

The SBP Transcription Factors in Arabidopsis and Rice and their Evolution in Plants

Guo Anyuan 2006.5.10

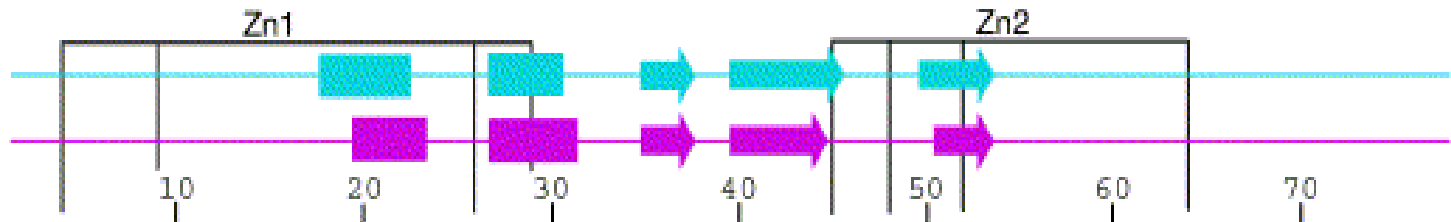


SBP TFs



- SQUAMOSA promoter Binding Protein
- SBP domain: 79 aa DNA binding domain

a



SPL4	51	LRLCQVDRCTADMKEAKLYHRRHKVCEVHAKASSVFLSGLNQRFCQQCSRPHDLQBFDEAKRSCRRRLAGHNERRRKS
SPL5	60	SRLCQVDRCTVNLTEAKQYYRRHRVCEVHAKASAATVAGVRQRFCCQCSRPHQLPFDEAKRSCRRRLAGHNERRRKI
SPL9	71	IPLCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRPHQLPFDEAKRSCRRRLAGHNERRRKF
SPL1	104	-AVCQVENCEADLSKVKDYHRRHKVCEMHSKATSATVEGILQRFCQQCSRPHLLQBFDEGKRSCRRRLAGHNKRRRKT
SPL12	124	AICCQVDNCGADLSKVKDYHRRHKVCEIHSKATTALVGGIMQRFCQQCSRPHVLEBFDEGKRSCRRRLAGHNKRRRKA
SPL3	53	--VCQVESCTADMSKAKQYHRRHKVCFHAKAPHVRI SGLHQRFCQQCSRPHALSFDEAKRSCRRRLAGHNERRRKS
SPL6	121	NPLCQVYGCCKDLSSSKDYHRRHRVCEAHSKTSVVI VNGLEQRFCQQCSRPHFLSBFDDGKRSCRRRLAGHNERRRK-
SPL10	173	VPRCQIDGCELDLSSSKDYHRRHRVCEHSKCPKVVVSGLERRFCCQCSRPHAVSEFDEKKRSCRKRLSHHNARRRKF
SPL11	172	VPRCQIDGCELDLSSAKGYHRRHKVCEKHSKCPKVVVSGLERRFCCQCSRPHAVSEFDEKKRSCRKRLSHHNARRRKF
SPL2	166	TPHCQVEG CNLDLSSAKDYHRRHRI CENHSKFPKVVVSGVERRFCCQCSRPHCLSEFDEKKRSCRRRLSDHNARRRKF
SPL8	185	TPRCQAEGCNADLSHAKHYHRRHKVCEFHASKASTVVAAGLSQRFCQQCSRPHLLSEFDNGKRSCRKRLADHNRRRKR-
SPL7	135	VARCQVPDCEADISELKGYHRRHRVCLRCATASFVVL DGENKRYCQQCGKPHLLPDFDEGKRSCRRKLERHNNRRRKR
		** * :. * * : :*: * . . * :*:*****: ** : :** *****: * ** **:

SBP TFs

- First found in *Antirrhinum majus* in 1985
- Binding site: TNCGTACA
- Function
 - flower development
 - ligule and auricle development
 - sporogenesis
 - architecture development and sensitivity to FB1
 - controlling the phenotype of maize (*tga1*)



SBPs in Arabidopsis and Rice



- 16 in Arabidopsis

- At1g76580 duplicated from AtSPL14, but lost SBP domain

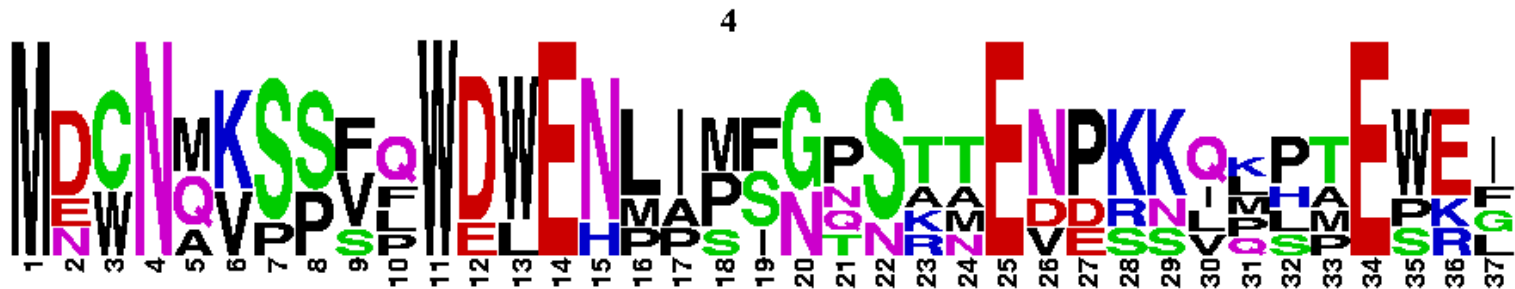
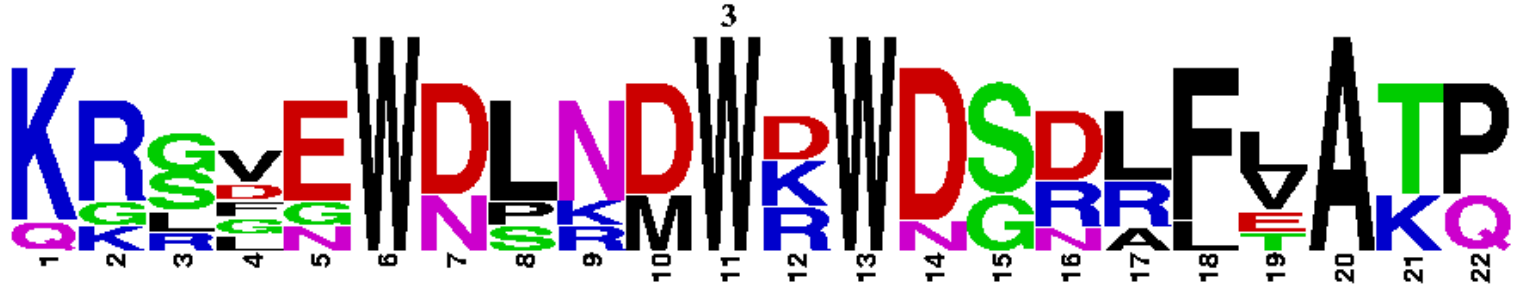
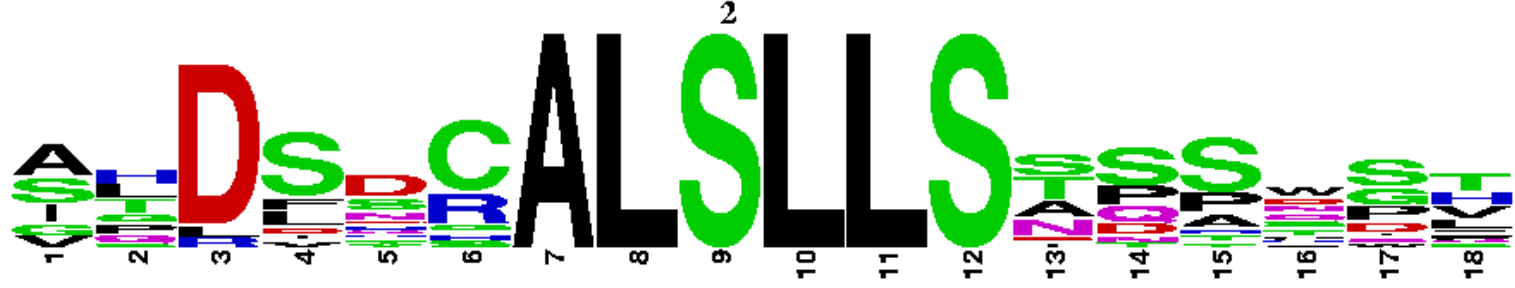
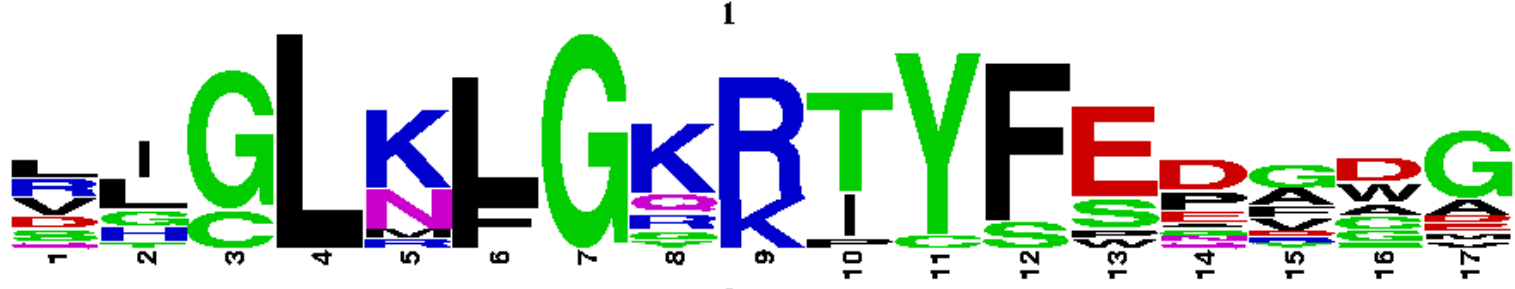
- 18 in Rice

- A complete SBP domain divided by a TAA stop codon into two genes:

LOC_Os11g30380 LOC_Os11g30370



4 Protein Motifs



Motifs



- Protein motifs: 1,2,3,4

- Exon motifs:

- GTGCTCTCTCTTTCTGTCA

- ALSLLS (motif 2)

- IIb,c,d,e,f,g (except IIa in all group II)

- MicroRNA complementary site

- CGCCACCGCCGCCGCCGCCGCCGCCGCCGCCG
code repeat Pro or Ala in 6 OsSBPs



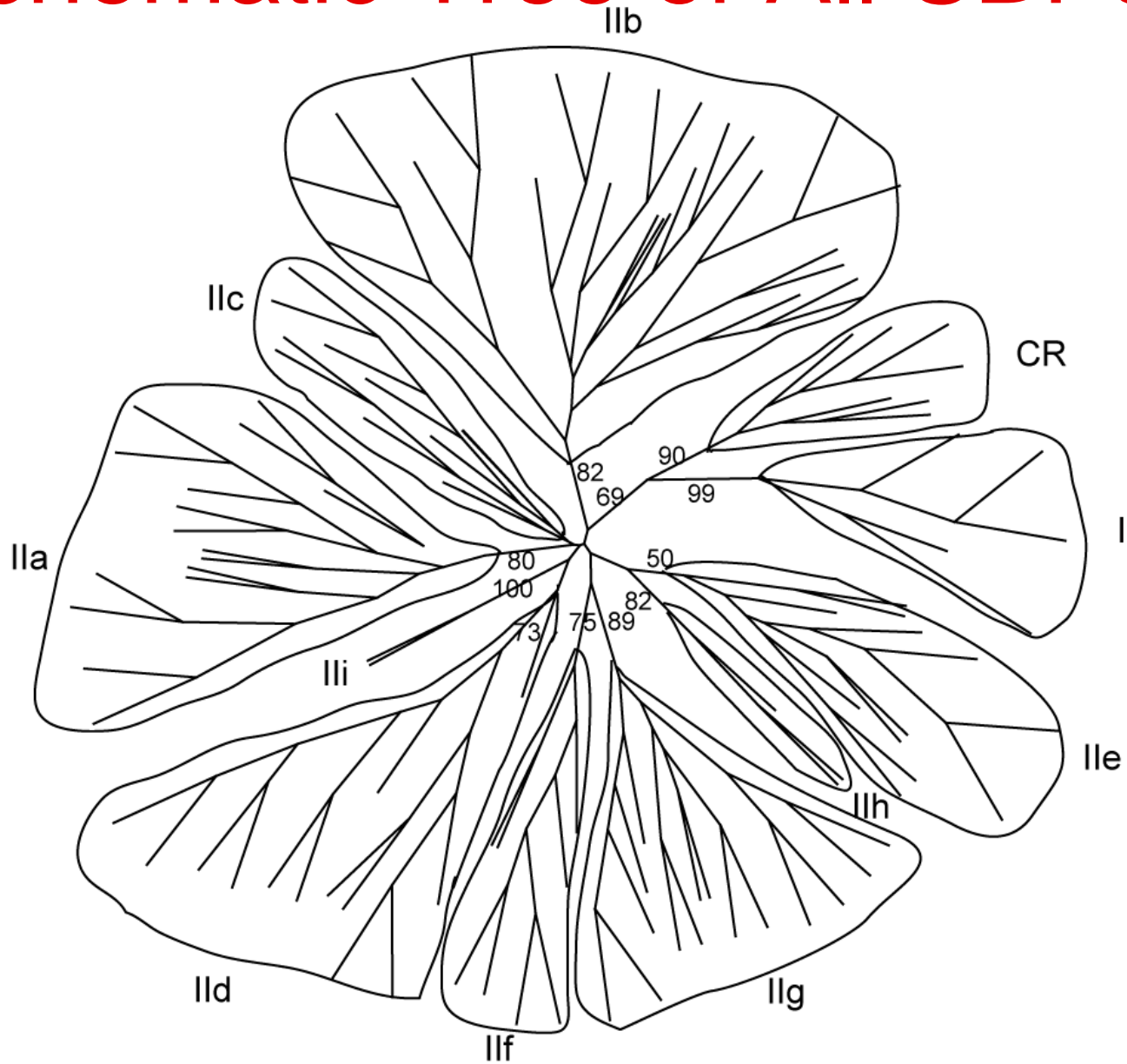
SBPs in Model Plants



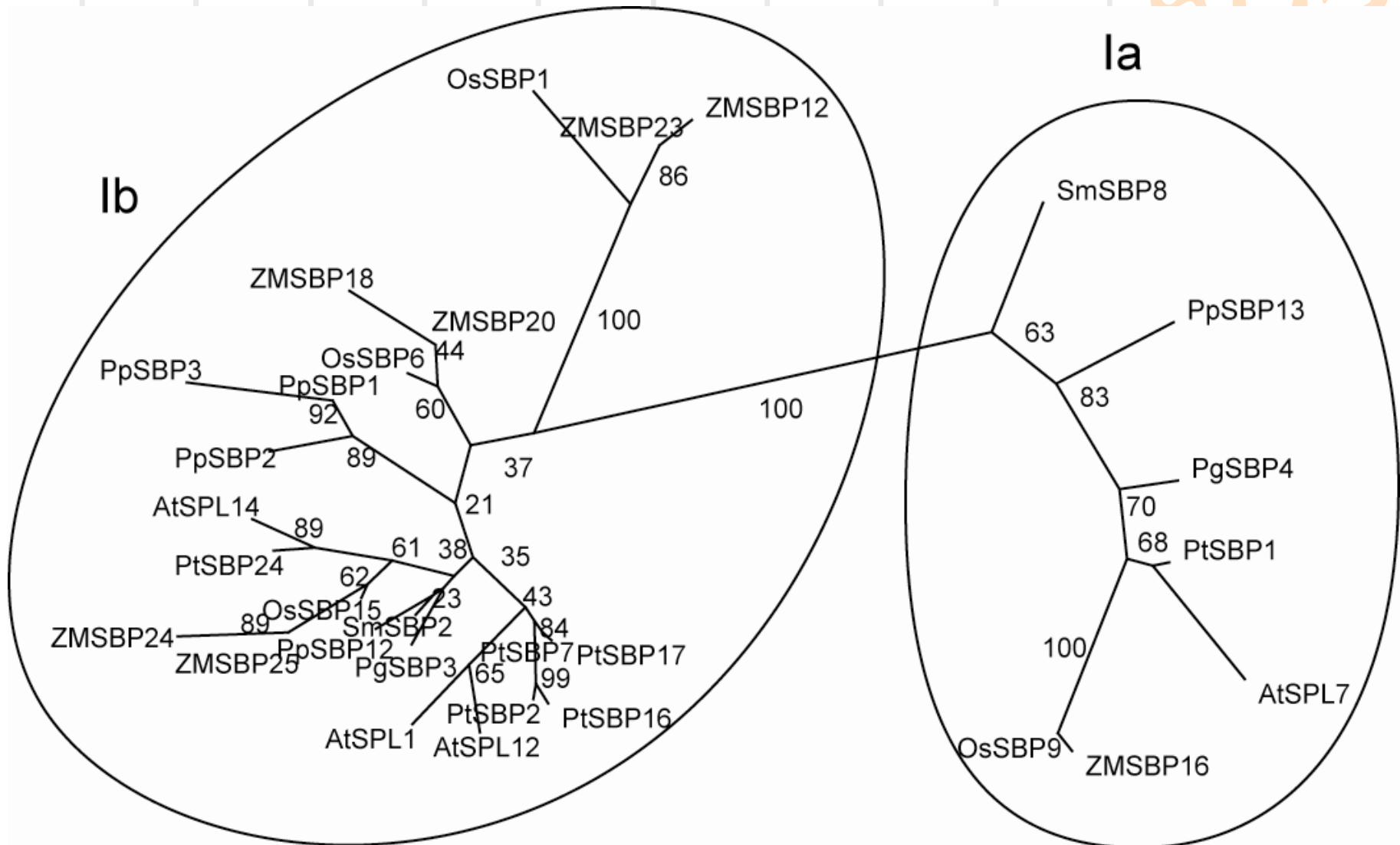
- Green alga (*Chlamydomonas reinhardtii* 19)
- Moss (*Physcomitrella patens* 14)
- Fern (*Selaginella moellendorffii* 13)
- Gymnosperms (pine 4, spruce 4 from EST)
- Dicots: *Arabidopsis* (16), poplar (24)
- Monocots: Rice (18), maize (33)



Schematic Tree of All SBPs



Groups of Many Exons Gene



Motif of Group I



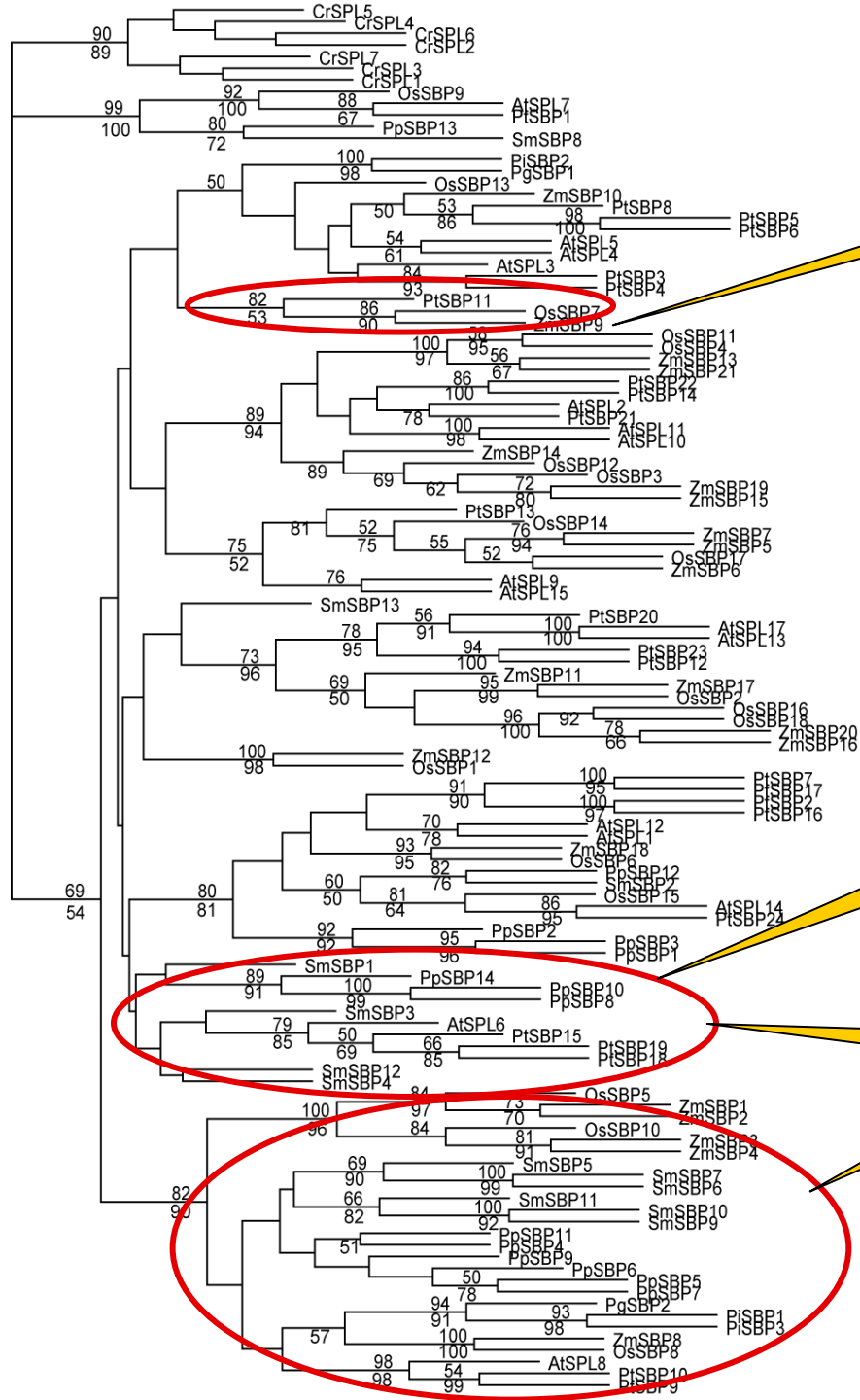
- In all subgroup Ia proteins
- 120 aa after SBP domain
- Even more conserved than SBP domain
- Also have an intron in it
- CrSPL1 has part of it

AtSPL7 309 DNKSAYSTVCPTGRISFKLYDWNPAEFPRRLRHQIFQWLANMPVELEGYIRPGCTILTVFIAMPEIMWAKLSKD 382

|.|.|.|.|.:|.|.|.|.|.:|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.:|.|.|.|.|.:|

OsSBP9 351 DTKSTYSSSCPTGRVSVFKLYDWNPAEFPRRLRHQIFEWLSSMPVELEGYIRPGCTILTVFVAMPQHMWDKLSKD 424





CR
I
IIc
IIh
IIg
IIe
IIe
IIe
IIe
IIe
IIi
IIi
IIi
IIc
IIb

No AtSPL

No OsSBP and ZmSBP

PpSBP SmSBP expansion



Motifs



- All SmSBPs in subgroup IIa have the motif 1 and not have the microRNA site

- PpSBPs and SmSBPs in IIb have both motif1 and the microRNA site



- PpSBPs and SmSBP in Ib have motif 1





Additional AA SBPs in Cereals

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ruler 1.....10.....20.....30.....40.....50.....60.....70.....80..
OsSPL6 ACQVEGCTADLTGV-RD-YHRRHKVCEMHAKATTAVVGN-TVQRFCCQCSRFBPLQEFDEGKRSCRRRLAGHNRRRRRKT RPE
OsSPL15 MCQVDDCRADLTNA-KD-YHRRHKVCEIHGKTTKALVGN-QMQRFCQCCSRFBPLSEFDEGKRSCRRRLAGHNRRRRRKTQPT
OsSPL1 CCQVDGCTVNLSSA-RD-YNKRHKVCEVHTKSGVVRIKN-VEHRFCQCCSRFBFLQEFDEGKKSRSRLAQHNRRRRRKVQVQ
OsSPL16 SCAVDGCKEDLSKC-RD-YHRRHKVCEAHSKTPLVVVSG-REMRFCQCCSRFBLLQEFDEAKRSCRKRLDGHNRRRRRKPQPD
OsSBP18 SCAVDGCKADLSKH-RD-YHRRHKVCEPHSKTPVVVSG-REMRFCQCCSRFBLLGEFDEAKRSCRKRLDGHNRRRRRKPQAD
OsSPL2 ACSVEGCAADLSKCVRD-YHRRHKVCEAHSKTAVVTVAG-QQRFCCQCCSRFBLLGEFDEEKRSCRKRLDGHNRRRRRKPQPD
OsSPL3 HCQVEGCNVDLSSA-KP-YHRKHRVCEPHSKTLKVIVAG-LERRFCQCCSRFBHGLAEFDQKKRSCRRRLHDHNARRRRKPQPE
OsSPL12 YCQVEGCKVDLSSA-RE-YHRKHKVCEAHSKAPKIVVSG-LERRFCQCCSRFBHGLAEFDQKKKSCRRRLSDHNARRRRKPQQE
OsSPL4 RCQVEGCGVELVGV-KD-YHRKHRVCEAHSKFPRVVVAG-QERRFCQCCSRFBHALSEFDQKKRSCRRRLYDHNARRRRKPQTD
OsSPL11 RCQVEGCGLELGGY-KE-YYRKHVCEPHTKCLR VVVAG-QDRRFCQCCSRFBHAPSEFDQEKRSCRRRLSDHNARRRRKPQTD
OsSPL5 RCQAEGCKADLSAA-KH-YHRRHKVCFHAKAAAVLAAG-KQRFCCQCCSRFBHVLAEFDEAKRSCRKRLTEHNRRRRRKPTAG
OsSPL10 RCQAEGCKADLSGA-KH-YHRRHKVCEYHAKASVVAASG-KQRFCCQCCSRFBHVLTEFDEAKRSCRKRLAEHNRRRRRKPAAA
SoSPL2 SCQADGCRADLSGA-KH-YHRRHKVCEHHTKDSVVTADGCTQQCFCHQCSRFBHVLTEFDEVNRSRKRLAEHNRRRRRKPAAT
OsSPL8 RCQAEGCKADLSSA-KR-YHRRHKVCEHHSKAPVVVTAGGLHQRFCCQCCSRFBLLDEFDDAKKSCRKRLADHNRRRRRKS KPS
ZMSBP8 RCQAEGCKADLSSA-KR-YHRRHKVCEHHSKAPVVVTAGGLHQRFCCQCCSRFBLLDEFDDAKKSCRKRLADHNRRRRRKS KPS
ZMSBP32 RCQAEGCKADLSGA-KR-YHRRHKVCDHHSKAPVVVTAGGMHQRFCCQCS-----
SoSPL1 RCQAERCNANLMTDEKP-YNRRHKVCEAHSKAPVVLVAG-LRQRFCCQCCSRFBHLS-----
ZMSBP15 RCQAERCNANLMTTEKP-YNRRHKVCEAHSKAPVVLVAG-LRQRFCCQCCSRIB-----
OsSPL13 RCQVERCGVDLSEA-GR-YNRRHKVCQTHSKEPVVLVAG-LRQRFCCQCCSRFBHELTEFDDAKRSCRRRLAGHNERRRRKSAAD
OsSBP17 RCQVEGCGVDLSGV-KP-YYCRHKVCYMHAKAPIVVVAG-LEQRFCCQCCSRFBHQLPEFDQEKKSCRRRLAGHNERRRRKPTPG
ZMSBP5 RCQVDGCNVDLTDV-KPAYCRHKVCKMHSKEPRVLVNG-LEQRFCCQCCSRFBHQLPEFDQLKKSCRKRLAGHNERRRRPPPG
OsSPL14 RCQVEGCGADLSGI-KN-YYCRHKVCFMHSKAPRVVAG-LEQRFCCQCCSRFBLLPEFDQGKRSCRRRLAGHNERRRRPQTP
OsSPL7 RCQVEGCDITLQGV-KE-YHRRHKVCEVHAKAPRVVHG-TEQRFCCQCCSRFBHVLAEFDDAKKSCRRRLAGHNERRRRSNAS
OsSPL9 KCQVPGCEADIREL-KG-YHRRHRVCLRCAHAAAVMLDG-VQKRYCQCCGKFHILLDFDEDKRSCRRKLERHNKRRRRKPD S

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Arabidopsis and Rice SBP Gene Duplication

- Ath: between 14.5-20.4 and 83-86 MYA
 - AtSPL10 AtSPL11 tandem Dup
 - (AtSPL1, AtSPL12), (AtSPL4, AtSPL5), (AtSPL9, AtSPL15), and (AtSPL14, At1g76580)

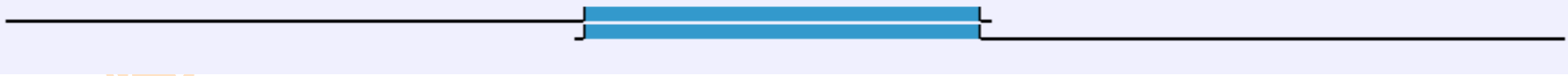
- Rice

- (OsSBP3, OsSBP12), (OsSBP4, OsSBP11), (OsSBP5, OsSBP10) (Chr2,Chr6)
- (OsSBP16, OsSBP18)

Non-plant SBP-like



- Find 2 from NCBI dbEST:
 - CV968636 (*Phytophthora infestans*)
Similar with tomato BF096268(225bp with 99% identity and 70 AA with 100% identity



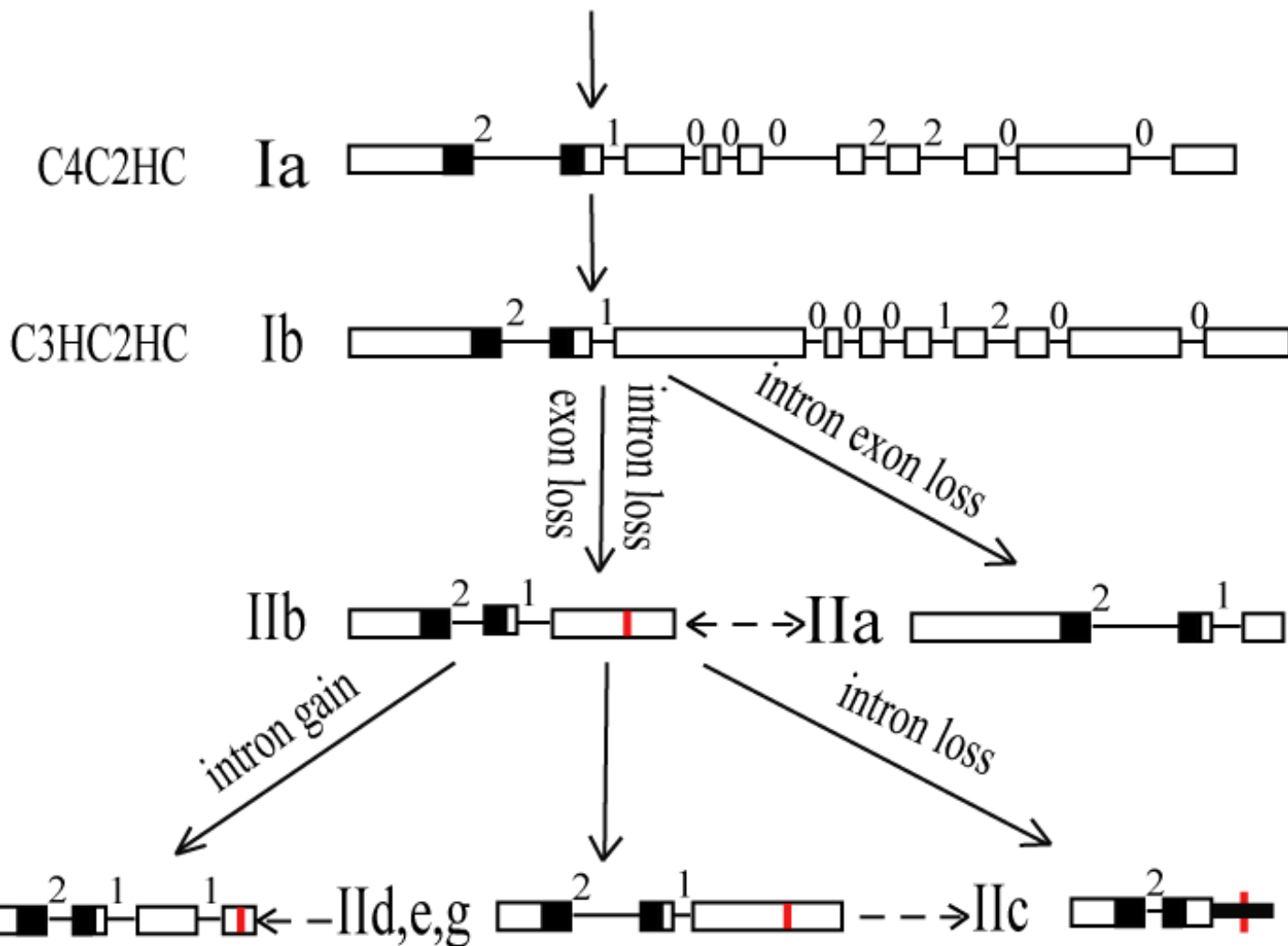
- DN479436 (*Alternaria brassicicola*)
850 bp length
86-295bp similar with At1g04410 (91%)
302-408bp similar with AtSPL3 (88%)



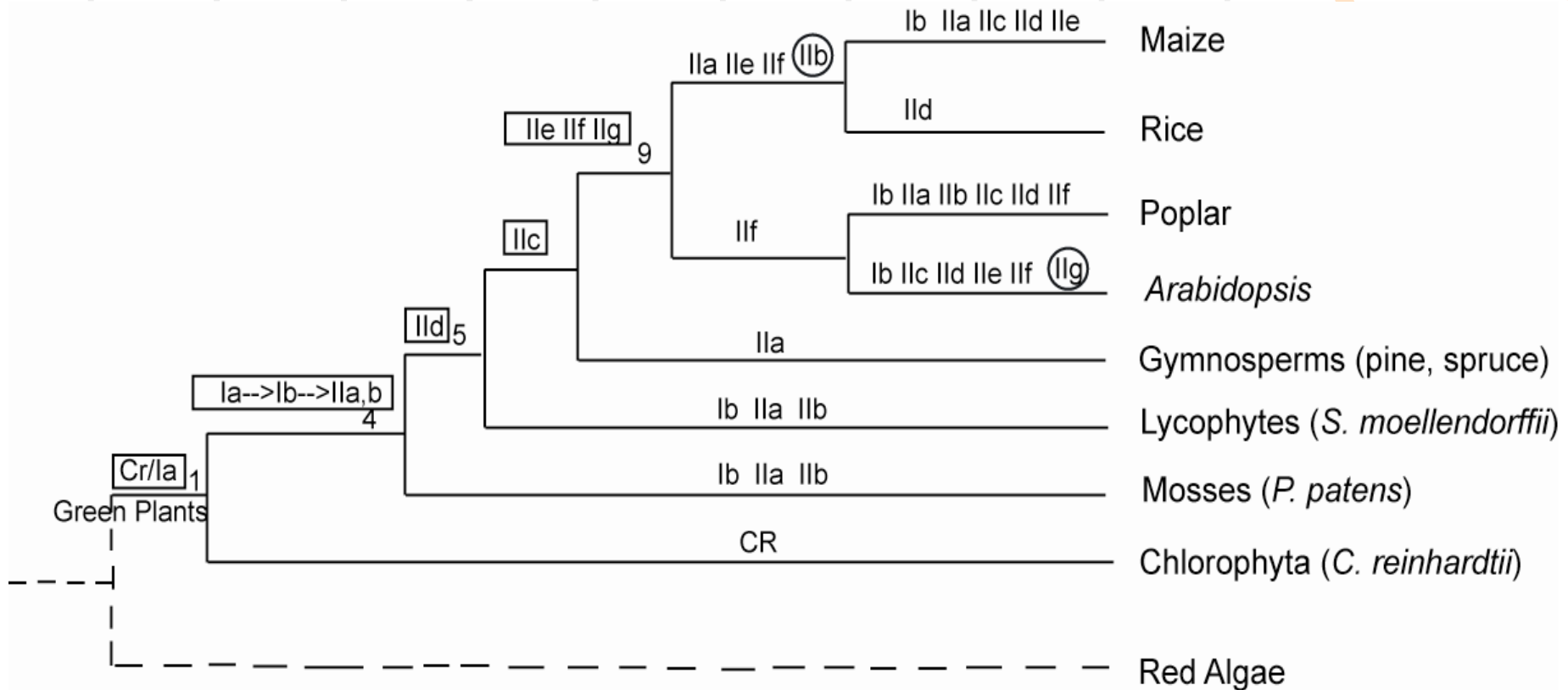
Evolutionary Model of SBP Gene Structure



SBP ancestor \longrightarrow CrSPLs



The Origin, Evolution, and Duplication Model of SBP Genes



Function



- Subgroup Ia: Function unknown
 - C4C2HC zinc finger
 - Only one gene of each organism
 - High conserved in each lineage
- Expansion diff in lower and high plants
 - IIa: 1 in At (AtSPL8 sporogenesis), but 6PpSBPs, 6SmSBPs (~50%)
 - IIb: 1 AtSPL, 3 PtSBPs, lost in rice & maize, expansion in Sm and Pp



SBP in other plants



- From TGI:cotton (14), sugarcane (20), soybean (14), tomato (10), barley (8), and wheat (11)
- Ath(16), rice(18),maize(33)

