

Supplementary Table 2 | Intra- and interspecific variation of closely related species, number of intra-individual polymorphic sites (*ITS*)

A) *Stuckenia pectinata* (genotypes 1a–b, 2a–e, and intraspecific hybrids), *S. striata*, and *S. striata* × *S. sp.*

Species (isolate)	Position in alignment (ITS 1 ITS 2)																												polym. sites (accessions)	
	62	75-6	107	111	131	139-140	149	155	163-4	177	233	236	423	458	492-3	505	552	559	561	562	584	597	601	646-9	660	662	676	680-1		729
<i>S. pectinata</i> genotype 1a (133, 981)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	0 (2)
<i>S. pectinata</i> genotype 1a (1010, 1935)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	0 (2)
<i>S. pectinata</i> genotype 1a (2071, 2116)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	0 (2)
<i>S. pectinata</i> genotype 1a (2448, 2465)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	0 (2)
<i>S. pectinata</i> genotype 1a (2541, 2545, 2561)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	0 (3)
<i>S. pectinata</i> genotype 1a (2705-2708)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	0 (4)
<i>S. pectinata</i> genotype 1a (2026)	m	AC	G	C	G	GC	C	T	TG	T	k	C	T	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	2
<i>S. pectinata</i> genotype 1a (2724-2726)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	cl-	A	C	G	A	T	T	AACC	T	A	C	GC	R	1 + indel (3)
<i>S. pectinata</i> genotype 1a (989)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	y	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	1
<i>S. pectinata</i> genotype 1a (2694)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	N	N	N	N	N	N	N	NNNN	N	N	N	NN	N	(0)
<i>S. pectinata</i> genotype 1a (2795)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	A	y	G	A	T	T	AACC	T	M	y	GC	A	3
<i>S. pectinata</i> genotype 1a (3201)	C	AC	G	C	G	GC	C	T	TG	T	G	C	T	C	AA	C	C	R	C	G	A	T	T	AACC	T	A	C	GC	A	1
<i>S. pectinata</i> genotype 1a (2695-2699)	C	AC	G	C	G	km	C	T	TG	T	G	C	T	C	AA	C	C	A	y	G	A	T	T	AACC	T	A	C	GC	A	3 (5)
<i>S. pectinata</i> gt 1a × gt 1b (2689)	C	AC	G	C	G	GC	C	T	TG	T	k	C	Y	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	2
<i>S. pectinata</i> gt 1a × gt 1b (1023, 2589)	C	AC	G	C	G	GC	C	T	TG	T	G	C	y	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	1 (2)
<i>S. pectinata</i> gt 1a × gt 1b (2538)	C	AC	G	C	G	GC	C	T	TG	T	G	C	y	C	AA	C	C	r	C	G	A	T	T	AACC	T	A	C	GC	A	2
<i>S. pectinata</i> gt 1a × gt 1b (2210-2212)	C	AC	G	C	G	GC	C	T	TG	T	G	C	y	C	AA	C	cl-	A	C	G	A	T	T	AACC	T	A	C	GC	R	2 + indel (3)
<i>S. pectinata</i> gt 1a × gt 1b (2213)	C	AC	G	C	G	GC	C	T	TG	T	G	C	y	C	AA	C	cl-	A	C	G	A	W	T	AACC	T	A	C	GC	R	3 + indel
<i>S. pectinata</i> gt 1a × gt 1b (2586)	C	AC	G	C	G	GC	C	T	TG	T	G	C	y	C	AA	C	cl-	A	C	G	A	T	T	AACC	T	A	C	GC	r	2 + indel
<i>S. pectinata</i> gt 1a × gt 1b (2587)	C	AC	G	C	G	GC	C	T	TG	T	G	C	y	C	AA	C	cl-	A	C	G	A	T	T	AACC	T	A	C	GC	r	2 + indel
<i>S. pectinata</i> genotype 1b (2040)	C	AC	G	C	G	GC	C	T	TG	T	G	C	C	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	0
<i>S. pectinata</i> gt 1b × gt 2b (2228) major	C	AC	G	C	G	GC	C	T	TG	T	G	C	C	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	N	NN	N	0 (allele)
<i>S. pectinata</i> gt 1a × gt 2a (2090) ¹	C	AC	s	s	G	KM	C	w	TG	T	G	C	y	C	AA	C	C	A	C	G	A	T	T	AACC	T	A	C	GC	A	6
<i>S. pectinata</i> gt 1a × gt 2a (2796)	C	AC	s	s	G	GC	C	T	TG	T	G	C	y	C	AA	C	C	A	C	G	r	T	T	wmCs	T	A	C	GC	A	7
<i>S. pectinata</i> gt 1b × gt 2a (2690)	C	AC	S	S	G	GC	C	T	G	T	G	C	C	S	AA	C	C	A	C	G	R	T	T	wmCs	T	A	C	GC	A	7
<i>S. pectinata</i> gt 1a × gt 2b (1711)	C	AC	S	S	R	GC	C	T	tg/-	T	G	C	Y	C	AA	C	C	A	C	G	R	T	T	wmCs	T	A	C	GC	A	8 + indel
<i>S. pectinata</i> gt 1a × gt 2e (2228) minor	C	TT	C	G	G	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	N	NN	N	0 (allele)
<i>S. pectinata</i> gt 2c × gt 2d (2283) c4	C	TT	C	G	G	GC	C	T	TG	T	G	C	C	C	--	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0 (clone)
<i>S. pectinata</i> gt 2c × gt 2d (3210) c4	C	TT	C	G	G	GC	C	T	TG	T	G	C	C	C	--	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0 (clone)
<i>S. pectinata</i> gt 2b × gt 2c (3225) minor	C	TT	C	G	G	GC	C	T	TG	T	G	C	C	C	--	C	C	A	C	R	G	T	T	TCCG	T	A	C	GC	A	1 (allele)
<i>S. pectinata</i> genotype 2a (2797)	C	AC	C	G	G	GC	C	T	TG	T	G	C	C	s	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	1
<i>S. pectinata</i> genotype 2a (1837)	C	AC	C	G	G	GC	C	T	TG	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0
<i>S. pectinata</i> genotype 2a (1841)	C	AC	C	G	G	GC	C	T	TG	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0
<i>S. pectinata</i> genotype 2a (2051)	C	AC	C	G	G	GC	C	T	TG	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0
<i>S. pectinata</i> genotype 2a (2484-2488)	C	AC	C	G	G	GC	C	T	TG	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0 (5)
<i>S. pectinata</i> gt 2a × gt 2b (1869)	C	AC	C	G	r	GC	C	T	tg/-	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	1 + indel
<i>S. pectinata</i> genotype 2b (2644)	C	AC	C	G	r	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	r	G	T	T	TCCG	T	A	C	GC	A	2
<i>S. pectinata</i> genotype 2b (2920)	C	AC	C	G	r	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	1
<i>S. pectinata</i> genotype 2b (1650)	C	AC	C	G	G	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0
<i>S. pectinata</i> genotype 2b (1652)	C	AC	C	G	G	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	GC	A	0
<i>S. pectinata</i> gt 2c × gt 2d (3210) c9	C	AC	C	G	G	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	TT	A	0 (clone)
<i>S. pectinata</i> gt 2c × gt 2d (2283) c2	C	AC	C	G	G	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	G	G	T	T	TCCG	T	A	C	TT	A	0 (clone)
<i>S. pectinata</i> gt 2b × gt 2c (3225) major	C	AC	C	G	G	GC	C	T	--	T	G	C	C	C	AA	C	C	A	C	R	G	T	T	TCCG	T	A	C	GC	A	1 (allele)
<i>S. striata</i> (2185)	C	AC	C	G	G	GC	y	T	TG	t/-	G	C	C	C	--	C	C	A	C	G	G	T	k	TCCG	y	A	C	GC	A	3 + indel
<i>S. striata</i> (3029)	C	AC	C	G	G	GC	y	T	TG	t/-	G	C	C	C	--	C	C	A	C	G	G	T	k	TCCG	y	A	C	GC	A	3 + indel
<i>S. striata</i> (1034)	C	AC	C	G	G	GC	Y	T	TG	--	G	s	C	C	--	C	C	A	C	G	G	T	G	TCCG	T	A	C	GC	A	2
<i>S. striata</i> × <i>S. sp.</i> (855) c3	C	AC	C	G	G	GC	C	T	TG	--	G	C	C	C	--	C	C	A	C	G	G	T	G	TCCG	T	A	C	GC	A	0 (clone)

¹ In the second half of this sequence, the additive character states of genotype 2 are missing (confirmed by several independent amplifications and sequencing reactions), probably as a result of gene conversion.

Legend: Variable positions are shown. Colors are for better distinction of the variation. Samples in bold cover the variation and were used for tree construction.
c: cloned sequences, major/minor: dominant ribotype/underrepresented ribotype in sequence electropherogram.

Supplementary Table 2 | Intra- and interspecific variation of closely related species, number of intra-individual polymorphic sites (*ITS*)

B) *Stuckenia amblyphylla*, *S. pamirica*, *S. filiformis* (genotypes 1 and 2 and intraspecific hybrids), ***S. vaginata*** (genotypes 1, 2a and 2b), and a hybrid involving ***S. filiformis* genotype 1** (second parent probably *S. vaginata*)

Species (isolate)	Position in alignment (ITS 1 ITS 2)														polym. sites (accessions)
	52	116	146-147	226	488	568	612	615	620	648	649	658	664	713-716	
<i>S. amblyphylla</i> (2602)	G	A	–	T	A	C	T	C	G	T	C	T	A	–	0
<i>S. amblyphylla</i> (2603)	G	A	–	T	A	C	T	C	G	T	C	T	A	–	0
<i>S. pamirica</i> (1753)	A	A	AC	T	C	T	T	C	G	T	C	W	C	TATG/–	1 + indel
<i>S. filiformis</i> genotype 1 (1987, 1989, 1992, 2006, 2288, 2290, 2291, 2296, 2297, 2298, 2322, 3216, 3217, 3218, 3229, 3248, 3252)	A	A	–	T	C	T	T	C	G	T	C	T	C	–	0 (17)
<i>S. filiformis</i> genotype 1 × genotype 2 (1060)	R	A	–	T	C	T	T	C	G	T	C	T	C	–	1
<i>S. filiformis</i> genotype 1 × genotype 2 (1703)	R	A	–	T	C	T	T	C	G	T	C	T	C	–	1
<i>S. filiformis</i> genotype 1 × genotype 2 (1985)	R	A	–	T	C	T	T	C	G	T	C	T	C	–	1
<i>S. filiformis</i> genotype 1 × <i>S. vaginata</i> (2446)*	R	A	–	Y	C	T	T	S	G	T	C	T	C	–	3*
<i>S. filiformis</i> genotype 1 × <i>S. vaginata</i> (2452)*	r	A	–	Y	C	T	T	S	G	T	C	T	C	–	3*
[second parent of 2446 and 2452, predicted sequence]	G	A	–	C	C	T	T	G	G	T	C	T	C	–	–
<i>S. filiformis</i> genotype 2 (1187, 1941, 2108, 2134, 2440, 2453, 2462, 2463, 2464, 2543, 2793, 2794, 3192)	G	A	–	T	C	T	T	C	G	T	C	T	C	–	0 (13)
<i>S. filiformis</i> genotype 2 (2095)	G	A	–	T	C	T	T	C	G	Y	C	T	C	–	1
<i>S. filiformis</i> genotype 2 (2461)	G	A	–	T	C	T	T	C	G	T	S	T	C	–	1
<i>S. vaginata</i> genotype 1 (1919)	G	A	–	T	C	T	T	C	T	T	C	T	C	–	0
<i>S. vaginata</i> genotype 1 (2052)	G	A	–	T	C	T	T	C	T	T	C	T	C	–	0
<i>S. vaginata</i> genotype 1 (2097)	G	A	–	T	C	T	T	C	T	T	C	T	C	–	0
<i>S. vaginata</i> genotype 1 (2132)	G	A	–	T	C	T	T	C	T	T	C	T	C	–	0
<i>S. vaginata</i> genotype 2a (1063)	G	G	–	T	C	T	T	C	G	T	C	T	C	–	0
<i>S. vaginata</i> genotype 2a (1976)	G	G	–	T	C	T	T	C	G	T	C	T	C	–	0
<i>S. vaginata</i> genotype 2a (1999)	G	G	–	T	C	T	T	C	G	T	C	T	C	–	0
<i>S. vaginata</i> genotype 2b (2016)	G	G	–	T	C	T	A	C	G	T	C	T	C	–	0

* hybrids with an unknown genotype of another species, according to cpDNA similar to *S. vaginata*

Groenlandia densa: three identical sequences, no polymorphisms, no close relatives

Legend: Variable positions are shown. Colors are for better distinction of the variation. Samples in bold cover the variation and were used for tree construction. c: cloned sequences, major/minor: dominant ribotype/underrepresented ribotype in sequence electropherogram.