

## 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

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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 ( $\pi$ ) 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)	GTAAAATCAAGTCCACCRCG	Levin et al. (2003)
<i>psbA</i> (F)	GTTATGCATGAACGTAATGCTC	Kress and Erickson (2007)
<i>trnH</i> (R)	CGCGCATGGTGGATTCACAAATCC	Kress and Erickson (2007)
<i>ITS</i> leu1 (F)	GTCCACTGAACCTTATCATTTAG	Bolson et al. (2015)
<i>ITS</i> 4 (R)	TCCTCCGCTTATGATATGC	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/ $\mu$ L.



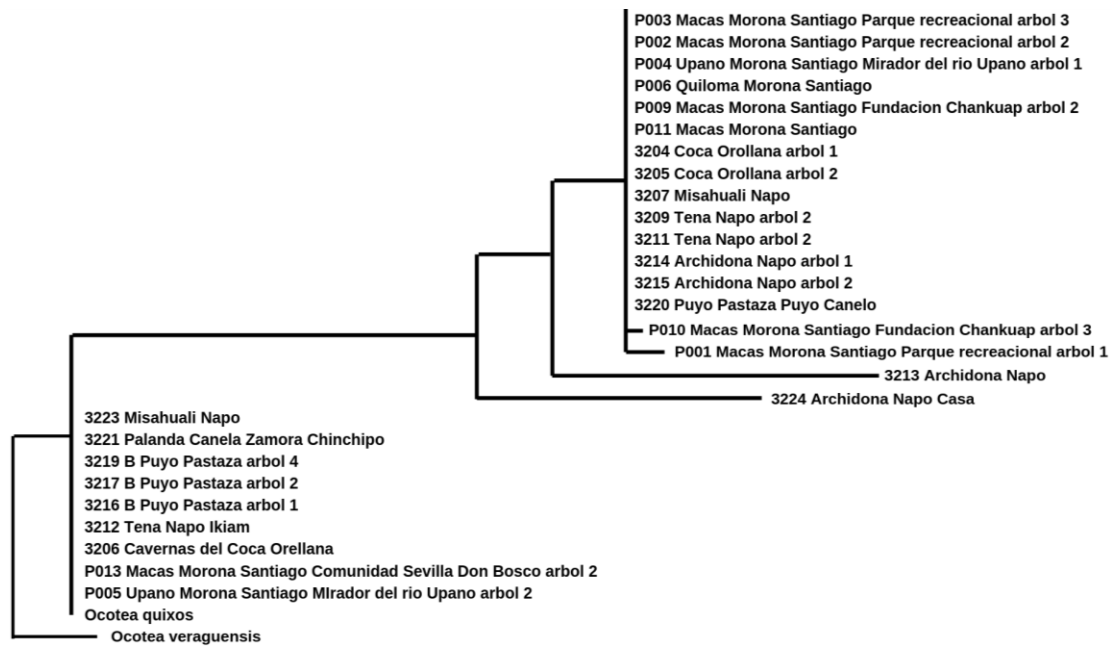
**Figure 1.** DNA extraction with previous washings following the protocol of Porebski et al. (1997), and the simple extraction protocol of foliar DNA by Doyle and Doyle (1987), agarose gel at 1%. (Note: First molecular marker, samples 3204-3215 (+), sample 3213 (-))

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



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



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

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

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; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
	559	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ( <i>rbcL</i> ) gene, partial cds; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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; chloroplast	100%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
	562	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ( <i>rbcL</i> ) gene, partial cds; chloroplast	100%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
	564	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ( <i>rbcL</i> ) gene, partial cds; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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; chloroplast	98%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
	507	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ( <i>rbcL</i> ) gene, partial cds; chloroplast	98%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
30A <i>rbcLa</i>	567	<i>Ocotea quixos</i> voucher COAH:81083 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ( <i>rbcL</i> ) gene, partial cds; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
	559	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ( <i>rbcL</i> ) gene, partial cds; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
	560	<i>Ocotea quixos</i> voucher COAH:81062 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit ( <i>rbcL</i> ) gene, partial cds; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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; chloroplast	100%	100%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>

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

16A <i>psbA-trnH</i>	506	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	98%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
19A <i>psbA-trnH</i>	497	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
22A <i>psbA-trnH</i>	497	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	98%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
23A <i>psbA-trnH</i>	505	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
24A <i>psbA-trnH</i>	501	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
25A <i>psbA-trnH</i>	467	<i>Lindera benzoin</i> voucher SERC-1076419278 <i>trnH-psbA</i> intergenic spacer, partial sequence; chloroplast	96%	95%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
26A <i>psbA-trnH</i>	505	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
27A <i>psbA-trnH</i>	504	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
28A <i>psbA-trnH</i>	488	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	97%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
29A <i>psbA-trnH</i>	496	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
30A <i>psbA-trnH</i>	505	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	95%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
31A <i>psbA-trnH</i>	422	<i>Ocotea quixos</i> chloroplast <i>psbA-trnH</i> intergenic spacer region	98%	99%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>

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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
36A <i>psbA-trnH</i>	445	<i>Lindera benzoin</i> voucher SERC-1076419278 <i>trnH-psbA</i> intergenic spacer, partial sequence; chloroplast	99%	95%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
1C <i>ITS</i>	405	<i>Brassica oleraceae</i> var. <i>capitata</i> 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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
2C <i>ITS</i>	734	<i>Brassica oleraceae</i> var. <i>capitata</i> 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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3C <i>ITS</i>	495	<i>Brassica oleraceae</i> var. <i>capitata</i> 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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
4C <i>ITS</i>	671	<i>Brassica oleraceae</i> var. <i>capitata</i> 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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
6C <i>ITS</i>	460	<i>Brassica oleraceae</i> var. <i>capitata</i> 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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cg">https://blast.ncbi.nlm.nih.gov/Blast.cg</a>
9C <i>ITS</i>	507	<i>Brassica oleraceae</i> var. <i>capitata</i> 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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
10C <i>ITS</i>	611	<i>Brassica oleraceae</i> var. <i>capitata</i> 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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>



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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>



3214 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3215 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3216 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3217 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3219 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3220 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3221 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3223 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>
3224 <i>ITS</i>	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%	<a href="https://blast.ncbi.nlm.nih.gov/Blast.cgi">https://blast.ncbi.nlm.nih.gov/Blast.cgi</a>