

COMPARISON OF THE GENETIC VARIABILITY OF THREE REGIONS OF CHLOROPLAST DNA AND NUCLEAR DNA IN ISHPINGO (*OCOTEA QUIXOS*) COMING FROM FIVE PROVINCES OF THE ECUADORIAN AMAZON

SALAZAR, P.^{1*} – RIVAS, P. I.¹ – MÁTYÁS, B.² – KAROLYS, G.^{1,3}

¹*Faculty of Sciences, Engineering in Biotechnology of Human Resources, Universidad Politécnica Salesiana, Av. 12 de Octubre 2422 and Wilson, Quito, Ecuador
(phone: +593-2-396-2900; fax: +593-2-396-2800)*

²*Grupo de Investigación en Ciencias Ambientales (GRICAM), Universidad Politécnica Salesiana, Rumichaca y Morán Valverde s/n, Quito, Ecuador
(phone: +593-2-396-2900; fax: +593-2-396-2800)*

³*Grupo de I+D en Ciencias Aplicadas a los Recursos Biológicos (GIDCARB), Universidad Politécnica Salesiana, Av. 12 de Octubre 2422 and Wilson, Quito, Ecuador
(phone: +593-2-396-2900; fax: +593-2-396-2800)*

**Corresponding author*

email: psalazarc@est.ups.edu.ec; phone: +593-9-271-6930

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Abstract. *Ocotea quixos* (Lam.) Kosterm. (Ishpingo) is a tree that grows in humid tropical forests in South America (310-1200 masl). It is used for food and medicine, since it possesses essential oils with antiplatelet and antithrombotic properties, among others. In Ecuador, the wild populations of Ishpingo have been reduced ecosystem transformation, deforestation and clonal cultivation. This study compared the genetic variability of three regions of chloroplast DNA (i.e., *matK*, *rbcLa* and *psbA-trnH*) and one nuclear region (i.e., ITS) in Ishpingo from 5 provinces of the Ecuadorian Amazon. Based on the obtained alignments, the phylogeny was performed by using the maximum likelihood criterion with a bootstrap of 1000 replicates and with the Jukes-Cantor correction. The genetic variability was determined using the DNA conservation coefficient and the Nei (π) nucleotide variability coefficient. The nucleotide variability of *matK*, *rbcLa* and *psbA-trnH* regions was low ($\pi \leq 0.005$) due to their high conservation degrees. The ITS region presented a superior variability ($\pi = 0.11$) by grouping the samples that were analyzed into two clades. The regions that were analyzed were not useful for the study of genetic variability in Ishpingo. Therefore, it is recommended that new chloroplast and nuclear DNA regions be analyzed to allow studies on the population genetics of this species in Ecuador to be carried out.

Keywords: *Ocotea*, *chloroplast*, *DNA*, *Amazonia*, *genetic variability*

Introduction

Ocotea quixos (Lam.) Kosterm. (Ishpingo, Ishpink or Canela Amazónica), is a perennial tree that reaches a height of 2 to 25 m (Cazorla, 2013; Palacios, 2016). It is distributed in the humid tropical forests of the Amazonian region of Colombia, Ecuador, Peru and Brazil (310-1200 masl) (Cárdenas et al., 2015).

In 2007, *Ocotea quixos* was banned from commercialization for six months due to the significant reduction from wild populations (Grijalva et al., 2012). In the Ministerial Agreement No. 167, published in the official Register No. 18 on February 8, 2007, it was reported that the main causes of the population reduction of *Ocotea quixos* are the

expansion of the road network, the transformation of ecosystems, deforestation and the clonal cultivars of the species (Ministerio del Ambiente de Ecuador, 2010).

The lack of genetic studies on the *Ocotea quixos* populations of Ecuador suggests that the genetic variability of Ishpingo may be declining. The objective of this study is to compare the genetic variability of the three regions of chloroplast DNA (i.e., *matK*, *rbcLa*, *psbA-trnH*) and a region of nuclear DNA (i.e., ITS) in *Ocotea quixos* to establish possible regions for future population genetics studies on Ishpingo.

Materials and methods

Botanical samples and the 38 foliar tissue samples of Ishpingo (*Ocotea quixos*) species were collected. The samples were obtained from 11 locations in 5 provinces of the Ecuadorian Amazon, where Ishpingo is traditionally cultivated. Botanical specimens were morphologically identified with the help the herbarium of Pontificia Universidad Católica del Ecuador.

Prewashes were performed according to the division protocol of polyphenols and polysaccharides as proposed by Porebski et al. (1997). After washing, Doyle and Doyle's simple foliar DNA extraction protocol (1987) was performed. To determine the presence of the DNA, a horizontal electrophoresis was performed in agarose gel at 1%.

The chloroplast DNA regions (i.e., *matK*, *rbcLa*, *psbA-trnH*) and the nuclear ITS region, defined for the Barcode system, were amplified by specific primers (Table 1).

Table 1. Primers for the amplification of DNA regions

Primers	Sequence (5'→3')	Reference
<i>matK</i> -1RKIM (F)	ACCCAGTCCATCTGGAAATCTTGGTTC	Lahaye et al. (2008)
<i>matK</i> -3FKIM (R)	CGTACAGTACTTTTGTGTTTACGAG	Lahaye et al. (2008)
<i>rbcLa</i> (F)	ATGTCACCACAAACAGAGACTAAAGC	CBOL Plant Working Group et al. (2009)
<i>rbcLa</i> (R)	GTAAAATCAAGTCCACCRGC	Levin et al. (2003)
<i>psbA</i> (F)	GTTATGCATGAACGTAATGCTC	Kress and Erickson (2007)
<i>trnH</i> (R)	CGCGCATGGTGGATTCACAAATCC	Kress and Erickson (2007)
ITS leu1 (F)	GTCCACTGAACCTTATCATTTAG	Bolson et al. (2015)
ITS 4 (R)	TCCTCCGCTTATTGATATGC	White et al. (1990)

The sequencing and purification of the samples were carried out at the company MacroGen (South Korea) using Sanger's simple sequencing method.

The sequencing analysis was carried out using the MEGA7 program. The MUSCLE algorithm was used to align the sequences, maximum likelihood trees were used for the phylogeny, and the Bootstrap method was performed with 1000 replications. The substitutions that were assessed were nucleotides, and Jukes-Cantor's substitution model (Jukes and Cantor, 1969) was used. The trees were rooted following the criteria of external groups or "outgroups", using the species *Ocotea veraguensis* and *Ocotea porosa*. The genetic variability was analyzed with the conservation coefficient, and Nei's variability nucleotide coefficient was determined by the "estimation analysis of

diversity with the specific data model” (Nei and Li, 1979) and was estimated with Tamura-Nei’s model (Tamura et al., 2013).

Results and discussion

The DNA of 35 samples was obtained (Fig. 1) once the washings were done. The DNA obtained had no signs of degradation and was pollution-free; the band obtained corresponded to the expected size: > 2000 pb with a concentration of approximately 40-100 ng/μL.



Figure 1. DNA extraction with previous washings following the protocol of Porebski et al. (1997), and the simple extraction protocol of foliar DNA by Doyle and Doyle (1987), agarose gel at 1%. (Note: First molecular marker, samples 3204-3215 (+), sample 3213 (-))

Out of the 35 sequences of the ITS region obtained, 28 consensus sequences were achieved. The average length of the sequence was 777 pb.

The region presented 428 polymorphic areas, a conservation region coefficient of 0.298 and a nucleotide variability coefficient of 0.1137. ITS presents a low conservation rate due to the great length variability of the sequence, and its incomplete concerted evolution led to the presence of divergent homologous copies within the samples (China Plant BOL Group et al., 2011).

The phylogenetic tree of the ITS region presented two clades; the samples grouped in the first clade were associated with the *Ocotea quixos* control sequence, and in the second clade, a polyphyletic grouping was observed with a branch support of 100% (Fig. 2). The presence of two clades may be because ITS has higher discrimination levels and interspecific variability followed by Gao et al. (2010); however, new studies have proven that there are several limitations associated with the ITS region, especially in phylogenetic inference (Gardes and Bruns, 1993), such as in the existence of extensive variations in genome sequences, which are determined by the formation events of duplications, the genomic accommodation of pseudogenes and an incomplete homogenization arrangement). These phenomena create relationships of paralog

sequences that potentially confuse the accuracy of phylogenetic reconstruction. Homoplasy is higher in ITS than in other DNA regions due to the orthologous/paralogs confusion, compensatory change in bases, problems in alignment due to the accumulation of deletions, and errors in the sequence (Grudinski et al., 2014). Despite being a quasi-universal sequence used in plants for phylogenetic studies, its complex and unpredictable evolutionary behaviour reduces its usefulness in phylogenetic analyses. The use of single-copy nuclear genes is suggested by Alvarez and Wendel (2003).

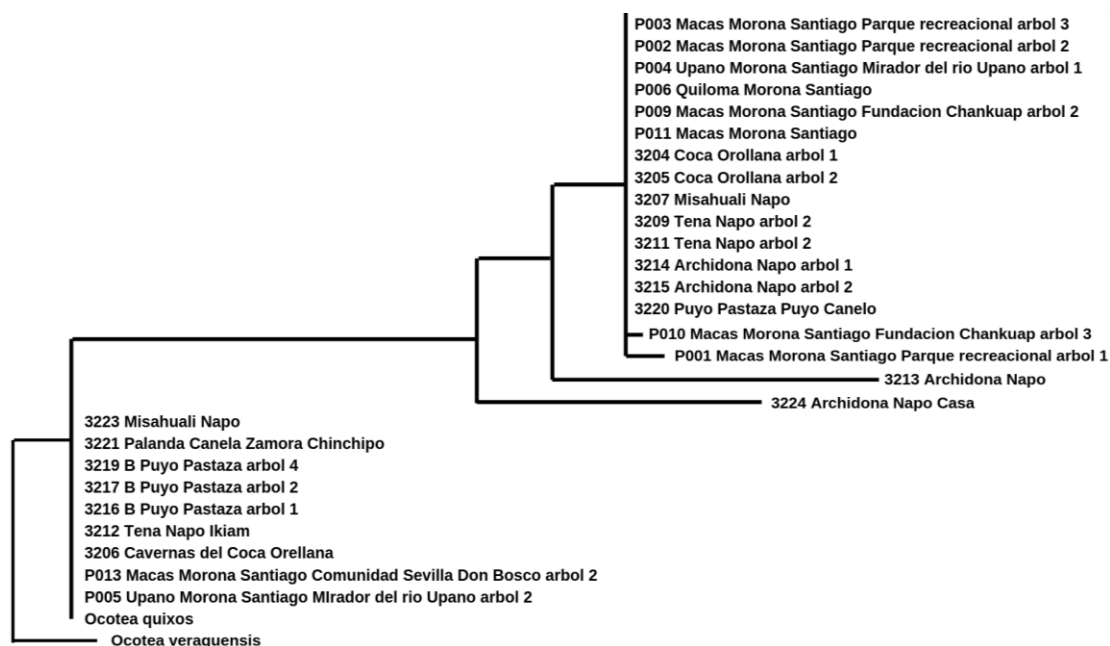


Figure 2. Maximum likelihood tree ITS region. (Note: A defined clade and a grouped clade can be observed with the *O. quixos* sequence obtained from GenBank using the MEGA 7 program)

Comparison of nucleotide variability among the regions *matK*, *rbcLa*, *psbA-trnH* and ITS: The *psbA-trnH* region has a variability coefficient of $\pi = 0.0051$ higher than those of the *matK* and *rbcLa* regions. This region has mononucleotide repetitions that increase its variability (Kress and Erickson, 2007). Despite this increase, the nucleotide variability coefficient is low <0.1 , as mentioned by Jakobsson et al. (2013), and does not provide high nucleotide substitution rates due to its short length in the *Ocotea* genus, so its nucleotide variability is low (Liu et al., 2012).

The ITS region presented the highest variability coefficient ($\pi = 0.1137$) among the four regions. One of the main reasons for this increase in the genetic variability is due to the homology problem of the sequences that this region has; i.e., the appearance of divergent copies in the samples, which can lead to an increase in the genetic variability, stated by Hollingsworth (2011) and Hollingsworth et al. (2011).

Conclusions

DNA regions *matK*, *rbcLa* and *psbA-trnH* in *Ocotea quixos* are preserved (nucleotide variation coefficient $\pi \leq 0.005$) for the study of genetic variability in this

population. The ITS region had highest substitution rates in nucleotides ($\pi = 0.1137$) in the sequences of the *Ocotea quixos*. This variability is associated with the amount of inscriptions in the DNA sequence that increase the nucleotide variability. The genetic variability coefficient obtained in the DNA regions of *Ocotea quixos* was low ($\pi = 0-0.1137$), which suggests that the genetic variability of the species is threatened by deforestation and the cultivation of clones.

Considering our study findings, we highly recommend to continue our research in order to establish possible regions for future population genetics studies on Ishpingo.

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APPENDIX

Primers for the amplification of DNA regions

#	Query length	Description	Query cover	Identity	Reference
1D <i>matK</i>	895	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	94%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
2D <i>matK</i>	902	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	94%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3D <i>matK</i>	856	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
4D <i>matK</i>	859	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
5D <i>matK</i>	859	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
6D <i>matK</i>	845	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
7D <i>matK</i>	851	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
8D <i>matK</i>	845	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
9D <i>matK</i>	855	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
11D <i>matK</i>	857	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
12D <i>matK</i>	860	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
13D <i>matK</i>	847	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	96%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
14D <i>matK</i>	812	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
17A <i>matK</i>	813	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
18A <i>matK</i>	800	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
19A <i>matK</i>	727	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
20A <i>matK</i>	850	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
21A <i>matK</i>	849	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
22A <i>matK</i>	782	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
23A <i>matK</i>	811	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
24A <i>matK</i>	821	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

25A <i>matK</i>	762	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
26A <i>matK</i>	820	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
27A <i>matK</i>	778	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
28A <i>matK</i>	807	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
29A <i>matK</i>	778	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
30A <i>matK</i>	852	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
31A <i>matK</i>	797	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
32A <i>matK</i>	793	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
33A <i>matK</i>	858	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
34A <i>matK</i>	809	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
35A <i>matK</i>	826	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi#alnHdr_9931066
36A <i>matK</i>	784	<i>Nectandra</i> sp. 1 AN410 maturase-like (<i>matK</i>) gene, partial sequence; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
1A <i>rbcLa</i>	564	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
2A <i>rbcLa</i>	572	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	99%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3A <i>rbcLa</i>	565	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
4A <i>rbcLa</i>	565	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
5A <i>rbcLa</i>	524	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
6A <i>rbcLa</i>	565	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
7A <i>rbcLa</i>	565	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

8A <i>rbcLa</i>	540	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	540	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
9A <i>rbcLa</i>	565	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	565	<i>Ocotea quixos</i> voucher COAH:81063 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
10A <i>rbcLa</i>	563	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	563	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
11A <i>rbcLa</i>	521	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	521	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
13A <i>rbcLa</i>	566	<i>Ocotea quixos</i> voucher COAH:81063 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
14A <i>rbcLa</i>	567	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
16A <i>rbcLa</i>	389	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	389	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
17A <i>rbcLa</i>	563	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	563	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

18A <i>rbcLa</i>	504	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	504	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
19A <i>rbcLa</i>	564	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	564	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
20A <i>rbcLa</i>	519	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	99%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	519	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	99%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
21A <i>rbcLa</i>	510	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	510	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
22A <i>rbcLa</i>	556	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	556	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
23A <i>rbcLa</i>	564	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	564	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
24A <i>rbcLa</i>	507	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	507	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

25A <i>rbcLa</i>	559	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	559	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
26A <i>rbcLa</i>	562	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	562	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
27A <i>rbcLa</i>	564	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	564	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
28A <i>rbcLa</i>	507	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	98%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	507	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	98%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
30A <i>rbcLa</i>	567	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
31A <i>rbcLa</i>	559	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	559	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
33A <i>rbcLa</i>	560	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
	560	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphospahte carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
34A <i>rbcLa</i>	565	<i>Ocotea cymbarum</i> voucher COAH:66878 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (<i>rbcL</i>) gene, partial cds; chloplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

	565	<i>Ocotea quixos</i> voucher COAH:81063 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, partial cds; chloroplast	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
1B <i>psbA-trnH</i>	488	<i>Ocotea purpurea</i> voucher Lundell 21170 PsbA (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	99%	97%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
2B <i>psbA-trnH</i>	494	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	96%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3B <i>psbA-trnH</i>	433	<i>Ocotea moschata</i> photosystem II protein D1 (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
5B <i>psbA-trnH</i>	499	<i>Ocotea botrantha</i> voucher s.n. PsbA (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	97%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
6B <i>psbA-trnH</i>	498	<i>Ocotea botrantha</i> voucher Wernisch s.n. PsbA (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	97%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
7B <i>psbA-trnH</i>	498	<i>Ocotea botrantha</i> voucher Wernisch s.n. PsbA (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	97%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
8B <i>psbA-trnH</i>	441	<i>Ocotea cuneata</i> voucher 1079133346 PsbA 9psbA) gene, partial cds; and <i>psbA- trnH</i> intergenic spacer, complete sequence; chloroplast	97%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
9B <i>psbA-trnH</i>	489	<i>Ocotea purpurea</i> voucher Lundell 21170 PsbA (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	98%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
10B <i>psbA-trnH</i>	440	<i>Ocotea cuneata</i> voucher 1079133346 PsbA 9psbA) gene, partial cds; and <i>psbA- trnH</i> intergenic spacer, complete sequence; chloroplast	97%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
11B <i>psbA-trnH</i>	1078	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	44%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
12B <i>psbA-trnH</i>	573	<i>Ocotea quixos</i>	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
13B <i>psbA-trnH</i>	496	<i>Ocotea botrantha</i> voucher Wernisch s.n. PsbA (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	98%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
14B <i>psbA-trnH</i>	495	<i>Ocotea purpurea</i> voucher Lundell 21170 PsbA (psbA) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (trnH) gene, partial sequence; chloroplast	97%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

16A <i>psbA-trnH</i>	506	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
17A <i>psbA-trnH</i>	500	<i>Ocotea purpurea</i> voucher Lundell 21170 PsbA (<i>psbA</i>) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (<i>trnH</i>) gene, partial sequence; chloroplast	97%	97%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
18A <i>psbA-trnH</i>	504	<i>Ocotea botrantha</i> voucher Wernisch s.n. PsbA (<i>psbA</i>) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (<i>trnH</i>) gene, partial sequence; chloroplast	96%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
19A <i>psbA-trnH</i>	497	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
20A <i>psbA-trnH</i>	494	<i>Ocotea purpurea</i> voucher Lundell 21170 PsbA (<i>psbA</i>) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (<i>trnH</i>) gene, partial sequence; chloroplast	98%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
21A <i>psbA-trnH</i>	492	<i>Ocotea purpurea</i> voucher Lundell 21170 PsbA (<i>psbA</i>) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (<i>trnH</i>) gene, partial sequence; chloroplast	98%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
22A <i>psbA-trnH</i>	497	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
23A <i>psbA-trnH</i>	505	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
24A <i>psbA-trnH</i>	501	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
25A <i>psbA-trnH</i>	467	<i>Lindera benzoin</i> voucher SERC-1076419278 <i>trnH-psbA</i> intergenic spacer, partial sequence; chloroplast	96%	95%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
26A <i>psbA-trnH</i>	505	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
27A <i>psbA-trnH</i>	504	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
28A <i>psbA-trnH</i>	488	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	97%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
29A <i>psbA-trnH</i>	496	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
30A <i>psbA-trnH</i>	505	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
31A <i>psbA-trnH</i>	422	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	98%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
32A <i>psbA-trnH</i>	401	<i>Ocotea cuneata</i> voucher 1079133346 PsbA (<i>psbA</i>) gene, partial cds; and <i>psbA-trnH</i> intergenic spacer, complete sequence; chloroplast	98%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
33A <i>psbA-trnH</i>	474	<i>Ocotea purpurea</i> voucher Lundell 21170 PsbA (<i>psbA</i>) gene, partial cds; <i>psbA-trnH</i> intergenic spacer, complete sequence; and tRNA-His (<i>trnH</i>) gene, partial sequence; chloroplast	100%	97%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

34A <i>psbA-trnH</i>	402	Lauraceae sp. MAG2009 voucher NL 110192 <i>PsbA</i> (<i>psbA</i>) gene, partial cds; and <i>psbA-trnH</i> intergenic spacer, partial sequence chloroplast	99%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
35A <i>psbA-trnH</i>	330	<i>Ocotea cuneata</i> voucher 1079133346 <i>PsbA</i> (<i>psbA</i>) gene, partial cds; and <i>psbA-trnH</i> intergenic spacer, complete sequence; chloroplast	97%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
36A <i>psbA-trnH</i>	445	<i>Lindera benzoin</i> voucher SERC-1076419278 <i>trnH-psbA</i> intergenic spacer, partial sequence; chloroplast	99%	95%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
1C <i>ITS</i>	405	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	71%	96%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
2C <i>ITS</i>	734	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	99%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3C <i>ITS</i>	495	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
4C <i>ITS</i>	671	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	98%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
5C <i>ITS</i>	683	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	90%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
6C <i>ITS</i>	460	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cg
9C <i>ITS</i>	507	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
10C <i>ITS</i>	611	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	61%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

11C ITS	627	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
13C ITS	694	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	89%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3204 ITS	593	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3205 ITS	712	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3206 ITS	647	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	94%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3207 ITS	559	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3209 ITS	709	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3211 ITS	620	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3212 ITS	513	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	86%	94%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3213 ITS	719	Uncultured eukaryote clone CMH360 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 28S ribosomal RNA gene, and 45S rDNA intergenic spacer, partial sequence	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi

3214 ITS	709	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3215 ITS	701	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	100%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3216 ITS	591	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	100%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3217 ITS	678	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	89%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3219 ITS	512	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3220 ITS	359	<i>Brassica oleraceae</i> var. capitata 18S ribosomal RNA gene, internal transcribed spacer 1, 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 45S rDNA intergenic spacer, complete sequence	99%	100%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3221 ITS	668	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	91%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3223 ITS	641	<i>Ocotea quixos</i> internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	95%	99%	https://blast.ncbi.nlm.nih.gov/Blast.cgi
3224 ITS	542	<i>Tripodanthus belmirensis</i> voucher Nickrent 5050 internal transcribed spacer 1, partial sequence; 5.8 ribosomal RNA gene, internal transcribed spacer 2, 26S ribosomal RNA gene, and 26S rDNA intergenic spacer, partial sequence	99%	92%	https://blast.ncbi.nlm.nih.gov/Blast.cgi