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

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SBP TFs

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

- Fist found in Antirrhinum majus in 1990.
- 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

1. GLKGNFEDSG
2. ALSLLS
3. KRGVEDLNWDWDSLFATP
4. MDCNKMSSWDWENFLMPSNTTTNPKKQKPTFENKALPSINNDNDDPDPLMKPQG
Motifs

- **Protein motifs:** 1,2,3,4

- **Exon motifs:**
  - GTGCTCTCTCTCTTCTGTCA
  - ALSLLS (motif 2)
  - Iib,c,d,e,f,g (except Ila in all group II)
  - MicroRNA complementary site
  - CGCCACCGCGCCGCGCCGCGCCGCGCCGCGCGCGCGCGCGCGCG
    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
No AtSPL

No OsSBP and ZmSBP

PpSBP SmSBP expansion
Motifs

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

- PpSBPs and SmSBPs in Iib have both motif 1 and the microRNA site

- PpSBPs and SmSBP in Ib have motif 1
Additional AA SBPs in Cereals

ruler

OsSPL16 ACQVEGCTADLTGV-RD-YHRHKVCEHMHAKATTAVGVN-TVQRFCQQCSRFHPLQEFDEKGKSCRRRLAGHNNRRRKKTRPE
OsSPL15 MCQVDDCRADLTNA-KD-YHRHKVCEIHGTKTALVGQ-QMQRFCQQCSRFHPLSEFDEKGKSCRRRLAGHNNRRRKTQPT
OsSPL11 CCQVDGCTVNLSSA-RD-YNHRHKVEVHTKSQGVR1KN-XVHFRFCQQCSRFHPLQEFDEGKSKCRRLAGHNNRRRKTQPT
OsSPL16 SCAVDCGKEDLSKCRD-YPHRHKVCEAHSTPLVYVSVG-REMRFQCCSRFHLLQEFDFAKRKCRKLKDGHNNRRRKPQFD
OsSPL18 SCAVDCGKADLSKH-RD-YHRHKVCEPHSTPVVYVSG-REMRFQCCSRFHLLGEFDFAKRKCRKLKDGHNNRRRKPQAD
OsSPL12 ACSVDCGCAADLSKVQRD-YHRHKVEAHSSTAVTVVAG-QQQRFQCCSRFHLLGEFDFAKRKCRKLKDGHNNRRRKPQAP
OsSPL13 HCQVGECNVDLSKSA-KP-YHRHKVCEPHSTKLVAVG-LERRFCQQCSRFHGLAEFDQKKKCRRRLSDHNNRRRKPQOE
OsSPL12 YCQVGECNVDLSA-RE-YHRHKVCEAHSKAPKVIVSG-LERRFCQQCSRFHGLAEFDQKKKCRRRLSDHNNRRRKPQOE
OsSPL14 RCQVGECGVELVKG-KD-YHRHKVCEAHSKFPVYVAG-GERRFQCCSRFHALSEFQKKKCRRRLSDHNNRRRKPQTD
OsSPL11 RCQVGECGLEGGY-KE-YHRHKVCEPHKCLYVYVAG-QDRRFQCCSRFPASEFDQKRSRRRLSDHNNRRRKPQTD
OsSPL15 RCQAEGCCKALSSAA-KH-YHRHKVCDFHAKAAAVLAAAG-KQQRFCQQCSRFHLMAEFDFAKRKCRKLTDHNNRRRKPAG
OsSPL10 RCQAEGCCKALSSA-KH-YHRHKVCYHAKASVAASQG-KQQRFCQQCSRFHLTEFDFAKRKCRKLAEHNNRRRKPAA
OsSPL12 SCQADGRCVNLSSA-KH-YHRHKVEHHTKDSTVLGAG-TCQCFHCSQRFHLTEFDVNSRKRKCRKLAEHNNRRRKPAG
OsSPL18 RCQAEGCCKALSSA-KR-YHRHKVCEHSHKALEVTVTAGL-HFQRFQCCSRFHLLDEFDFAKRKCRKLADHNNRRRKSPP
ZMSBP8 ZMSBP9 ZMSBP12 RCQAEGCCKALSSA-KH-YHRHKVCEHSHKALEVTVTAGL-HFQRFQCCSRFHLLDEFDFAKRKCRKLADHNNRRRKSPP
ZMSBP32 ZMSBP34 ZMSBP32 RCQAEGCCKALSSA-KH-YHRHKVCEHSHKALEVTVTAGL-HFQRFQCCSRFHLLDEFDFAKRKCRKLADHNNRRRKSPP
Arabidopsis and Rice SBP Gene Duplication

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

- **Rice**
  - $(\text{OsSBP3, OsSBP12}), (\text{OsSBP4, OsSBP11}), (\text{OsSBP5, OsSBP10}) \text{ (Chr2,Chr6)}$
  - $(\text{OsSBP16, OsSBP18})$
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
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
  - Ila: 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)