

Kashin, A. S., Kritskaya, T. A., Parkhomenko, A. S. and Schanzer, I. A. 2019. Genetic polymorphism in *Chondrilla* (Asteraceae) in the south of European Russia and the nature of *Chondrilla juncea* L. – Nordic Journal of Botany 2019: e02420

Appendix 1

Table A1. Diagnostic characters used to identification of taxa of the genus *Chondrilla*.

subgenus	section	series	species	IIPN	IIPH	HFN	SP	LW	LP	BPAL	BPAS	BL	BBA	AC	CS
Chondrilla				(7)8(9)		(9)11(12)									
	Arthrorhynchus		<i>laticoronata</i>							>5		1–2.5	1		0
	Chondrilla									≤5			0		
		Latifoliae					0	10–40	0						
			<i>canescens</i>				0	~10	0		1	2–5			2
			<i>latifolia</i>				1	20–40	1			3.5–5			3
		Junceae					2	0.5–3(6)	2						
			<i>brevirostris</i>								0	0.5–2.5			1
			<i>juncea</i>		0						3	3–6			4
			<i>graminea</i>		2						5	3–6			4
			<i>acantholepis</i>		1						4	3–6			4
Brachyrhynchus				5–7		5–7									
			<i>ambigua</i>	5		5						0.1–0.3		0	
			<i>pauciflora</i>	(5)6–7		(5)6–7						0.5–2		1	

IIPN inner involucre phyllaries number.

IIPH inner involucre phyllaries hairiness: 0 – without bristles; 1 – with hard, long, dense bristles on midrib; 2 – with short loose bristles on midrib.

HFN head florets number.

SP stem pubescence: 0 – dense cobwebby; 1 – glabrous to loosely hairy in middle part; 2 – glabrous.

LW stem leaf width, mm.

LP stem leaf pubescence: 0 – dense cobwebby; 1 – dense hirsute with stiff bristles on margins and midrib below; 2 – glabrous.

BPAL broad part of the achene length, mm.

BPAS broad part of the achene surface: 0 – broad, entire scales in 1-2 transversal rows; 1 – broad trilobate scales; 2 – muricate; 3 – muricate and scaly in upper 1/4–3/4; 4 – scaly in upper part only, scales of the upper row trilobate; 5 – scaly in upper part only, scales of the upper row bilobate.

BL beak length, mm.

BBA beak base articulation: 0 – lacking; 1 – well developed.

AC achene corona: 0 – lacking or nearly lacking; 1 – well developed.

CS corona scales: 0 – broadly spatulate; 1 – short and broad, blunt; 2 – trilobate with better developed middle lobe; 3 – ovate; 4 – narrow and acute in apical part.

Supplementary Table A2. ISSR primers used for *Chondrilla* species genotyping.

Primer name	Primer sequence 5'-3'	Number of polymorphic bands	Reference
ISSR 3	(AG) ₉ C	5	Dogan et al., 2007
ISSR 4	(AC) ₉ G	6	Dogan et al., 2007
ISSR 5	(AC) ₈ CG	15	Dogan et al., 2007
ISSR 18	(ACTG) ₅	7	Dogan et al., 2007
«Aster»	(TG) ₈ RC	15	Escaravage et al., 2011
UBC 807	(AG) ₈ T	7	Ryu and Bae, 2012
UBC 809	(AG) ₈ G	5	Ryu and Bae, 2012
UBC 810	(GA) ₈ T	6	Ryu and Bae, 2012
UBC 811	(GA) ₈ C	7	Ryu and Bae, 2012
UBC 813	(CT) ₈ T	7	Ryu and Bae, 2012
UBC 820	(GT) ₈ C	8	Ryu and Bae, 2012
UBC 834	(AG) ₈ YT	9	Ryu and Bae, 2012
UBC 835	(AG) ₈ YC	11	Ryu and Bae, 2012
UBC 836	(AG) ₈ YA	7	Ryu and Bae, 2012
UBC 841	(GA) ₈ YC	15	Ryu and Bae, 2012

Table A3. Partition of variance (AMOVA) within and among different species or groups of species of *Chondrilla*.

Groups tested	DF	Percentage of Variance
Plastid markers		
"ambigua", "acantholepis", "brevirostris", "canescens", "graminea", "juncea", "latifolia", "laticoronata"		
Among populations	7	84.07 ^{ns}
Within populations	32	15.93
"ambigua", "brevirostris", "laticoronata" vs. "acantholepis", "canescens", "graminea", "juncea", "latifolia"		
Among groups	1	85.65***
Within groups	6	4.55
"acantholepis", "canescens", "graminea", "juncea", "latifolia"		
Among populations	4	26.63 ^{ns}
Within populations	22	73.37
"ambigua" + "brevirostris"		
Among populations	1	-11.11 ^{ns}
Within populations	8	111.11
"ambigua" + "laticoronata"		
Among populations	1	55.53 ^{ns}
Within populations	6	44.47
"brevirostris" vs. "acantholepis", "canescens", "graminea", "juncea", "latifolia"		
Among groups	1	85.84***

Within groups	4	4.34
"ambigua" vs. "brevirostris", "laticoronata" vs. "acantholepis", "canescens", "graminea", "juncea", "latifolia"		
Among groups	2	83.13****
Within groups	5	6.06
"ambigua" vs. "brevirostris" vs. "laticoronata" vs. "acantholepis", "canescens", "graminea", "juncea", "latifolia"		
Among groups	3	83.68****
Within groups	4	5.22
ITS markers		
A group of all species		
Among populations	14	66.86 ^{ns}
Within populations	62	33.14
"brevirostris" + "ambigua"		
Among populations	1	36.77 ^{ns}
Within populations	14	63.23
"brevirostris" + "juncea"		
Among populations	1	54.19 ^{ns}
Within populations	29	45.81
"brevirostris" + "laticoronata"		
Among populations	1	5.06 ^{ns}
Within populations	14	94.94
"ambigua" vs. "brevirostris", "laticoronata" vs. "acantholepis", "canescens", "graminea", "juncea", "latifolia"		
Among groups	2	71.95****

Within groups	7	2.18
"ambigua" vs. "brevirostris" vs. "laticoronata" vs. "acantholepis", "canescens", "graminea", "juncea", "latifolia"		
Among groups	3	73.16***
Within groups	6	0.39

Note: *** $p(\text{observed value} \geq \text{random value}) \leq 0.0001$; ** $p(\text{obs.} \geq \text{rand.}) \leq 0.01$;

* $p(\text{obs.} \geq \text{rand.}) \leq 0.05$; ns, not significant.

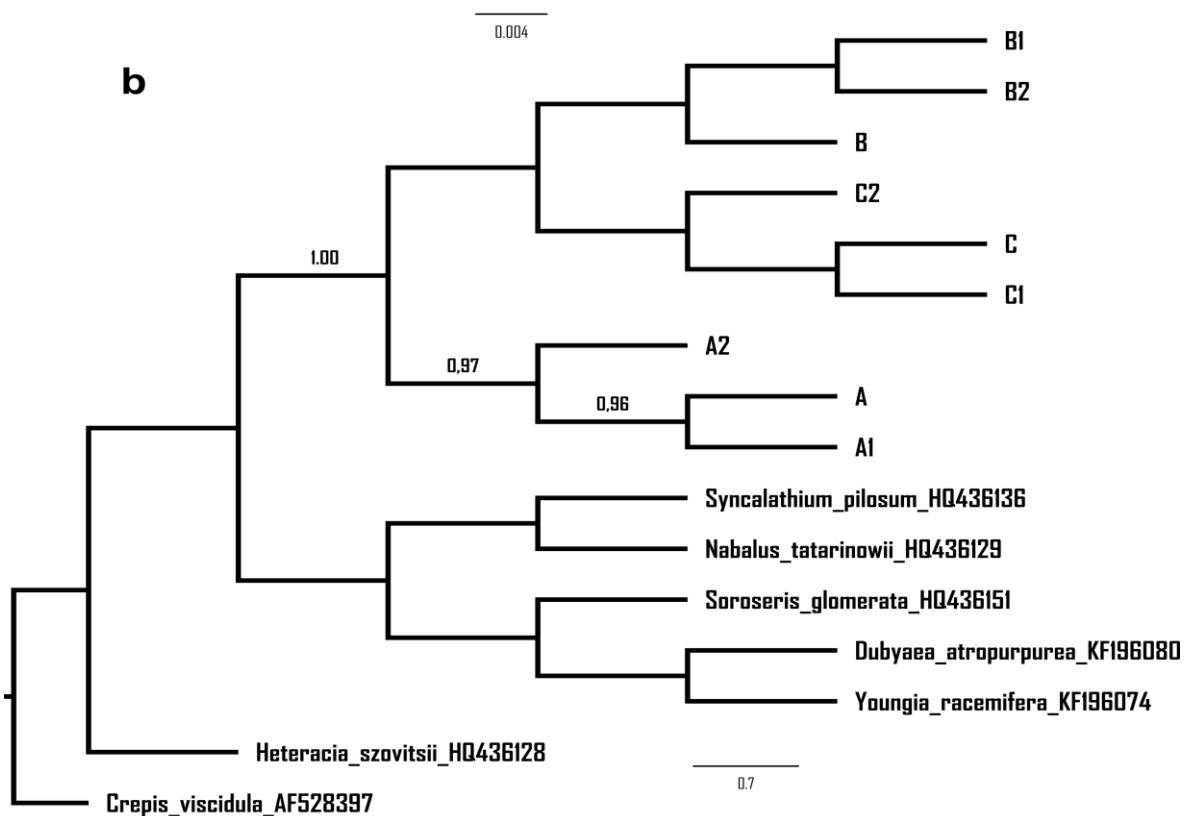
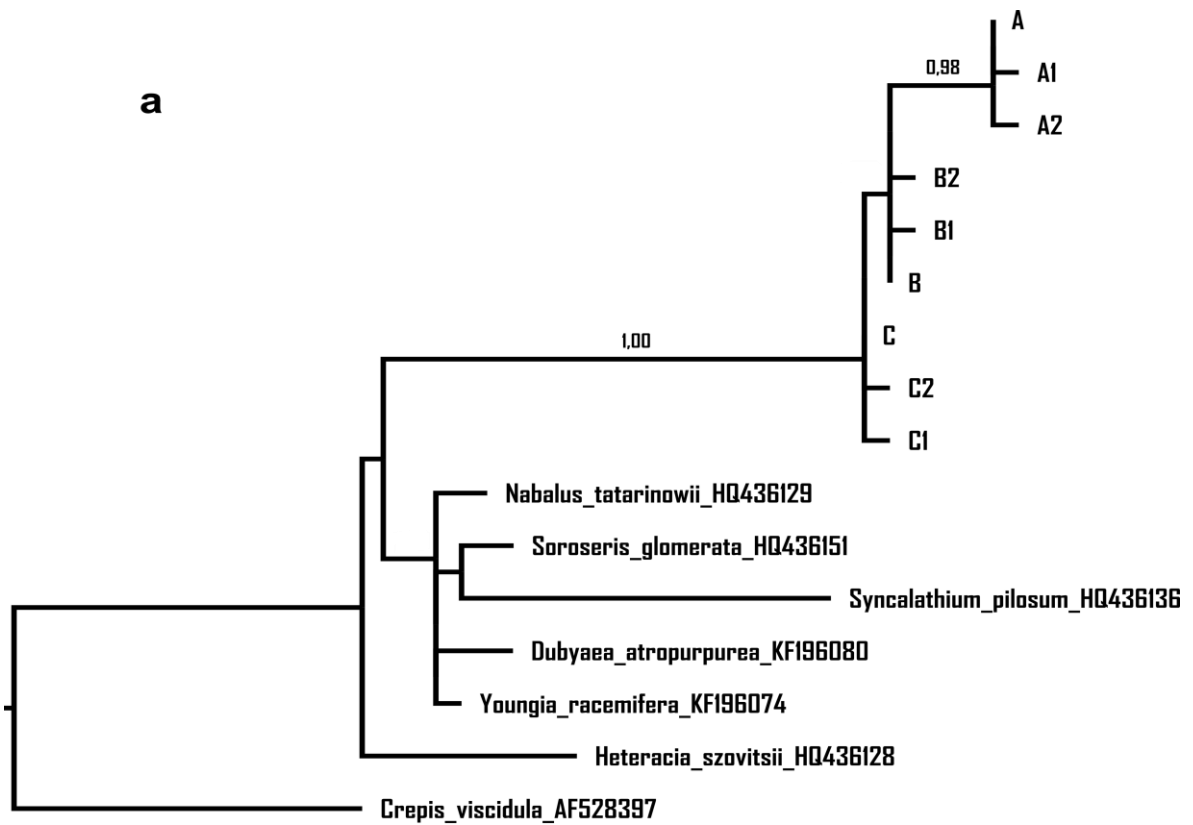


Figure A1. Rooted trees based on *Chondrilla* plastid haplotype data. Bootstrap values above 0.8 are shown above the branches.

a. The maximum likelihood tree with the highest log likelihood value. The C clade is sister to the A+B clade.

b. One of the ten shortest maximum parsimony trees. The A clade is sister to the B+C clade.

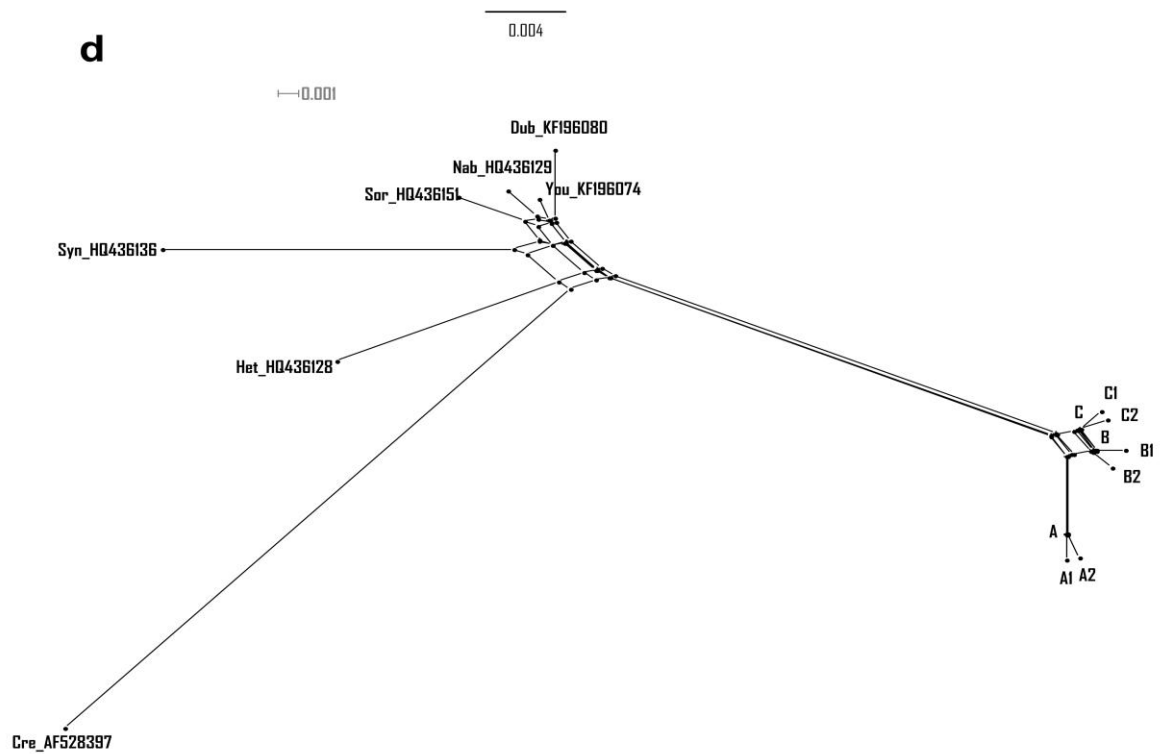
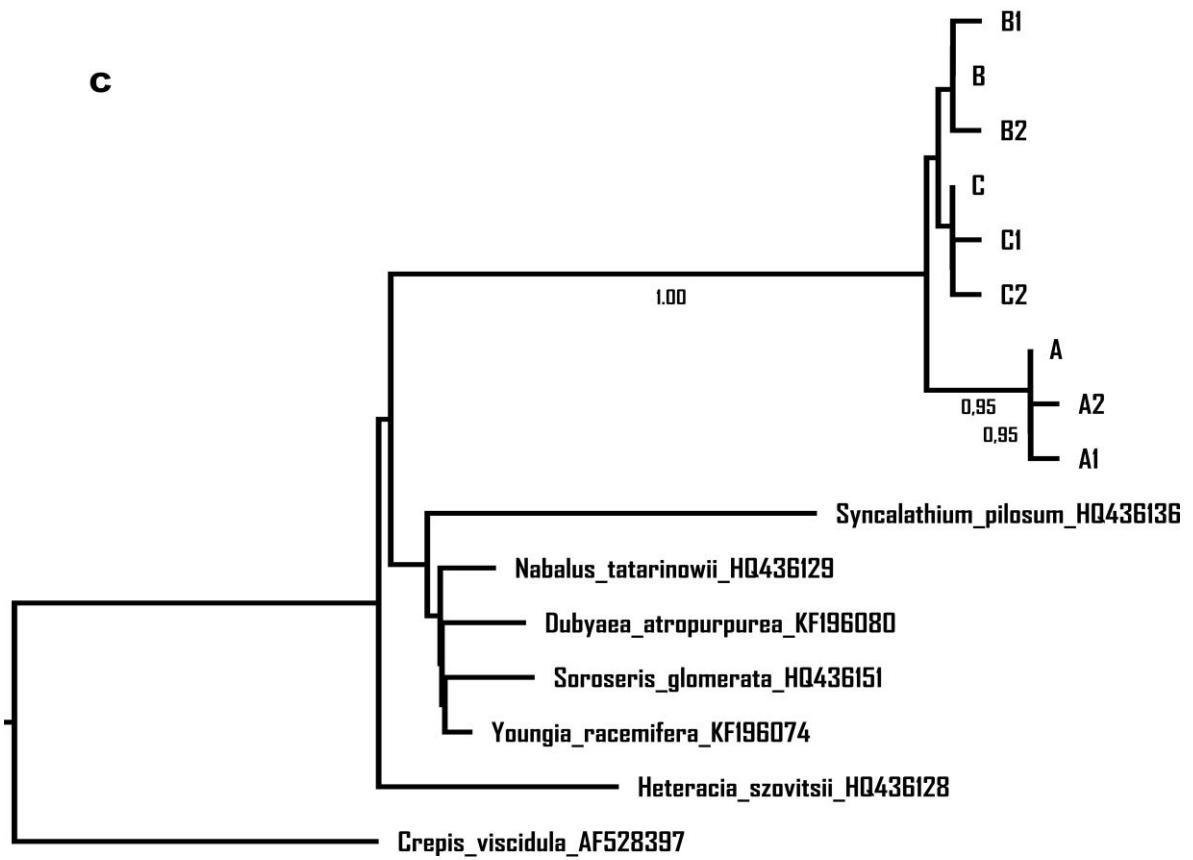


Figure A1 (continued).

c. The neighbor joining tree. The A clade is sister to the B+C clade.

d. The neighbor net network. The A clade is sister to the B+C clade.

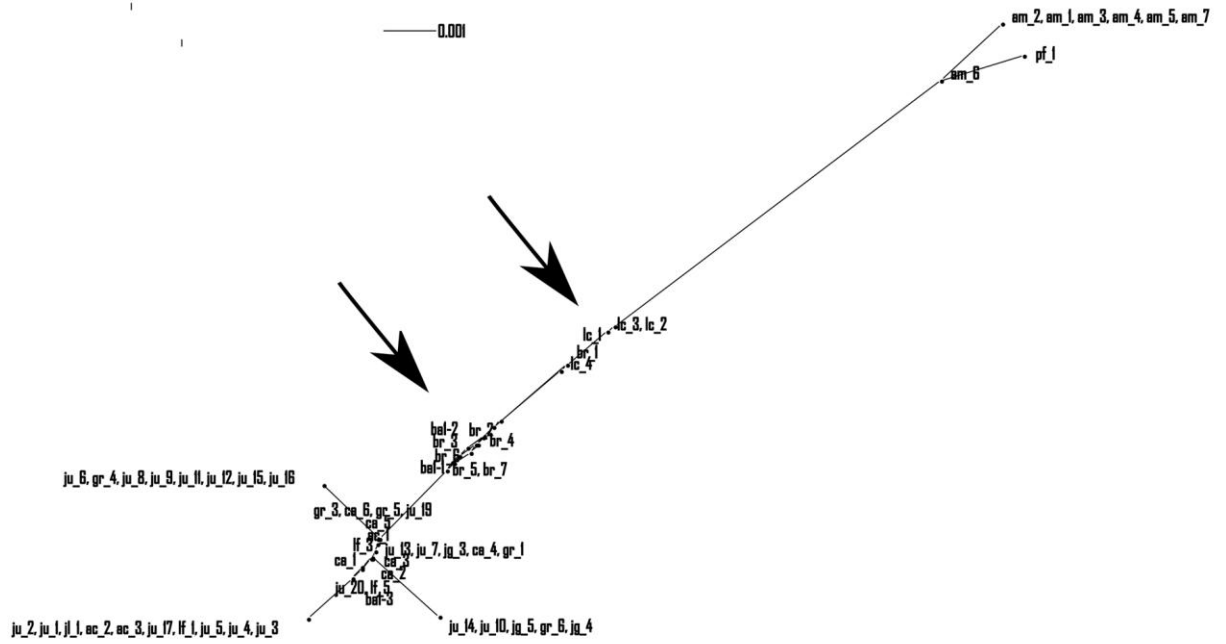


Figure A2. The Neighbor Net network based on the complete ITS sequence dataset, including the sequences possessing ambiguities in multiple sites. Designation of individual samples corresponds to the Table 1. Arrows mark the positions of *C. laticoronata* and *C. brevisrostris* (+ *C. brevisrostris/C. ambigua* intermediates).

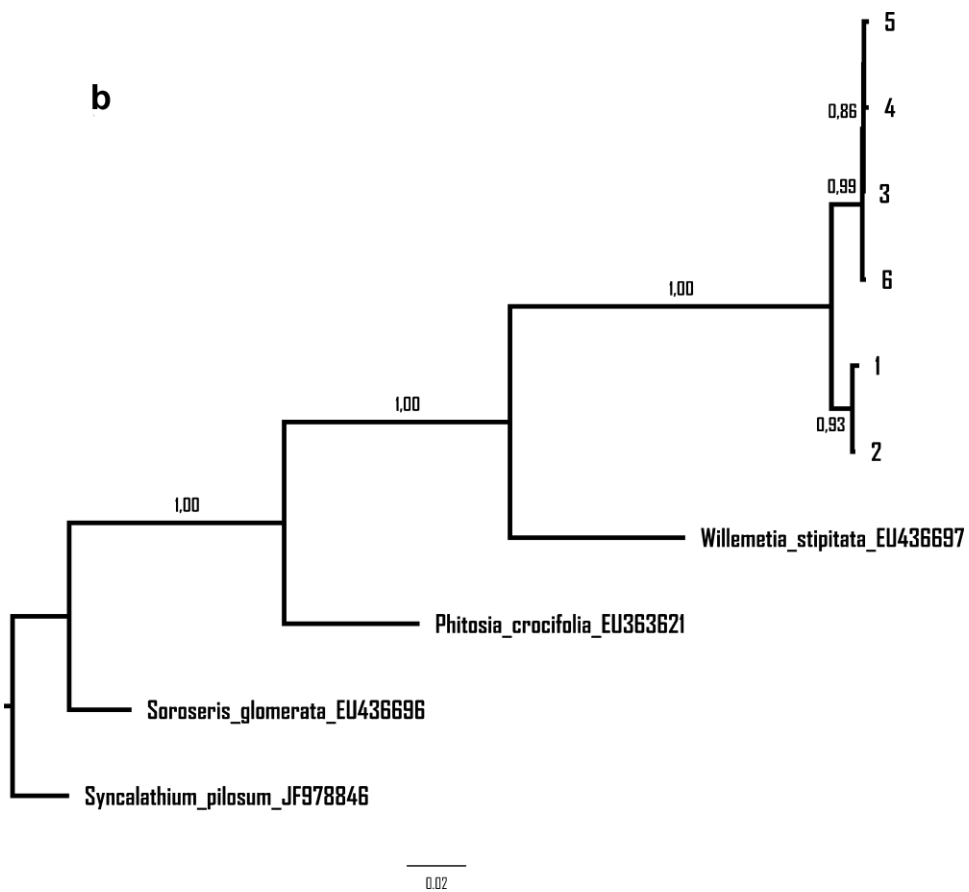
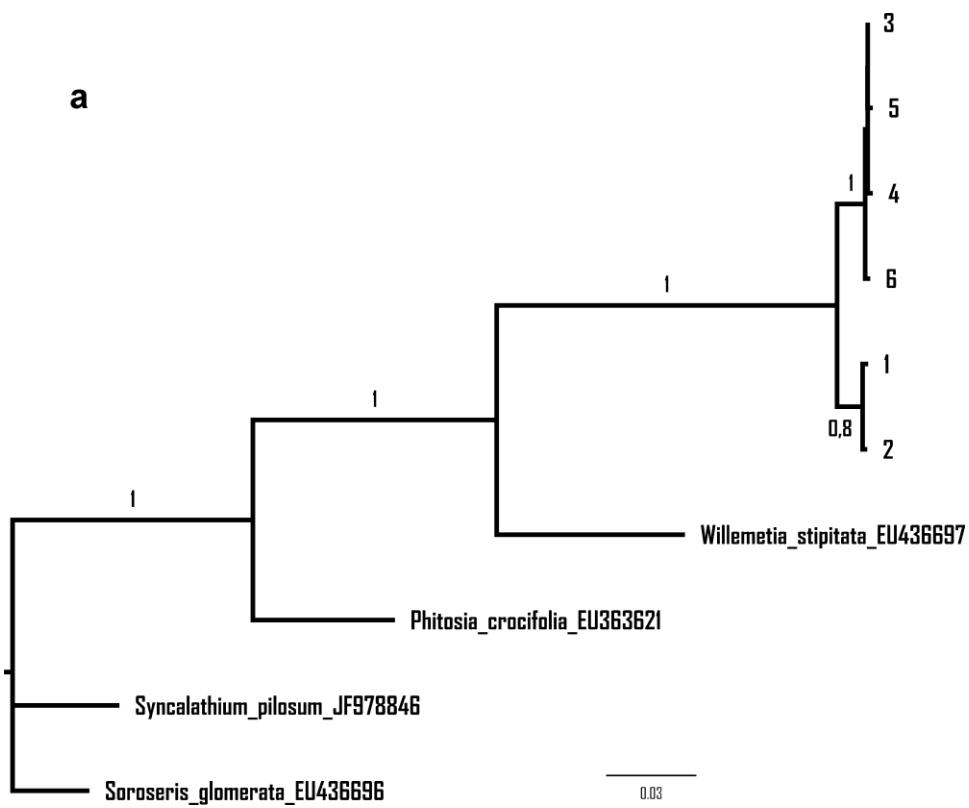


Figure A3. Rooted trees based on *Chondrilla* ITS ribotype dataset. Bootstrap values above 0.8 are shown above the branches. Ribotype designations are the same as in Fig. 3.

a. Maximum likelihood tree.

b. Neighbor joining tree.

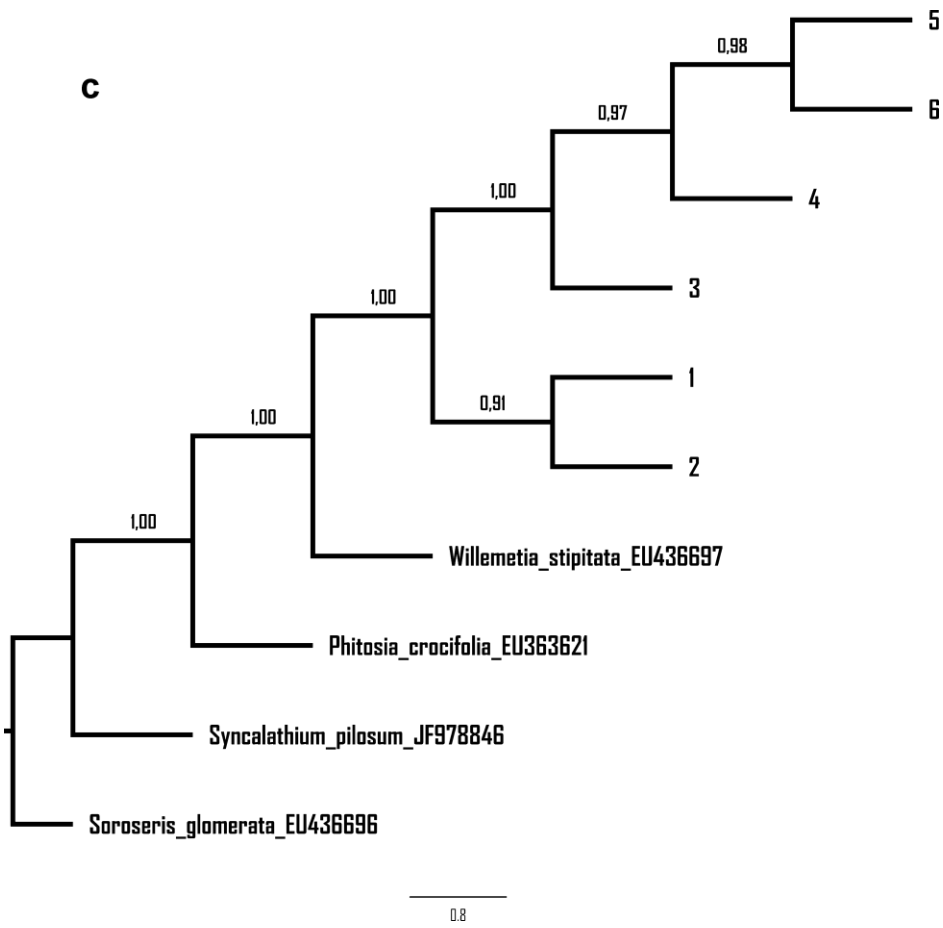


Figure A3. (continued).
c. Strict consensus maximum parsimony tree.