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## 大豆SBP转录因子家族的预测分析

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摘要: SBP转录因子基因家族是一个植物的特异转录因子家族, SBP基因都含有一段保守的核苷酸序列即DNA结合结构域, 又称为SBP盒 (SBP-box), SBP盒编码的蛋白质序列称SBP结构域 (SBP-domain), 含79个氨基酸残基, 并具有高度保守性。该研究通过对拟南芥、水稻等植物已知的转录因子与大豆基因组数据比对, 并设置一系列严格的筛选标准, 共得到44条新的大豆SBP转录因子; 又通过基因分析注释以及启动子功能预测, 进一步发现这些转录因子参与生长发育、逆境胁迫响应、激素应答、抗霉菌应答、光合作用等调控过程。

Abstract: In transcription factor family, SBP is a specific group only found in plant. The genes in this family contain a conservative nucleotide sequences namely DNA-binding domain, also called SBP-box, which encodes the SBP-domain including 79 amino acid residues and is highly conservative. With homology alignment, all previously known SBP from Arabidopsis, Oryza sativa and other plant species were blasted against the soybean genome sequences to mining novel SBP TFs in soybean by a series of strict filtering criteria. In total, 44 members in SBP TFs were identified and predicted. These transcription factors were predicted and verified to be involved in soybean growth and development, adversity response, hormone response, resistance to mold response and photosynthesis control process.

### 参考文献/References:

- [1]Klein J, Saedler H, Huijser P, et al. A new family of DNA binding proteins includes putative transcriptional regulators of the Antirrhinum majus floral meristem identity gene SQUAMOSA [J]. Molecular and General Genetics, 1996, 250(1): 7-16.
- [2]Yamasaki K, Kigawa T, Inoue M, et al. Arabidopsis?SBP-domain fragment with a disrupted C-terminal zinc-binding site retains its tertiary structure[J]. FEBS Letters, 2006, 580(8): 2109-2116.
- [3]Stone J M, Liang X, Neel E R, et al. Arabidopsis?AtSPL14, a plant-specific SBP-domain transcription factor, participates in plant development and sensitivity to fumonisin B1[J]. The Plant Journal, 2005, 41(5): 744-754.
- [4]Cardon G, Hohmann S, Huijser P, et al. Molecular characterization of the Arabidopsis?SBP-box genes[J]. Gene, 1999, 237(1): 91-104.

- [5] Birkenbihl R P, Jach G, Saedler H, et al. Functional dissection of the plant-specific SBP-domain: overlap of the DNA-binding and nuclear localization domains[J]. *Journal Molecular Biology*, 2005, 352(3): 585-596.
- [6] Moreno M A, Harper L C, Dellaporta S L, et al. Freeling M liguleless1 encodes a nuclear-localized protein required for induction of ligules and auricles during maize leaf organogenesis[J]. *Genes Development*, 1999, 16(3): 620-628.
- [7] Cardon G, Hohmann S, Huijser P, et al. Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a novel gene involved in the floral transition[J]. *The Plant Journal*, 1997, 12(2): 367-77.
- [8] Wang H, Nussbaum-Wagler T, Li B, et al. The origin of the naked grains of maize[J]. *Nature*, 2005, 436(10): 714-719.
- [9] Huijser P, Klein J, Lonnig W E, et al. Bracteomania, an inflorescence anomaly, is caused by the loss of function of the MADS-box gene squamosa in *Antirrhinum majus*[J]. *EMBO Journal*, 1992, 11(4): 1239-1249.
- [10] Kropat J, Tottey S, Birkenbihl R P, et al. A regulator of nutritional copper signaling in *Chlamydomonas* is an SBP domain protein that recognizes the GTAC core of copper response element[J]. *Proceedings of the National Academy of Sciences of the United States of America*, 2005, 102(51): 18730-18735.
- [11] Lannenpan M, Jananen I, Haltta-Vuori M, et al. A new SBP-box gene BpSPL1 in silver birch (*Betula pendula*)[J]. *Physiologia Plantarum*, 2004, 120(3): 491-500.
- [12] Manning K, Tar M, Poole M, et al. A naturally occurring epigenetic mutation in a gene encoding an SBP-box transcription factor inhibits tomato fruit ripening[J]. *Nature Genetics*, 2006, 38: 948-952.
- [13] Unte U S, Sorensen A M, Pesaresi P, et al. SPL8, an SBP-box gene that affects pollen sac development in Arabidopsis[J]. *Plant Cell*, 2003, 15(4): 1009-1019.
- [14] Wu G, Poethig R S. Temporal regulation of shoot development in Arabidopsis thaliana by miR156 and its target SPL3[J]. *Development*, 2006, 133(18): 3539-3547.
- [15] Yamasaki K, Kigawa T, Inoue M, et al. A novel zinc-binding motif revealed by solution structures of DNA-binding domains of Arabidopsis SBP-family transcription factors[J]. *Journal Molecular Biology*, 2006, 337: 49-63.
- [16] Maeo K, Tokuda T, Ayame A, et al. An AP2-type transcription factor, WRINKLED1, of Arabidopsis thaliana binds to the AW-box sequence conserved among proximal upstream regions of genes involved in fatty acid synthesis[J]. *Plant Journal*, 2009, 60(3): 476-487.

#### 相似文献/References:

- [1] 赵艳, 刘晓鑫, 张庆林, 等. 大豆种子特异性启动子研究进展[J]. (article.aspx?type=view&id=201001035) *大豆科学*, 2010, 29(01): 151. [doi:10.11861/j.issn.1000-9841.2010.01.0151]
- ZHAO Yan, LIU Xiao-xin, ZHANG Qing-lin, et al. Advances of Studies on Seed-specific Promoters of Soybean[J]. *Soybean Science*, 2010, 29(02): 151. [doi:10.11861/j.issn.1000-9841.2010.01.0151]
- [2] 刘冬冬, 王洋, 柏锡. 大豆 Glyma08g02580 及其同源蛋白的生物信息学分析[J]. (article.aspx?type=view&id=201405005) *大豆科学*, 2014, 33(05): 648. [doi:10.11861/j.issn.1000-9841.2014.05.0648]
- LIU Dong-dong, WANG Yang, BAI Xi. Bioinformatics Analysis on Transcription Factor Glyma08g02580 and Its Homology Proteins[J]. *Soybean Science*, 2014, 33(02): 648. [doi:10.11861/j.issn.1000-9841.2014.05.0648]
- [3] 刘德泉, 郭文云, 何则铭, 等. 大豆胚发育期酵母双杂交文库的构建及与bHLH转录因子互作蛋白的筛选[J]. (article.aspx?type=view&id=201505007) *大豆科学*, 2015, 34(05): 789. [doi:10.11861/j.issn.1000-9841.2015.05.0789]
- LIU De-quan, GUO Wen-yun, HE Ze-ming, et al. Yeast Two-hybrid cDNA Library Construction of Soybean Embryo Developmental Phase and Screening of Proteins Interacting with Soybean bHLH Transcription Factor[J]. *Soybean Science*, 2015, 34(02): 789. [doi:10.11861/j.issn.1000-9841.2015.05.0789]
- [4] 成舒飞, 端木慧子, 陈超, 等. 大豆 MYB 转录因子的全基因组鉴定及生物信息学分析[J]. (article.aspx?type=view&id=201601008) *大豆科学*, 2016, 35(01): 52. [doi:10.11861/j.issn.1000-9841.2016.01.0052]
- CHENG Shu-fei, DUANMU Hui-zi, CHEN Chao, et al. Whole Genome Identification of Soybean MYB Transcription Factors and Bioinformatics Analysis[J]. *Soybean Science*, 2016, 35(02): 52. [doi:10.11861/j.issn.1000-9841.2016.01.0052]
- [5] 郭文雅, 崔艳梅, 喻德跃, 等. 野生大豆 GsAP1 基因的克隆及功能分析[J]. (article.aspx?type=view&id=201606006) *大豆科学*, 2016, 35(06): 919. [doi:10.11861/j.issn.1000-9841.2016.06.0919]
- GUO Wen-ya, CUI Yan-mei, YU De-yue, et al. Cloning and Functional Analysis of GsAP1 in Wild Soybean[J]. *Soybean Science*, 2016, 35(02): 919. [doi:10.11861/j.issn.1000-9841.2016.06.0919]

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