

## ***New Phytologist* Supporting Information**

Article title: **The evolutionary dynamics of ancient and recent polyploidy in the African semi-aquatic species of the legume genus *Aeschynomene***

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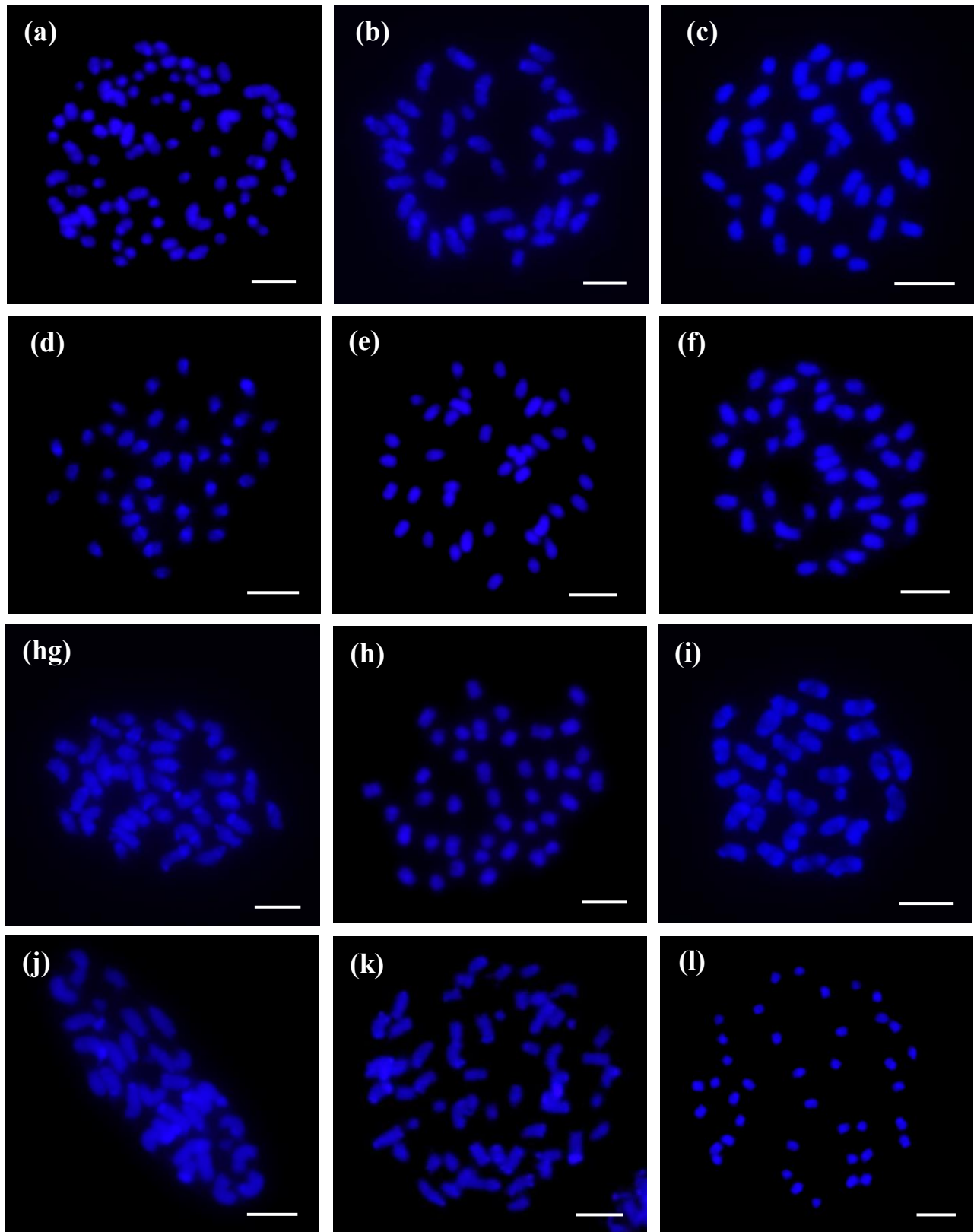
The following Supporting Information is available for this article:

**Fig. S1** Somatic metaphases in different *Aeschynomene* species

**Fig. S2** Alignment of the coding sequence (partial or complete) of single-copy nuclear genes

**Table S1** Genes and SSR markers used in this study

**Table S2** GenBank numbers for the sequences used in the phylogenetic analyses

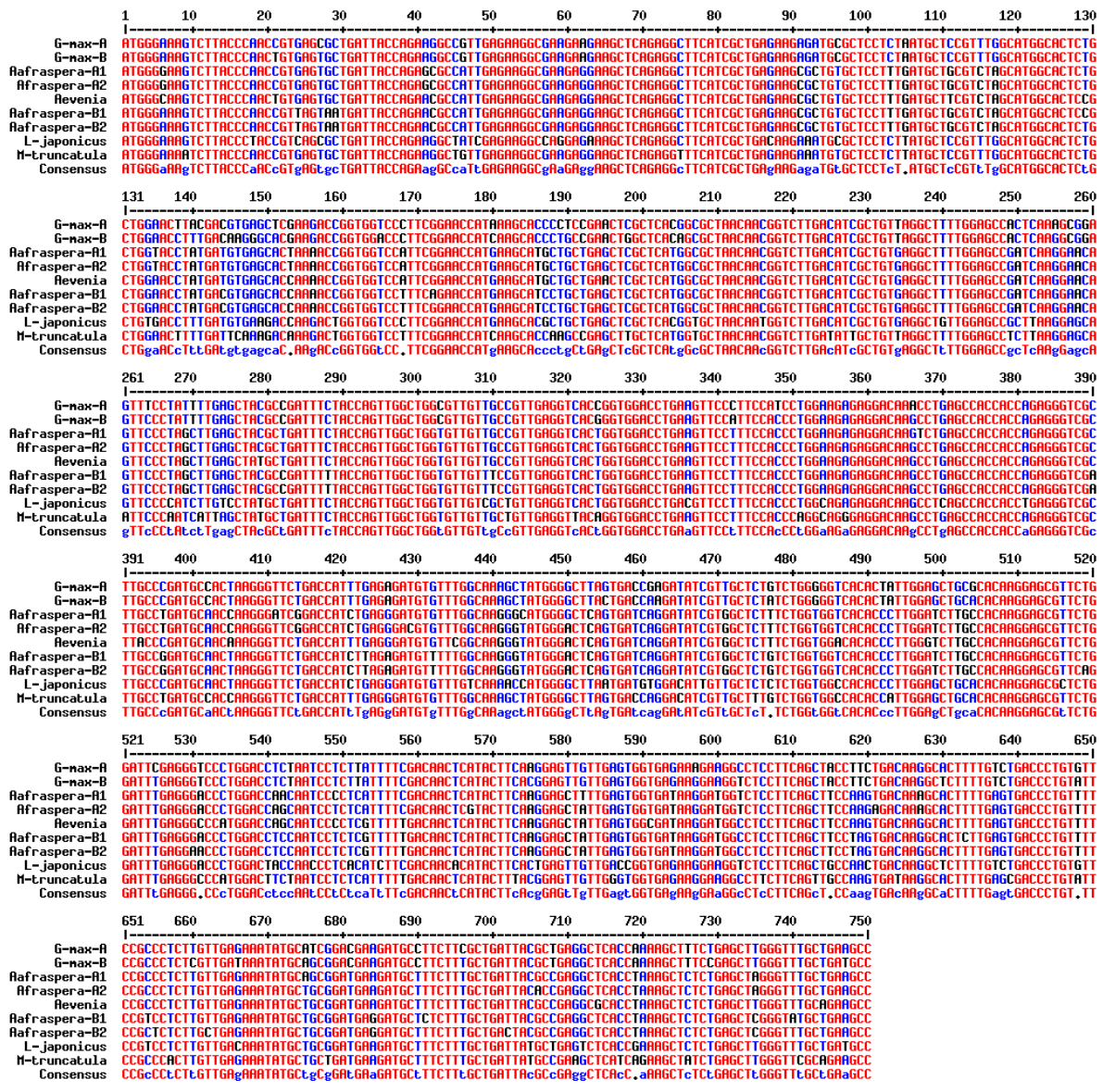


**Fig. S1 Somatic metaphases in different *Aeschynomene* species**

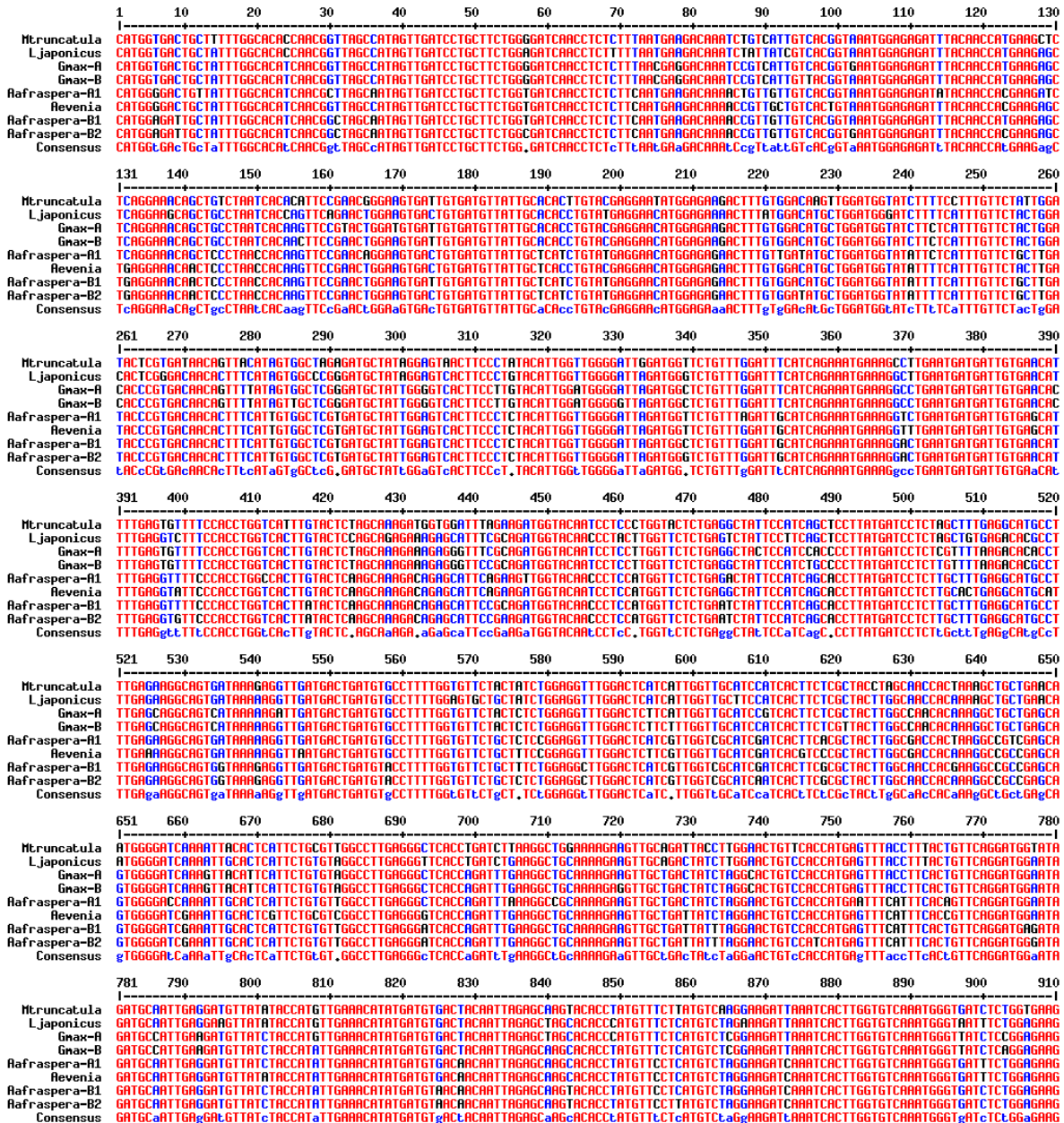
DAPI staining of root-tip mitotic chromosomes for (a) *A. afraspera*-1, (b) *A. aspera*-47, (c) *A. crassicaulis*-13, (d) *A. cristata*-169, (e) *A. elaphroxylon*-112, (f) *A. fluitans*-118, (g) *A. nilotica*-53, (h) *A. pfundii*-54, (i) *A. schimperi* “grandiflora”-123, (j) *A. schimperi*-49, (k) *A. schimperi*-126, (l) *A. uniflora*-61. Numbers following the species names refer to the accession code figuring in Table 1. Bars, 5  $\mu$ m.

**Fig. S2 Alignment of the coding sequence (partial or complete) of single-copy nuclear genes (a) *APX2*, (b) *AS2*, (c) *eil1α*, (d) *PIP2;7*, (e) *SUS*, (f) *TIP1;1* of *Medicago truncatula*, *Lotus japonicus*, the A and B components of the *Glycine max* genome, the A1-A2-B1-B2 components of the *A. afraspera* genome and *A. evenia*. The aligned sequences were used to calculate the rate of silent substitution per synonymous site for molecular dating of the divergences of the different *Aeschynomene* genomes and lineages.**

(a) Alignment of *APX2* sequences



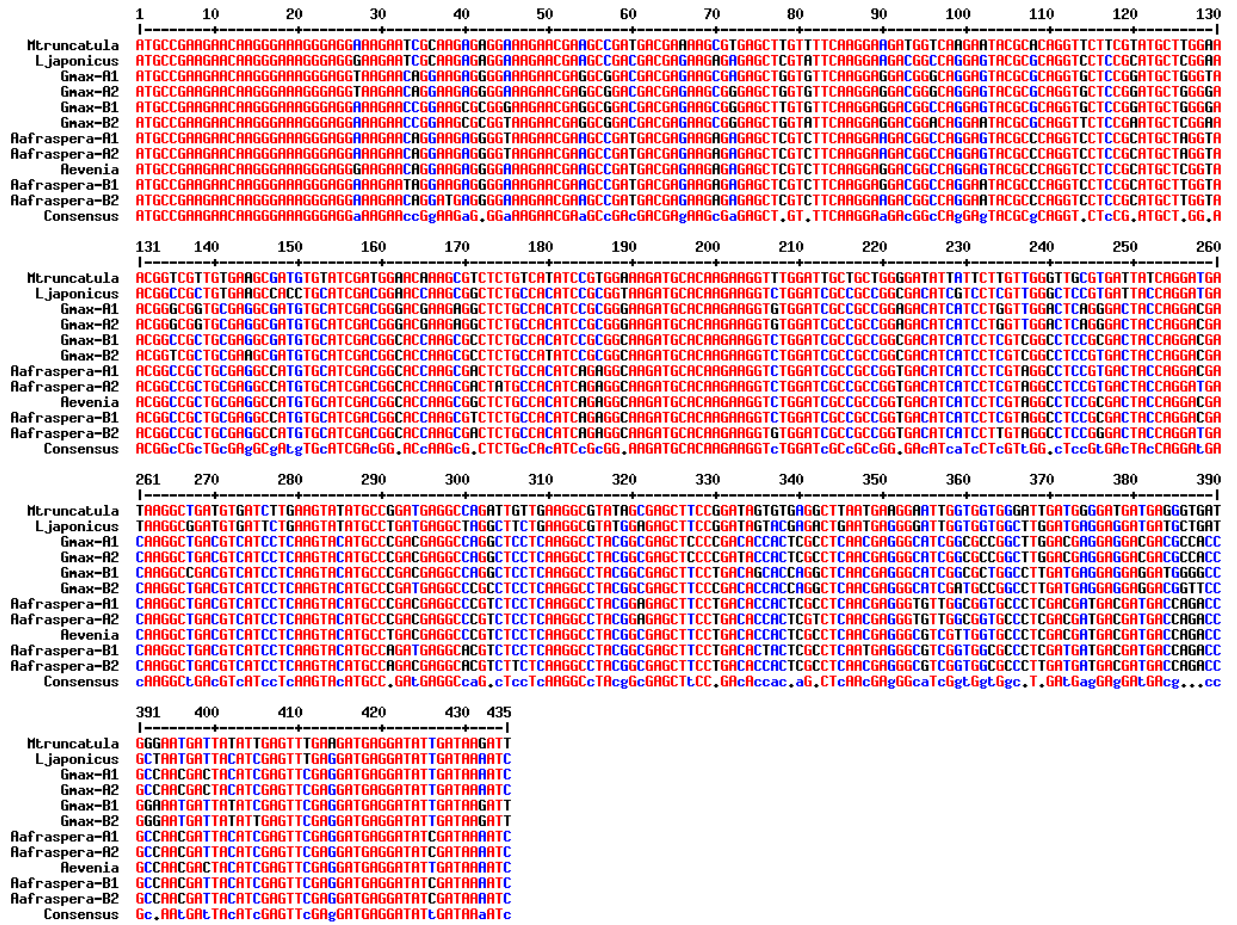
(b) Alignment of AS2 sequences



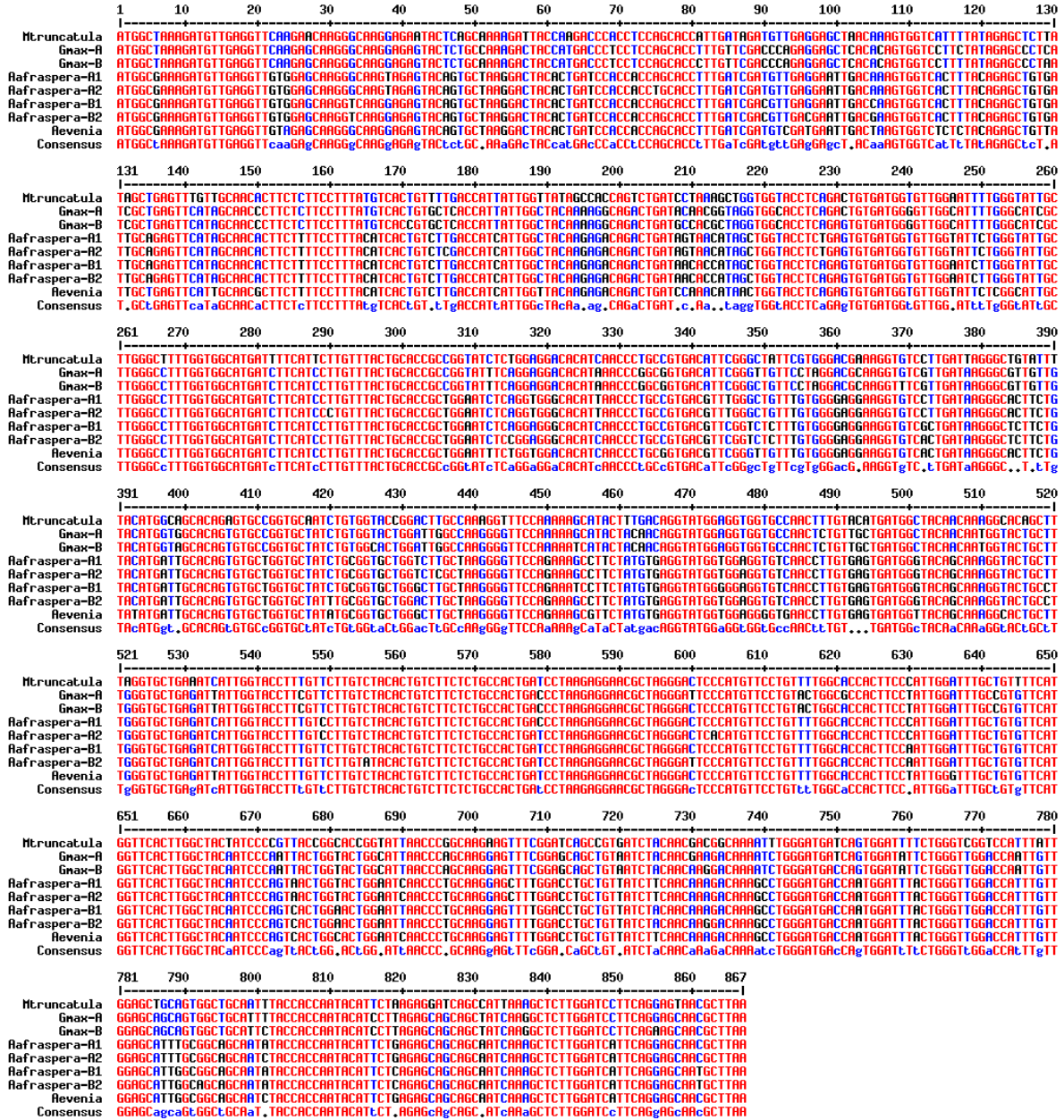
(b) Alignment of AS2 sequences continued

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Mtruncatula	GATCTGATGAGATATTGGTGGATATCTGACTTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGAGGCAAAATAAATCAAC														
L.japonicus	GATCTGATGAGATATTGGTGGTACTTGACTTCCATAGGACCTAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCTAAATAATCAAC														
Gmax-A	GATCTGATGAGATATTGGAGGGTATCTGACTTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCAAAATAAATCAAC														
Gmax-B	GATCTGATGAGATATTGGAGGGTATCTGACTTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCAAAATAAATCAAC														
Rafraspera-A1	GTTCTGATGAGATCTTTGGAGGGTATCTTTACTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCAAAATAAATCAAC														
Revenia	GCTCTGATGAGATCTTTGGAGGGTATCTTTACTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCAAAATAAATCAAC														
Rafraspera-B1	GTTCTGATGAGATCTTTGGAGGGTATCTTTACTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCAAAATAAATCAAC														
Rafraspera-B2	GTTCTGATGAGATCTTTGGAGGGTATCTTTACTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCAAAATAAATCAAC														
Consensus	Ga7CTGATGAGATCTTTGGAGGGTATCTTTACTTCCARAGGCCACCAACARAGGAGAGTTCCACACAGAACATGCCGARGATCAAGGCCTCCACCAATATGATTGCCAGGCAAAATAAATCAAC														
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Mtruncatula	CTTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
L.japonicus	ATTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
Gmax-A	ATTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
Gmax-B	ATTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
Rafraspera-A1	ATTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
Revenia	ATTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
Rafraspera-B1	ATTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
Rafraspera-B2	ATTTGCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
Consensus	aTTTCTGGGGCTAGAGGCCAGGTTCCATTTTGGACRAGGATTTTCARTGTTGCARTGATATTGATCCCGAGTATAGATGATTAACGAGCAGAGGCACATTGAGAGGTATATCTCGAGG														
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Mtruncatula	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
L.japonicus	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
Gmax-A	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
Gmax-B	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
Rafraspera-A1	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
Revenia	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
Rafraspera-B1	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
Rafraspera-B2	AAGGCTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
Consensus	AaggGcTTCGATGATGAGAGCACTCTTATCTGCCAAGCACATTTATACAGGCGAGAGGACCAATTCAGTGTGGTGGTGGTATAGTGGATTGATGGCCTAAGGCTCATGTCGCAAAACATGTGA														
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Mtruncatula	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGATCTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
L.japonicus	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGATCTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
Gmax-A	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGATCTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
Gmax-B	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGATCTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
Rafraspera-A1	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGCTTACTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
Revenia	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGCTTACTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
Rafraspera-B1	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGCTTACTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
Rafraspera-B2	CTGATAGGATGATCTTATGCTGGTAACTATCTCCACACACACCCARARACCAAGGAGGCTTACTACTACAGARTGATCTTTGGAGGTTCTCCCCAGAACCTCAGCAGAGGCTTACTGTTCCCTGG														
Consensus	CTGaAaaATGATCTTATGCTGGTAACTATCTCCcCacAACACCCcAaaaACCAAGGaGcaTACTACTACAGARTGATCTTTGGAGGTTCTCCcCacAGAcTCAGCTAGGCTACTGCTCCcGG														
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Mtruncatula	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
L.japonicus	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
Gmax-A	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
Gmax-B	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
Rafraspera-A1	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
Revenia	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
Rafraspera-B1	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
Rafraspera-B2	AAGGCAACCTGTTGATGATGACACAGCTAAGGCTGTTGAGTGGATGCTCTTGGTCCAGAACCTTATGCTCTTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACCGAARACCTTTG														
Consensus	AAGGCaAagctGtGAtGAtGAcAcAgCtAaAgCtGtGAGTGGaTgCtCtTGGTCCaGaaCctTATGCTCtTGGTATGAGCAGCAGCTTGGAGTTCATGATTCAGCTTACGAAACcagAACaactTg														
	1561	1570	1580	1590	1600	1610	1620	1629							
Mtruncatula	GTCACAAACCTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
L.japonicus	ATCACAAACCTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
Gmax-A	ATCACAAAGGGTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
Gmax-B	ATCACAAAGGGTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
Rafraspera-A1	GTCACAAAGCTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
Revenia	GTCACAAAGCTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
Rafraspera-B1	GTCACAAAGCTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
Rafraspera-B2	GTCACAAAGCTGTGAAATTTGAGAGGATATACCAAGAGCTTCCAGTTGAGGTTGCCATTCAAGGC														
Consensus	gTCACAAagctGtGAAatTTGAGAGGAtATACCAAGAGctTCCAGTTGAGGTTGCCattCAAGGC														

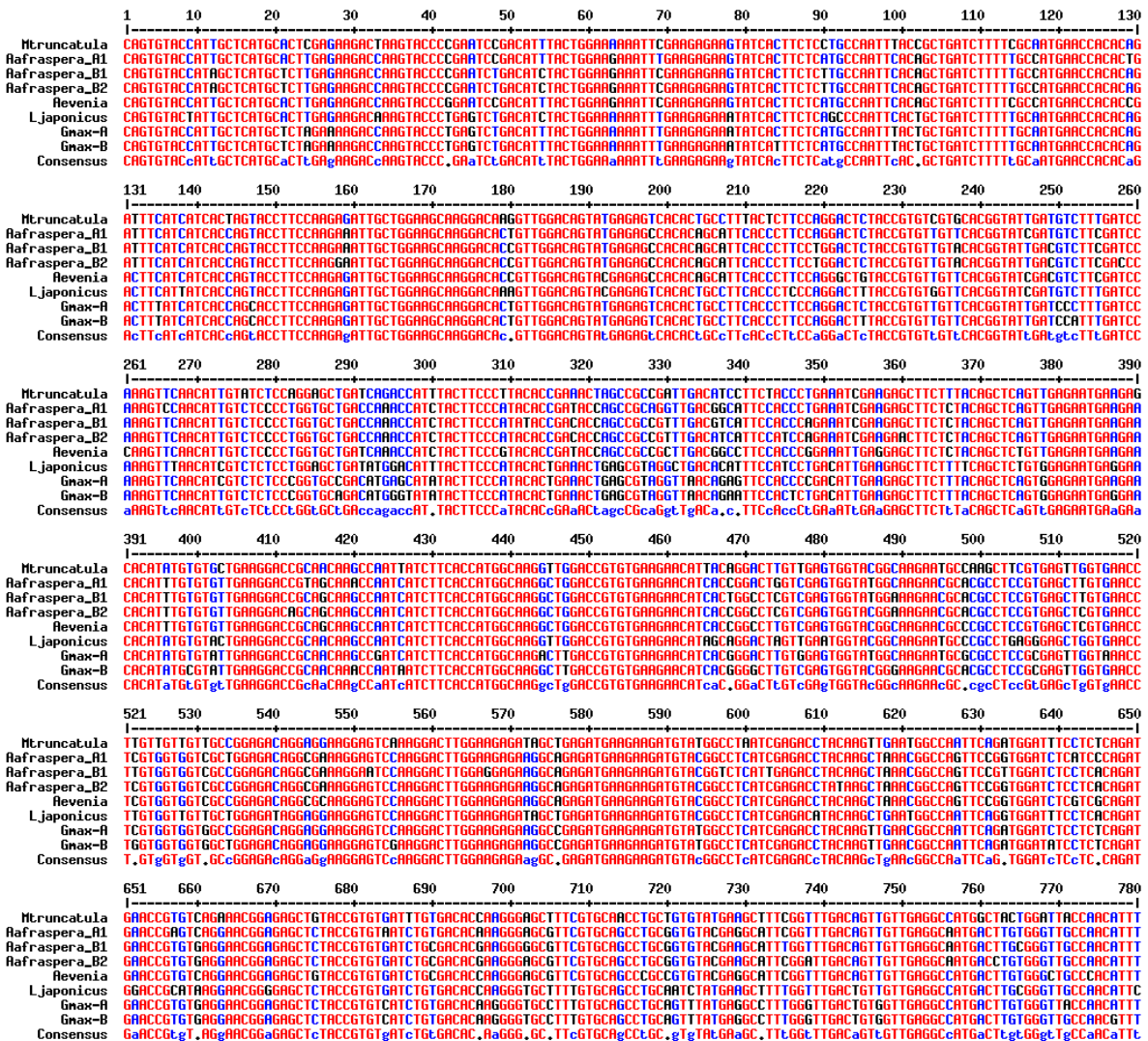
(c) Alignment of *elf1α* sequences



(d) Alignment of *PIP2;7* sequences



(e) Alignment of *SUS* sequences

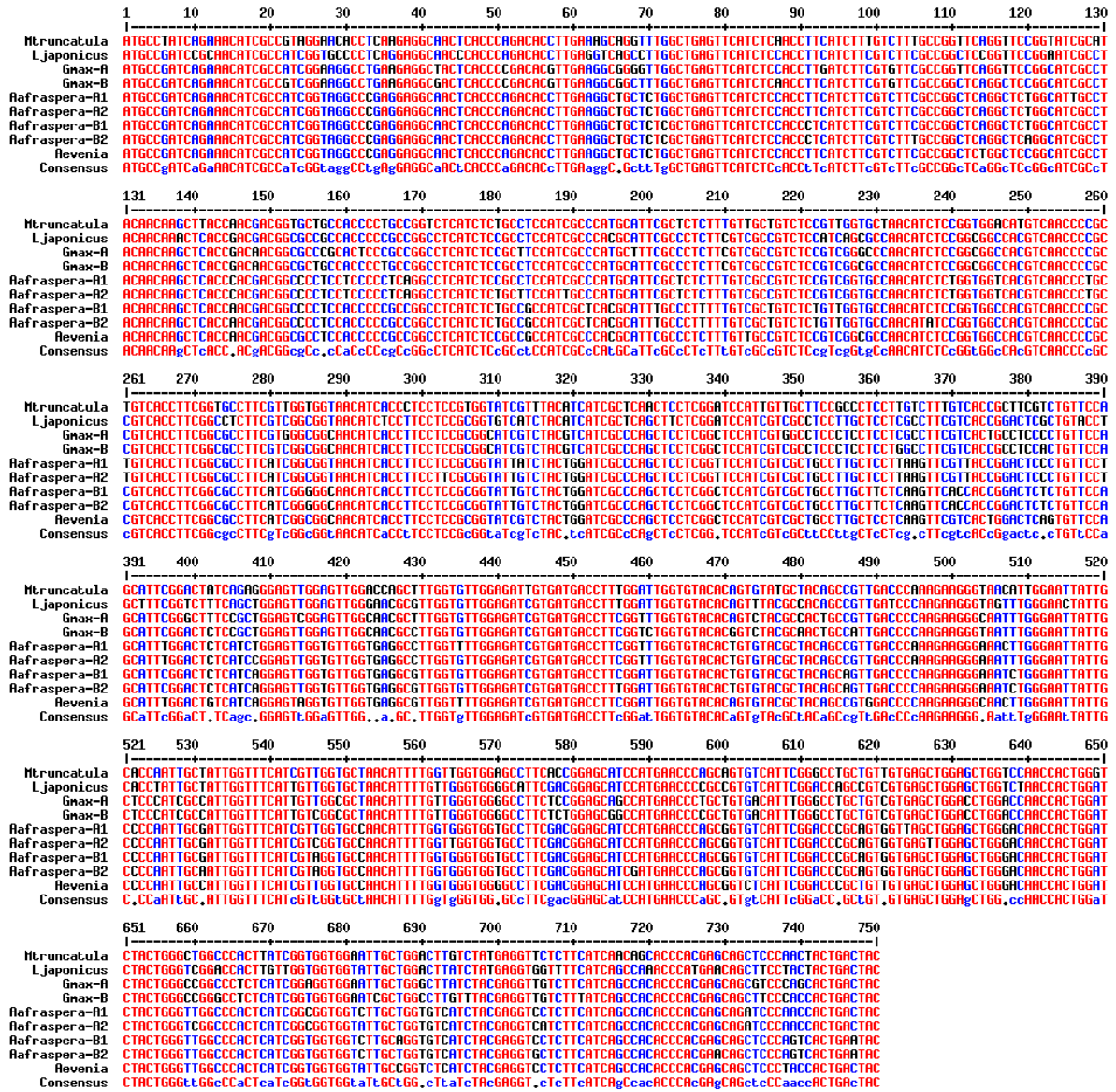




(e) Alignment of *SUS* sequences continued

	781	790	800	810	820	830	840	850	860	870	880	890	900	910
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Rafraspera_A1	GCACATGCAATGGTGGCTCTGCTGAGATCATTGTCATGGAAATCAGGGTTCCACATTGACCCCTACCATGGTACCCGCTGCTGATCTCCTCGTTGATTTCTTTGAGAGGTCAGGTTGATCCAT													
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Revenia	GCCACCTGCATGGTGGCTCTGCTGAGATCATTGTCATGGAAATCAGGGTTCCACATTGACCCCTACCATGGTACCCGCTGCTGATCTCCTCGTTGATTTCTTTGAGAGGTCAGGTTGATCCAT													
L.japonicus	GCCACCTGCATGGTGGCTCTGCTGAGATCATTGTCATGGAAATCAGGGTTCCACATTGACCCCTACCATGGTACCCGCTGCTGATCTCCTCGTTGATTTCTTTGAGAGGTCAGGTTGATCCAT													
Gmax-A	GCCACATGCATGGTGGCTCTGCTGAGATCATTGTCATGGAAATCAGGGTTCCACATTGACCCCTACCATGGTACCCGCTGCTGATCTCCTCGTTGATTTCTTTGAGAGGTCAGGTTGATCCAT													
Gmax-B	GCCACATGCATGGTGGCTCTGCTGAGATCATTGTCATGGAAATCAGGGTTCCACATTGACCCCTACCATGGTACCCGCTGCTGATCTCCTCGTTGATTTCTTTGAGAGGTCAGGTTGATCCAT													
Consensus	GCcAc..TgcAATGGTGGcCTGCTGAGATCATTGT..CATGGAAATCTcGG..TTCcAcATTGAcCCcTACCATGGcGcCgTcGCTGcGATcCTcCTGTTGAgTTCCTTTGAgAg..gCAAgGcTcGATcCAc													
	911	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040
Mtruncatula	CTCAGCTGGGACAGATCTCCAGGGTGGTCTCCAGCGTATTGAGGAGAGTACACATGGACATATACTCTCAGAGGCTCTTACACTCAGCTGGTGTCTATGGCTCTGGAGACATGTGTACACCTCGA													
Rafraspera_A1	CTCAGCTGGGACAGATCTCCAGGGTGGTCTCCAGCGTATTGAGGAGAGTACACATGGACATATACTCTCAGAGGCTCTTACACTCAGCTGGTGTCTATGGCTCTGGAGACATGTGTACACCTCGA													
Rafraspera_B2	CTCAGCTGGGACAGATCTCCAGGGTGGTCTCCAGCGTATTGAGGAGAGTACACATGGACATATACTCTCAGAGGCTCTTACACTCAGCTGGTGTCTATGGCTCTGGAGACATGTGTACACCTCGA													
Revenia	CTCAGCTGGGACAGATCTCCAGGGTGGTCTCCAGCGTATTGAGGAGAGTACACATGGACATATACTCTCAGAGGCTCTTACACTCAGCTGGTGTCTATGGCTCTGGAGACATGTGTACACCTCGA													
L.japonicus	CTCAGCTGGGACAGATCTCCAGGGTGGTCTCCAGCGTATTGAGGAGAGTACACATGGACATATACTCTCAGAGGCTCTTACACTCAGCTGGTGTCTATGGCTCTGGAGACATGTGTACACCTCGA													
Gmax-A	CTCAGCTGGGACAGATCTCCAGGGTGGTCTCCAGCGTATTGAGGAGAGTACACATGGACATATACTCTCAGAGGCTCTTACACTCAGCTGGTGTCTATGGCTCTGGAGACATGTGTACACCTCGA													
Gmax-B	CTCAGCTGGGACAGATCTCCAGGGTGGTCTCCAGCGTATTGAGGAGAGTACACATGGACATATACTCTCAGAGGCTCTTACACTCAGCTGGTGTCTATGGCTCTGGAGACATGTGTACACCTCGA													
Consensus	CTcAGCTGGGAcAa..ATCTCcCAgGGcGGcTCCAGcGcTATtGAGGAgAgTAcAcATGGAcATAtACTCTcAGAgGcCTcTtAcAcTcAGcTGGtGtCTAtGGcTcTGGAgAcATGtGtAcAcCTcGAc													
	1041	1050	1060	1070	1080	1090	1100	1110	1120	1128				
Mtruncatula	CCGCTTGGAGGCCCGCTATCTTGGATGTTCTATGCTCTCAGATCCCGCAATGGCTGAGCTGTGCCCTAGCTGTGGAGG													
Rafraspera_A1	CCGCTTGGAGGCCCGCTATCTTGGATGTTCTATGCTCTCAGATCCCGCAATGGCTGAGCTGTGCCCTAGCTGTGGAGG													
Rafraspera_B2	CCGCTTGGAGGCCCGCTATCTTGGATGTTCTATGCTCTCAGATCCCGCAATGGCTGAGCTGTGCCCTAGCTGTGGAGG													
Revenia	CCGCTTGGAGGCCCGCTATCTTGGATGTTCTATGCTCTCAGATCCCGCAATGGCTGAGCTGTGCCCTAGCTGTGGAGG													
L.japonicus	CCGCTTGGAGGCCCGCTATCTTGGATGTTCTATGCTCTCAGATCCCGCAATGGCTGAGCTGTGCCCTAGCTGTGGAGG													
Gmax-A	CCGCTTGGAGGCCCGCTATCTTGGATGTTCTATGCTCTCAGATCCCGCAATGGCTGAGCTGTGCCCTAGCTGTGGAGG													
Gmax-B	CCGCTTGGAGGCCCGCTATCTTGGATGTTCTATGCTCTCAGATCCCGCAATGGCTGAGCTGTGCCCTAGCTGTGGAGG													
Consensus	cCgCtTgGAgGcCcGcTAtcTtGgATGtTcTATGcTcTcAGATccCGcAAATGGcTgAGcTgTgCcCtAGcTgTgGAgG													

(f) Alignment of *TIP1;1* sequences



**Table S1** Genes and SSR markers used in this study

**(a)** Transcriptomic data

Gene	<i>A. evenia</i> Single gene	<i>A. afraspera</i> "A1 copy"	<i>A. afraspera</i> "A2 copy"	<i>A. afraspera</i> "B1 copy"	<i>A. afraspera</i> "B2 copy"
<i>APX2</i>	Ae-Eve14159	CL62Contig2 CL66Contig1	CL62Contig1	CL66Contig3	CL66Contig2
<i>AS2</i>	Ae-Eve08216	CL10Contig4 ADL0ADA11YM05	CL10Contig1 (partial sequence)	CL10Contig2 CL72Contig2	CL10Contig3 CL72Contig1
<i>eiF1a</i>	Ae-Eve24102	Obtained by PCR and sequencing	-	ADL0ADA12YO19	ADL0ADA7YI19
<i>PIP2;7</i>	Ae-Eve09630	CL2Contig1 CL2Contig2	CL2Contig4 CL34Contig3	CL2Contig7 CL34Contig4	CL2Contig3
<i>SUS</i>	Ae-Eve02139	CL30Contig2 CL40Contig2	-	CL30Contig3 CL40Contig2	CL30Contig1 CL40Contig2
<i>TIP1;1</i>	Ae-Eve17222	CL3Contig1	CL3Contig3 ADL0ACA14YK02CM1	CL3Contig4	CL3Contig2 CL79Contig1

**(b)** Gene primers

Gene	Forward primer	Reverse primer	PCR product size
<i>eiF1a</i>	F: ATGCCGAAGAACAAGGGAAA F	R1: ATCAATATCCTCATCCTCGAACTC R2: ATCGATATCCTCATCCTCGAAC	429 pb 429 pb
<i>SUS</i>	F1: GAAGGACCGTAGCAAACCAA F2: ACCATGGCAAGGCTGGAC F:	R: CCCAGTGAGAAGGATCAACC R	515 pb 486 pb
<i>ITS</i>	GTCCACTGAACCCTTATCATTTAGAGG	R: GCCGTTACTAAGGGAATCCTTGTTAG	704 pb
<i>matK</i>	trnK685F: GTATCGCACTATGTATCATTTGA F1: ACCCTATCCTATTCATCTGGAAA F2: CGATTTTTCGAATATGCAG	trnK2R: CCCGGAAGTACTAGTCGGATGG	1900 pb for sequencing for sequencing

**Table S1** Genes and SSR markers used in this study continued

**(c) SSR primers**

Gene	Forward primer	Reverse primer	Type
AaSSR1	GGTTGTTAGGGTTTTGATTGC	GAAGAAGAGGGGCTTCTTGG	(AG)13
AaSSR2	AAATATTTTGGCAAGATTA AAAACG	AGCTCCGTACCCGTTTCAG	(AG)14
AaSSR3	CCCAAATTTCTGGAGCAAC	TGGTACACAACAAGCCAAACA	(TA)12
AaSSR4	ATGGATTCTGCTAGGGGTTG	TTGAATCCTCAAATCCAAAGC	(TA)11
AaSSR5	AGGGTGCATTCTTGAGACC	GGAAATTAGAGTGAGGAAGTGCTG	(AT)13
AaSSR6	TGATAATGCAATTCCCTCTTTT	TTCCCACTTCAACCCCAATA	(AT)11
AaSSR7	GAAAATGGTTAATGAGAGAGAAAA	CCACAAGTACACAACAACA AAAA	(AT)11
AaSSR8	TTTCTTGGTGGTACTTCAGC	AGGAAGCTTGAGTGCAGCAT	(CT)13
AaSSR9	ACCAAGTGCTGCCATCTTGT	GGCAAACAAAGGAAGTGGTC	(AT)12
AaSSR10	TCGGCAGCATA CAGGGATAC	GGAAAAGGACATTGCCTCAA	(TTA)13
AaSSR11	GAGTCAA AAGGTGAACTTGGA	GGGTAAGATAGTCACCAATTGACA	(TA)11
AaSSR12	GTTGGCTTCCCTTTCTGTTG	ACATAGGAAATTAGGTACAAACACG	(AT)11
AaSSR13	GCTGCAACTATGATCCACCA	TTTTTGGGTTTCATCAACATT	(AT)11
AaSSR14	AACCACTAGCAGGGGTGATG	CCAAAACAGGGGAAAACAGA	(TA)6
AaSSR15	AAGTGTCCGTCGCCACTAAG	TGCAGTCCCCATCACAATTA	(GA)8
AaSSR16	GGAAGGTGCAGCACAAATGTA	TTTTATCACGCATGGGACCT	(TA)6
AaSSR17	GAATTGCCCTCTCTTCCTC	CCTGTCCTCGTGGCTTTTAC	(TC)6
AaSSR18	CAAATGCTCATGGATGCAAA	AGGGGTATCCCTGAAAAAGC	(AT)10
AaSSR19	CGTGAGGTT CAGGAGTCACA	TCATTGGCAATCAAATCAACA	(AT)8
AaSSR20	ATGGTTCATCACAGCACAGC	GGGCCATCCTCAAGAAATTA	(TG)6
AaSSR21	TTTCCAAACAGGGCCAAATA	ATTCAGAACCCCATCCATCA	(AT)10
AaSSR22	CGCCAAAGGTCACAACAAA	GCCCCAACAGAAA ACTTGAA	(CT)7
AaSSR23	CCATACTGTCGTTGGGAACC	TCAA AAGAGGAAGAACCGTGA	(GT)6
AaSSR24	GGAACAGGCAGAGCATGAAT	GAAGGAGGAGGGGGAGAAG	(AG)9
AaSSR25	TTGACGGCCTAGTCGATCTT	CACACATCACAACACCACCA	(AT)8
AaSSR26	ATAATGGGTGTTTGGGGTTG	CCACCGACAACTTATCCAAG	(TA)6
AaSSR27	GACCAAATGCCCTTGAAAA	TAAATAATTGCAGCCCCAAA	(AT)7
AaSSR28	GAAAGCCATGTCGATCCAGT	CGGACACATTTTGATCATGG	(AG)7
AaSSR29	TCAGCTGCAACGCACTTTAC	CGCAGGAGAAGGAGACAAAG	(TC)9
AaSSR30	GATAAAACCCTTACCTTCCTC	ATGGAGCGGACGTTGTA CTT	(CA)7
AaSSR31	GCCTTCGATTCCATCTCTTC	TGGAACCTTCTAGGCTGCAC	(TC)7
AaSSR32	AACTCAACTAAACCTCTTGCC TTT	GTTTCCCTGCTTGGACTTGA	(TC)9
AaSSR33	CAGCAGCAGAGGAGTGTTCA	TGCATTCTTG TACAGAAAAACAAA	(AT)11
AaSSR34	CGGGGATTTGTAGCAGACAC	TCCTTGAGGCATTTCTGAC	(AG)10
AaSSR35	GGCGTGAAGACGAGACAGAC	GTACGTCCCTTCCCCAATCT	(GA)8
AaSSR36	TGGGAGCTCGTTCTCACTTT	TGCAATGAAATTACTCCATACACA	(AT)9

**Table S2** GenBank numbers for the sequences used in the phylogenetic analyses

Species	LSTM code	Voucher	<i>eiFla</i>	<i>SUS</i>	<i>ITS</i>	<i>matK</i>
<i>A. afraspera</i>	1	LSTM1	KT821096 KT821097 KT821098	KT821123 KT821124 KT821125	FM242584*	KT821176
	2	LSTM2			FM242585*	KT821177
	225	CIAT 22491			KT821150	KT821178
	227	IRRI 14142			KT821151	KT821179
	228	IRRI 14143			KT821152	KT821180
<i>A. aspera</i>	47	IRRI 013020	KT821099 KT821100	KT821126 KT821127	FM242623*	KT821181
	264	LSTM264			KT821153	KT821182
	266	LSTM266			KT821154	KT821183
	294	LSTM294			KT821155	KT821184
<i>A. crassicaulis</i>	13	LSTM13	KT821101 KT821102	KT821128 KT821129	FM242594*	KT821185
<i>A. cristata</i>	169	ILRI 16880	KT821119 KT821120	KT821146 KT821147	KT821169	KT821206
<i>A. elaphroxylon</i>	112	LSTM112	KT821105 KT821106	KT821132 KT821133	KC540624*	KT821187
	148	IRRI 12148			KT821156	KT821188
	159	ILRI 010590			KT821157	KT821189
<i>A. evenia</i>	76	CIAT22838	KC163232*	KC163271*	KC163299*	KT821190
<i>A. fluitans</i>	118	CPI 052338	KT821107 KT821108	KT821134 KT821135	KC540622*	KT821191
	119	CPI 073047			KT821158	KT821192
<i>A. nilotica</i>	53	IRRI 014040	KT821109 KT821110	KT821136 KT821137	KC560767*	KT821193
	247	IRRI 14152			KT821159	KT821194
<i>A. pfundii</i>	54	LSTM54	KT821111 KT821112	KT821138 KT821139	FM242629*	KT821195

**Table S2** GenBank numbers for the sequences used in the phylogenetic analyses continued

<i>A. schimperi</i> "grandiflora"	123	ILRI 000659	KT821113 KT821114	KT821140 KT821141	KT821160	KT821196
	124	ILRI 001170			KT821161	KT821197
	138	CIAT 22523			KT821162	KT821198
<i>A. schimperi</i>	49	IRRI 012146	KT821103 KT821104	KT821130 KT821131	FM242625*	KT821186
	59	IRRI 012156			FM242633*	KT821199
	125	ILRI 002056			KT821163	KT821200
	126	ILRI 009675			KT821164	KT821201
	128	ILRI 013490			KT821165	KT821202
	129	ILRI 013814	KT821115 KT821116 KT821117 KT821118	KT821142 KT821143 KT821144 KT821145	KT821166	KT821203
	171	IRRI 012059			KT821167	KT821204
	309	LSTM309			KT821168	KT821205
	<i>A. uniflora</i>	61	IRRI 013158	KT821121 KT821122	KT821148 KT821149	FM242635*
114		CPI 052333			KT821170	KT821208
137		CPI 060164			KT821171	KT821209
213		ILRI 700			KT821172	KT821210
318		LSTM318			KT821173	KT821211
319		LSTM319			KT821174	KT821212
320		LSTM320			KT821175	KT821213

\*, Sequences previously published.