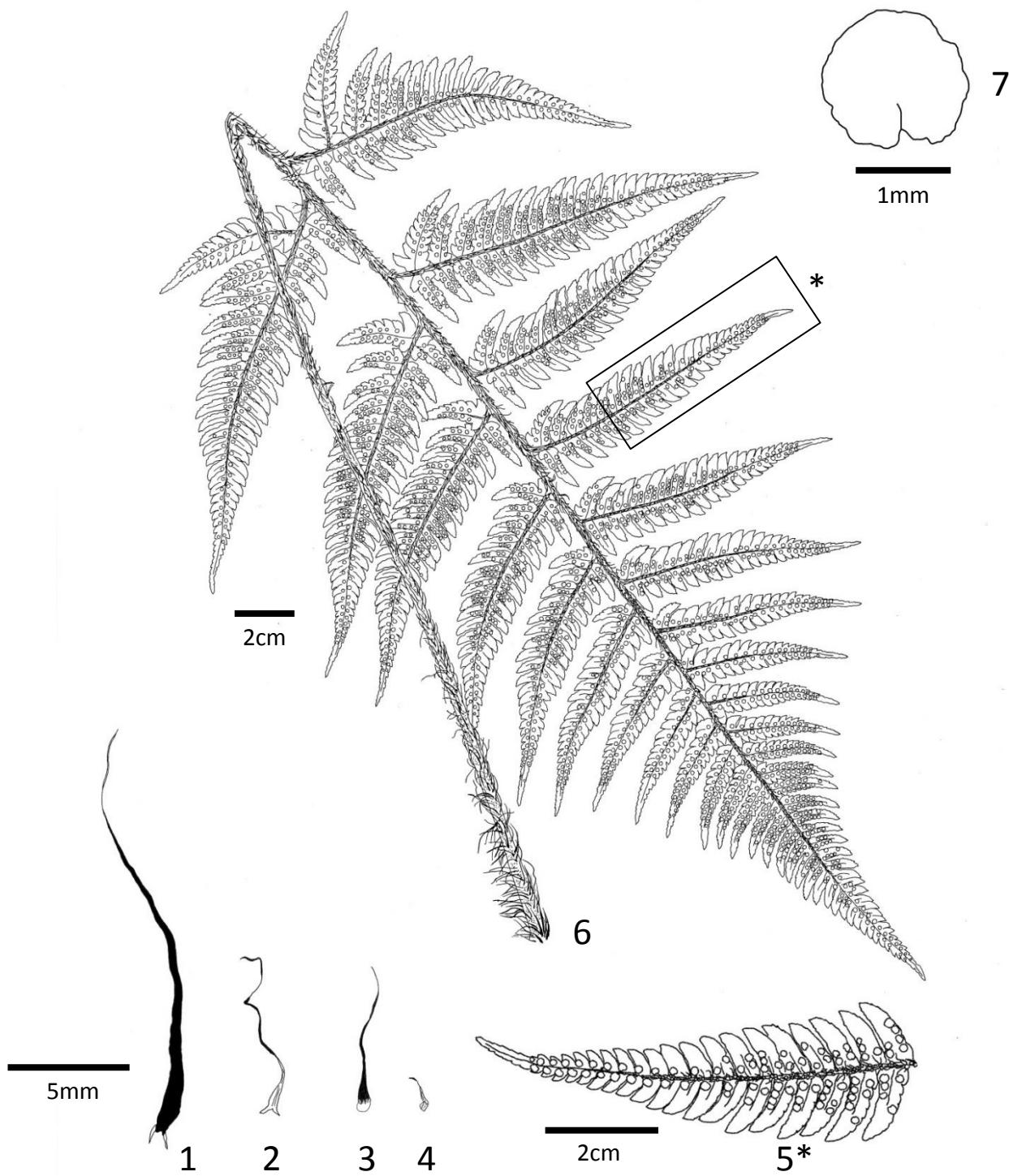


Figure 3-11a. *Dryopteris subhikonensis* K.Hori et N.Murak. 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of upper pinnae. 6: abaxial surface of frond. 7: indusium. (drawn from type specimen of MAK 449117).



Figure 3-11b. The distribution map of *Dryopteris subhikonensis* K. Hori. et N. Murak. in Japan.

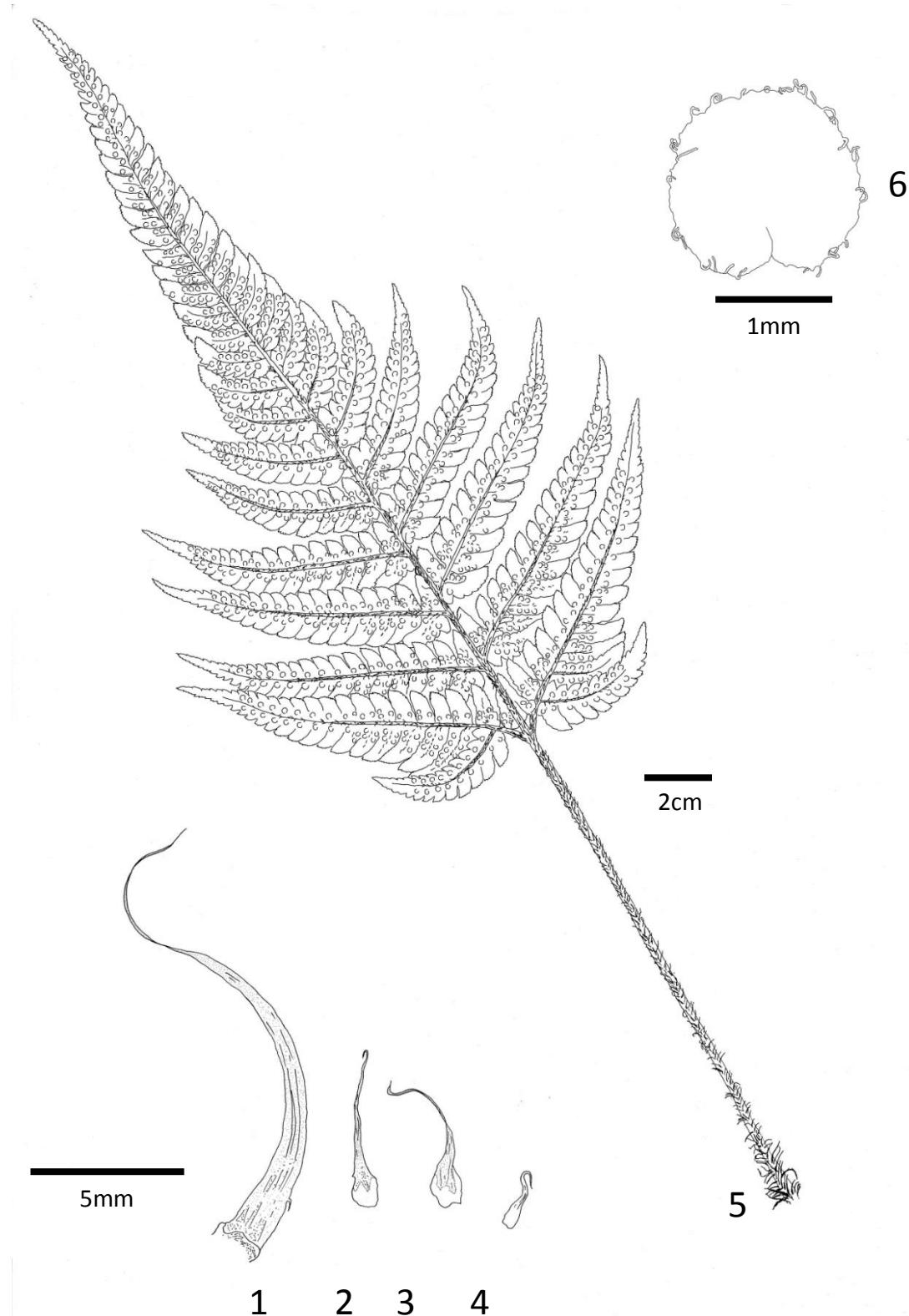


Figure 3-12a. *Dryopteris varia* (L.) Kuntze 1-4: Morphology of the scales on basal petioles, upper petioles, rachis and pinna rachises. 5: abaxial surface of frond. 6: indusium. (drawn from the specimen of MAK449120).



Figure 3-12b. The distribution map of *Dryopteris varia* (L.) Kuntze in Japan.

Appendix 3-1. Additional specimens of the *Dryopteris varia* complex are examined. Only the name of the first collector is shown.

Species	TNS	MAK	MBK	PE	Year	Month	Date	Coll.	Locality
<i>D. varia</i>	363460				1975	12	17	M. Yokota	Hiroshima pref., Aki county, Gamagari town
<i>D. varia</i>	359446				1980	1	27	S. Mitani	Kagawa pref., Shouzu county, Tonosho town
<i>D. varia</i>	359536				1976	5	23	S. Mitani	Kagawa pref., Sakaide city, Mt. Iino
<i>D. varia</i>	360805				1974	12	15	S. Mitani	Kagawa pref., Takamatsu city, Yashima
<i>D. varia</i>	374190				1975	5	11	S. Mitani	Kagawa pref., Takamatsu city, Mt. Mineyama
<i>D. varia</i>	359487				1980	2	3	S. Mitani	Kagawa pref., Mitoyo county, Mino town
<i>D. varia</i>	346302				1985	12	26	T. Miyazaki	Kochi pref., Takaoka county, Nakatosa town
<i>D. varia</i>	371466				1978	1	15	K. Yamaoka	Kochi pref., Tosashimizu city, Kubotsu
<i>D. varia</i>	371493				1976	4	4	T. Kouzai	Kochi pref., Takaoka county, Ochi town
<i>D. varia</i>	366907				1976	2	21	Y. Kougami	Kochi pref., Tosa city, Izuma
<i>D. varia</i>	366354				1976	7	4	T. Kouzai	Kochi pref., Aki city, Iogi
<i>D. varia</i>	361883				1978	9	10	T. Kouzai	Kochi pref., Muroto city, Hane town, Nakakawachi
<i>D. varia</i>	346260				1978	3	21	K. Tamaki	Kochi pref., Hata county, Ootsuki town, Kashiwajima
<i>D. varia</i>	347284				1978	3	22	K. Tamaki	Kochi pref., Tosashimizu city, Shimokawaguchi
<i>D. varia</i>	368370				1977	5	28	T. Kouzai	Kochi pref., Tosashimizu city, Matsuo
<i>D. varia</i>	346296				1979	3	4	K. Yamaoka	Kochi pref., Takaoka county, Nakatosa town
<i>D. varia</i>	346253				1974	10	21	T. Nakaike	Kochi pref., Tosashimizu city, Kubotsu
<i>D. varia</i>	346282				1976	6	13	T. Kouzai	Kochi pref., Muroto city, Kiragawa town, Nichinann
<i>D. varia</i>	346310				1977	12	28	K. Yamaoka	Kochi pref., Tosa city, Usa town
<i>D. varia</i>	346309				1977	12	28	K. Yamaoka	Kochi pref., Tosa city, Takaoka town
<i>D. varia</i>	346366				1972	12	23	S. Mitsuta	Kochi pref., Takaoka county, Ochi town
<i>D. varia</i>	361391				1982	8	30	N. Niwaki	Saga pref., Fujitsu county, Ureshino town, Yunoda
<i>D. varia</i>	359257				1975	11	2	Y. Kurashige	Saga pref., Ogi county, Ushizu town
<i>D. varia</i>	359437				1975	4	27	H. Koike	Saga pref., Kashima city, Mikawachi
<i>D. varia</i>	359482				1976	5	2	T. Baba	Saga pref., Fujitsu county, Ureshino town, Kogui
<i>D. varia</i>	359347				1975	3	21	M. Koike	Saga pref., Taku city, Kitataku town
<i>D. varia</i>	359752				1973	10	4	S. Komaki	Mie pref., Kumano city
<i>D. varia</i>	359797				1976	5	2	Y. Nakajima	Mie pref., Minamimuro county, Mihamo town
<i>D. varia</i>	359662				1975	11	22	A. Yamamoto	Mie pref., Owase city, Oosoneura
<i>D. varia</i>	363640				1989	1	8	K. Seto	Mie pref., Kitamuro county, Kiinagashima
<i>D. varia</i>	363550				1967	10	19	H. Ito	Mie pref., Owase city, Yukino beach
<i>D. varia</i>	900768				1978	3	27	R. Ito	Mie pref., Owase city, Hayata
<i>D. varia</i>	359682				1979	10	14	A. Minami	Yamaguchi pref., Kumage county, Kaminoseki town
<i>D. varia</i>	359772				1988	9	19	H. Masaki	Yamaguchi pref., Shimomatsu city, Kannonn
<i>D. varia</i>	359916				1977	9	6	A. Minami	Yamaguchi pref., Hikari city, Ushima Island
<i>D. varia</i>	360124				1990	8	7	A. Minami	Yamaguchi pref., Iwakuni city, Hashirajima Island
<i>D. varia</i>	360222				1976	4	11	H. Masaki	Yamaguchi pref., Boufu city, Nojimaakazaki
<i>D. varia</i>	345235				1980	8	14	A. Minami	Yamaguchi pref., Kumage county, Kaminoseki town
<i>D. varia</i>	361930				1982	2	14	A. Minami	Yamaguchi pref., Yanai city, Heigunn
<i>D. varia</i>	361885				1953	9	28	K. Oka	Yamaguchi pref., Kaminoseki town, Iwaishima Island
<i>D. varia</i>	361791				1964	10	19	S. Miyake	Yamaguchi pref., Boufu city, Mukojima Island
<i>D. varia</i>	361746				1989	1	25	A. Minami	Yamaguchi pref., Yanai city, Hizumi
<i>D. varia</i>	361705				1956	11	10	T. Hashimoto	Shiga pref., Hino town, Mt. Yotsugase
<i>D. varia</i>	361615				1985	8	18	T. Yamanaoka	Kagoshima pref., Kimotsuki county, Sata town
<i>D. varia</i>	360627				1960	1	24	T. Yamanaoka	Kagoshima pref., Imizu city, Ayukawa
<i>D. varia</i>	361480				1975	4	4	M. Hioki	Kagoshima pref., Kajiki city, Takaika
<i>D. varia</i>	361435				1985	1	21	M. Kawabata	Kagoshima pref., Kagoshima city, Hirakawa town
<i>D. varia</i>	361345				1986	10	26	T. Kariyazaki	Kagoshima pref., Minamitane town, Shimama
<i>D. varia</i>	361841				1987	4	17	T. Kariyazaki	Kagoshima pref., Minamitane town, Nojiri
<i>D. varia</i>	361526				1988	6	15	T. Kariyazaki	Kagoshima pref., Nishinoomote city, Sumiyoshi
<i>D. varia</i>	360331				1986	10	12	T. Kariyazaki	Kagoshima pref., Nishinoomote city, Waseda river
<i>D. varia</i>	359997				1984	3	4	K. Kawahara	Kagoshima pref., Yubisuki city, Mt. Uomidake
<i>D. varia</i>	360267				1980	3	16	M. Shiroto	Kagoshima pref., Akune city, Kuronohama
<i>D. varia</i>	359401				1985	1	21	M. Kawabata	Kagoshima pref., Kagoshima city, Hirakawa town, Mt. Eboshidake
<i>D. varia</i>	360175				1977	8	5	K. Takesako	Kagoshima pref., Soo county, Shibushi town, Mt. Gozaisyodake
<i>D. varia</i>	334578				1975	10	25	N. Miyaji	Kagoshima pref., Nishinoomote city, Furuta
<i>D. varia</i>	1219419				1977	1	27	T. Nakaike	Kagoshima pref., Kumage county, Nakatane town, Adakaiso
<i>D. varia</i>	1219424				1974	3	23	K. Takesako	Kagoshima pref., Satsuma county, Shimokoshiki village
<i>D. varia</i>	1219429				1977	1	29	K. Takesako	Kagoshima pref., Kawanabe county, Bountotsu town, Jinnoo
<i>D. varia</i>	1219431				1977	2	6	K. Takesako	Kagoshima pref., Kawanabe county, Kasasa town
<i>D. varia</i>	1219434				1975	2	26	K. Kawahara	Kagoshima pref., Imizu county, Nagashima town
<i>D. varia</i>	1219436				1977	1	16	K. Takesako	Kagoshima pref., Kaseda city, Mt. Nagaya
<i>D. varia</i>	360069				1959	9	10	T. Yamanaoka	Kagoshima pref., Tarumi city, Enoshima
<i>D. varia</i>	360427				1973	7	8	K. Takesako	Kagoshima pref., Kagoshima county, Yoshida town
<i>D. varia</i>	360337				1973	12	12	K. Takesako	Kagoshima pref., Aira city, Kamou town
<i>D. varia</i>	360063				1976	8	2	K. Takesako	Kagoshima pref., Kimotsuki county, Satta town
<i>D. varia</i>	397423				1976	8	4	K. Takesako	Kagoshima pref., Kimotsuki county, Nejime town
<i>D. varia</i>	362470				1985	1	21	M. Kawabata	Kagoshima pref., Kagoshima city, Hirakawa town
<i>D. varia</i>	362110				1976	7	21	K. Takesako	Kagoshima pref., Aira city, Fukuyma town, Isowaki
<i>D. varia</i>	360846				1986	5	10	T. Kariyazaki	Kagoshima pref., Nishinoomote city, Tenmyogakura
<i>D. varia</i>	361210				1976	3	31	A. Yamamoto	Kagoshima pref., Satsuma county, Shimokoshiki village
<i>D. varia</i>	363469				1959	8	28	M. Shiroto	Kagoshima pref., Kimotsuki county, Sata town
<i>D. varia</i>	1219466				1940	5	23	K. Ochi	Kagoshima pref., Ibusuki city, Yamakawa town
<i>D. varia</i>	1219471				1982	9	25	K. Kawahara	Kagoshima pref., Ibusuki city, Higashikata

General Discussion

In this thesis, I have attempted to clarify the origin of the apogamous species of the *Dryopteris varia* complex on the basis of the “hybridization cycle hypothesis” by Lin *et al.* (1992). Lin *et al.* (1992) discovered unequal meiosis in the triploid apogamous sporophytes of *D. pacifica* (now *D. hikonensis* according to my new classification system), which produces diploid apogamous gametophytes and diploid apogamous sporophytes. The hybridization cycle hypothesis, which was proposed based on the finding of unequal meiosis, is the most effective way to explain the origin of morphological and genetic variations in a triploid apogamous fern complex. Later, Yamamoto (2013) discovered that a triploid apogamous species, *D. erythrosora*, can produce triploid apogamous hybrids through hybridization with a related diploid sexual species, *D. caudipinna*, under experimental conditions of their artificial crossing experiments. However, it is unclear how hybridization cycles contribute to the genetic diversification of a triploid apogamous fern complex in nature. This thesis is the first study that elucidated the hybrid origins of each species of a triploid apogamous fern complex considering the hybridization cycle hypothesis.

In Chapter 1, I clarified the reticulate evolution of the *Dryopteris varia* complex through hybridization between triploid apogamous species and diploid sexual species using a nuclear single copy gene, *PgiC*, as the nuclear genetic marker. The *PgiC* sequences of each diploid sexual species of the *D. varia* complex were distinguished and named as follows: *D. varia*, A; *D. saxifraga*, B; *D. protobissetiana*, C; *D. caudipinna*(+*D. koidzumiana*), D; *D.*

chinensis, E; *D. insularis*, M. Moreover, each apogamous species of the complex had two or three of the *PgiC* sequences in those of the diploid species as follows: *D. pacifica* (α), A+C; *D. pacifica* (β), A+B+C; *D. pacifica* (γ), A+C+D; *D. bissetiana*, B+C; *D. sacrosancta*, A+C+E; *D. kobayashii*, B+C+E; *D. insularis* var. *chichisimensis*, A+C+M. Thus, some of the triploid apogamous species had three *PgiC* sequences, suggesting that recurrent reticulation should have occurred through hybridization cycles.

Dryopteris protobissetiana, one of the diploid sexual species of the *D. varia* complex listed above, was a new species, which I fortunately discovered in Yakushima Island. Thousands of specimens of the *D. varia* complex have been collected from the entire area of Japan. However, only a few specimens of *D. protobissetiana* have been collected from the narrow areas of the western and southern parts of Yakushima Island. It was difficult to find them from the large number of specimens because each species of the complex demonstrates continuous morphological variation. *Dryopteris protobissetiana* is considered to be endemic to Yakushima Island because I was unable to find a specimen of this species even among those collected from the nearby Islands of Yakushima, such as the Amami Islands, Kuchinoerabu Island, Tanegashima Island, the Tokara Islands as well as from China, Korea, or Taiwan. The genome of *D. protobissetiana* (Type C) was widely shared by most members of the triploid apogamous species of the *D. varia* complex in contrast to the geographical distribution area of *D. protobissetiana*, which is narrower than that of the other members of the complex. It is likely that *D. protobissetiana* was widely distributed in Japan

earlier but that its distribution range shrank due to competition and/or repeated hybridization with related diploid sexual and triploid apogamous species of the *D. varia* complex.

In Chapter 1, it is important to note that I discovered some members of the *Dryopteris varia* complex with the nuclear *PgiC* sequences of *D. caudipinna* and *D. chinensis*, which are not members of the complex but which belong to other section or subgenus of *Dryopteris*. Furthermore, this finding helped to solve the issues regarding the origin of large morphological variations in the *D. varia* complex. The contributions of these two species to the diversification of the *D. varia* complex have never been conceived because clear differences in morphological characteristics are observed between them. *Dryopteris caudipinna* is a diploid sexual species mainly distributed in the Izu Islands, the Oki Islands, and Tsushima Island and rarely distributed in mainland Japan. *Dryopteris chinensis*, from which only triploid apogamous cytotype was reported, is distributed in Japan and surrounding countries. I found that the *PgiC* sequence of this species is shared by the triploid apogamous members of the *D. varia* complex: *D. kobayashii* and *D. sacrosancta*. Later, I fortunately discovered the diploid sexual cytotype of *D. chinensis* from Miyazaki Prefecture, Japan by checking thousands of specimens in the herbaria (MAK, TNS). The diploid sexual cytotype of *D. chinensis* was not found probably because its distribution area is much narrower than that of the triploid apogamous cytotype.

Dryopteris caudipinna and *D. chinensis* have never been included as

members of the *D. varia* complex because of the large differences in their morphological characteristics from the complex. However, in a molecular phylogenetic tree based on the nucleotide sequences of the plastid *rbcL* gene (Figure 1-2, 2-10), these two species seemed to be relatively closely related to the *D. varia* complex in the entire genus of *Dryopteris*. This means that morphological characteristics do not necessarily reflect phylogenetic relationships. Therefore, for elucidating the origin of triploid apogamous fern species, it is indispensable to collect geographically and phylogenetically wide samples and examine their reproductive mode and ploidy level. I collected such samples and conducted all of the analyses in this study.

In Chapter 2, I analyzed five nuclear markers—*AKI*, *Esterase*, *GapCp*, *G6pdh*, and *PgiC*—for the same plant materials as in Chapter 1 and additional materials of the *Dryopteris varia* complex to clarify whether chromosome recombination by recurrent reticulation through hybridization cycles occurs. As a result, the genotypes of each sample, including triploid apogamous individuals, were the same among the five nuclear loci. Recurrent reticulations accompanying chromosomal recombination seem to occur only a few times in the *D. varia* complex because the genotypes (allele combinations) were the same among the five nuclear loci used in this study as nuclear genetic markers. The genotypes (allele combinations) of each sample of the apogamous species of the complex were the same among the five nuclear loci: apogamous cytotype of *D. varia*, A; diploid apogamous *D. pacifica* (α), AC; triploid apogamous *D. pacifica* (α), AAC, ACC, or A/C (A/C means either AAC or ACC); *D.*

pacifica (β), ABC; *D. pacifica* (γ), ACD; *D. bissetiana*, BCC or B/C; *D. sacrosancta*, ACE; *D. kobayashii*, BCE; *D. insularis* var. *insularis* (diploid apogamous), M (MM); *D. insularis* var. *chichisimensis*, ACM. The individuals which had allele of one nuclear marker had the genotypes “AAC” did not have the genotypes “ACC.” Similarly, the individuals which had allele of one nuclear marker had the genotypes “BCC” did not have the genotypes “BBC.” However, for “BBC”, I could not distinguish from “BCC” because there was not enough genetic variation in *D. saxifraga* (B). If more nuclear markers were analyzed, I may have been able to distinguish these genotypes and discuss whether there are chromosomal recombinations. Furthermore, in this study, I used only five nuclear markers, which are inadequate to uncover whether chromosomal recombination occurred in the whole genome because the base chromosome number of *Dryopteris* is 41 (Takamiya 1996). In the future, I would like to analyze nuclear markers covering loci on each of the 41 chromosomes.

In Chapter 3, I revised the classification of the *Dryopteris varia* complex based on the genome constitutions estimated by the five nuclear markers. Specifically, I revised *D. pacifica* (Nakai) Tagawa because the results in Chapter 2 clearly revealed that this apogamous species contains three species with different genome constitutions. The three types, α , β , and γ , of *D. pacifica* should be considered as distinct species. Moreover, the name *D. pacifica* (Nakai) Tagawa is an illegitimate name of *D. pacifica* Christ, which was published 13 years earlier than the former. I attributed the α type to *D. hikonensis* (H. Ito) Nakaike. I described the β type as *D. subhikonensis*

K.Hori et N.Murak and the γ type as *D. erythrovaria* K.Hori et N.Murak (Figure 3-1). The taxonomical problems of the apogamous fern complex have seldom been well resolved. Specifically, former Japanese pteridologists have considered that a clear classification is impossible for the apogamous species of the *D. varia* complex (Tagawa 1959, Iwatsuki 1995). This thesis is the first study that could revise the classification of the apogamous fern complex containing several triploid apogamous species on the basis of a clear standard: their genome constitutions.

This thesis is one of the best case studies on the evolution of the apogamous fern complex. Fern taxonomists should pay attention to several points when they discuss the evolutionary histories of the apogamous fern complex. Searches for diploid sexual species that are sources producing diversities of triploid apogamous species are indispensable. Even if DNA analyses using many nuclear genetic markers are performed without analyzing materials of diploid sexual species that contributed to the formation of the apogamous fern complex, it is impossible to identify the genomes contained in each apogamous species. However, it is difficult to completely collect all diploid sexual members as materials. Recent studies on the reticulate evolution of ferns had the problem of “missing diploid” (Dyer *et al.* 2012, Jaruwattanaphan *et al.* 2013, Sessa *et al.* 2012). Further, in the present study, it was most important to find the diploid sexual type *Dryopteris protobissetiana* in Yakushima Island and the diploid sexual type of *D. chinensis* from Miyazaki Prefecture, as previously noted. Without analyzing them, I could not have resolved the complicated reticulate

evolution in the *D. varia* complex (Figure 3-1).

Fern taxonomists who wish to solve problems in the apogamous fern complex may first have to survey diploid sexual species or cytotypes, but diploid sexual species are often distributed in restricted areas like in the case of *Dryopteris protobissetiana*, *D. caudipinna*, and the diploid sexual cytotype of *D. chinensis* in this study. Therefore, the sampling of plant materials from wide geographical areas is needed. Many specimens of ferns have been collected from all over the world and deposited in herbaria. Therefore, the distributions of diploid sexual species or cytotypes can be estimated by using these specimens. Counting spore numbers per sporangium in herbarium specimens is quite effective for discovering the localities of diploid sexual species, though 64 spores per sporangium do not necessarily indicate diploid sexual species because there are many polyploid sexual species in ferns (Takamiya 1996). To solve this problem, ploidy analysis and counting chromosomes using living stocks are necessary. Therefore, fern taxonomists have to conduct both methods to solve the taxonomical problems of the apogamous fern complex.

Once plant samples of almost all diploid sexual species are obtained, fern taxonomists have to develop nuclear DNA markers to distinguish their genomes. The plastid *rbcL* gene is the most frequently used DNA marker to distinguish biological species (Yatabe *et al.* 2009, Yamada *et al.* 2016). However, this gene is maternally inherited and is thus useful only for determining maternal parental species. *GapCp* and *PgiC* genes are the widely used biparentally inherited nuclear DNA markers of ferns (Dyer *et*

al. 2012, Grusz *et al.* 2009, Ishikawa *et al.* 2002, Jaruwattanaphan *et al.* 2013, Sessa *et al.* 2012). However, the reported PCR primers for these genes are often mismatched to various taxa of ferns. It is becoming easier to design new PCR primers because the databases of the transcriptome in ferns are also being enriched. In this study, I was able to search for effective nuclear genes to resolve the genome constitutions of the members of the apogamous fern complex using such databases. Presently, enzyme genes, which have been used for allozyme electrophoretic analyses, are most effective in estimating the genome constitutions of apogamous ferns. PCR–SSCP analysis using acrylamide gels is a useful method to distinguish several alleles in each individual. However, in the future, analyses using dozens or hundreds of nuclear markers will be easily conducted through cost reductions in high-throughput sequencing.

It is still debatable whether fern taxonomists should use several nuclear markers because the allele constitutions of the five nuclear loci were concordant in the *Dryopteris varia* complex. If apogamous ferns do not cause chromosomal recombinations through unequal meiosis, there will be no problem in estimating genome constitutions and discussing the evolution of the apogamous fern complex using only one biparental nuclear marker. However, if some apogamous ferns cause chromosomal recombinations through unequal meiosis, pteridologists must use several nuclear DNA markers to resolve reticulate evolution of the apogamous fern complex. To answer this question, similar studies to this study using several unlinked nuclear genetic markers of several phylogenetically distant apogamous fern

complexes should be conducted.

If chromosomal recombinations does not occur in several groups of apogamous ferns, they might have some mechanisms which retains their original genome constitutions derived from diploid sexual progenitors. This phenomenon is hard to explain only by natural selection. If such hybridization cycles as shown in Figure 2-1 reoccur, the resultant apogamous species can display huge amounts of interclonal genetic variation. In the case of $x = 41$, chromosome constitutions can display a maximum of $3^{41} = 3.6472996e+19$ patterns in a triploid apogamous species as mentioned in Chapter 2. This means that offspring with the original genome constitution are not likely to be produced by chance. Therefore, there might be some mechanism particular to triploid apogamous species using in unequal meiosis to select chromosomes derived from a particular diploid sexual species. For example, only red chromosomes are selected when reduced spores are produced. Alternatively, triploid apogamous species having three different genomes originating from three diploid sexual species (e.g. *Dryopteris sacrosancta* was shown to have genomes from *D. varia*, *D. protobissetiana*, and *D. chinensis* in this study) might have some mechanism to stop unequal meiosis. If such a mechanism is uncovered in future studies, our understanding of apogamous ferns will be further deepened.

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Summary in Japanese

複数の核遺伝マーカーを用いたイタチシダ類（オシダ科）の無配生殖種における網状進化
の解明（英文）

シダ植物には、二次的に有性生殖をやめて無配生殖と呼ばれる無性生殖を行っているものが少なくない。無配生殖とは、前葉体が胞子体を形成するとき受精をせずに次世代の胞子体を形成する生殖様式のことである。無配生殖種の子孫は親と遺伝的に同一（クローン）となり、形態や遺伝的多様性は少ないと考えられる。しかし、実際は無配生殖種にも幅広い形態変異や遺伝的多様性がみられることが多い。その理由を説明するための仮説として、三倍体無配生殖種が稀に不等減数分裂を起こして二倍体の精子を生じ（父親）、それが別の二倍体有性生殖種（母親）の一倍体の卵細胞と受精・交雑することが考えられている（Lin et al. 1995, Yamamoto 2012）。無配生殖種には大きな遺伝的多様性が見られるので、遠縁な二倍体有性生殖種も含めて交雑している可能性が考えられる。

そこで本研究では、無配生殖種を多く含み、形態的・遺伝的にも非常に多様なイタチシダ類を材料に用いることにした。日本では、ナンカイイタチシダ *Dryopteris varia*、イワイタチシダ *D. saxifraga*、モトイタチシダ *Dryopteris protobissetiana*、オオイタチシダ *Dryopteris pacifica*、ヤマイタチシダ *D. bissetiana*、リョウトウイタチシダ *D. kobayashii*、ヒメイタチシダ *D. sacrosancta* の 7 種がこの類として認識されている。これらのうち、2 倍体有性生殖型が知られているのはナンカイイタチシダ、イワイタチシダ、モトイタチシダだけである。これらの種における系統関係を、母性遺伝する葉緑体 *rbcL* 遺伝子と両性遺伝する核シングルコピー領域の 1 つである *PgiC* (phosphoglucose isomerase) 遺伝子の塩基配列情報を用いて調べた。その結果、イタチシダ類の核 *PgiC* 遺伝子には A, B, C, D, E の 5 タイプがあることが分かり、それぞれナンカイイタチシダ、イワイタチシダ、モトイタチシダ、ハチジョウベニシダ、ミサキカグマのものに対応した。さらに、イタチシダ類の無配生殖種の核 *PgiC* 遺伝子の型は、ヤマイタチシダ(BC)、オオイタチシダ(AC, ABC, ACD)、リョウ

トウイタチシダ(BCE)、ヒメイタチシダ(ACE)のように複数のタイプの *PgiC* 遺伝子を合わせもっていたことから、これらは複数の有性生殖種と無配生殖種の交雑によって起源したものであることが分かった。また、ハチジョウベニシダとミサキカグマの核 *PgiC* 遺伝子(D, E)がイタチシダ類に含まれていることも明らかになり、遠縁な種が交雫を起こしたことが強く示唆された。さらに、3種類の核 *PgiC* 遺伝子をもつイタチシダ類の無配生殖種があることから、2種類の核ゲノムをもった無配生殖種が別の2倍体有性生殖種と交雫を起こすことにより、新たな遺伝子型の3倍体無配生殖種が生じたと考えられる。

ところが、シダの無配生殖種群のほとんどは、胞子形成時に減数分裂を生じ、イタチシダ類もその例外ではない。交雫と減数分裂を繰り返せば、遺伝子座位ごとにゲノムの組み合わせが異なっている可能性がある。そこで次に、複数の核シングルコピー遺伝子座位を用いてゲノム構成を推定することにした。*AK1*、*Esterase*、*GapCp*、*G6pdh* の4遺伝子座におけるDNA塩基配列の解析を行った結果、ゲノム構成は *PgiC* 遺伝子と一致した。二倍体有性生殖種のモトイタチシダ *D. protobissetiana* では少なくとも *AK1* と *Esterase* が連鎖していないことも明らかになった。このことは、イタチシダ類の無配生殖種は、世代を重ねても基本的にはそのゲノム構成が固定していること、すなわち有性生殖種との交雫は少數回しか起きていないことを強く示唆している。

最後に、この結果をもとにイタチシダ類の分類学的再検討・新種記載を行った。従来、オオイタチシダに充てられていた *D. pacifica* という学名は、Christによってサモア産の別種に与えられていたので非合法名である。オオイタチシダには AC, ABC, ACD の3種類のゲノム構成をもつ個体があることが分かったので、これらをそれぞれ、オオイタチシダ *D. hikonensis*, *D. subhikonensis* (新種), *D. erythrovaria* (新種) として整理した。