

**genome-wide analysis of the spl family transcription ...** - genome-wide analysis of the spl family transcription factors and their responses to abiotic stresses in maize hu-de maoa,b,li-juanyub, zhan-jie lib, yan yanb, ran hanb,huijiub,mengmab a state key laboratory of crop stress biology for arid areas and college of plant protection, northwest a&f university, yangling, shaanxi 712100, china

**molecular characterization and expression analysis of the ...** - molecular characterization and expression analysis of the ... (spl) genes encode plant-specific transcription factors ... to perform a genome-wide analysis of the spl family, taking advantage of the full birch genome sequence (unpublished data). here we searched the birch genome assembly

**genome-wide binding analysis of the ... - plant cell** - genome-wide binding analysis of the transcription activator ideal plant architecture1 reveals a complex network regulating rice plant architecture ... the iconic feature of spl proteins is the conserved sbp-box. in arabidopsis, the sbp-box contains a dna binding domain, directly targeting a core sequence, gtac (birkenbihl ...

**genomic organization, differential expression, and ...** - genomic organization, differential expression, and interaction of squamosa promoter-binding-like ... precursors were identified in the rice genome. sequence and experimental analysis suggested that ... plant spl proteins were classified into six subgroups based on the

**genomic organization, differential expression, and ...** - to date, the analysis of spl proteins has mainly focused on information garnered from genome sequences of arabidopsis thaliana and oryza sativa, and there has been limited classification of spl proteins of flowering plants, especially upland cotton (gossypium hirsutum). upland cotton is an important economic crop that provides fiber,

**genome-wide analysis of cyclins in maize zea mays** - genome-wide analysis of cyclins in maize (zea mays) x. hu1, x. cheng 2, h. jiang 2, s. zhu, ... since then, more than 70 plant cyclins have been isolated from various plant species. in animals, multiple cyclins have been identified in several species, of which several have been ... the overall analysis of the complete genome of maize revealed ...

**analysis of the female gametophyte transcriptome of** - analysis of the female gametophyte transcriptome of ... the extensive data on the transcription of the plant genome are derived primarily from the sporophytic generation. there ... 2001), a study of the female gametophyte transcriptome has not been performed at the whole-genome level. we have previously described a gene called sporo-

**molecular characterization of squamosa promoter binding ...** - to demonstrate a correlation between spl-like gene expression and fruit load in fruit trees. however, further analyses are required to strengthen these relationships. in the current work, we performed a functional analysis of the citrus spl in arabidopsis. the results showed it was able to promote flowering, while

**negative regulation of anthocyanin biosynthesis in ...** - negative regulation of anthocyanin biosynthesis in arabidopsis by a mir156-targeted spl transcription factor woa ... flavonoids are major plant phenylpropanoid metabolites found throughout the plant kingdom, including the model species ... the arabidopsis genome contains 11 spl genes that are targeted by mir156. these spl genes can be ...

**biotechnological and genomic analysis for salinity ...** - biotechnological and genomic analysis for salinity tolerance in sugarcane kalpana sengar, r.s. sengar and ashu singh tissue culture lab, college of biotechnology, sardar vallabh bhai patel university ... and plant genome evolution. search for new models. plant physiol 138: 127-130.

**arabidopsis transcription factors spl1 and spl12 confer ...** - spl12 confer plant thermotolerance at reproductive stage lu-men chao 1,4, yao-qian liu2, dian-yang chen 1, ... the arabidopsis thaliana genome encodes 17 spl members, which form two major classes. class i contains five (spl1, 7, 12, 14, and 16) large proteins of more than 800 amino ... motif analysis by smart (schultz et al., 1998) ...

**cloning and characterization of spl-family genes in the ...** - genome-wide analysis has revealed that 17 members of the spl family genes are present in arabidopsis (birkenbihl et al., 2005; guo et al., 2008). to date, a large number of spls have been discovered in various plant species, such as green algae, moss, tomato, rice, maize, and silver

**research article open access mutant sk156 spl15 in a ...** - to repress spl (squamosa promoter binding protein-like) genes [2-4], which are plant-specific transcription factors containing the sbp

(squamosa promoter binding protein) box [5]. in arabidopsis, 11 spl genes are targeted by mir156 [2,4,6,7], and in silico full genome analysis showed that no other genes in arabidop- **function annotation of an sbp-box gene in arabidopsis ...** - analysis of the arabidopsis genome reveals 29 classes of transcription factors, 16 of which appear to be unique to plants [1]. one of these contains a dna binding domain referred to as the squamosa promoter ... that spl genes play a role in controlling plant development, we can infer that spl genes may not only ... list of genes that are ...

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