



**Taxonomické zhodnocení diverzity
na příkladu čeledi Potamogetonaceae**



Druh – soubor populací s jedinečným vývojovým původem a historií, tvořený navzájem si podobnými jedinci, kteří se mezi sebou mohou plodně křížit a jsou reprodukčně izolováni od jiných podobných skupin











a



b

Fig. 2. *Potamogeton alpinus* from Malšova Lhota, Czech Republic; a – specimen KAPLAN 96/681 collected in the field, b – specimen KAPLAN C 338 from cultivation; scale bars = 5 cm.



a



b

Fig. 3. *Potamogeton xfluitans* from Fußach, Austria; a – specimen KAPLAN 98/129 with floating leaves collected in the field, b – specimen KAPLAN C 983 with submerged leaves from cultivation; scale bars = 5 cm.

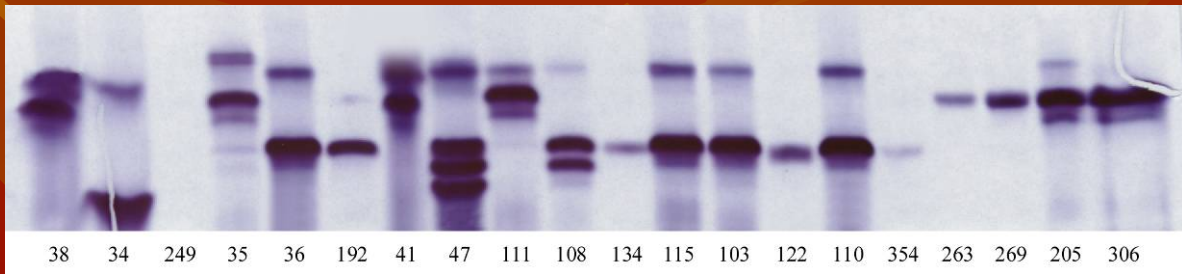
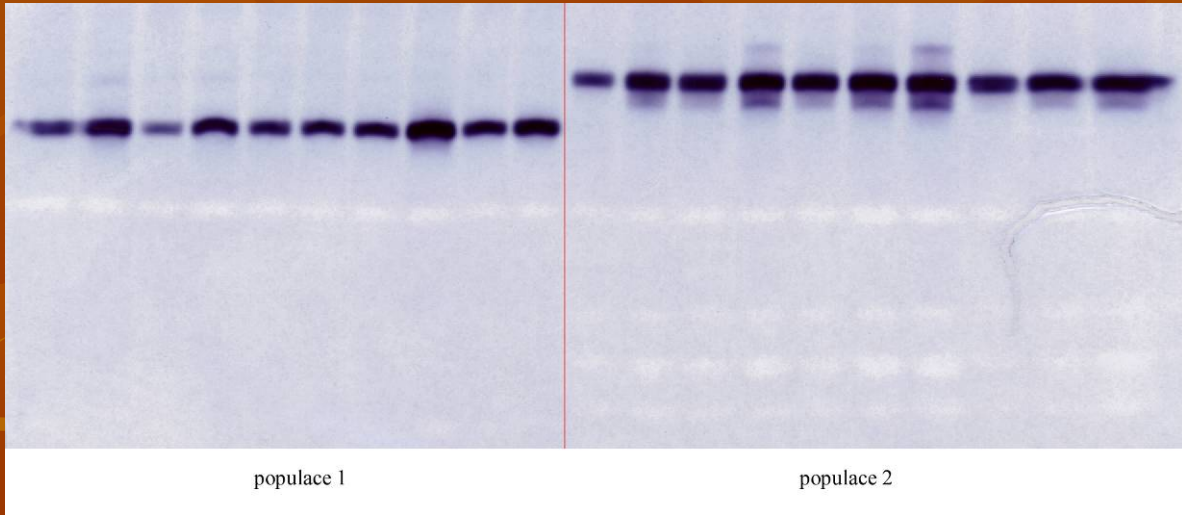
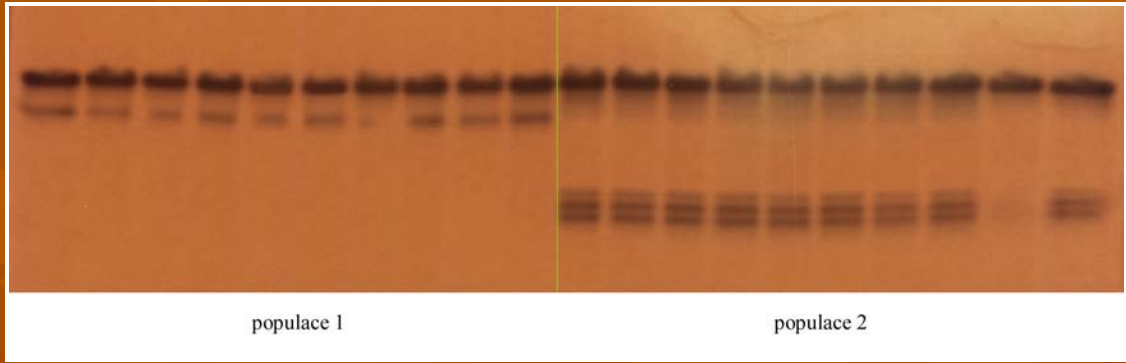


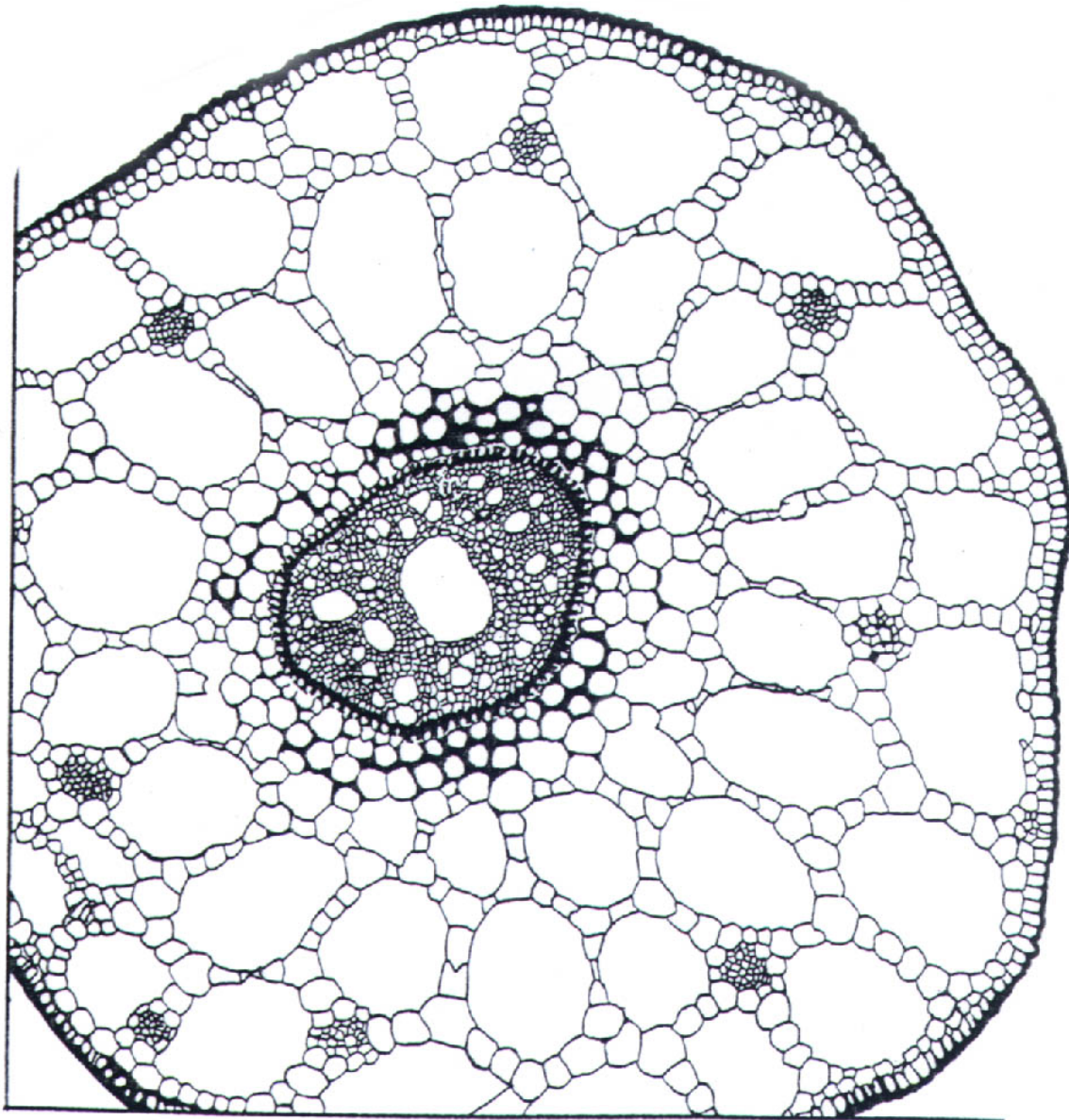
a



b

Fig. 4. *Potamogeton gramineus* from Česká Skalice, Czech Republic; a – specimen KAPLAN 97/831 collected in the field, b – specimen KAPLAN C 887 from cultivation; scale bars = 5 cm.







0658027 == 2528AD
 STEYNBERG, M.C.
 22415 == 6



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2528 AD	Grid Ref. Ruiterw.	Regio TRANSCAAL
MC Steynberg 6	Legit & No.	ANNO 1980.11.10

Potamogeton thunbergii Cham. & Schlecht.

Rust-der-Winterdam. By inloop. In volle
 sonlig
 Humusryke grond.
 Hidrofiet, kom hier-en-daar voor
 0,31 cm hoog met groen blomme

ex UP Herb.
 C. Reid Det. Verw. 7 L.F.D. 1504

Stem anatomy of *Potamogeton*
 examined by Z. KAPLAN, 2003

type of stele: proto trio oblong four bundles circular
 endodermis: O-type O-U-type U-type
 interlacunar bundles: absent present
 subepidermal bundles: absent present
 pseudohypodermis: absent present

Potamogeton schweinfurthii A. BENN.
 2003 det./rev. Z. KAPLAN

658027

HERB. HORT. KEW.



Potamogeton richardii SOLMS
 [syn. *P. thunbergii* auct.]

2002 det./rev. Z. KAPLAN

Stem anatomy of *Potamogeton*
 examined by Z. KAPLAN, 2002

type of stele: proto trio oblong four bundles circular
 endodermis: O-type O-U-type U-type
 interlacunar bundles: absent present
 subepidermal bundles: absent present
 pseudohypodermis: absent present



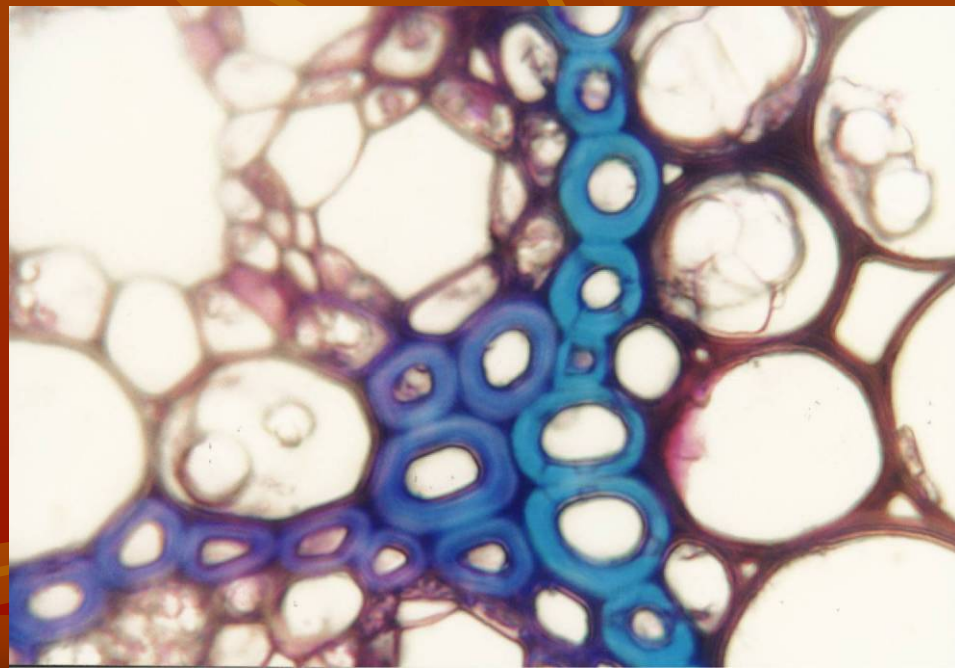
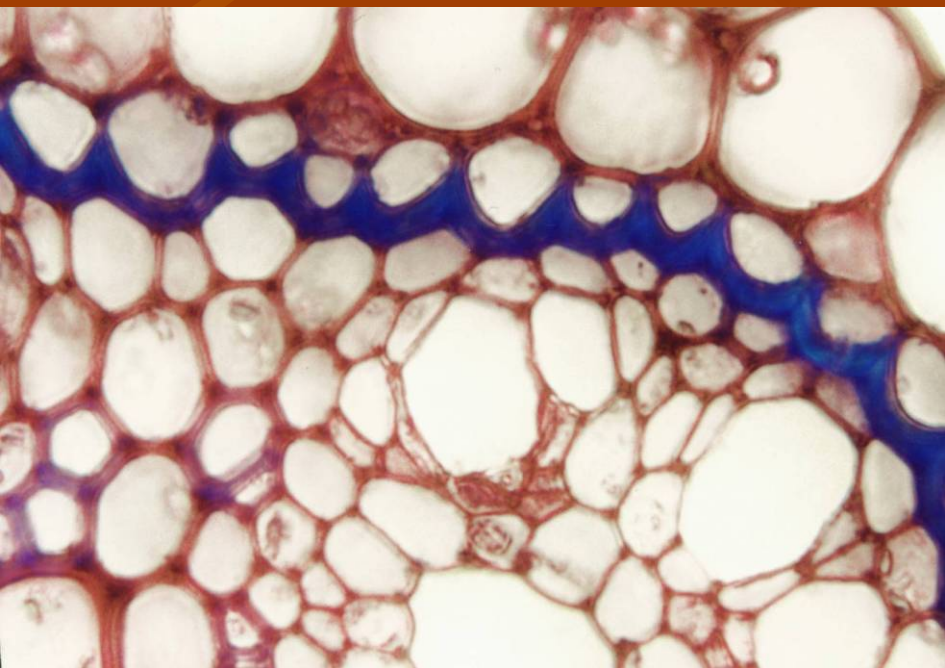
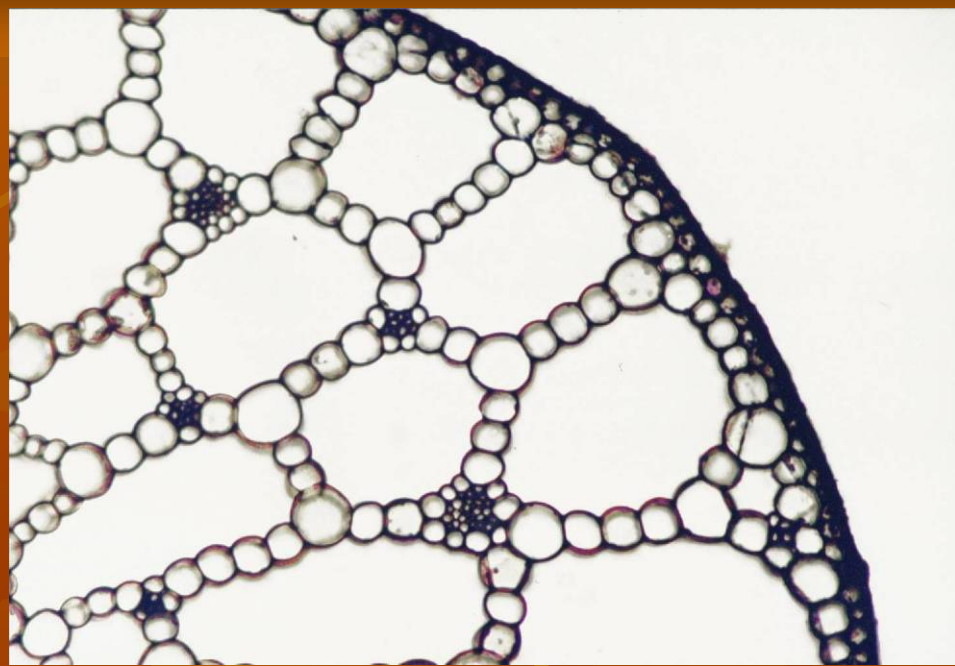
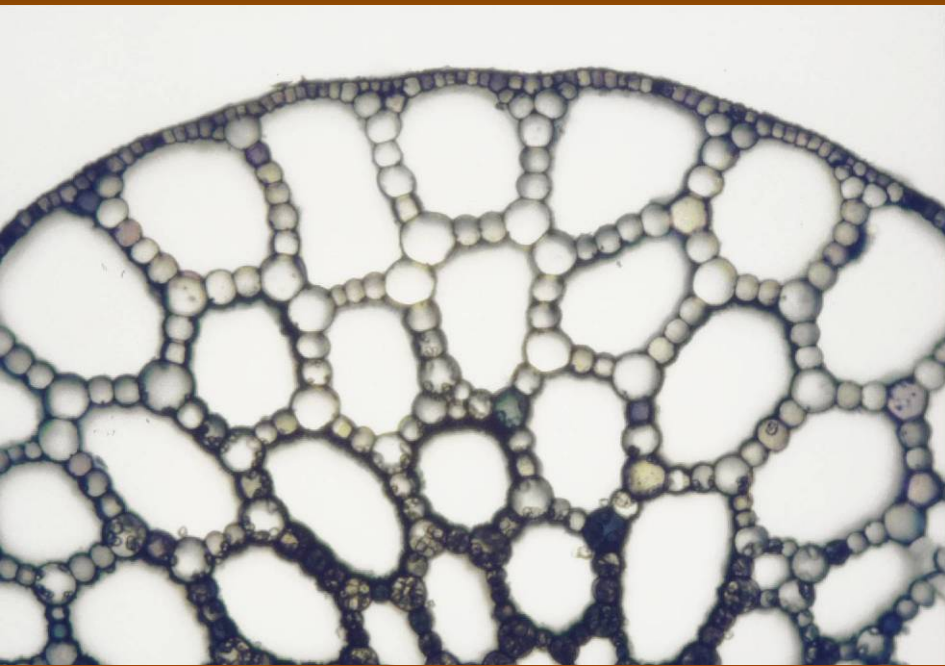
Distributed by the Missouri Botanical Garden Herbarium (MO)

PLANTS OF MALAWI *Potamogeton*
thunbergii Cham. & Schlecht.
Potamogeton richardii Solms

Floating on surface of pond,
 rooted in mud.

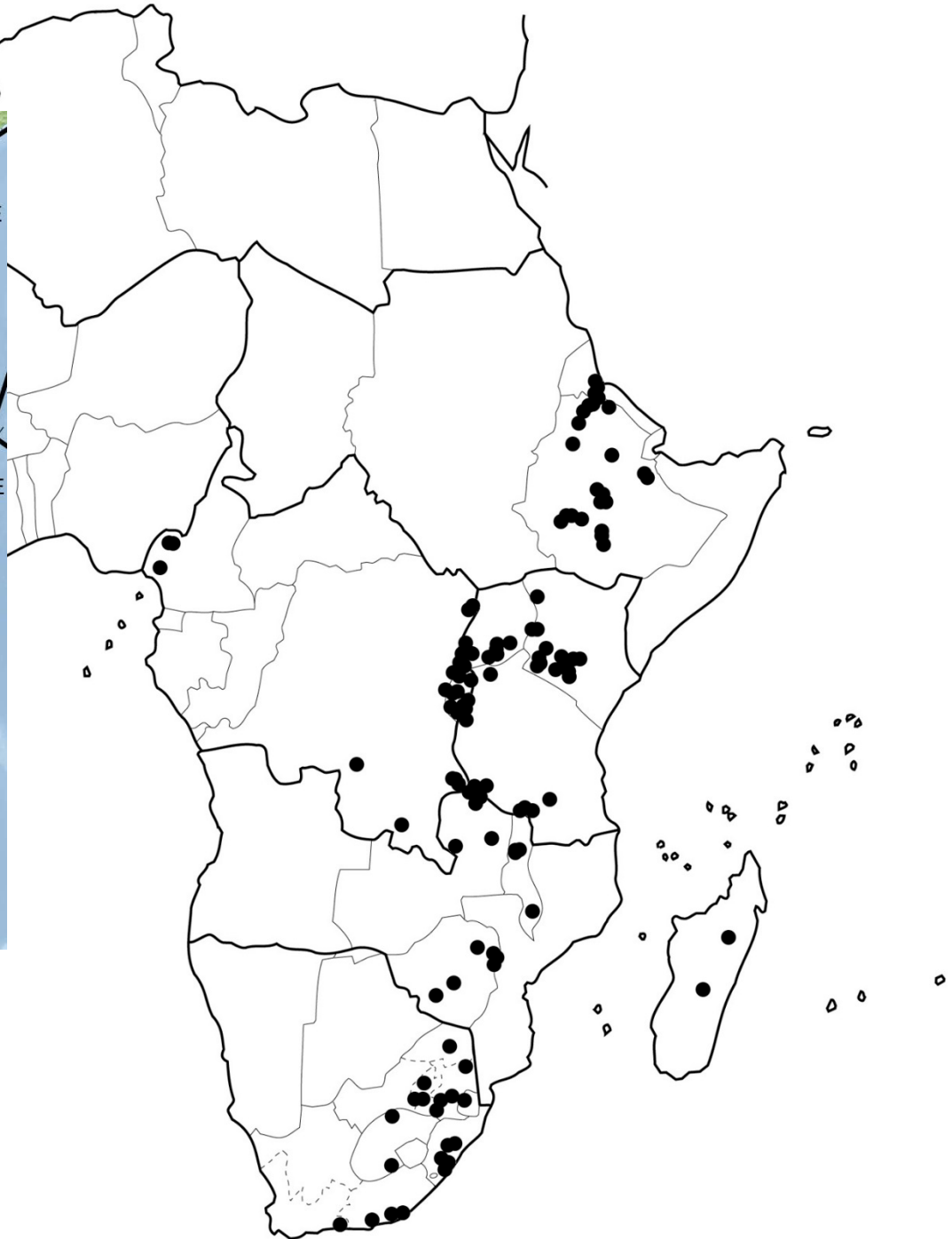
N. Prov., Nkhata Bay Dist.,
 Vipya Plateau, 36 mi. SW
 of Muzuu. 1670 m

Jan Pawek 13230 12 Nov 77















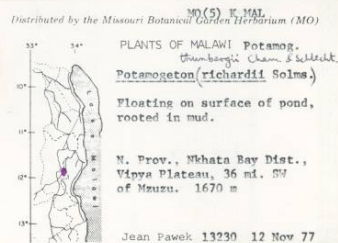




Potamogeton richardii SOLMS
[syn. *P. thunbergii* auct.]
2002 det./rev. Z. KAPLAN

Stem anatomy of *Potamogeton*
examined by Z. KAPLAN, 2002

type of stele:	proto	trio	oblong	four bundles	circular
endodermis:	O-type	O-U-type	U-type		
interlacunar bundles:	absent	present			
subepidermal bundles:	absent	present			
pseudohypodermis:	absent	present			



Potamogeton richardii

stanovení počtu chromozomů:

$$2n = 8x = 104$$

multigenové sekvenování:

sekvence druhů *P. nodosus* a *P. natans*

inkongruence mezi stromy založenými
na jaderné a chloroplastové DNA

závěr: alopolyloidní druh, který obsadil
volnou niku

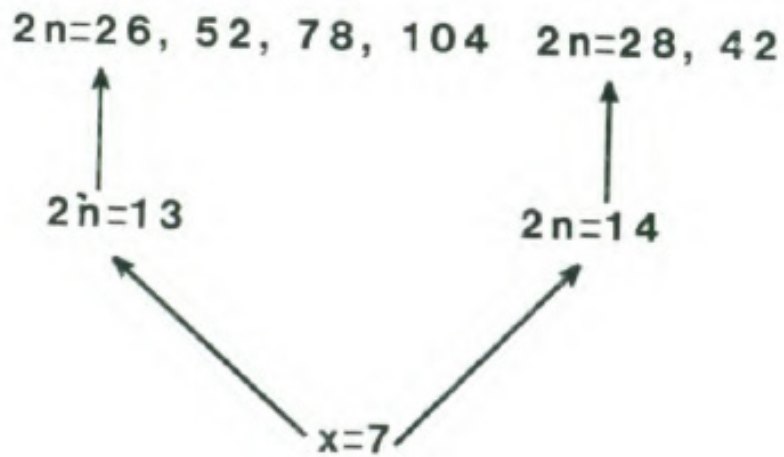
Table 5

Species of *Potamogeton* showing variation in chromosome number^a

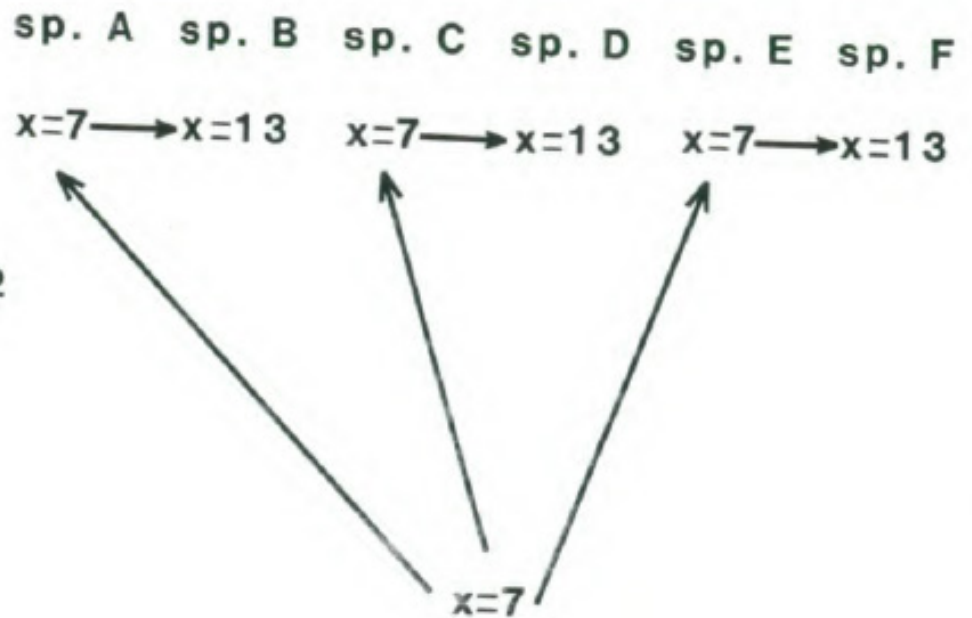
Species	Euploid	Aneuploid
<i>P. compressus</i>		$2n = 26, 28, 38-41$
<i>P. crispus</i>	$2n = 26, 52, 78$	$2n = 50, 56$
<i>P. distinctus</i>		$2n = 52, 56$
<i>P. filiformis</i>		$2n = \text{ca. } 66, 78$
<i>P. foliosus</i>	$2n = 14, 28$	$2n = 26$
<i>P. fryeri</i>		$2n = 42, 48, 52$
<i>P. indicus</i>		$2n = 42, 50, 52$
<i>P. maackianus</i>	$2n = 26, 52$	$2n = 56$
<i>P. natans</i>		$2n = 42, 52$
<i>P. oxyphyllus</i>		$2n = 26, 28$
<i>P. pectinatus</i>	$2n = 42, 84$	$2n = \text{ca. } 66, 76, 78, 80, 82, 86^b$
<i>P. perfoliatus</i>	$2n = 26, 52, 78$	$2n = 14, \text{ca. } 40, \text{ca. } 48$
<i>P. polygonifolius</i>		$2n = 26, 28$
<i>P. pusillus</i>		$2n = 26, 28$
<i>P. richardsonii</i>	$2n = 26, 52$	
<i>P. vaginatus</i>		$2n = 78, \text{ca. } 88$

^aWithin a species, chromosome numbers with a common denominator of 13 or 14 are arbitrarily classified as showing euploid variation, whilst those without these common denominators are classified as aneuploid. Agmatoploid variation has been ignored.

^bResults from preparations regarded as poor by Kalkman and Van Wijk (1984) have been omitted.



single origin hypothesis



multiple origin hypothesis

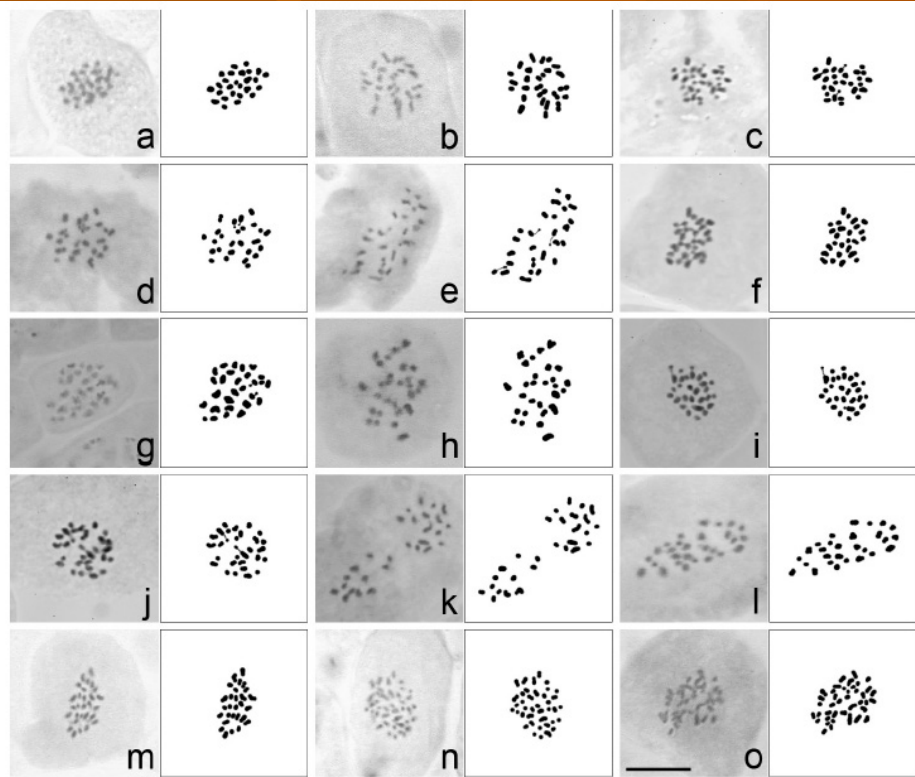


Fig. 1. – Chromosomes (photograph of the cytological preparation on the left with its interpretation on the right in each pair) of selected species and hybrids of *Potamogetonaceae* at the metaphase of the first meiotic division of the pollen mother cells (a) or at mitotic metaphase in somatic cells (b–o), arranged according to increasing chromosome number: a – *Potamogeton gramineus*, sample 2072, $n = 26$; b – *Potamogeton berchtoldii*, sample 1648, $2n = 26$; c – *P. berchtoldii* s. l., sample 1619, $2n = 26$; d – *P. foliosus*, sample 1593, $2n = 26$; e – *P. pusillus*, sample 1715, $2n = 26$; f – *P. trichoides*, sample 1903, $2n = 26$; g – *P. acutifolius*, sample 321, $2n = 28$; h – *P. cheesemani*, sample 950, $2n = 28$; i & j – *P. compressus*, sample 1962, $2n = 28$; k – *P. polygonifolius*, sample 1535, $2n = 28$; l – *P. spirillus*, sample 1695, $2n = 28$; m – *P. zosteriformis*, sample 1491, $2n = 28$; n – *P. pusillus*, sample 1133, $2n = 39$; o – *P. xgessnacensis*, sample 1286, $2n = 40$. Scale bar identical for all figures = 10 μm .

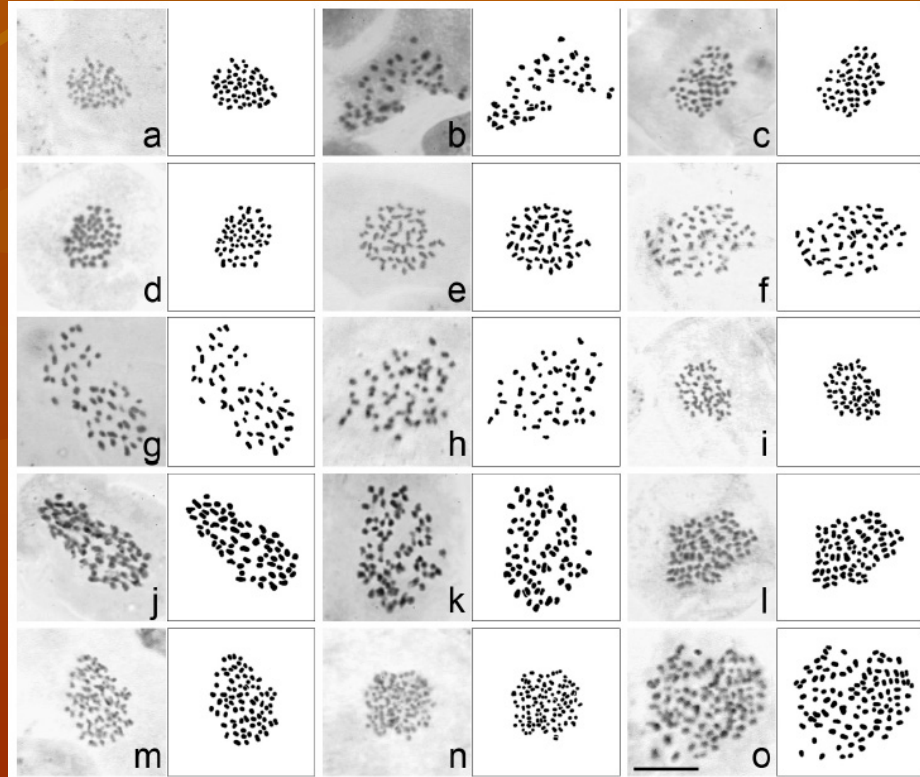
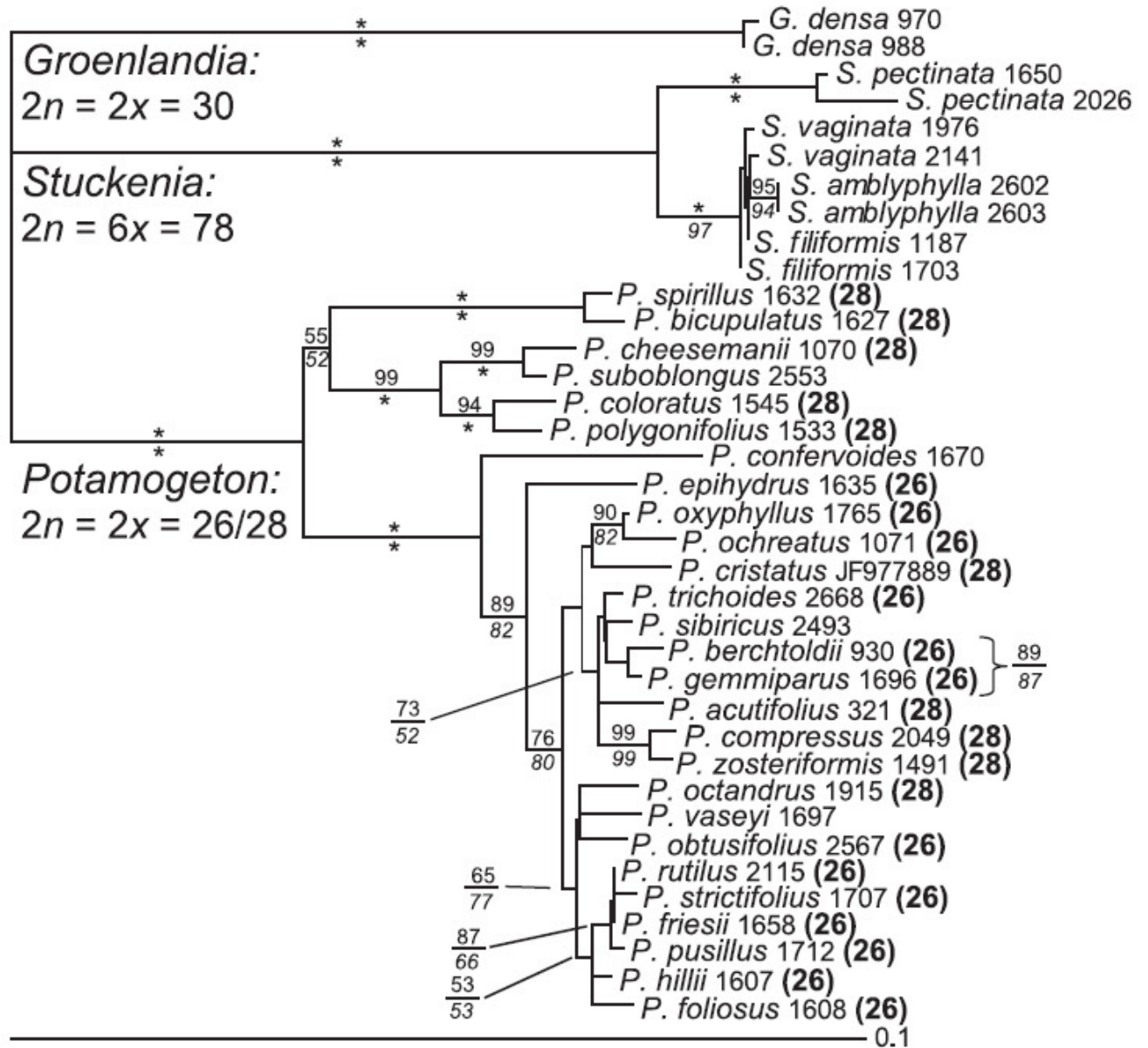
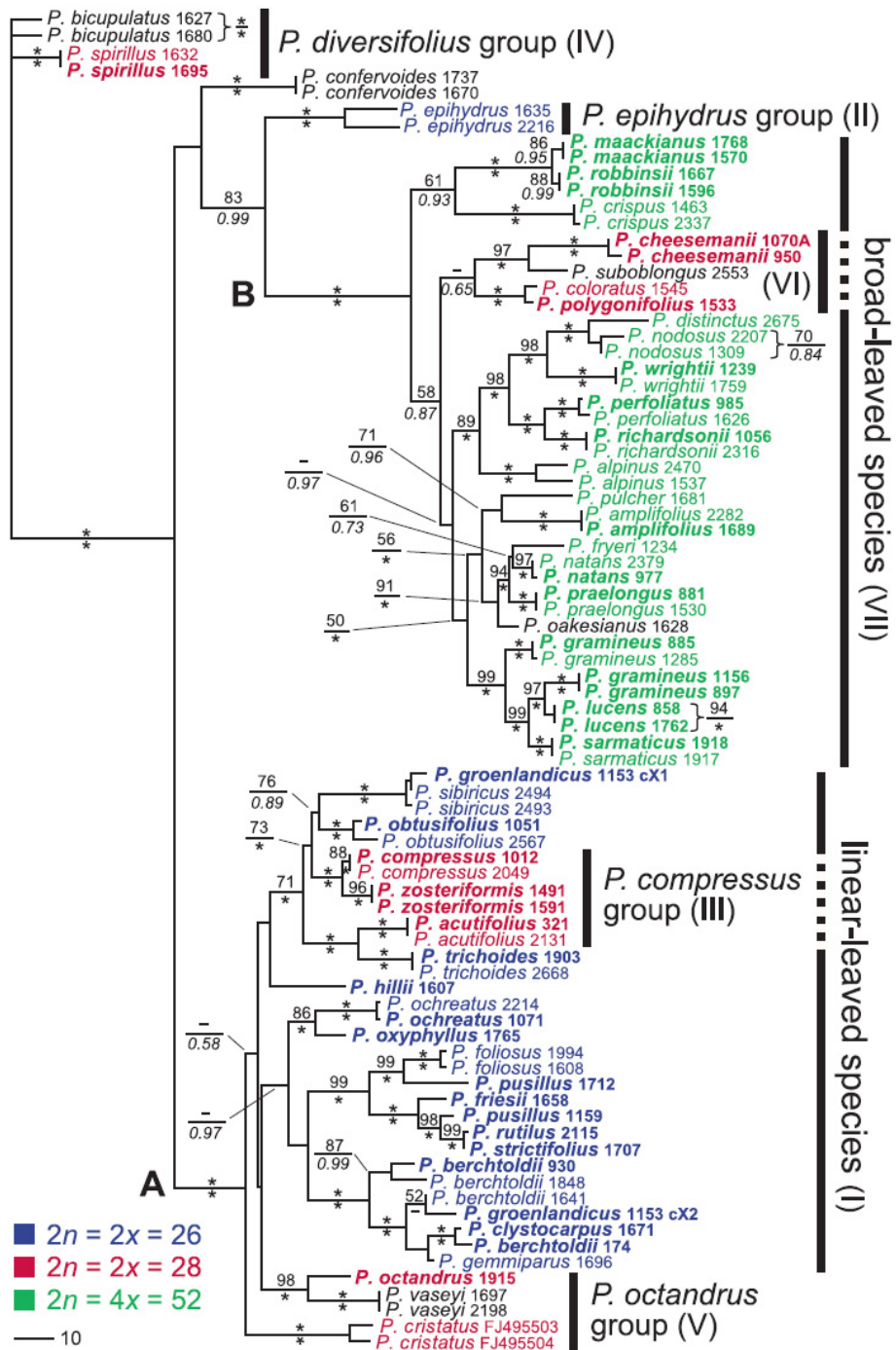


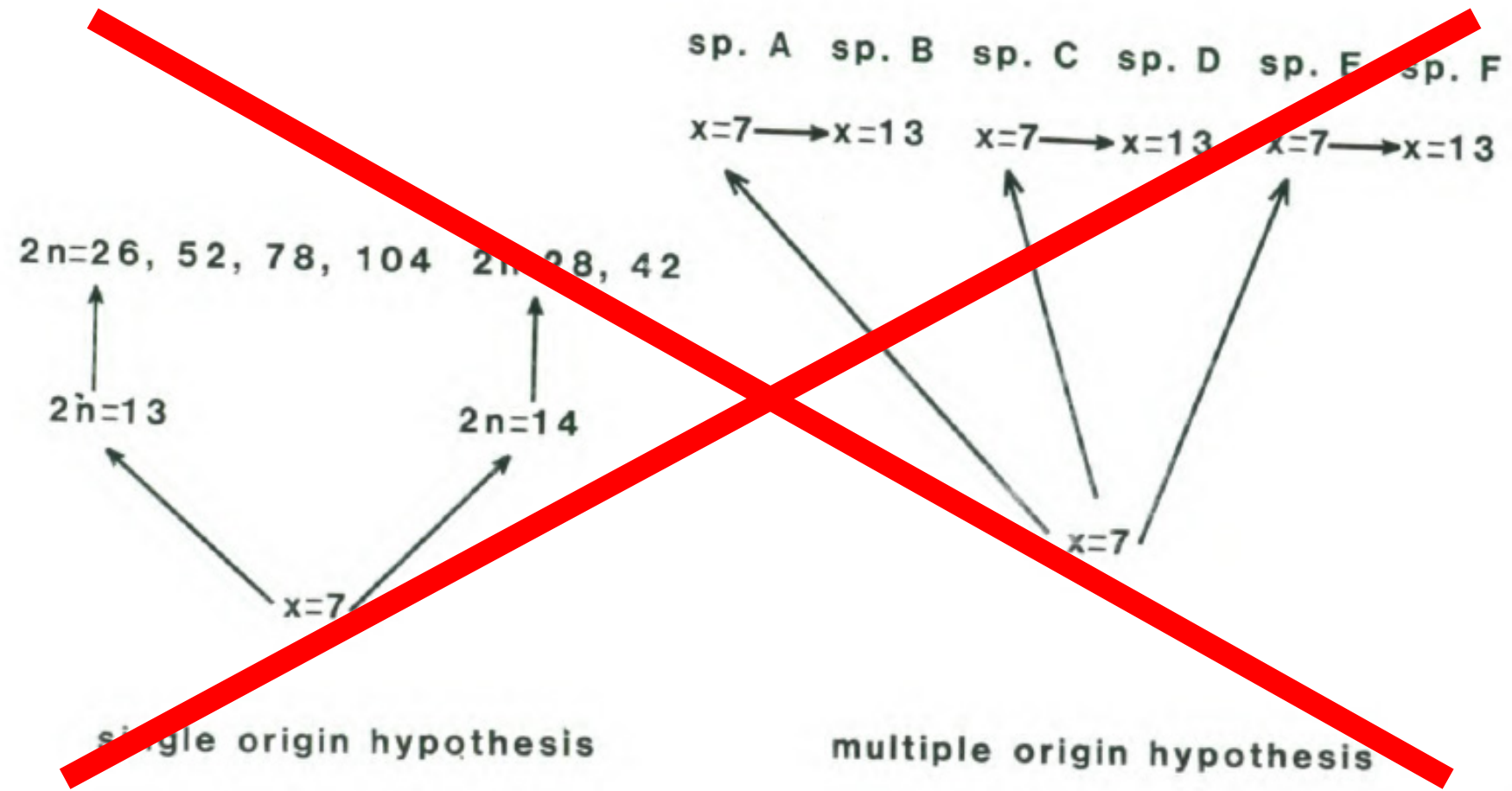
Fig. 2. – Chromosomes (photograph of cytological preparation on the left with its interpretation on the right in each pair) of selected species and hybrids of *Potamogetonaceae* at mitotic metaphase in somatic cells, arranged according to increasing chromosome number: a – *Potamogeton alpinus*, sample 338, $2n = 52$; b – *P. gramineus*, sample 885, $2n = 52$; c – *P. maackianus*, sample 1768, $2n = 52$; d – *P. natans*, sample 977, $2n = 52$; e – *P. perfoliatus*, sample 985, $2n = 52$; f – *P. perfoliatus*, sample 1002, $2n = 52$; g – *P. richardsonii*, sample 1056, $2n = 52$; h – *P. xnitens*, sample 879, $2n = 52$; i – *P. xundulatus*, sample 1025, $2n = 52$; j – *P. xlintonii*, sample 2119, $2n = 65$; k – *P. xsalicifolius*, sample 1017, $2n = 78$; l – *P. xtorssanderi*, sample 1006, $2n = 78$; m – *Stuckenia filiformis*, sample 1187, $2n = 78$; n – *Potamogeton illinoensis*, sample 856, $2n = 104$; o – *P. schweinfurthii*, sample 861, $2n = 104$. Scale bar identical for all figures = 10 μm .

Genus	Informal species group (in <i>Potamogeton</i>)	Species	Chromosome number determined in this study (2n)	Literature records (2n)
<i>Groenlandia</i>		<i>G. densa</i>	30	30
<i>Potamogeton</i>	I. linear-leaved species (excl. <i>P. compressus</i> group)	<i>P. berchtoldii</i>	26	26
		<i>P. clystocarpus</i>	ca 26	–
		<i>P. foliosus</i>	26	26 (28)
		<i>P. friesii</i>	26	26
		<i>P. gemmiparus</i>	26	–
		<i>P. groenlandicus</i>	26	26
		<i>P. hillii</i>	26	–
		<i>P. obtusifolius</i>	26	26
		<i>P. ochreateus</i>	26	–
		<i>P. oxyphyllus</i>	26	26 (28)
		<i>P. pusillus</i>	26	26
		<i>P. rutilus</i>	26	26
		<i>P. strictifolius</i>	26	–
	<i>P. trichoides</i>	26	26	
	II. <i>P. epihydrus</i> group	<i>P. epihydrus</i>	ca 26	26
	III. <i>P. compressus</i> group	<i>P. acutifolius</i>	28	(26)
		<i>P. compressus</i>	28	26, 28 (38–41)
		<i>P. zosteriformis</i>	28	–
	IV. <i>P. diversifolius</i> group	<i>P. spirillus</i>	28	–
	V. <i>P. octandrus</i> group	<i>P. octandrus</i>	28	28
		<i>P. cristatus</i>	–	28
	VI. broad-leaved species of the <i>P. polygonifolius</i> group	<i>P. cheesemani</i>	28	28
		<i>P. coloratus</i>	28	26
		<i>P. polygonifolius</i>	28	26, 28
	VII. majority of broad-leaved species	<i>P. alpinus</i>	52	52
		<i>P. amplifolius</i>	52	52
		<i>P. crispus</i>	52	52 (26, 48, 50, 56, 78)
		<i>P. distinctus</i>	ca 52	52 (56)
		<i>P. fryeri</i>	–	52 (42, 48)
		<i>P. gramineus</i>	52	52
		<i>P. lucens</i>	52	52
		<i>P. maackianus</i>	52	52 (56)
		<i>P. natans</i>	52	52 (42)
<i>P. nodosus</i>		52	52	
<i>P. perfoliatus</i>		52	52 (78)	
<i>P. praelongus</i>		52	52	
<i>P. richardsonii</i>		52	52	
<i>P. robbinsii</i>		ca 52	52	
<i>P. sarmaticus</i>	52	–		
<i>P. wrightii</i>	52	52 (48, 50, 51)		
VIII. broad-leaved species of the <i>P. illinoensis</i> group	<i>P. illinoensis</i>	104	104	
	<i>P. richardii</i>	ca 104	(42)	
	<i>P. schweinfurthii</i>	104	–	
<i>Stuckenia</i>	<i>S. filiformis</i>	78	78	
	<i>S. pectinata</i>	78	78 (70–87)	
	<i>S. striata</i>	78	–	
	<i>S. vaginata</i>	78	78 (ca 88)	

ancestor:
 $2n = 2x = 26$







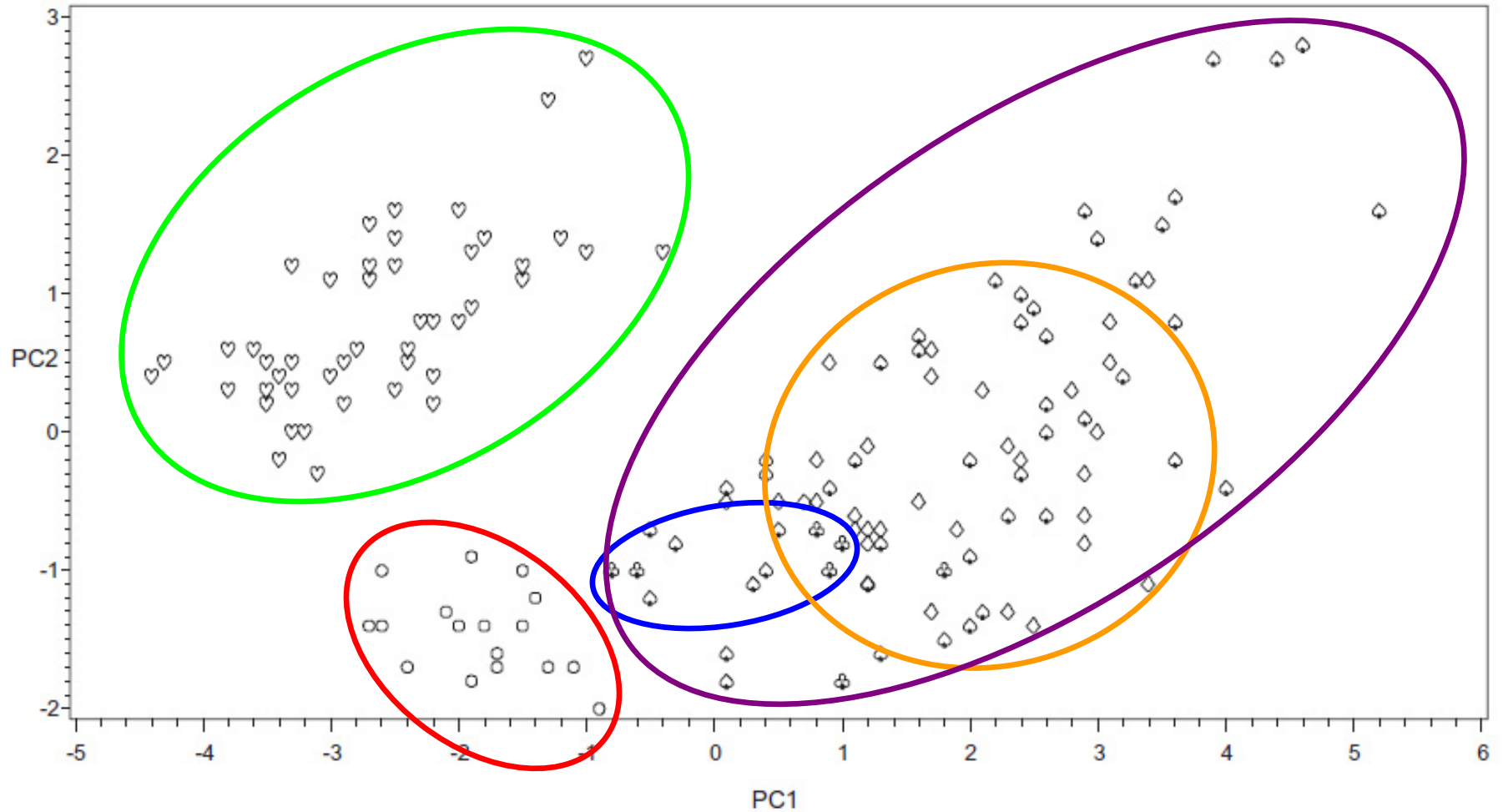
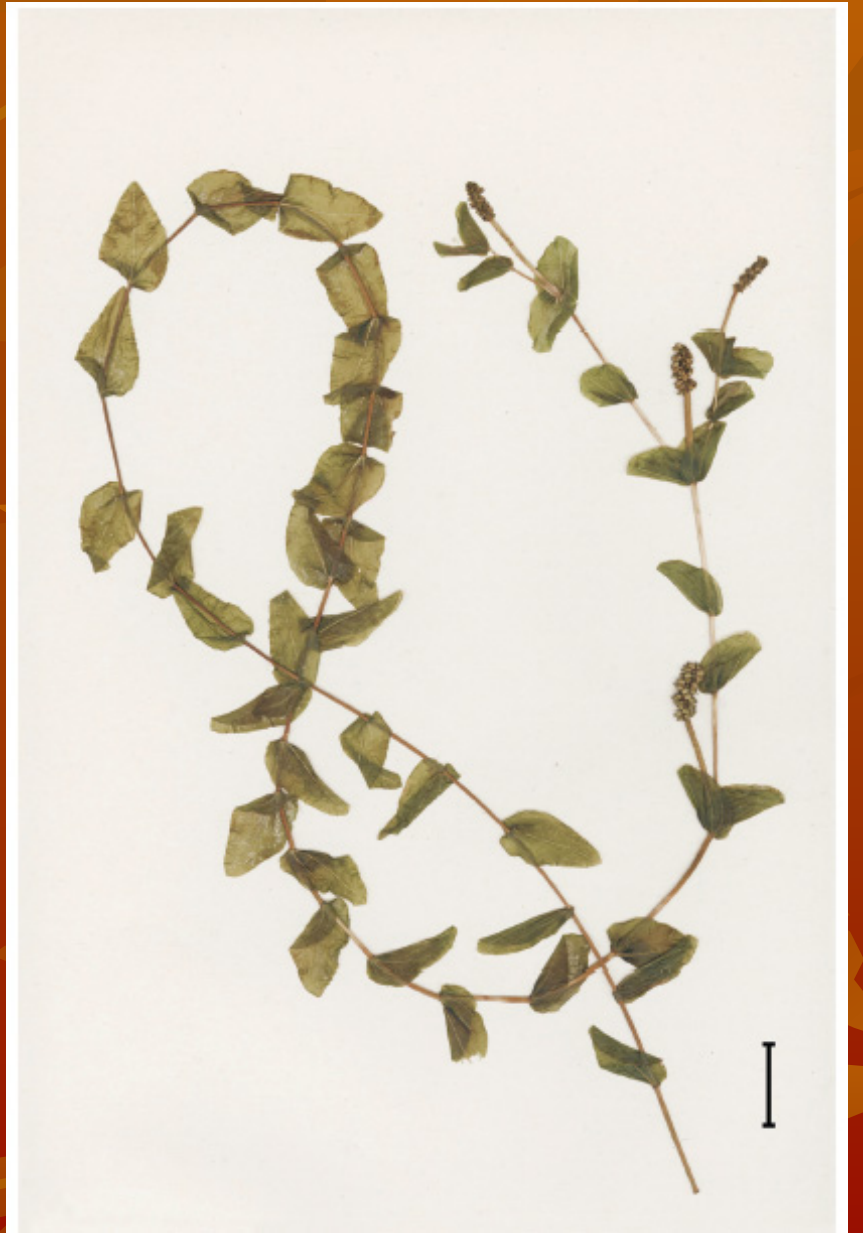
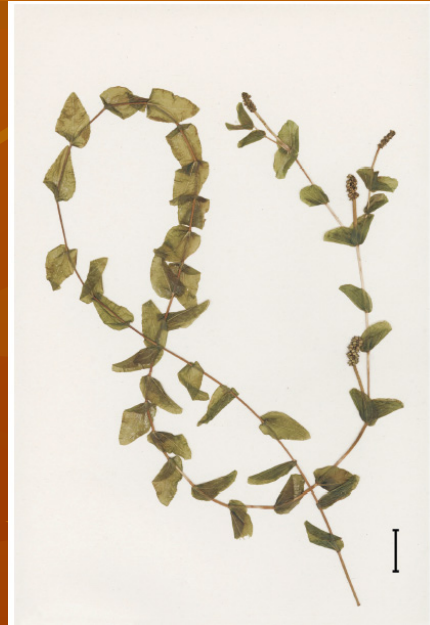
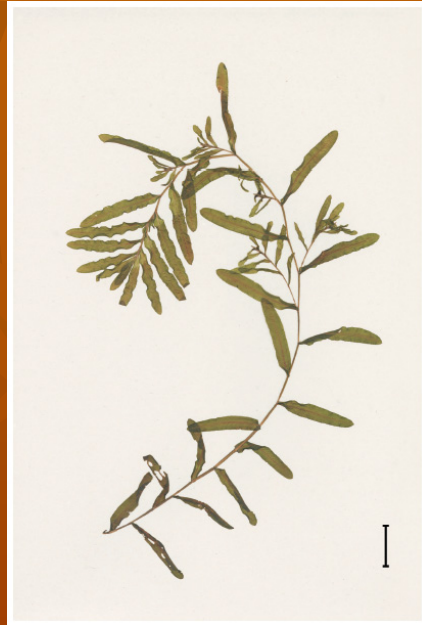


Figure 3. Principal component analysis of the *Potamogeton compressus* group based on ten morphological characters and the complete set of data. Heart, *P. acutifolius*; spade, *P. compressus*; club, *P. henningii*; circle, *P. manchuriensis*; diamond, *P. zosteriformis* (see also Table 3: PCA1). The first two axes explain 57.1% and 11.6% of the variation, respectively.





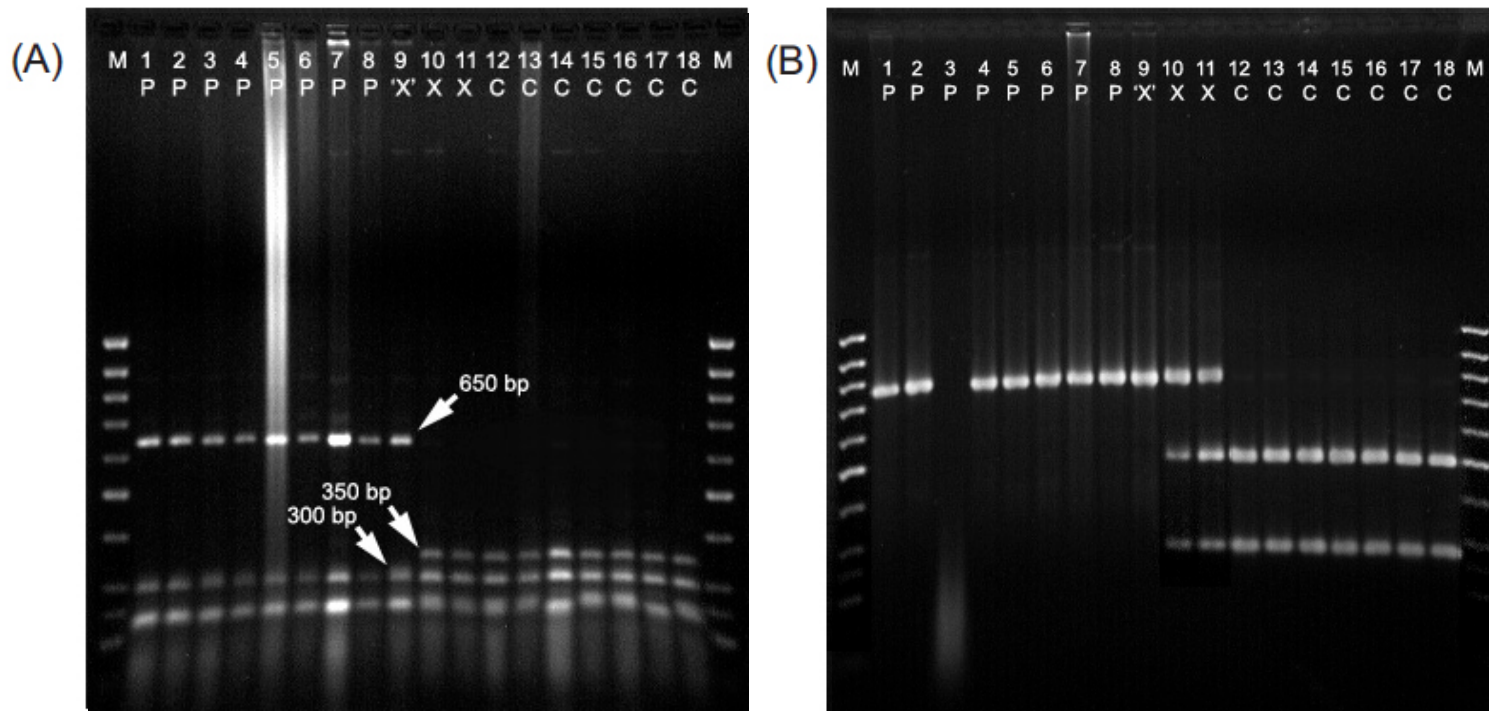
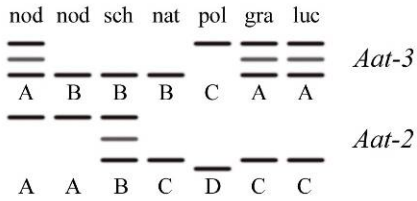
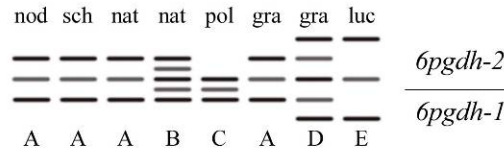


Fig. 8. **(A)** – RFLP of the *trnK-trnQ* intergenic spacer of chloroplast DNA. The *P. perfoliatus*-specific (P) fragment (650 bp) is cut into two fragments in the *P. crispus*-specific (C) samples; the smaller one (300 bp) runs – according to the relative brightness of bands in samples with similar DNA concentration (e.g. compare 1–4 to 15–18 or 7 to 14) – along with a fragment of similar length that is present in both species. The sample 1470 originally suspected to be *P. ×cooperi* but later identified as a narrow-leaved form of *P. perfoliatus* (“X”) in track 9 shows the *P. perfoliatus* pattern (for discussion see text). The two true hybrids (X) show the *P. crispus* haplotype indicating their maternal origin from this species in both cases. Identity of samples (compare Table 1): 1 – 1002, 2 – 979, 3 – 985, 4 – 1467, 5 – 1469, 6 – 840, 7 – 1481, 8 – 1471, 9 – 1470, 10 – 1248, 11 – 1420, 12 – 1463, 13 – 1485, 14 – 1483, 15 – 1464, 16 – 1466, 17 – 1473, 18 – 1472. **(B)** – RFLP of the internal transcribed spacer. 1–8 (P): *P. perfoliatus*; 9 (“X”): sample originally incorrectly suspected to be *P. ×cooperi* (see text) showing only the *P. perfoliatus* pattern (uncut PCR product, 768 bp); 10–11 (X): true hybrids showing the ITS variants of both parental taxa; 12–18 (C): *P. crispus* (273 and 495 bp fragments, respectively). Sample 3 was degraded for unknown reasons, but also had the *P. perfoliatus* pattern (not shown). Identity of samples (compare Table 1): 1 – 1002, 2 – 979, 3 – 985, 4 – 1467, 5 – 1469, 6 – 840, 7 – 1481, 8 – 1471, 9 – 1470, 10 – 1248, 11 – 1420, 12 – 1463, 13 – 1485, 14 – 1483, 15 – 1464, 16 – 1466, 17 – 1473, 18 – 1472.

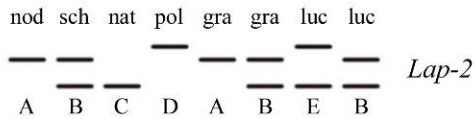
AAT



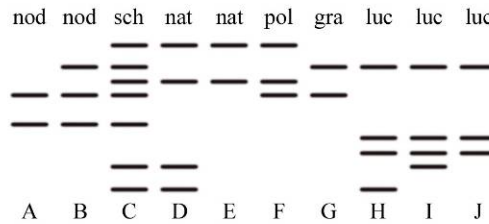
6PGDH



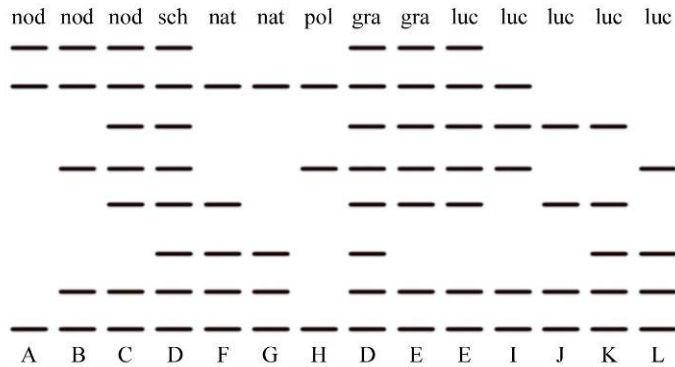
LAP



EST



SOD



ADH

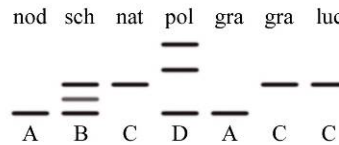


Fig. 8. – Enzyme phenotypes of AAT, ADH, LAP, EST, SOD and 6PGDH present in samples of *Potamogeton nodosus* (nod), *P. xschreberi* (sch), *P. natans* (nat), *P. polygonifolius* (pol), *P. gramineus* (gra) and *P. lucens* (luc). All enzymes migrated anodally (towards the bottom of the figure). Size of the bands and distances between them within an enzyme system are printed in 72% of the actual size they were on the gel. In the dimeric systems AAT, ADH and 6PGDH, supposed mono- and homomeric bands are illustrated in black, bands corresponding to supposed heterodimers are given in grey. The secondary bands that appeared in some samples at ADH and SOD are not shown. Alphabetical codes below the banding patterns denote the different locus or enzyme phenotypes of polymorphic enzymes.

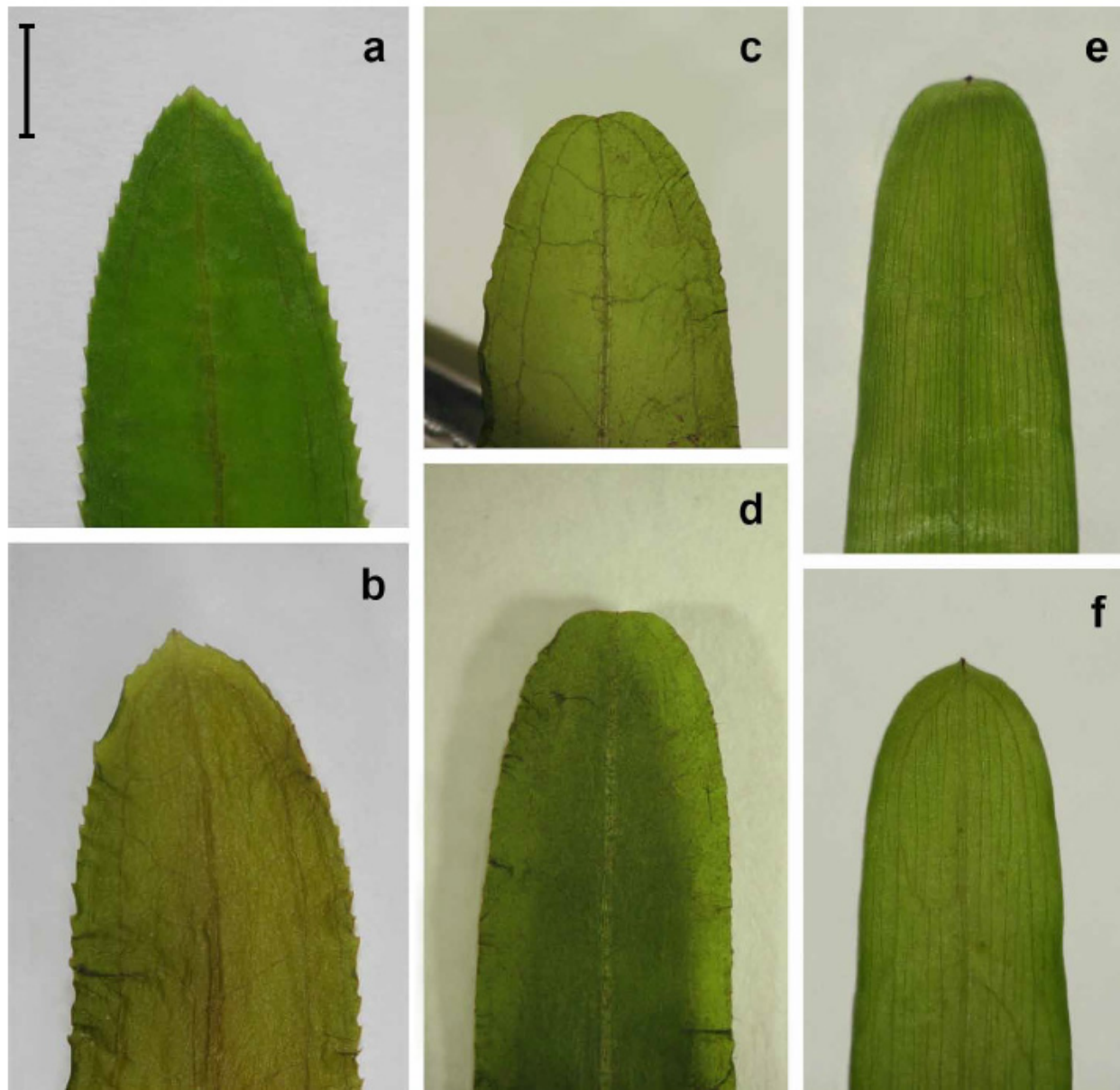


Fig. 4. Shape of leaf apex: a, *P. crispus* (Kaplan 08-646), b, *P. crispus* (Kaplan 08-384), c & d, *P. xjacobsii* (Hellquist 17201 & Sainty), e & f, *P. ochreatus* (Kaplan 1071). Scale bar identical for all figures: 2 mm.

Table 3. Nucleotide sequence variation and ITS ribotypes of *Potamogeton crispus*, *P. ochreatus* and their hybrid, *P. xjacobsii*.

Taxon	Position in alignment ¹																																										
	55	70	75	86	87	130	198	202	222	235	247	249	250	251	264	270	274	403	448	453	459	461	464	465	469	477	513	514	523	525	528	531	567	594	595	602	606	613	655	658	659	662	663
<i>P. ochreatus</i>	T	A	T	A	A	C	A	G	G	T	G	A	C	T	A	T	A	C	C	C	C	A	T	C	T	G	C	C	-	T	C	C	T	C	T	T	G	C	A	C	C	-	-
<i>P. xjacobsii</i> clone 11	T	A	T	A	A	C	A	G	G	T	G	A	C	T	A	T	A	C	C	C	C	A	T	C	T	G	C	C	-	T	C	C	T	C	T	T	G	C	A	C	C	-	-
<i>P. crispus</i> (Europe)	C	T	A	A	T	T	A	A	C	A	T	T	T	A	G	-	G	T	A	T	T	T	C	T	T	A	T	T	T	T	G	-	T	C	C	A	T	C	A	-	C	A	
<i>P. crispus</i> (India)	C	T	A	A	T	T	T	A	C	A	T	T	T	A	G	-	K	T	A	T	T	T	C	T	T	A	T	T	T	K	T	G	-	T	C	T	A	T	C	A	-	C	A
<i>P. crispus</i> (Australia)	C	T	A	A	T	T	T	A	C	A	T	T	T	A	G	-	G	T	A	T	T	T	C	T	T	A	T	T	T	T	G	-	T	C	T	A	T	C	A	-	C	A	
<i>P. xjacobsii</i> clone 3	C	T	A	G	T	T	T	A	C	A	T	T	T	A	G	-	G	T	A	T	T	T	C	T	T	A	T	T	T	T	G	-	T	C	T	A	T	C	A	-	C	A	
<i>P. xjacobsii</i> clone 6	C	T	A	G	T	T	T	A	C	A	T	T	T	A	G	-	G	T	A	T	T	T	C	T	A	A	T	T	T	T	G	-	T	C	T	A	T	C	A	-	C	A	
<i>P. xjacobsii</i> clone 15	C	T	A	A	T	T	T	A	C	A	T	T	T	A	G	-	G	T	A	T	T	T	C	T	T	A	T	T	T	T	G	-	T	C	T	A	T	C	A	-	C	A	

¹ position 86: intra-individual polymorphism in the hybrid sample (also apparent in direct sequencing); positions 198 and 602: intraspecific polymorphisms in *P. crispus* differing between Australian/Indian and European samples; positions 274 and 525: intra-individual polymorphisms in Indian *P. crispus* (K = G or T); position 469: polymerase error in *P. xjacobsii* clone 6. The alignment starts with the first base after the forward primer sequence. Only positions that differ among the sequences are shown.

Table 3

Character states in the ITS region differing between the parents, and cloned sequences of hybrids.

Taxon	Position in alignment ^a
	1 11122222222444444444444444555555556666666666666667 55788912380244556704455566667777112236790013455556667881 58014530022279011322727803460179343847152635134580124564
<i>P. perfoliatus</i> 979	TTATCTTTCTTGGACTTAYGTCACATC-TTGTCC-CGTGTTGCGATCGC--TTTCC
<i>P. perfoliatus</i> 985	TTATCTTTCTTGGACTTACGTCACATC-TTGTCC-CGTGTTGCGATCGC--TTTCC
<i>P. perfoliatus</i> 1002	TTATCTTTCTTGGACTTACGTCACATC-TTGTCC-CGTGTTGCGATCGC--TTTCC
<i>P. perfoliatus</i> 1470	TTATCTTTCTTGGACTTACGTCACATC-TTGTCC-CGTGTTGCGATCGC--TTTCC
<i>P. ×cognatus</i> 1226 clone 10	TTATCTTTCTTGGACTTACGTCACATC-TTGTCC-CGTGTTGCGATCGC--TTTCC
<i>P. ×cognatus</i> 1226 clone 1	TTATCTTTCTTGGACTTACGTCACATC-TTGTCC-CGTGTTGCGATCGC--TTTCC
<i>P. ×cognatus</i> 1226 clone 2	TCATCTTTCTTGGACTTACGTCACATC-TTGTCC-CGTGTTGCGATCGC--TTTCC
<i>P. ×cognatus</i> 1226 clone 7	TCAAGGACTTGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAC
<i>P. ×cognatus</i> 1226 clone 5	TCAAGGACTTGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAC
<i>P. ×cognatus</i> 1226 clone 4	TCAAGGACTCGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAT
<i>P. ×cognatus</i> 1226 clone 12	TCAAGGACTCGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAT
<i>P. praelongus</i> 881	TCAAGGACTCGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAT
<i>P. praelongus</i> 1530	TCAAGGACTCGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAT
<i>P. ×undulatus</i> 1025 clone 14	TCAAGGACTCGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAT
<i>P. ×undulatus</i> 1025 clone 1	TCAAGGACTCGGGACTCACTGCTACCCCCGCCT-CATACCATAG---CCACCCAT
<i>P. ×undulatus</i> 1025 clone 3 ^b	TCAAGGACTCGGGACTCATGATTTTCT-TTACTTTTA-GCCATGGTCCA-ACCCCT
<i>P. ×undulatus</i> 1025 clone 4	CCTAGGACTCACTTTATGTGATTTTCT-TTACTTTTA-GCCATGGTCCA-ACCCCT
<i>P. crispus</i> 1463	CCTAGGACTCACTTTATGTGATTTTCT-TTACTTTTA-GCCATGGTCCA-ACCCCT
<i>P. crispus</i> 1464	CCTAGGACTCACTTTATGTGATTTTCT-TTACTTTTA-GCCATGGTCCA-ACCCCT
<i>P. crispus</i> 1472	CCTAGGACTCACTTTATGTGATTTTCT-TTACTTTTA-GCCATGGTCCA-ACCCCT
<i>P. crispus</i> 1473	CCTAGGACTCACTTTATGTGATTTTCT-TTACTTTTA-GCCATGGTCCA-ACCCCT

^a Positions are numbered from the first base after the forward primer^b Recombinant clone (not submitted to GenBank)

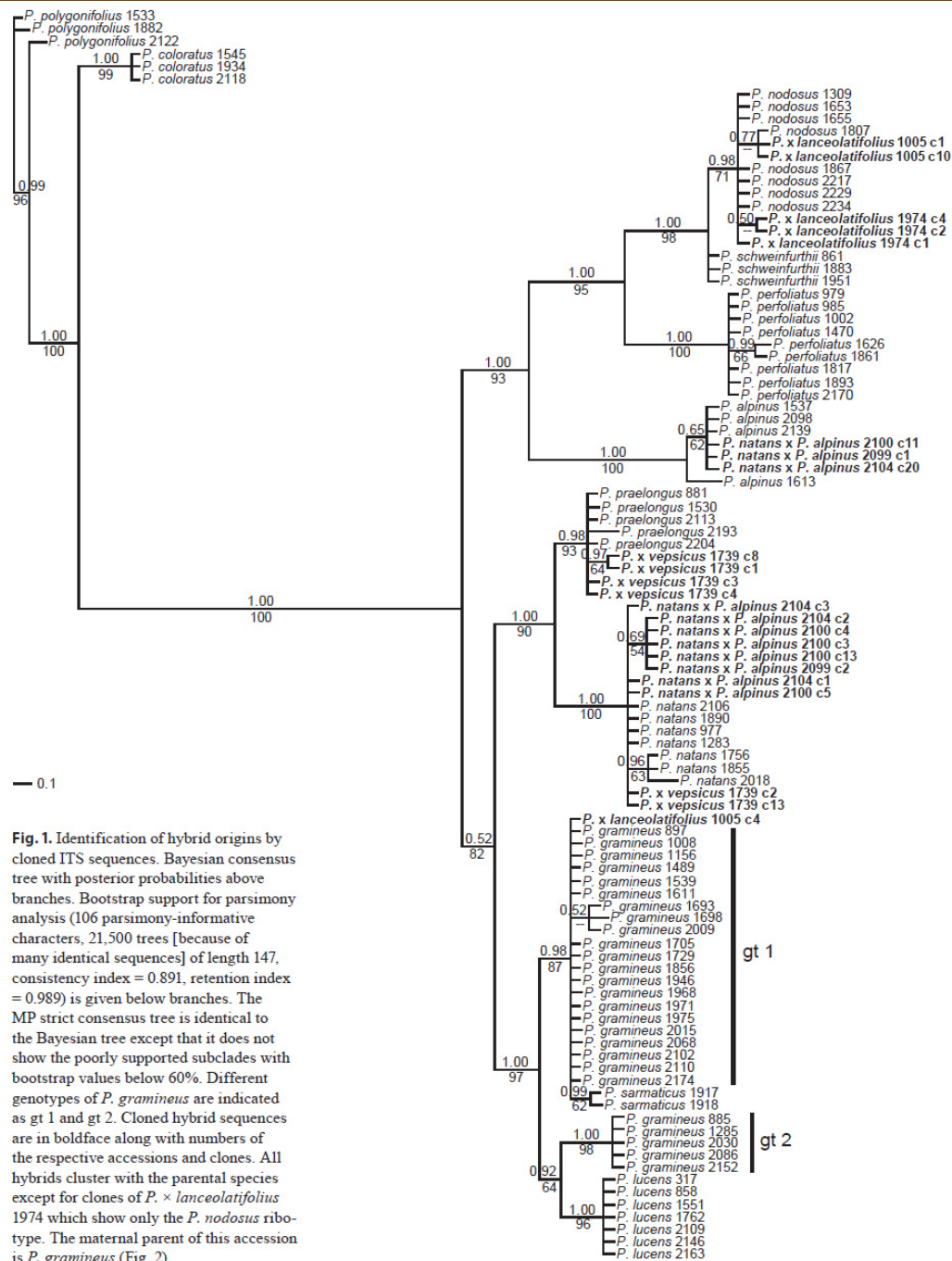


Fig. 1. Identification of hybrid origins by cloned ITS sequences. Bayesian consensus tree with posterior probabilities above branches. Bootstrap support for parsimony analysis (106 parsimony-informative characters, 21,500 trees [because of many identical sequences] of length 147, consistency index = 0.891, retention index = 0.989) is given below branches. The MP strict consensus tree is identical to the Bayesian tree except that it does not show the poorly supported subclades with bootstrap values below 60%. Different genotypes of *P. gramineus* are indicated as gt 1 and gt 2. Cloned hybrid sequences are in boldface along with numbers of the respective accessions and clones. All hybrids cluster with the parental species except for clones of *P. x lanceolatifolius* 1974 which show only the *P. nodosus* ribotype. The maternal parent of this accession is *P. gramineus* (Fig. 2).



PLANTE SUECLE

Potamogeton decipiens Nt. β Torssanderi Tis.

(Titel. Potam. exsicc. Suec. Fasc. II. 75.)

Skånskf. Vårdinge s:n, sjån Sillen.

den 29^{de} 1848
A. P. B., Lönner

J. G. Laurell.

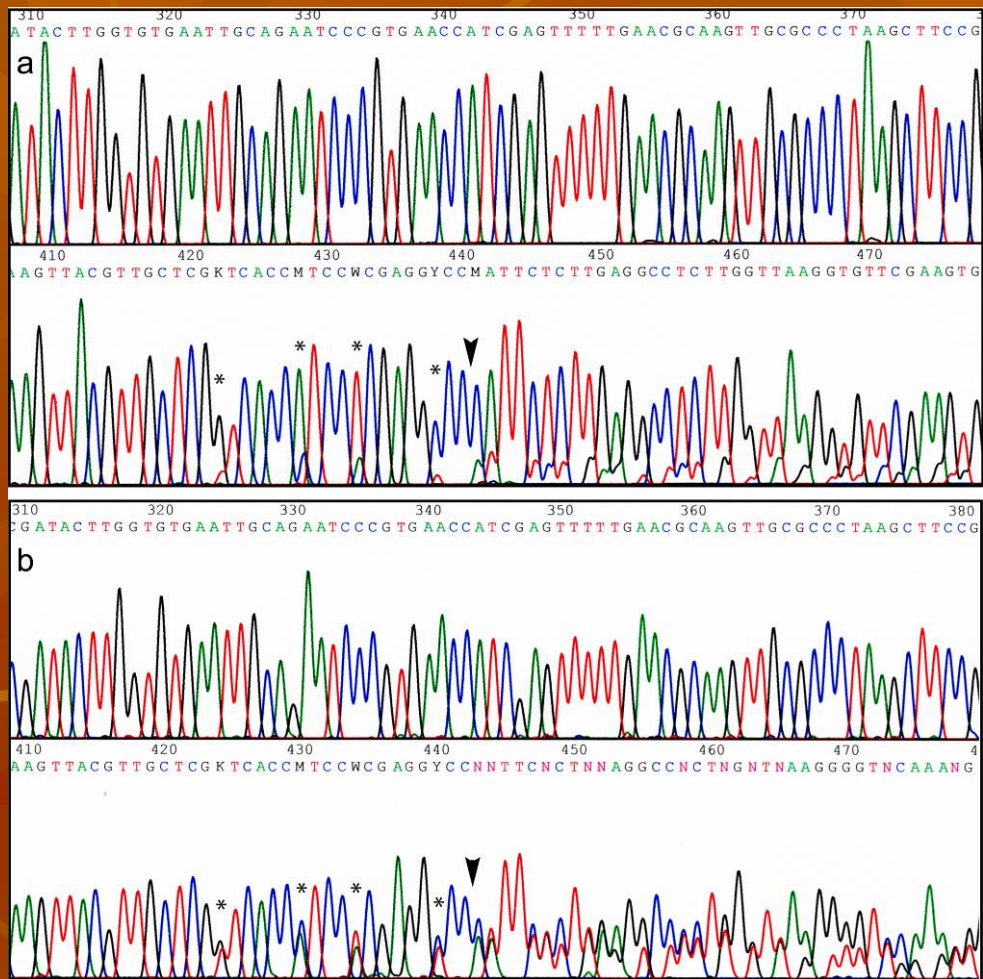
Potamogeton \times *torssanderi* (TISELIUS) DÖRFLER
[= *P. gramineus* L. \times *P. lucens* L. \times *P. perfoliatus* L.]
2005

rev. Z. KAPLAN

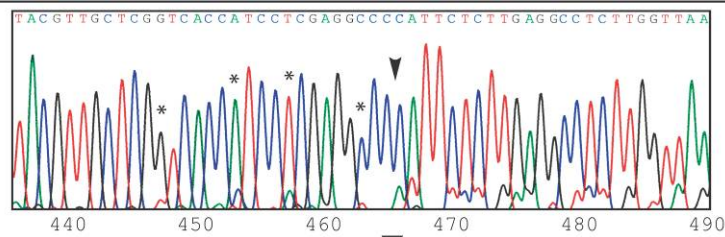
Herb. Vocke

Herb. Goettingen

1848/49

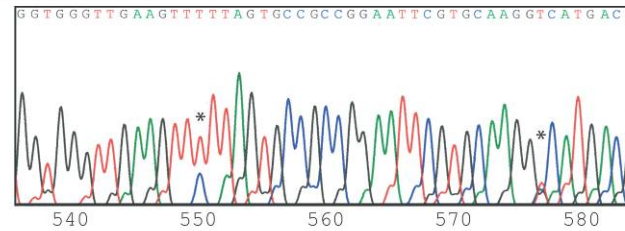


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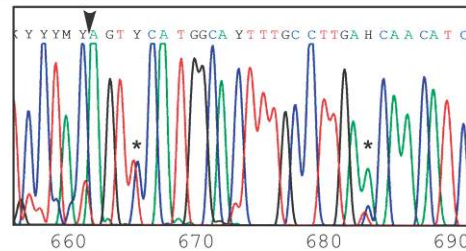
perf-979 TACGTTGCTCGTTCACCCCTCCACGAGGTCCATTTTCTTGAGGCTCTTGTTAAG
 perf-1002 TACGTTGCTCGTTCACCCCTCCACGAGGTCCATTTTCTTGAGGCTCTTGTTAAG
 torss-1006 TACGTTGCTCGKTCACCMTC CGAGGYCCATTCTTGAGGCCCTTGTTAA
 lucens-858 TACGTTGCTCGGTACCATCCTCGAGGCCCATTCCTTGAGGCCCTTGTTAA
 lucens-317 TACGTTGCTCGGTACCATCCTCGAGGCCCATTCCTTGAGGCCCTTGTTAA
 gramin-1285 TACGTTGCTCGGTACCATCCTCGAGGCCCATTCCTTGAGGCCCTTGTTAA
 gramin-897 TACGTTGCTCGGTACCATCCTCGAGGCCCATTCCTTGAGGCCCTTGTTAA

B



perf-979-rv GTGGTGGTTGAAGTTTTTAGTGCCGCCGGAATTCGTGCAAGGGCATGA
 perf-1002-fw GTGGGTTGAAGTTTTTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG
 perf-979 GGTGGGTTGAAGTTTTTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG
 torss-1006-fw GGTGGGTTGAAGTTTYYTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG
 torss-1006-rv GGTGGGTTGAAGTTTYYTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG
 lucens-858 GGTGGGTTGAAGTWTTTTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG
 lucens-317 GGTGGGTTGAAGTTTTTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG
 gramin-1285 GGTGGGTTGAAATTTTTTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG
 gramin-897 GGTGGGTTGAAGTTCTTAGTGCCGCCGGAATTCGTGCAAGGGCATGACGG

C



perf-979-rv GTTCCTAGTTCATGGCATTTCGCTTGATCAACATC
 perf-1002-fw CCTAGTTCATGGCATTTCGCTTGATCAACATCGCG
 torss-1006-fw TCCTACAGTYCATGGCACTTCGCTTGATCAACATC
 torss-1006-rv KYYYMYAGTYCATGGCAYTTTGCCTTGAHCAACATC
 lucens-858 TCCTACAGTCCATGGCACTTCGCTTGAAACAACATC
 lucens-317 TCCTACAGTCCATGGCACTTCGCTTGAAACAACATC
 gramin-1285 TCCTACAGTCCATGGCACTTCGCTTGACCAACATC
 gramin-897 TCCTACAGTTCATGGCACTTWTGCCTTGACCAACATC

8x



6x

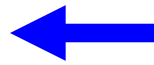
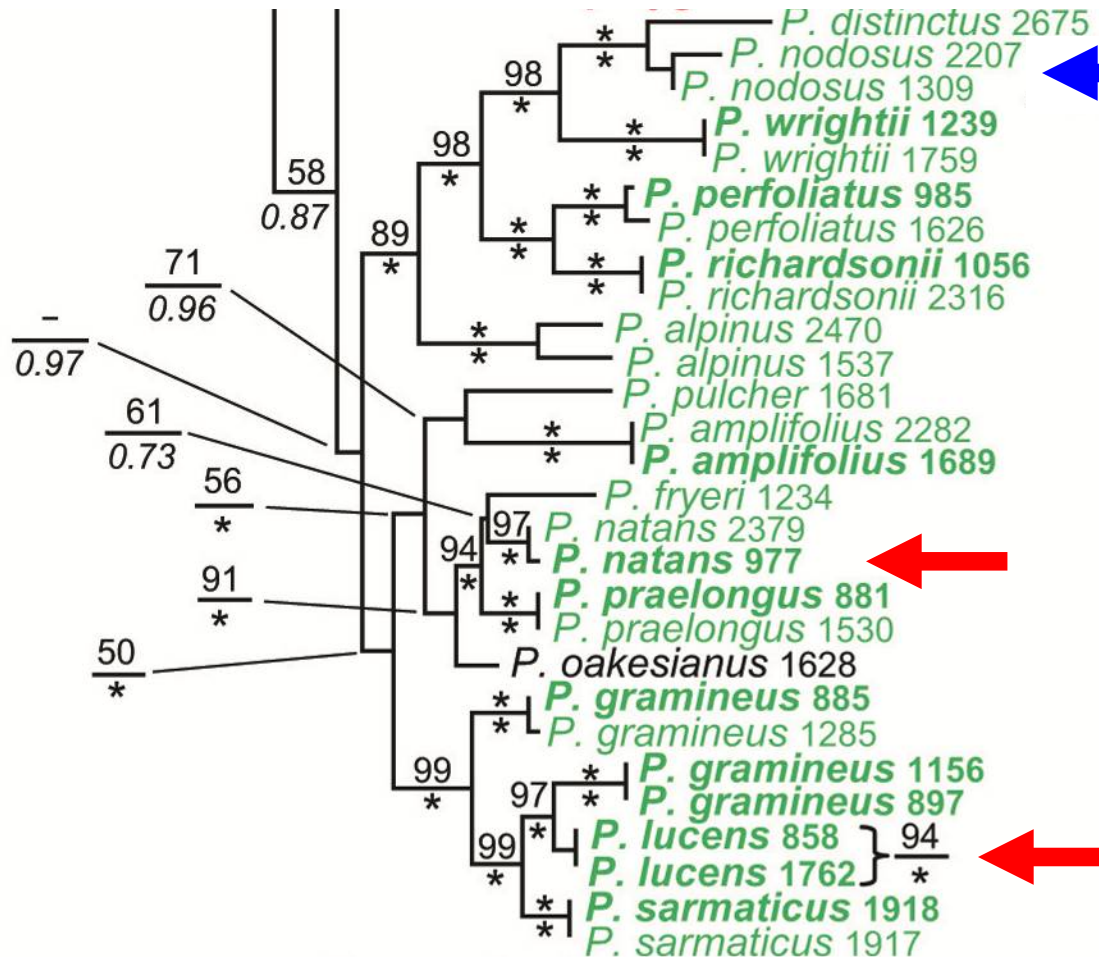


4x











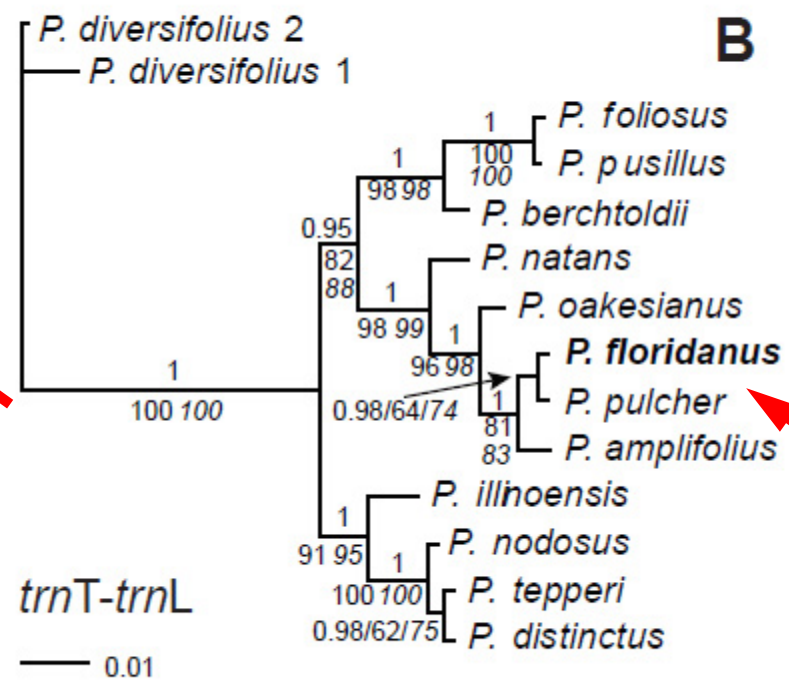
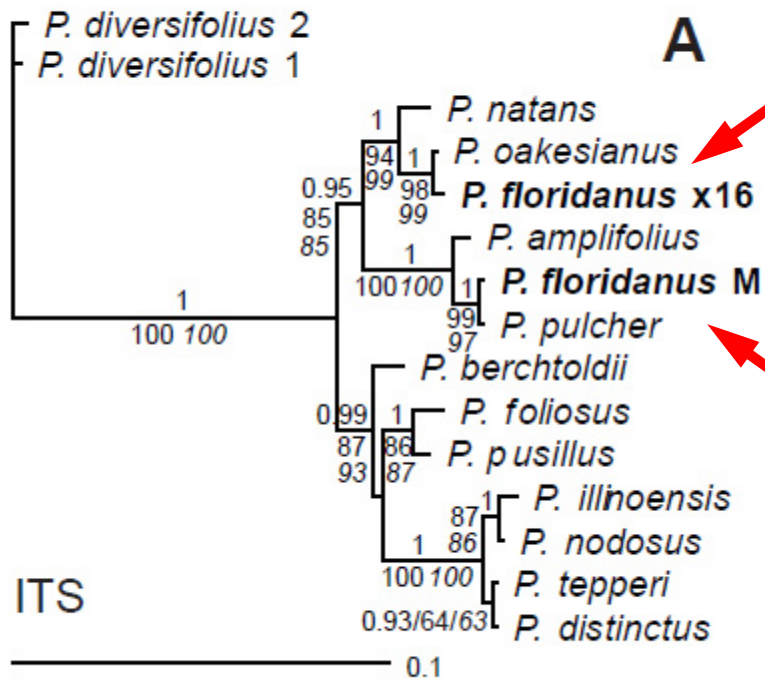


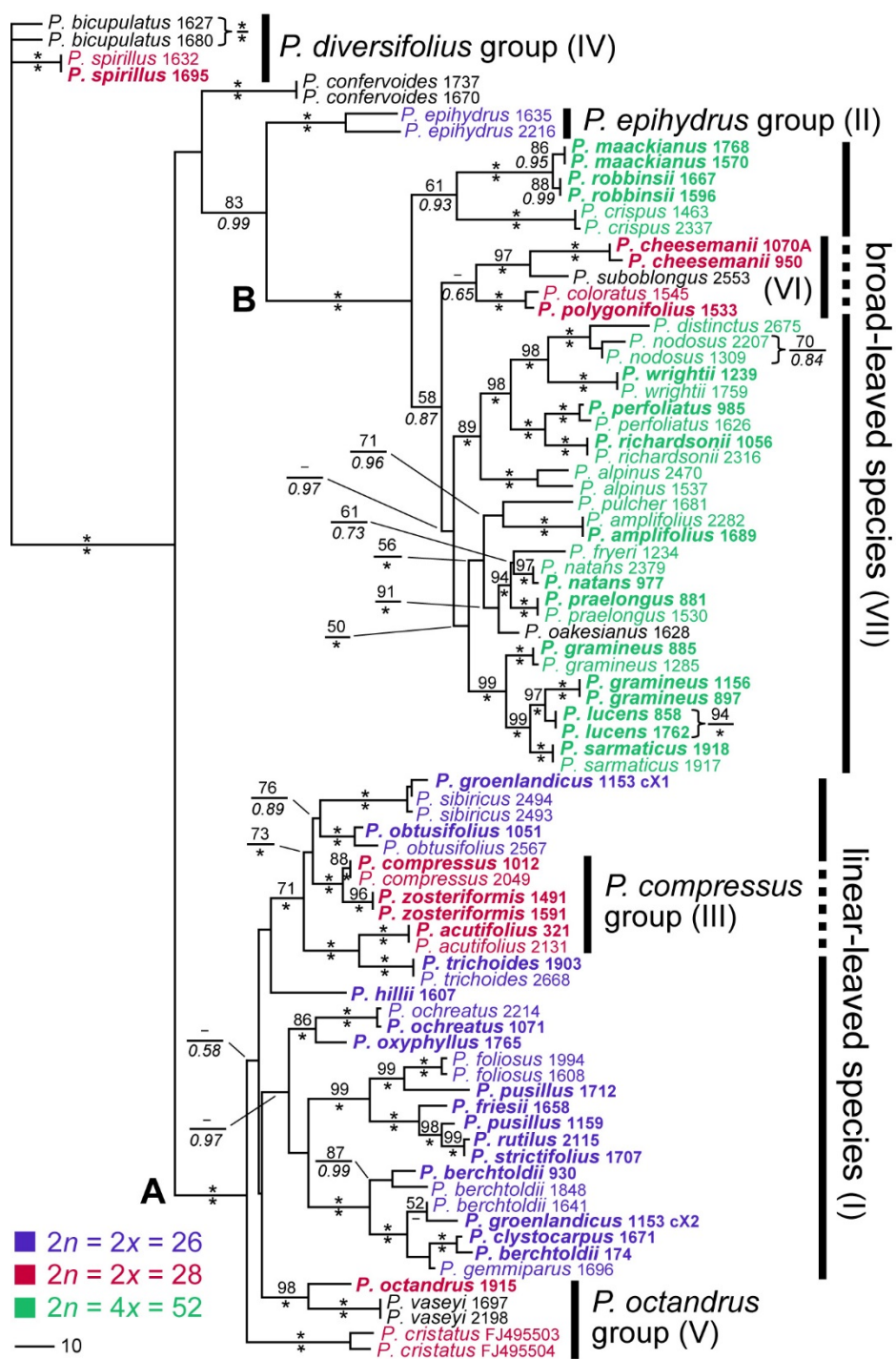
A *P. floridanus* (*P. oakesianus* × *P. pulcher*)

Sample	Position in alignment																											
	34	36	40	61	65	79	80	117	127	130	132	134	140	150	153	166	183	199	208	210	221	223	226	239	246	254	262	286
oak_DQ786479	G	A	T	T	T	C	A	G	A	C	T	G	G	T	A	C	T	G	A	T	T	G	A	C	C	T	G	T
oak_1628	G	A	T	T	T	y	A	G	A	C	T	G	G	T	A	C	T	G	A	T	T	G	A	C	C	T	G	T
Moak_1628	G	A	T	T	T	C	A	G	A	C	T	G	G	T	A	C	T	G	A	T	T	G	A	C	C	T	G	T
flor_DQ786478	G	A	T	T	T	C	R	G	A	S	K	G	R	K	R	S	T	S	A	A	Y	G	A	C	M	T	G	T
flor_2536	S	R	W	K	K	H	R	K	R	S	K	K	R	K	R	S	Y	S	W	W	Y	S	R	S	M	K	K	Y
pul_1681	C	r	A	G	G	w	G	T	G	G	G	w	A	G	G	G	C	C	T	A	C	C	k	G	A	G	T	C
Mpul_1681	C	G	A	G	G	A	G	T	G	G	G	T	A	G	G	G	C	C	T	A	C	C	G	G	A	G	T	C

← Lindqvist et al. 2006

← Kaplan et al. 2018



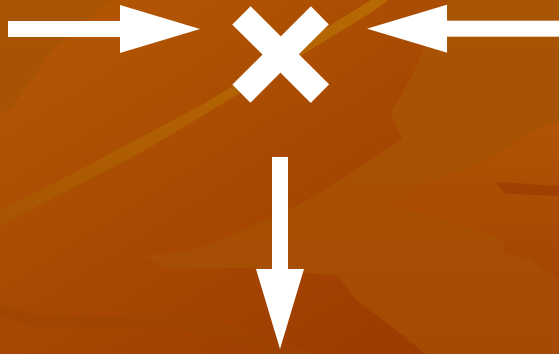




×



Potamogeton oakesianus



Potamogeton pulcher



Potamogeton × *floridanus*











Phenetic Difference



A

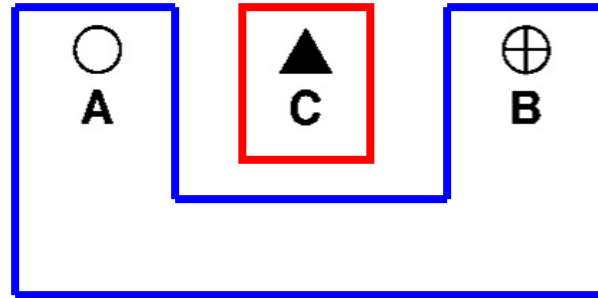


C



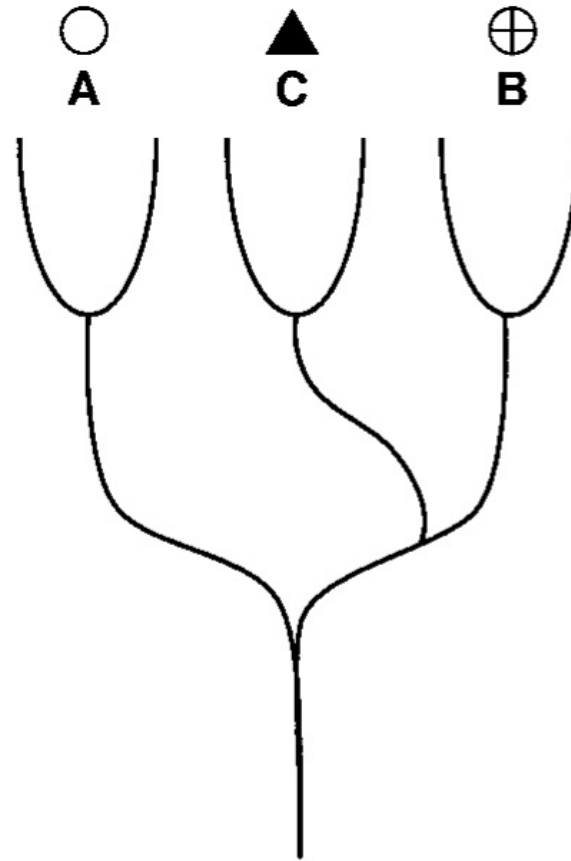
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Phenetic Difference



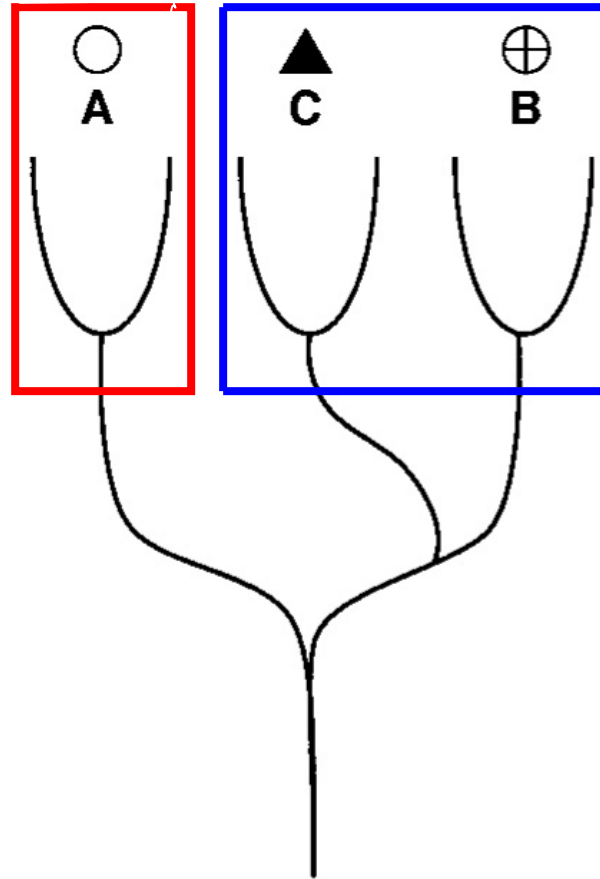
Phenetic Difference

Genealogy



Phenetic Difference

Genealogy



Phenetic Difference

