



# OPEN Genome-wide identification of lipid transfer proteins in *Sorghum bicolor* and discovery of flower-specific promoters

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*Sorghum bicolor* is a drought- and heat-tolerant cereal widely cultivated in arid regions. However, like other important grasses, it is susceptible to ergot disease caused by *Claviceps* species, which infect ovary tissues and reduce grain yield. To combat this disease, targeted biotechnological strategies are needed. In this study, we conducted a genome-wide identification and classification of lipid transfer proteins (LTPs) in *S. bicolor*, uncovering 68 putative genes grouped into five families. In silico analyses of gene expression and promoter sequences identified two LTP genes, *SbLTP1.4* and *SbLTP1.5*, as strong candidates for flower-specific biotechnological applications. Their promoters were functionally tested in transgenic *Arabidopsis thaliana*, revealing distinct spatial and stress-responsive expression profiles. The *SbLTP1.4* promoter was active in stigmas, floral peduncles, styles, and young leaves, and was strongly induced by both biotic and abiotic stress. In contrast, *SbLTP1.5* promoter displayed low and stigma-specific expression, with no detectable stress responsiveness. Promoter analysis also revealed conserved transcription factor binding sites across orthologous genes in other economically important grasses, supporting the potential transferability of this strategy to related species. These findings introduce novel tissue-specific promoters for the targeted expression of antimicrobial proteins in reproductive tissues, offering a promising tool to control *Claviceps* infections and enhance crop resilience in cereals and forage grasses.

**Keywords** Lipid transfer proteins, Genome-wide, Flower tissue-specific promoters, *Sorghum bicolor*

*Sorghum* (*Sorghum bicolor* [L.] Moench) is an important cereal crop widely cultivated for both forage and grain. Its remarkable tolerance to drought, elevated temperatures, and high water-use efficiency makes it an ideal crop for arid and semi-arid regions. Forage sorghum is widely grown as a drought-resistant alternative to maize in arid subtropical to warm temperate regions. It holds promise as a biofuel source on marginal lands unsuitable for food production<sup>1</sup>. Being a C4 plant, sorghum boasts improved photosynthetic efficiency and reduced water loss in hot and dry environments—valuable amidst current global climate change, limited access to fertilizers, and diminishing arable land<sup>2</sup>. However, sorghum faces challenges from Ergot, a disease caused by fungi belonging to the genus *Claviceps*. Ergot infects young, often unfertilized ovaries, replacing the seeds with dark mycelial masses called sclerotia. The alkaloids produced by the fungus severely impact the health of humans and warm-blooded animals. Ergot-related issues also affect commercial seed production in infected crops<sup>3</sup>.

Non-specific lipid transfer proteins (LTPs) were discovered approximately 30 years ago<sup>4</sup>. These proteins are abundant, secreted, soluble, cysteine (Cys)-rich, and typically small, with a molecular size usually below 10 kDa<sup>5–7</sup>. LTPs proteins family evolved after plants adapted to land, as they are present in liverworts, mosses, and other land plants but not in algae. They are classified into five major types (LTP1, LTP2, LTP-C, LTP-D, and LTP-G) based on the spacing between the Cys residues in the eight-cysteine motif, the polypeptide sequence identity, and the position of evolutionarily conserved introns<sup>6,8</sup>. Although the in vivo functions of LTPs

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remain unclear, accumulating evidence suggests diverse roles for LTPs in plant physiology. These roles include involvement in cutin synthesis,  $\beta$ -oxidation, somatic embryogenesis, allergenic properties, plant signaling, and plant defense against phytopathogens<sup>5,6</sup>.

LTP genes exhibit complex expression patterns, both temporally and spatially, making them excellent candidates for tissue-specific expression studies. Numerous studies have demonstrated LTP expression in floral organs<sup>5,7,9</sup>. These genes are notably active during early flower development and are highly expressed in inflorescences across a range of plant species. High transcript levels have been reported in young developing inflorescences of carrot and *Arabidopsis thaliana*, the sepals of unopened tobacco flowers, the flower buds of broccoli, the microspores of rapeseed, and the corolla and carpel of *Gerbera hybrida*. While some LTPs exhibit exclusive expression in floral tissues, others are expressed in multiple organs<sup>10</sup>.

In addition to their floral-specific expression, many LTP genes respond to various environmental signals, including salinity, drought, extreme temperatures, heavy metals, and biotic stresses such as bacterial and fungal pathogen attacks<sup>5,6,11</sup>. These dual characteristics—floral-specific expression and environmental responsiveness—underscore the suitability of LTP promoters for targeted gene expression in floral organs, particularly for strategies aimed at combating stresses like fungal infections.

Plant genetic engineering plays a pivotal role in introducing valuable traits that enable crops to thrive with reduced dependence on pesticides, fungicides, and fertilizers, while enhancing stress resistance. Using organ-specific, developmentally and stress-induced promoters is vital for genetically modifying plants. While constitutive and non-specific promoters are useful in proof-of-concept experiments, their application in genetically improved crops presents potential drawbacks<sup>12,13</sup>. Overexpression of proteins in excessive amounts or at unnecessary times can strain cellular energy reserves<sup>14</sup> or result in undesirable pleiotropic effects in transgenic plants<sup>15,16</sup>. One way to minimize these problems is by using endogenous regulatory regions from promoters with well-defined developmental expression patterns<sup>17,18</sup>. Thus, achieving precise temporal and tissue-specific expression of foreign genes through promoter control is crucial<sup>17,19</sup>.

This study performed a genome-wide identification of LTP genes in *S. bicolor* and classified them based on structural analysis and in silico expression patterns to identify flower tissue-specific promoters. Given the specificity of *Claviceps* infection in sorghum, stigma-specific promoters for expressing antifungal compounds in floral organs represent a promising strategy to disrupt the infection process by preventing the germination of ascospores or the development of infectious hyphae. Since *Claviceps* targets several agriculturally important species, including Sorghum, Zea, Pennisetum, Setaria, and others, this approach has the potential to significantly reduce economic losses and improve the productivity of food and forage crops. These findings highlight the functional diversity of LTPs in *S. bicolor* and establish tissue-specific promoters as valuable tools for targeted antimicrobial protein expression, laying a foundation for enhancing crop resilience and combating ergot disease in cereals and forages.

## Results

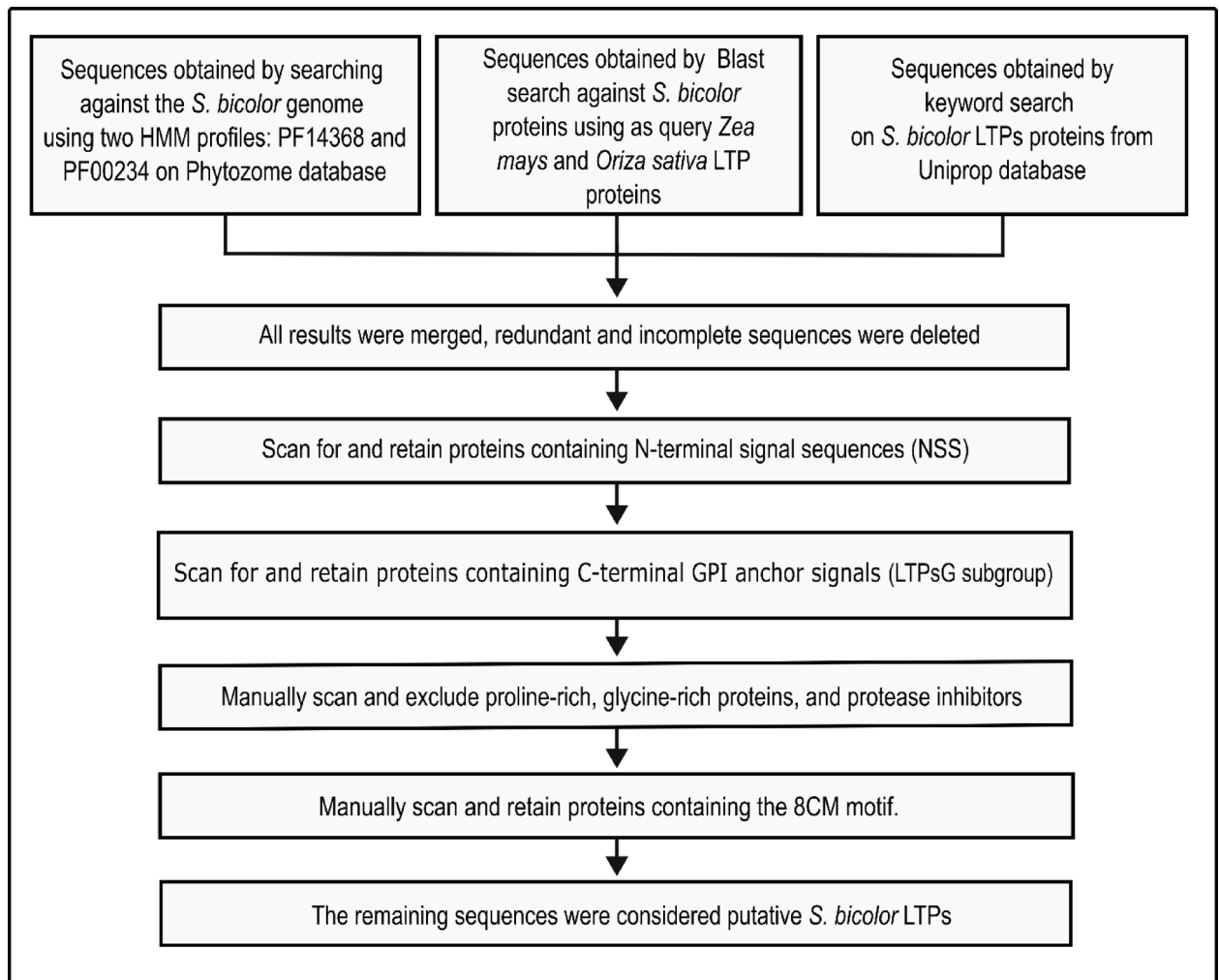
### Identification and classification of putative LTPs genes in the *S. bicolor* genome

To identify all putative, non-redundant LTPs genes within the *S. bicolor* genome, we conducted an exhaustive search and data mining process according to the workflow chart presented in Fig. 1. First, we retrieved putative LTPs sequences from *S. bicolor* genome using two hidden Markov models (HMM) profiles developed for protease inhibitor, seed storage and LTP proteins (PF14368 and PF00234). Subsequently, we performed a Blastp search using previously reported LTPs protein sequences in *Z. mays* and *O. sativa*<sup>20</sup> and a keyword search against the Uniprot database. These additional methods led to the discovery of novel sequences, which were integrated with the initial dataset. We removed redundant sequences, resulting in 116 non-redundant amino acid sequences.

LTPs are typically produced as pre-proteins, which include an N-terminal signal peptide necessary for their correct secretion to their subcellular location<sup>21</sup>. To ensure the inclusion of proteins with such signal peptides, we conducted N-terminal signal sequence (NSS) prediction and excluded proteins lacking in them (Table S2). On the other hand, the members of the LTP-G protein subgroup are characterized by having a C-terminal motif that undergoes post-translational modification in the endoplasmic reticulum through adding a GPI moiety<sup>21</sup>. This modification enables the protein to anchor to the outer side of the plasma membrane<sup>20</sup>. Therefore, we also conducted predictions for C-terminal glycosylphosphatidylinositol (GPI) anchor signals. Finally, we excluded sequences belonging to alpha-amylase/trypsin inhibitors, proline-rich proteins or hybrid proline-rich proteins, and glycine-rich proteins (Table S2). The remaining deduced protein sequences were thoroughly examined for the presence of the characteristic 8CM motif of LTPs, and proteins lacking these motifs were removed. Consequently, a total of 68 sequences were isolated, identified as putative LTP genes in the *S. bicolor* genome, and designated as SbLTPs (Table 1, Table S2).

Applying the classification system developed by Edstam et al.<sup>8</sup> This pattern of conservation and diversification underscores the importance of gene duplication and subsequent adaptation in the evolution of LTPs, with different types evolving to fulfill specific roles in response to environmental pressures and unique functional requirements., we categorized the sequences into five LTP types. Proteins that met the LTP criteria but did not align with any of the five LTP groups, due to the 8CM motifs or intron position not precisely matching the pattern described by Edstam et al.<sup>8</sup> were assigned to the non-determined (ND) category. In the ND category, we found two subgroups that, according to the phylogenetic analysis (Fig. S4), are related to groups LTP-G and LTP-D. In the case of the Type G proteins, these appear to have lost the GPI-anchor site (Table 1). Specifically, we identified 9 LTP-1, 7 LTP-2, 2 LTP-C, 12 LTP-D, 20 LTP-G, and 18 LTP-ND.

To analyze the sequence characteristics of SbLTPs, we performed a multiple sequence alignment using the deduced mature proteins from the 68 SbLTP for each LTP subgroup (Fig. 2). The main characteristic of all plant LTPs is the presence of a highly conserved 8CM ( $C_1$ -Xn- $C_2$ -Xn- $C_3$ - $C_4$ -Xn- $C_5$ - $C_6$ -Xn- $C_7$ -Xn- $C_8$ ), which enables the formation of four disulfide bonds, crucial for stabilizing the three-dimensional structure of the



**Fig. 1.** Workflow diagram of data mining tools used for the identification of SbLTP sequences.

protein, allowing it to interact with lipids and facilitate their transfer between biological membranes<sup>22</sup>. Each LTP subgroup has a characteristic arrangement of the 8CM motif, with the spacing and specific sequence varying between types (Table 1; Fig. 2). Additionally, a high conservation of other amino acids (P, L, V, Y) is observed, which differ among subtypes and could be essential for their function and/or functional specificity<sup>23</sup>. Regarding the CXC motif, type 1 SbLTP displayed variability in the residues at the X position (Ser, Gly, Glu, Asn, Ala, Arg), with five sequences having hydrophilic residues and four sequences having hydrophobic residues. On the other hand, types 2, C, D, and G SbLTPs exhibited hydrophobic residues at this position.

### Chromosomal locations and gene duplication of putative SbLTPs

The chromosome locations of each gene were determined using information from the NCBI Genome Browser, and a physical map was constructed (Fig. 3). The exact positions of *SbLTPs* on chromosomes are detailed in Table S3. The chromosomal location analysis revealed that the 68 *SbLTP* genes were unevenly distributed across the ten *S. bicolor* chromosomes, with most genes organized into clusters. The largest clusters are on chromosomes 1, 2, and 3, with the highest numbers of *SbLTP* genes found on chromosomes 1 (15) and 2 (18), while chromosome 4 had the lowest number (1). LTPs are predominantly situated towards the distal ends of the chromosomes, often away from the centromere regions on both arms. However, several chromosomes lacked SbLTPs in specific regions, such as the short arms of chromosomes 4, 6, 9, and 10, as well as the long arm of chromosome 8. Additionally, we identified five tandem LTP repeats in the *S. bicolor* genome: (1) *SbLTP2.1/SbLTP2.2*, (2) *SbLTPnd15/SbLTPnd16*, (3) *SbLTPd5/SbLTPd6*, (4) *SbLTP1.4/SbLTP1.5* and (5) *SbLTPd7/SbLTPd11*. Each tandem repeat comprised genes of the same LTP type, indicating they likely originated from gene duplication events.

To analyze evolutionary relationships, a phylogenetic tree of LTPs from *A. thaliana*, *O. sativa*, and *S. bicolor* was constructed. Our analysis confirmed the Edstam classification, showing that the five groups in the SbLTP classification align with types 1, 2, C, D, and G from the other species, with some overlap in types D and G (Fig. S2). Types 1, 2, and C formed distinct clades with over 95% bootstrap support, indicating a common ancestor for each group. LTPs-G were further divided into three clades, and LTPs-D into two, reflecting additional

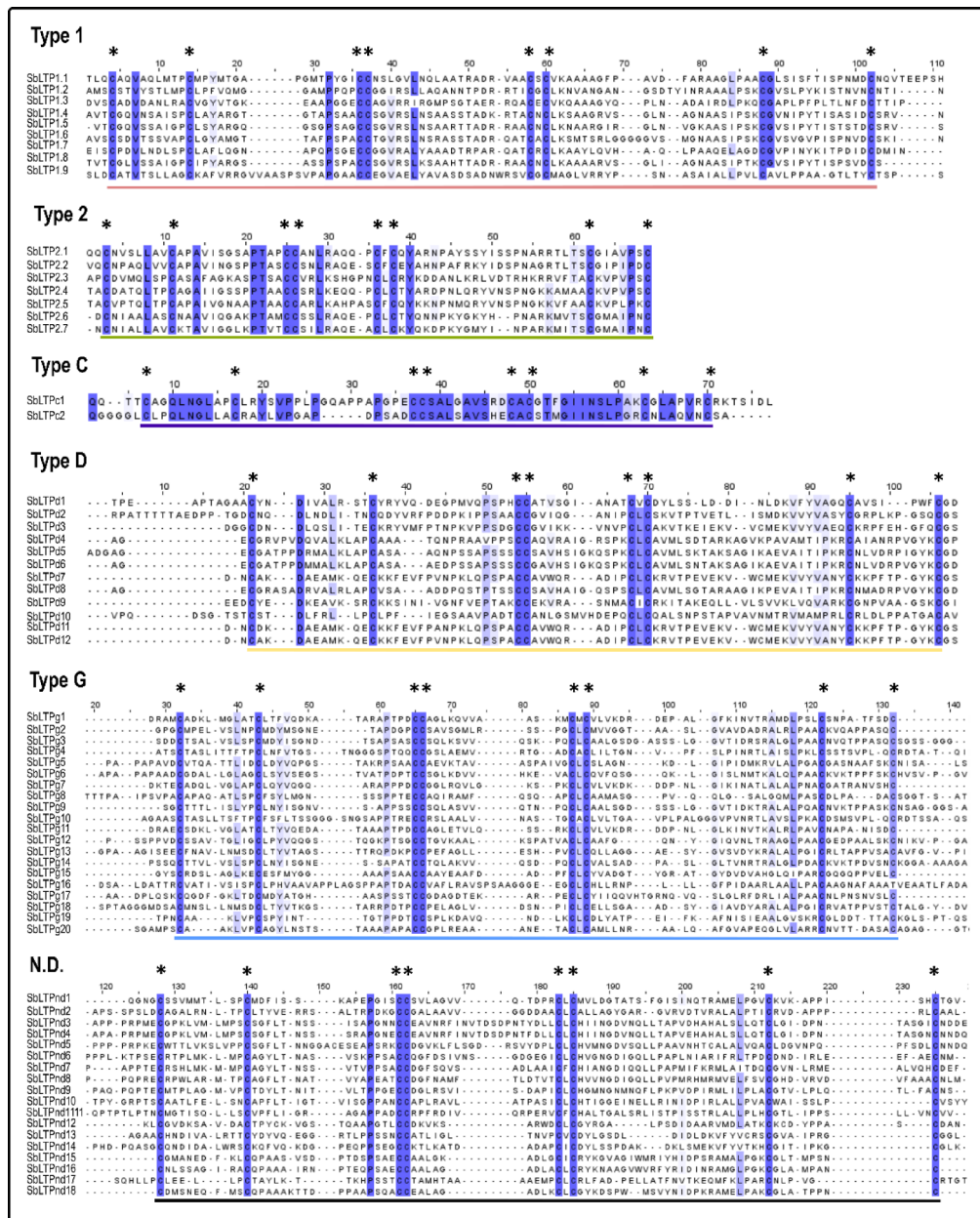
Protein Name	Full protein	Mature peptide (aa)	pI	MW	GPI anchor signal	Intron number	Intron position *	Eight Cysteine Motif (ECM)															
Type 1																							
SbLTP1.1	135	107	5.52	10782.49	No	1	5	C1	9	C2	15	C3	0	C4	19	C5	1	O6	22	C7	13	C8	
SbLTP1.2	124	95	8.91	9900.48	No	1	5	C1	9	C2	14	C3	0	C4	19	C5	1	O6	21	C7	13	C8	
SbLTP1.3	126	93	6.34	9713.10	No	1	5	C1	9	C2	14	C3	0	C4	19	C5	1	O6	22	C7	13	C8	
SbLTP1.4	124	93	9.10	9071.23	No	1	5	C1	9	C2	14	C3	0	C4	19	C5	1	O6	22	C7	13	C8	
SbLTP1.5	120	93	9.30	9142.27	No	0	-	C1	9	C2	14	C3	0	C4	19	C5	1	O6	22	C7	13	C8	
SbLTP1.6	127	96	8.74	9350.65	No	1	5	C1	9	C2	14	C3	0	C4	19	C5	1	O6	25	C7	13	C8	
SbLTP1.7	116	92	4.56	9707.09	No	1	5	C1	9	C2	14	C3	0	C4	19	C5	1	O6	21	C7	13	C8	
SbLTP1.8	114	90	9.10	8786.10	No	1	3	C1	9	C2	14	C3	0	C4	19	C5	1	O6	22	C7	13	C8	
SbLTP1.9	148	116	8.51	11532.32	No	1	5	C1	9	C2	21	C3	0	C4	20	C5	1	O6	21	C7	12	C8	
Type 2																							
SbLTP2.1	99	68	8.75	7053.10	No	0	-	C1	7	C2	13	C3	0	C4	8	C5	1	O6	23	C7	6	C8	
SbLTP2.2	96	68	6.67	7172.18	No	0	-	C1	7	C2	13	C3	0	C4	8	C5	1	O6	23	C7	6	C8	
SbLTP2.3	98	74	9.22	8014.39	No	0	-	C1	7	C2	13	C3	0	C4	9	C5	1	O6	23	C7	6	C8	
SbLTP2.4	98	69	8.72	7143.28	No	0	-	C1	7	C2	13	C3	0	C4	8	C5	1	O6	23	C7	6	C8	
SbLTP2.5	105	71	9.47	7436.83	No	0	-	C1	7	C2	13	C3	0	C4	9	C5	1	O6	23	C7	6	C8	
SbLTP2.6	90	65	8.71	6898.04	No	0	-	C1	7	C2	13	C3	0	C4	8	C5	1	O6	21	C7	6	C8	
SbLTP2.7	92	65	9.03	6999.49	No	0	-	C1	7	C2	13	C3	0	C4	8	C5	1	O6	21	C7	6	C8	
Type C																							
SbLTPc1	117	75	8.52	7583.85	No	1	1	C1	9	C2	19	C3	0	C4	9	C5	1	O6	12	C7	6	C8	
SbLTPc2	103	67	5.38	6621.62	No	1	1	C1	9	C2	14	C3	0	C4	9	C5	1	O6	12	C7	6	C8	
Type D																							
SbLTPd1	113	84	4.08	8944.09	No	1	4	C1	10	C2	16	C3	0	C4	10	C5	1	O6	20	C7	7	C8	
SbLTPd2	124	102	4.75	10745.21	No	1	4	C1	10	C2	17	C3	0	C4	9	C5	1	O6	22	C7	9	C8	
SbLTPd3	112	87	8.60	9714.46	No	1	4	C1	10	C2	17	C3	0	C4	9	C5	1	O6	11	C7	10	C8	
SbLTPd4	119	91	9.65	9348.17	No	1	4	C1	14	C2	14	C3	0	C4	11	C5	1	O6	24	C7	10	C8	
SbLTPd5	118	95	8.86	9609.17	No	1	4	C1	14	C2	14	C3	0	C4	12	C5	1	O6	24	C7	10	C8	
SbLTPd6	118	92	8.19	9284.81	No	1	4	C1	14	C2	14	C3	0	C4	12	C5	1	O6	24	C7	10	C8	
SbLTPd7	108	87	8.74	9866.66	No	1	4	C1	10	C2	17	C3	0	C4	9	C5	1	O6	11	C7	10	C8	
SbLTPd8	112	91	8.21	9239.63	No	1	4	C1	14	C2	14	C3	0	C4	11	C5	1	O6	24	C7	10	C8	
SbLTPd9	120	92	8.99	9896.69	No	1	4	C1	10	C2	16	C3	0	C4	9	C5	1	O6	23	C7	9	C8	
SbLTPd10	199	174	8.21	17752.58	No	1	4	C1	9	C2	14	C3	0	C4	12	C5	1	O6	24	C7	10	C8	
SbLTPd11	108	87	8.58	9882.61	No	1	4	C1	10	C2	17	C3	0	C4	9	C5	1	O6	11	C7	10	C8	
SbLTPd12	103	71	8.40	7757.80	No	0	-	C1	2	C2	8	C3	0	C4	9	C5	1	O6	14	C7	7	C8	
Type G																							
SbLTPg1	196	166	7.65	17199.96	Yes	2	-	C1	9	C2	16	C3	0	C4	12	C5	1	O6	26	C7	8	C8	
SbLTPg2	187	155	4.75	15151.21	Yes	2	-	C1	9	C2	14	C3	0	C4	12	C5	1	O6	25	C7	9	C8	
SbLTPg3	161	133	6.13	12506.98	Yes	1	4	C1	9	C2	15	C3	0	C4	12	C5	1	O6	28	C7	9	C8	
SbLTPg4	199	167	5.57	16886.45	Yes	2	-	C1	10	C2	17	C3	0	C4	12	C5	1	O6	24	C7	8	C8	
SbLTPg5	176	152	8.19	14521.70	Yes	2	-	C1	9	C2	16	C3	0	C4	14	C5	1	O6	23	C7	9	C8	
SbLTPg6	213	180	8.64	17459.99	Yes	2	-	C1	9	C2	16	C3	0	C4	12	C5	1	O6	24	C7	9	C8	
Continued																							

Protein Name	Full protein	Mature peptide (aa)	pI	MW	GPI anchor signal	Intron number	Intron position *	Eight Cysteine Motif (ECM)															
								C1	9	C2	14	C3	0	C4	12	C5	1	C6	26	C7	9	C8	
SbLTPg7	196	169	6.87	16925.32	Yes	2	-	C1	9	C2	14	C3	0	C4	12	C5	1	C6	26	C7	9	C8	
SbLTPg8	217	181	4.32	17669.15	Yes	0	-	C1	9	C2	14	C3	0	C4	12	C5	1	C6	22	C7	6	C8	
SbLTPg9	184	151	8.70	14515.45	Yes	2	-	C1	9	C2	14	C3	0	C4	12	C5	1	C6	26	C7	9	C8	
SbLTPg10	212	183	8.54	17799.26	Yes	1	4	C1	9	C2	16	C3	0	C4	12	C5	1	C6	24	C7	9	C8	
SbLTPg11	211	181	8.47	18159.66	Yes	2	-	C1	9	C2	16	C3	0	C4	12	C5	1	C6	26	C7	8	C8	
SbLTPg12	168	146	8.81	13945.10	Yes	2	-	C1	9	C2	16	C3	0	C4	14	C5	1	C6	22	C7	9	C8	
SbLTPg13	191	164	5.54	16042.46	Yes	2	-	C1	9	C2	16	C3	0	C4	12	C5	1	C6	25	C7	9	C8	
SbLTPg14	181	152	8.19	14685.61	Yes	0	-	C1	9	C2	14	C3	0	C4	12	C5	1	C6	25	C7	9	C8	
SbLTPg15	199	164	3.99	16864.06	Yes	2	-	C1	9	C2	14	C3	0	C4	12	C5	1	C6	26	C7	9	C8	
SbLTPg16	215	188	5.02	18665.62	Yes	2	-	C1	9	C2	21	C3	0	C4	18	C5	1	C6	24	C7	20	C8	
SbLTPg17	181	156	6.29	16142.26	Yes	2	-	C1	9	C2	14	C3	0	C4	12	C5	1	C6	29	C7	9	C8	
SbLTPg18	211	179	5.11	17679.17	Yes	2	-	C1	9	C2	16	C3	0	C4	12	C5	1	C6	25	C7	9	C8	
SbLTPg19	153	125	6.71	12766.55	Yes	2	-	C1	6	C2	14	C3	0	C4	12	C5	1	C6	25	C7	8	C8	
SbLTPg20	179	149	8.52	14179.07	Yes	2	-	C1	6	C2	16	C3	0	C4	12	C5	1	C6	25	C7	8	C8	
ND																							
SbLTPnd1	180	147	4.64	14972.17	No	2	-	C1	9	C2	14	C3	0	C4	12	C5	1	C6	25	C7	9	C8	
SbLTPnd2	197	169	8.45	16585.12	No	1	64	C1	9	C2	16	C3	0	C4	13	C5	1	C6	24	C7	9	C8	
SbLTPnd3	213	183	4.88	19277.18	No	2		C1	10	C2	15	C3	0	C4	20	C5	1	C6	26	C7	11	C8	
SbLTPnd4	210	183	5.22	19332.2	No	1	16	C1	10	C2	15	C3	0	C4	20	C5	1	C6	26	C7	11	C8	
SbLTPnd5	222	192	4.90	20220.40	No	1	19	C1	10	C2	8	C3	0	C4	17	C5	1	C6	18	C7	7	C8	
SbLTPnd6	174	145	4.81	15333.92	No	2		C1	9	C2	15	C3	0	C4	15	C5	1	C6	26	C7	11	C8	
SbLTPnd7	166	138	5.10	14753.43	No	2		C1	9	C2	15	C3	0	C4	13	C5	1	C6	26	C7	12	C8	
SbLTPnd8	194	165	4.89	17065.76	No	2		C1	9	C2	15	C3	0	C4	13	C5	1	C6	26	C7	12	C8	
SbLTPnd9	250	224	4.87	22493.45	No	1	4	C1	9	C2	15	C3	0	C4	12	C5	1	C6	26	C7	11	C8	
SbLTPnd10	173	148	5.56	15390.19	No	1	6	C1	9	C2	16	C3	0	C4	13	C5	1	C6	26	C7	7	C8	
SbLTPnd11	155	133	6.06	13811.18	No	1	4	C1	9	C2	14	C3	0	C4	13	C5	1	C6	26	C7	11	C8	
SbLTPnd12	106	78	7.61	8180.45	No	0		C1	3	C2	12	C3	0	C4	9	C5	1	C6	21	C7	1	C8	
SbLTPnd13	120	91	5.39	9554.01	No	2	227	C1	10	C2	16	C3	0	C4	10	C5	1	C6	17	C7	2	C8	
SbLTPnd14	126	98	6.08	10592.07	No	1	1	C1	10	C2	16	C3	0	C4	11	C5	1	C6	23	C7	7	C8	
SbLTPnd15	104	78	6.70	8170.52	No	0		C1	9	C2	16	C3	0	C4	9	C5	1	C6	26	C7	7	C8	
SbLTPnd16	105	77	8.74	8030.40	No	0		C1	9	C2	16	C3	0	C4	9	C5	1	C6	24	C7	7	C8	
Continued																							

Protein Name	Full protein	Mature peptide (aa)	pI	MW	GPI anchor signal	Intron number	Intron position *	Eight Cysteine Motif (ECM)														
SbLTPnd17	177	151	7.81	16470.09	No	1	28	C1	6	C2	13	C3	0	C4	12	C5	1	C6	25	C7	5	C8
SbLTPnd18	125	76	4.72	8028.27	No	0		C1	9	C2	17	C3	0	C4	9	C5	1	C6	24	C7	7	C8

**Table 1.** Putative LTPs isolated from the genome of *S. Bicolor*. The composition of the 8CM and some physicochemical characteristics of the LTPs are detailed in the table. The intron position corresponds to the number of nucleotides from the codon corresponding to the last cysteine of the 8CM to the intron. The accession number of the locus corresponding to each protein is detailed in supplementary table S2.





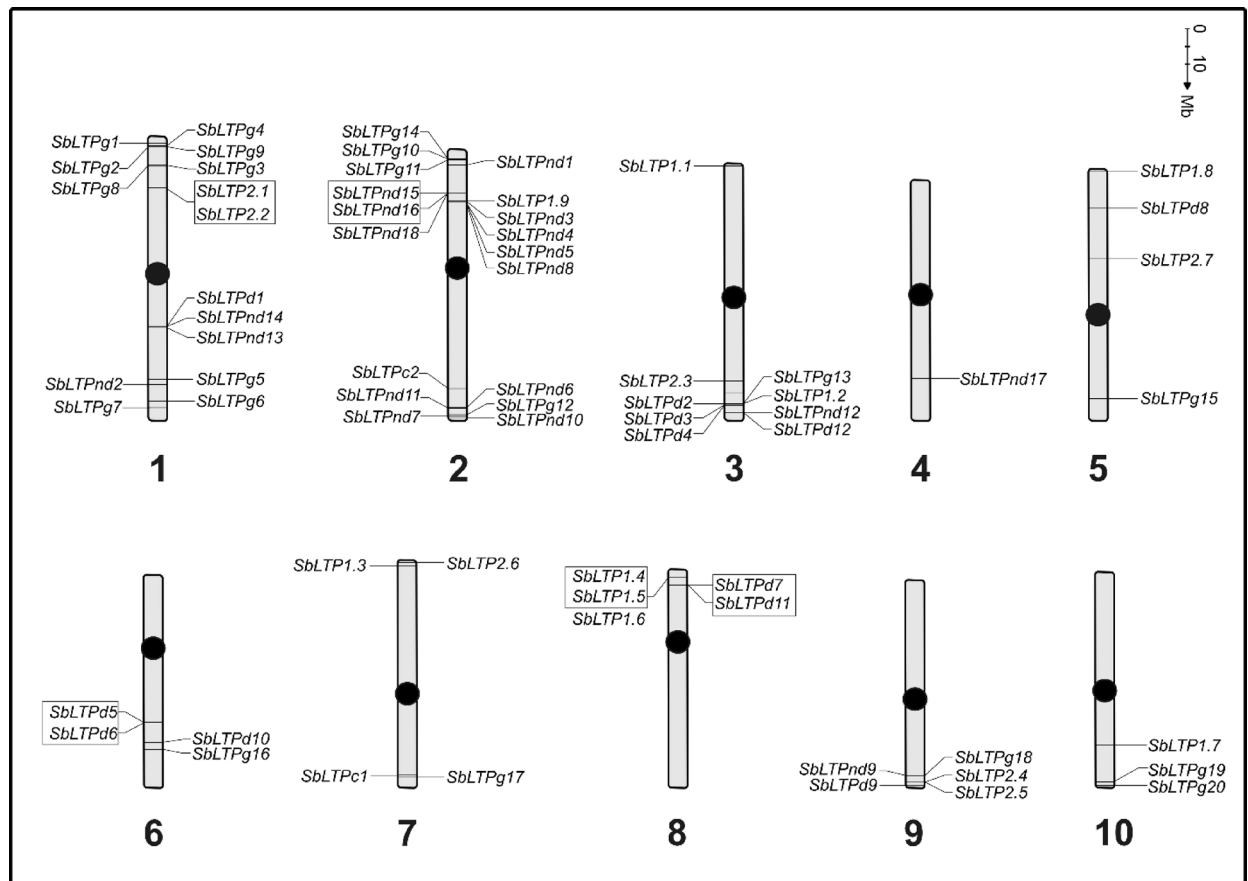
**Fig. 2.** Multiple sequence alignment of the SbLTP 8CM domain sequences. Protein sequences were aligned using MUSCLE and visualized with Jalview. The horizontal line indicates the 8CM domain, and asterisks (\*) mark the cysteine residues within the 8CM domain.

diversification. Notably, 9 ND SbLTPs (SbLTPnd3–SbLTPnd11) clustered with LTPs–G, suggesting these proteins may belong to the G group but could have lost the GPI anchor and undergone subfunctionalization to fulfill new roles distinct from their ancestral functions.

To further characterize the SbLTP proteins, we analyzed their theoretical isoelectric point (pI) and molecular weight (MW). As shown in Table 1, type G and ND SbLTPs have the highest molecular weights, averaging 15 kDa, while types 2 and C have the lowest, averaging 7 kDa. Regarding pI, LTPs–1, LTPs–C, LTPs–D, and LTPs–G show a range of both basic and acidic values, whereas LTPs–2 are predominantly basic (Table 1). Notably, LTPs 2.1/2.2 and ND15/ND16, which originated from tandem duplications (Fig. 3), exhibit significantly different pI values, one being basic and the other acidic. This variation suggests functional diversification resulting from these duplication events.

### In silico expression analysis and selection of candidate SbLTP genes for promoter characterization

Plant LTPs exhibit complex tissue-specific and developmental expression patterns<sup>11</sup>. To explore the expression profiles of all 68 predicted SbLTPs, we analyzed RNA-seq datasets from various tissues. Expression patterns



**Fig. 3.** Chromosomal localization of the putative SbLTP genes. Chromosomes are depicted by cylinders with the chromosome numbers indicated at the bottom of each cylinder. Gene names are listed along the sides of each chromosome correspond to the approximate locations of each LTP gene. The tandem-duplicated gene clusters are marked in boxes. Centromere positions are indicated with black circles to help distinguish the relative position of genes in chromosomal arms.

varied significantly among the different groups. Notably, only two SbLTGs (*SbLTP1.9* and *SbLTP2.4*) showed no detectable expression, which may indicate they function as pseudogenes or that their expression is limited to specific tissues or conditions not covered by the RNA-seq datasets (Fig. 4).

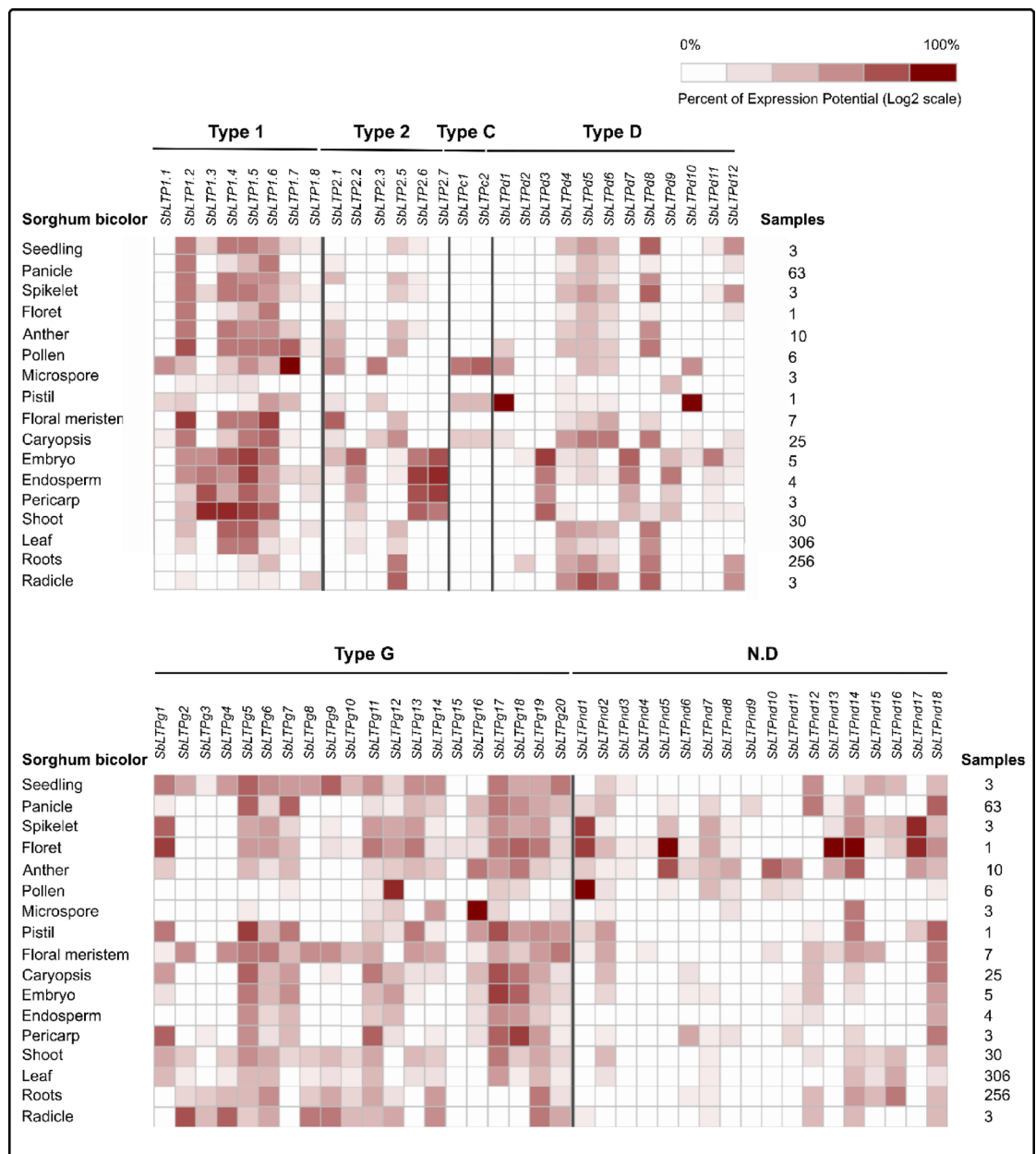
*SbLTP-1* genes are predominantly characterized by ubiquitous expression, with high levels in reproductive tissues and low or negligible levels in roots. In contrast, *SbLTP-2* and *SbLTP-D* genes exhibit low to intermediate expression levels and a more tissue-specific expression pattern. For example, *SbLTP2.2*, *SbLTP2.6*, and *SbLTP2.7*, *SbLTPd3*, *SbLTPd7* and *SbLTPd9* are exclusively expressed in seeds. *SbLTP-C* genes are specifically expressed in anthers and microspores, indicating a male-specific role in reproduction. Within the *SbLTP-G* group, there are both ubiquitous and tissue-specific expression profiles. In this group ubiquitous genes generally have strong to moderate expressions in roots and seedlings. The ND type LTGs mostly exhibit low, tissue-specific expression, except for *SbLTPnd-2*, *SbLTPnd-14*, and *SbLTPnd-18*, which show different patterns.

To identify promoters with high expression in target tissues, we focused on SbLTP genes with preferential and high expression in female reproductive tissues, particularly in pistils. To minimize the potential environmental impact of AMP expression, genes with high expression in roots or pollen were excluded. Based on these criteria, we identified eight candidate genes (*SbLTP1.2*, *SbLTP1.4*, *SbLTP1.5*, *SbLTP2.1*, *SbLTPg1*, *SbLTPg7*, *SbLTPg13*, and *SbLTPg16*) that met the requirements. Type 1 LTGs are known to respond to both biotic and abiotic stress<sup>24–28</sup> which makes them ideal candidates for promoters aimed at expressing biological control proteins. Given this, we chose *SbLTP1.4* and *SbLTP1.5* for further isolation and characterization of their promoters.

### Identification of conserved transcription factor binding sites in the LTP promoters of *S. bicolor* and related grass species

To identify conserved transcription factor (TF) binding sites within the promoters of selected SbLTP genes, we performed an in silico analysis using the MEME and TOMTOM software tools<sup>29,30</sup>. We examined the promoters *SbLTP1.4* and *SbLTP1.5*, as well as their orthologous genes in related grass species (*O. sativa*, *S. italica*, *Z. mays*, and *P. hallii*) to identify putative TFs involved in stress responses. MEME identified four *de novo* regulatory motifs (Fig. 5). The localization of consensus sequences for each identified TF on the promoter sequences is shown in Fig. S5.










**Fig. 4.** Expression profile of *SbLTP* genes across various anatomical structures. The data were obtained from the Genevestigator database and are represented using a color scale indicating expression levels according to the “percent of expression potential” (PEP) metric, shown on a log<sub>2</sub> scale. Genevestigator expression data for each gene can be retrieved using the corresponding locus ID listed in Table S2.

Motif 1 matches a cis-regulatory element recognized by AtMYB31, an R2R3-MYB transcription factor (TF) involved in regulating wax biosynthesis in reproductive tissues and playing a role in seed development in *A. thaliana*<sup>31</sup>. Additionally, MYB TFs, including AtMYB31, have been shown to modulate plant defense against fungal pathogens<sup>32,33</sup>. Furthermore, members of the MYB family are crucial for plant responses to abiotic stresses, enhancing salt and drought tolerance in species such as *Triticum aestivum*<sup>34</sup> and *A. thaliana*<sup>35</sup>.

Motif 2 corresponds to a cis-element recognized by AGL55 (AGAMOUS-like 55), a TF from the MADS-box family. AGL55 plays a critical role in regulating stamen and carpel identity and in determining floral meristem identity<sup>36</sup>.

Motif 3 corresponds to the binding regulatory elements for two transcription factors: DREB2C and ERF015. DREB (Dehydration Responsive Element Binding) TFs, part of the AP2/ERF family, play a significant role in plant responses to various stressors such as drought, high salinity, cold, and heat. These TFs enhance plant tolerance by binding to DRE/CRT cis-elements in the promoter regions of stress-responsive genes<sup>37</sup>. Specifically, DREB2C recognizes and binds to the consensus sequence 5'-[AG]CCGAC-3', mediating responses related to high salinity and abscisic acid (ABA)<sup>38</sup>. Additionally, DREB2C is upregulated during heat stress, indicating

	MEME			Match in JASPAR				
	De novo motif	E-value	Oc	Name	Sequence	Alignment	p-value	Function
1		4.4e-30	12/13	MA1738.1 (ATMYB31)			1.56e-07	Member of the R2R3 factor gene family; wax regulator associated with reproductive development. GO: Involved in response to auxin.
2		7.1e-12	13/13	MA1202.1 (AGL55)			3.43e-04	Plays a central role in regulating stamen and carpel identity and participates in meristem determinacy during flower development.
3		1.5e-06	13/13	MA0986.1 (DREB2C)			1.65e-03	Binding to the C-repeat/DRE element mediates high salinity and ABA inducible transcription. GO: Heat acclimation.
				MA1265.2 (ERF015)			2.16e-03	Binds to the GCC-box pathogenesis-related promoter element. May be involved in the regulation of gene expression by stress factors and by components of stress signal transduction pathways
4		6.5e-06	13/13	MA0564.1 (ABI3)			4.90e-04	Participates in abscisic acid-regulated gene expression during seed development. Regulates the transcription of SGR1 and SGR2 that are involved in leaf and embryo degreening. GO: Response to ABA and auxin, embryo development, plastid organization and mitochondria-nucleus signaling pathway.
				MA0581.1 (LEC2)			5.49e-04	Plays a central role in embryo development. Required for the maintenance of suspensor morphology, specification of cotyledon identity, progression through the maturation phase and suppression of premature germination. Ectopic expression promotes somatic embryogenesis. GO: Response to auxin, seed maturation and seed oilbody biogenesis.
				MA0565.1 (FUS3)			1.52e-03	Involved in gene regulation during late embryogenesis. Positively regulates the abundance of the ABI3 protein in the seed. Regulates developmental phase transitions and lateral organ development, and acts as a positive regulator of ABA signaling during germination. GO: Response to auxin, embryo development and negative regulation of gibberellin biosynthetic process.

**Fig. 5.** Conserved motifs and transcription factor binding sites identified in the promoter sequences of *LTP1.4* and *LTP1.5* and their orthologs from grass species. The Logo column displays the conserved sequences (*de novo* motifs) detected by the MEME tool, along with the occurrence (Oc) within the input sequences. The Name and Sequence columns provide the binding sequences of the TFs identified in the JASPAR Plants database. The figure also includes the significance of MEME motifs (E-value) and TFs (p-value), along with their associated biological functions as found in the UniProt database. GO: Gene Ontology.

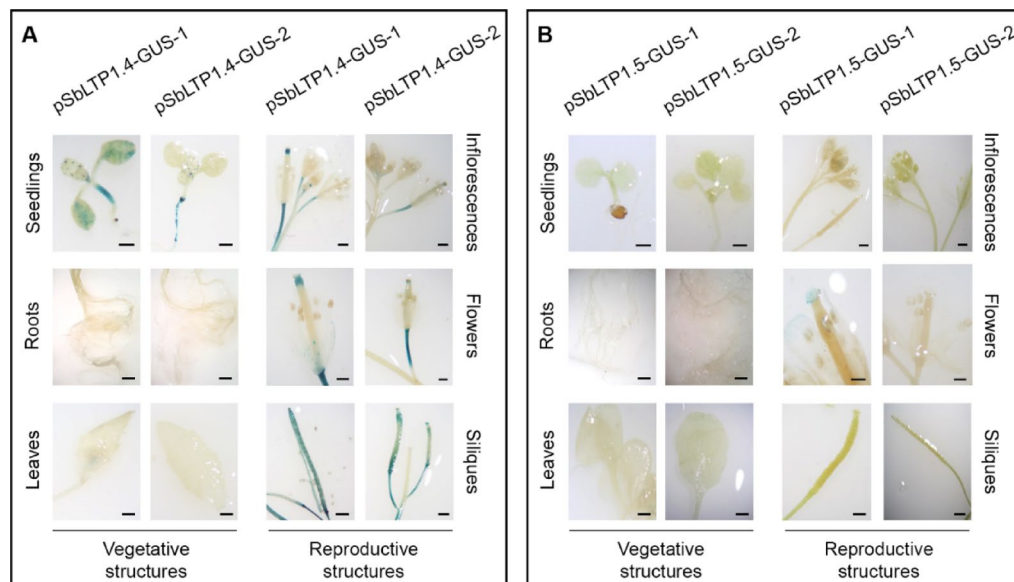
its involvement in heat acclimation in *A. thaliana*<sup>39</sup>. Conversely, ERF family genes exhibit varied expression patterns during plant growth and development, as well as in response to stress-related stimuli such as ethylene, jasmonic acid, and salicylic acid, or abiotic stress conditions<sup>40,41</sup>. ERF015 positively regulates responses to ABA and may contribute to plant tolerance to salinity and drought<sup>42</sup>.

Motif 4 corresponds to binding elements for ABI3, FUS3, and LEC2 transcription factors from the B3 family. These TFs form a regulatory network involved in embryo development, ABA signaling, and stress responses<sup>43</sup>. ABI3 is crucial for embryo development, ABA signaling, and tolerance to freezing, desiccation, and dehydration<sup>44–48</sup>. Interestingly, ABI3 from the desert moss *Syntrichia caninervis* was shown to enhance salinity and osmotic stress tolerance in *A. thaliana* transgenic plants<sup>49</sup>. FUS3 also plays a role in stress responses, including inhibition of seed germination at high temperatures and drought tolerance<sup>37,50</sup>.

### Spatio-temporal expression patterns of pSbLTP-GUS constructs in *A. thaliana* transgenic plants

Two independent homozygous lines for each construct (pSbLTP1.4-GUS-1, pSbLTP1.4-GUS-2, pSbLTP1.5-GUS-1 and pSbLTP1.5-GUS-2) were selected for spatial and temporal GUS expression analysis.

In six-day-old seedlings of the pSbLTP1.4-GUS-1 line, notable GUS expression was observed in leaf primordium trichomes, cotyledons, and hypocotyls. In 55-day-old pSbLTP1.4-GUS-1 plants, GUS expression was detected in the floral peduncle, receptacle, style, and stigma, but not in male reproductive structures. Expression was also noted in the silique valves (but not in seeds) and weakly in rosette leaves. The pSbLTP1.4-GUS-2 line showed a similar expression pattern, although with lower reporter gene intensity (Fig. 6A, Fig. S6). An evaluation throughout plant development confirmed that the expression of the pSbLTP1.4-GUS construct is restricted to the aerial parts of the plant (Fig. S7).



**Fig. 6.** Anatomical-specific expression profiling of the pSbLTP1.4-GUS (A) and pSbLTP1.5-GUS (B) constructs in transgenic *A. thaliana* plants. The expression patterns of the GUS reporter gene in vegetative and reproductive structures are shown for two homozygous lines of each construct. Seedling 0.2 mm. Flowers 0.5 mm. Inflorescences, siliques, leaves and roots 1 mm.

For the pSbLTP1.5-GUS construct, both transgenic lines generally exhibited very low or no detectable GUS expression in seedlings and adult plants (Fig. 6B, Fig. S7). Only the pSbLTP1.5-GUS-1 line showed specific expression of the reporter gene in the stigma (Fig. 6B). The wild-type plants used as a negative control in the experiment did not show any evident GUS signal (Fig. S8).

### Response of pSbLTP-GUS constructs to biotic and abiotic stresses in *A. thaliana* transgenic plants

To evaluate the response of the pSbLTP1.4-GUS and pSbLTP1.5-GUS constructs to various biotic and abiotic stress conditions, we subjected transgenic *A. thaliana* plants to a range of stressors, including *Pseudomonas syringae* infection, osmotic stress induced by mannitol, and high salinity stress.

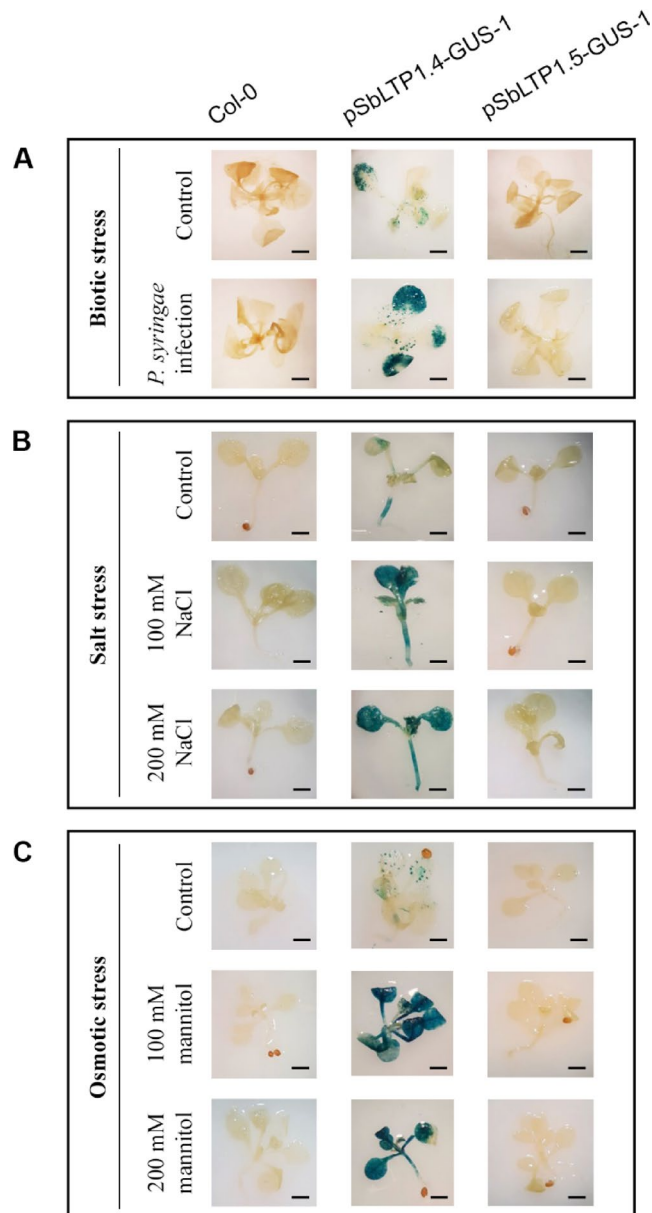
During the seedling stage, plants infected with *P. syringae* to simulate pathogen stress exhibited distinct responses. pSbLTP1.4-GUS seedlings displayed a marked increase in GUS expression, with intense reporter gene activity across the entire surface of cotyledons and leaves (Fig. 7A), indicating strong activation of the *SbLTP1.4* promoter under biotic stress. In contrast, pSbLTP1.5-GUS plants and non-transgenic controls showed only weak GUS staining, confined to the edges of cotyledons and trichomes of young leaves, regardless of infection presence (Fig. 7A).

Abiotic stress treatments further highlighted these differences. Saline conditions significantly increased GUS staining in pSbLTP1.4-GUS-1 transgenic plants. While control seedlings showed reporter gene activity limited to specific areas, such as cotyledons, leaf trichomes, and hypocotyls, exposure to 100 and 200 mM NaCl resulted in a notable increase in GUS expression throughout the entire seedling (Fig. 7B). A similar response was observed in seedlings treated with 100 and 200 mM mannitol (Fig. 7C). Conversely, transgenic seedlings carrying the pSbLTP1.5-GUS construct showed no reporter gene expression under any of the abiotic stress conditions tested (Fig. 7B,C).

To assess the stress response of the pSbLTP1.4 and pSbLTP1.5 promoters during plant adulthood, we conducted biotic and salt stress experiments on transgenic *A. thaliana* lines at the mature reproductive stage. Inoculation with *P. syringae* maintained the same pattern but markedly increased the intensity of GUS staining in pSbLTP1.4-GUS-1 plants relative to control plants. GUS expression was detected in the floral peduncle, receptacle, style, stigma, cauline leaves, and silique valves, but not in rosette leaf laminae (Fig. 8A) or roots (Fig. S7). At this stage, both promoters showed expression in female reproductive tissues. However, pSbLTP1.5-GUS-1 consistently exhibited very weak expression at the stigma and no detectable expression in other tissues. Additionally, saline treatment with 100 and 200 mM NaCl produced results like those observed under biotic stress for pSbLTP1.4-GUS-1 plants, with very strong blue staining in reproductive tissues, including siliques, and no significant differences between the two salt concentrations tested (Fig. 8B). In contrast, pSbLTP1.5-GUS-1 plants did not show any reporter gene signal in response to the stress conditions tested (Fig. 8).

### Discussion

*Claviceps* species cause ergot disease in cereals and forage grasses, forming sclerotia in place of grains and leading to considerable economic losses. This contamination affects flour quality due to ergot alkaloids, which are also harmful to mammals<sup>1,3,51</sup>. Due to the absence of known resistance genes, transgenic strategies targeting the



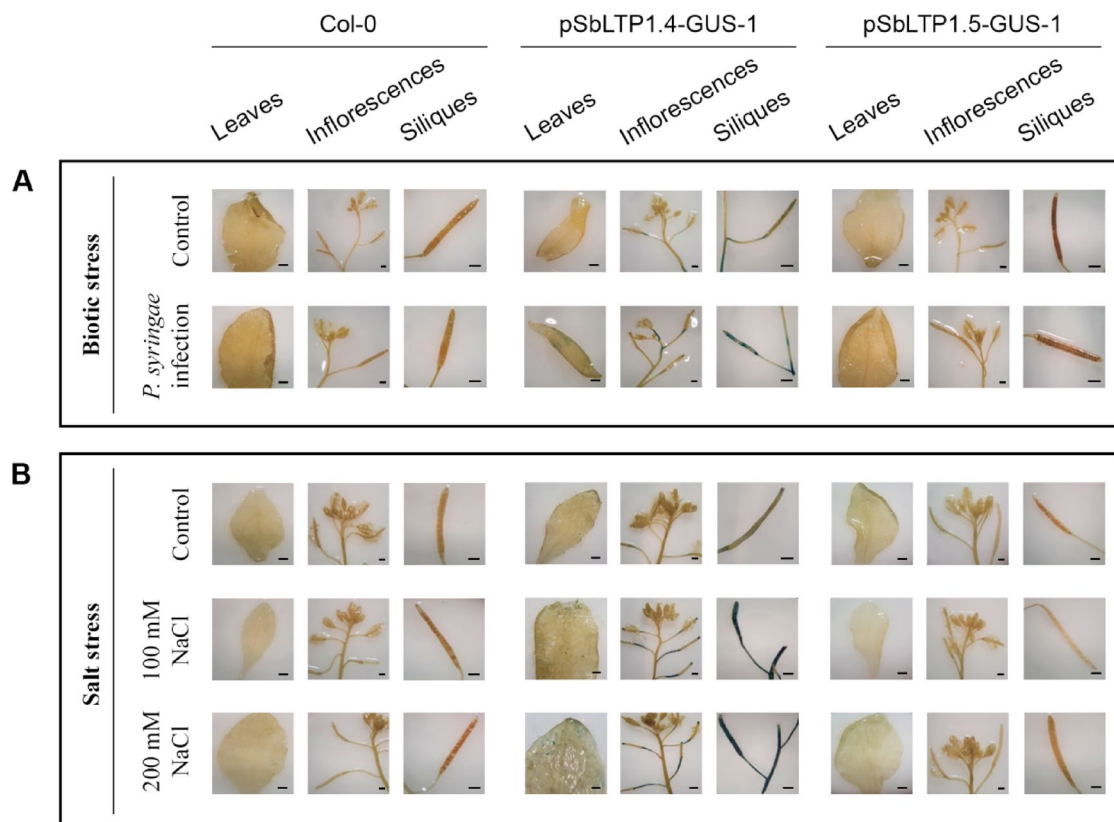
**Fig. 7.** Response of pSbLTP1.4-GUS and pSbLTP1.5-GUS constructs to biotic and abiotic stress at the seedling stage. Wild-type (Col-0) and transgenic *A. thaliana* seedlings (pSbLTP1.4-GUS and pSbLTP1.5-GUS) were inoculated with *P. syringae* (A) and exposed to salt stress (B) and osmotic stress (C). GUS expression was assessed 3 days post-inoculation for *P. syringae* and 24 h post-treatment for both salt and osmotic stress conditions. Seedlings 0.2 mm.

site of infection are promising. This study contributes to such efforts by identifying reproductive tissue-specific promoters from the LTP family in *S. bicolor*.

We identified 68 LTPs in the *S. bicolor* genome and classified them into five subfamilies using Edstam's classification system, which evaluates structural and biochemical features to provide a more robust framework than traditional approaches<sup>52</sup>. Our comprehensive analysis revealed LTPs that had not been previously identified in sorghum<sup>20</sup>.

Phylogenetic and structural analyses revealed that *S. bicolor* LTPs, along with those from *A. thaliana* and *O. sativa*, are distributed across all five subfamilies. The proportion of *S. bicolor* LTPs varied across subfamilies, with members of the same subgroup exhibiting conserved exon-intron structures. The presence of distinct clades for types LTPs type 1, 2, and C with over 95% bootstrap support suggests that these groups have maintained a strong evolutionary identity, likely due to essential functions preserved from a common ancestor. In contrast, the greater diversification observed in types G and D, which formed multiple clades, may reflect a higher degree of evolutionary flexibility, allowing these types to adapt to different functional roles. The clustering of the undetermined *SbLTPs* (ND) with the LTP-G group, together with the loss of the GPI anchor, suggests





**Fig. 8.** Response of pSbLTP1.4-GUS and pSbLTP1.5-GUS constructs to biotic and abiotic stress at the adult plant stage. Wild type (Col-0) and transgenic *A. thaliana* plants carrying the pSbLTP1.4-GUS and pSbLTP1.5-GUS constructs were subjected to biotic and abiotic stress conditions. Plants were inoculated with *P. syringae* (A) and exposed to salt stress (B). GUS expression was evaluated 3 days post-inoculation for bacterial infection and 48 hs post-treatment for both salt and osmotic stress. Leaves, inflorescences, siliques 1 mm.

that these genes may have undergone subfunctionalization or neofunctionalization, potentially acquiring specialized or novel roles distinct from those of their ancestral counterparts. Research on lipid transfer proteins (LTPs) shows that they are often organized in clusters, with many arising from tandem duplications<sup>53–56</sup>. We identified five tandem duplications, such as *SbLTP1.4/SbLTP1.5*, *SbLTP2.1/SbLTP2.2*, *SbLTPd5/SbLTPd6*, and *SbLTPd7/SbLTPd11* and *SbLTPnd15/SbLTPnd16*. While some pairs exhibited similar expression profiles, others did not; for example, *SbLTP2.1* is flower-specific, whereas *SbLTP2.2* is seed-specific. This pattern of conservation and diversification underscores the importance of gene duplication and subsequent adaptation in the evolution of LTPs, with different types evolving to fulfill specific roles in response to environmental pressures and unique functional requirements.

Two LTPs, *SbLTP1.4* and *SbLTP1.5*, were selected for promoter analysis based on their *in silico* expression patterns. Spatio-temporal evaluation revealed that both promoters drive gene expression exclusively in the aerial structures of the plant. This is likely related to cutin deposition associated with the lipid transport function characteristic of these proteins, which explains the absence of expression in roots<sup>57</sup>. In transgenic *A. thaliana* lines carrying the pSbLTP1.4-GUS construct, GUS staining was observed in vegetative structures such as the hypocotyl, cotyledons, and trichomes of leaf primordia. In reproductive structures, GUS expression was detected in peduncles, floral receptacles, styles, and stigmas, with no expression in male floral organs. These results align with the *in silico* expression profile of *SbLTP1.4* reported for sorghum. In contrast, the *SbLTP1.5* promoter exhibited very low activity, restricted solely to stigmas, which unexpectedly diverges from the *in silico* expression profile reported by Genevestigator. However, other transcriptomic studies in sorghum corroborate our findings, showing that *SbLTP1.5* displays significantly lower expression levels than *SbLTP1.4* in inflorescences<sup>9</sup>. This discrepancy highlights the limitations of transcriptomic methods like RT-PCR in distinguishing highly homologous genes. The high sequence similarity between these paralogs could bias detection toward the more abundant transcript. Therefore, heterologous promoter testing remains a valuable approach for assessing tissue-specific expression and resolving such ambiguities.

Stress assays revealed that pSbLTP1.4 is induced by *Pseudomonas syringae* infection, salt, and osmotic stress. This is consistent with the presence of binding sites for stress-related transcription factors such as AtMYB31, DREB2C, ABI3, and FUS3 in its promoter region. These TFs are known regulators of biotic and abiotic stress responses and have been shown to activate LTP genes in rice and maize<sup>32,33,58,59</sup>. Conversely, pSbLTP1.5 showed no detectable response to any stress treatment. Despite sharing similar predicted TF binding sites with

pSbLTP1.4, the absence of stress responsiveness suggests the involvement of additional regulatory elements not captured in our analysis. Interestingly, the expression profiles of the orthologous genes in *Setaria italica* mirror those observed in *S. bicolor*,<sup>60</sup> reinforcing the functional divergence observed between these promoters.

The contrasting patterns of SbLTP1.4 and SbLTP1.5 expression reflect an evolutionary strategy of functional specialization. SbLTP1.4 combines responsiveness to multiple stresses with broad reproductive and vascular tissue expression, possibly contributing to both defense and reproductive development. SbLTP1.5, on the other hand, shows low, stigma-specific expression, suggesting a specialized role in female reproductive biology, potentially in pollen interaction. The complementary expression patterns of these two paralogs highlight an evolutionary strategy to balance tissue-specific roles with environmental responsiveness, which could be exploited in biotechnological applications aimed at enhancing disease resistance specifically in reproductive tissues without compromising overall plant fitness.

In this context, tissue-specific promoters offer a powerful strategy for targeted disease control. While some studies have shown that constitutive AMP expression does not significantly affect the rhizosphere or mammalian microbiota<sup>61,62</sup> restricting expression to infection sites remains a safer strategy to minimize ecological and physiological risks. Both pSbLTP1.4 and pSbLTP1.5 exclude root expression, preserving the soil microbiome, and effectively target reproductive tissues where *Claviceps* initiates infection. These features make them promising tools for engineering resistance in cereals and forage grasses while minimizing off-target effects.

## Materials and methods

### In silico identification and classification of putative *S. bicolor* LTPs

HMM profiles PF14368 (probable lipid transfer; LTP\_2) and PF00234 (Protease inhibitor/seed-storage/LTP family; Tryp\_alpha\_amyl) were used to search against the *S. bicolor* genome (*Sorghum bicolor* v3.1.1) from the Phytozome database (<https://phytozome-next.jgi.doe.gov/>) using the HMMER 3.1 software (<http://hmmerr.org/>)<sup>66</sup>. Keyword searches were conducted on the UniProt website (<https://www.uniprot.org/>) using the queries “LTP sorghum bicolor” and “lipid transfer protein sorghum bicolor”. Additionally, a BLASTp search was performed against the *S. bicolor* genome in the NCBI database using *Zea mays* and *Oryza sativa* LTPs as queries<sup>20</sup>. All results were merged, eliminating duplicate entries and incomplete sequences. Since LTPs are secreted proteins, only those with a signal peptide were retained, and TargetP-2.0 was used to detect N-terminal signal sequences, removing proteins without them<sup>67</sup>. Sequences not directly related to LTPs, such as alpha-amylase/trypsin inhibitors, glycine-rich, proline-rich proteins, and hybrids, were excluded. The GPI Plant Prediction Server<sup>68</sup> was used to detect GPI (glycosylphosphatidylinositol) anchor recognition sites and predict potential omega sites for LTP proteins of subgroup G. As a final criterion, the presence of the 8CM was manually checked, and proteins lacking the essential cysteine residues were removed. The procedural scheme for isolating putative LTPs from the *S. bicolor* genome is summarized in Fig. 1.

### LTP classification and multiple sequence alignment

Edstam's classification scheme was used to group *S. bicolor* LTPs, which are based on sequence identity, spacing between the Cys residues, intron position in the 8CM, and the presence of (GPI) anchors as a post-translational modification<sup>8</sup>. The number and position of exons and introns were determined by comparing the coding sequences (CDSs) with their corresponding genomic DNA sequences obtained from NCBI (<https://www.ncbi.nlm.nih.gov/>). Theoretical molecular weight and isoelectric point were determined using ExPASy Compute pI/Mw tool ([https://web.expasy.org/compute\\_pi/](https://web.expasy.org/compute_pi/))<sup>69</sup>. A multiple sequence alignment of *S. bicolor* LTPs was performed using the T-coffee program with the Jalview web service (<https://www.jalview.org/>)<sup>70</sup>.

### Phylogenetic construction

The LTP amino acid sequences of *A. thaliana* and *O. sativa* were obtained from Duo et al.<sup>11</sup>. Multiple alignments of the mature proteins were carried out and the phylogenetic tree was built using IQ-TREE software<sup>71</sup> with the neighbour-joining (NJ) method and 1000 bootstrap replications. The results were then imported into the iTOL online service (<https://itol.embl.de/>) for visualization<sup>72</sup>.

### Chromosomal mapping and gene duplication

Genes were mapped on chromosomes by identifying their chromosomal position using the NCBI-Genome Data Viewer (<https://www.ncbi.nlm.nih.gov/genome/gdvr/>). Gene duplication was defined according to the following criteria: (1) the alignment length covered > 80% of the longer gene; (2) the aligned region had an identity > 80%; (3) only one duplication event was counted for tightly linked genes<sup>73</sup>. All the relevant genes identified in the *S. bicolor* genome were aligned using T-coffee<sup>74</sup> and identity percentages were calculated using the Sequence Manipulation Suite online software ([https://www.bioinformatics.org/sms2/ident\\_sim.html](https://www.bioinformatics.org/sms2/ident_sim.html))<sup>75</sup>.

### In silico expression profiling

The Genevestigator database<sup>76</sup> was used to perform expression analysis for the identified *S. bicolor* LTPs genes. RNA-seq data was used to develop a heat map of expression profiling in different anatomical parts using hierarchical clustering tool. Expression patterns were presented as “percent of expression potential” (PEP = average expression of a gene across all the samples in a particular tissue / maximum expression value across samples) and the results were visualized as a heat map using logarithm (log2) scale.

### Promoter analysis

Promoter sequences (1 kb upstream of the transcription start site) of the selected *S. bicolor* LTPs and their homologs in *O. sativa*, *Setaria italica*, *Z. mays*, and *Panicum hallii* were retrieved from NCBI GenBank (<https://www.ncbi.nlm.nih.gov/>). The MEME *de novo* motif detection tool (<http://meme-suite.org>)<sup>30</sup> was utilized to identify



novel sequence motifs within the promoter region of LTPs. Motif length (minimum of 6 and maximum of 15 nucleotides) and distribution type (zero or one occurrence per sequence - zoops) were specified. After obtaining the results, MEME motifs containing repetitive sequences were excluded, and the remaining motifs were analyzed using the TOMTOM website (<https://meme-suite.org/meme/tools/tomtom>)<sup>29</sup> to identify significant matches with known motifs in Jaspar Core Plants 2022<sup>77</sup>. Motifs that did not match known transcription factor binding sequences, or those that did but with low conservation, were discarded. Since the MEME zoops option enables the discovery of conserved motifs present at most once per sequence, we used the Jaspar 2022 database (<https://jaspar2022.genereg.net/>) and input the promoter sequences to identify additional sites corresponding to the transcription factors found. Results were obtained using the default 80% relative score threshold, and only those with a score greater than or equal to 0.85 were selected.

### Construction of SbLTP promoter-GUS fusions

Promoter sequences of the *SbLTP1.4* (LOC8067182) and *SbLTP1.5* (LOC8067183) genes were amplified from *S. bicolor* genomic DNA by PCR using specific primers (Table S1) and the Platinum™ Pfx DNA Polymerase (Invitrogen, Cat. No. 11708039). The obtained fragments (982 bp for the *SbLTP1.4* promoter and 998 bp for the *SbLTP1.5* promoter) were cloned into the pJET1.2 vector using the CloneJET PCR Cloning Kit (Thermo Fisher Scientific, Cat. No. K1231) following the manufacturer's instructions. The promoter sequences were then subcloned into the pKGWFS7 binary vector by Gateway technology using specific primers (Table S1). pKGWFS7 vector harbors the GUS reporter gene (coding for the enzyme beta-glucuronidase) downstream of the Gateway recombination site, allowing functional evaluation of the promoter sequences. The generated constructs (pSbLTP1.4-GUS and pSbLTP1.5-GUS) were confirmed by restriction enzyme analysis and DNA sequencing (Fig. S1 and S2).

### Transformation of *A. thaliana* and selection of transgenic plants

*Arabidopsis thaliana* Col-0 ecotype seeds were obtained from the Arabidopsis Biological Resource Center (ABRC). Transgenic lines were generated for transient assays to characterize the activity of the selected promoters. pSbLTP1.4-GUS and pSbLTP1.5-GUS constructs were separately introduced into *Agrobacterium tumefaciens* strain GV3101 using the MicroPulser electroporator (Bio-Rad, #1652100). The transformed bacteria were then used for the stable transformation of *A. thaliana* Columbia-0 (Col-0) plants by the floral dip method (Fig. S1 and S2). Transgenic lines were selected on MS medium (1/2 MS, 0.7% agar, pH 5.8) supplemented with kanamycin (50 mg/L), and the presence of the constructs was verified by PCR using specific primers that amplify an internal region of the promoters (Fig. S3 and Table S1). After two rounds of self-fertilization, homozygous lines (T2) were identified based on segregation analysis (Fig. S3). GUS expression assays were performed on *A. thaliana* plants from the T3 generation.

### Plant growth conditions

For adult plant experiments, wild-type and transgenic *A. thaliana* seeds were sown in pots containing a premix of GrowMix® Multipro substrate (TerraFertil). The pots were placed in a controlled growth chamber with a 16 h light / 8 h dark cycle at 23 °C, a light intensity of 150  $\mu\text{mol m}^{-2} \text{s}^{-1}$ , and 60% relative humidity. Plants were watered three times per week with Hakaphos Red fertilizer solution (Compo Expert), prepared and applied according to the manufacturer's guidelines. Pots were monitored to ensure consistent moisture levels throughout the growth period. For seedling assays, *A. thaliana* seeds were surface sterilized with chlorine gas (Cl<sub>2</sub>) for 2 h. After venting chlorine vapors, seeds were sown on 90 × 15 mm Petri dishes (8–10 seeds per plate) containing 1/2 MS medium (Sigma-Aldrich) with 0.7% agar, adjusted to pH 5.8. Plants were grown in growth chambers under a 16 h light / 8 h dark cycle at 23 °C, with a light intensity of 150  $\mu\text{mol m}^{-2} \text{s}^{-1}$ .

### Biotic stress treatments

Biotic stress treatment was performed by infecting *A. thaliana* seedlings with *Pseudomonas syringae* pv. tomato DC3000. For this purpose, 10 ml of KB medium supplemented with rifampicin (50  $\mu\text{g/ml}$ ) was inoculated with *P. syringae*, and then incubated under shaking at 28 °C overnight. The culture was diluted in sterile water containing 0.025% Silwet L77, and then dispersed on 14-day-old wild-type and transgenic *A. thaliana* plants. After three minutes, the excess culture was removed, and the plates were transferred to the growth chamber. A sterile water solution containing 0.025% Silwet L77 was used as a negative inoculation control. In each experiment, three plates were used for each line evaluated (Col-0, pSbLTP1.4-GUS-1, pSbLTP1.5-GUS-1). At 3 days post-inoculation (DPI), three plants from each plate were sampled, and GUS histochemical staining was performed. The experiments were repeated three times.

*P. syringae* inoculations were also performed on adult plants (55 days-old) using the method described by Moriconi et al.<sup>77</sup>. Shoots were dipped in a bacterial solution (OD<sub>600</sub>=0.7) containing 10 mM MgCl<sub>2</sub> and 0.2% Silwet L77 for 30 s. A sterile water solution containing 10 mM MgCl<sub>2</sub> and 0.2% Silwet L77 was used as negative control. Three plants of each line evaluated (Col-0, pSbLTP1.4-GUS-1, pSbLTP1.5-GUS-1) were inoculated. At 3 DPI, leaf, inflorescence, and silique samples were taken from each plant, and GUS histochemical staining was performed. The experiments were repeated three times.

### Abiotic stress treatments

For osmotic and salt stress assays 10-day-old seedlings grown under normal conditions were transferred to Petri dishes containing MS medium (1/2 MS, 0.7% agar, pH 5.8) supplemented with 0, 100 or 200 mM NaCl and 0, 100 or 200 mM mannitol, respectively. In each experiment, three plates (8 seedlings per plate) were used for each line evaluated (Col-0, pSbLTP1.4-GUS-1, pSbLTP1.4-GUS-2, pSbLTP1.5-GUS-1). After 24 h, three plants

were taken from each plate and GUS histochemical staining was performed. The experiments were repeated three times.

Salt stress treatment on adult plants (55 days old) was performed by irrigation with a solution of 0, 100 or 200 mM NaCl. Three plants of each line evaluated (Col-0, pSbLTP1.4-GUS-1, pSbLTP1.5-GUS-1) were used. After 48 h, leaves, inflorescences, and siliques were sampled and, GUS histochemical staining was performed. The experiments were repeated three times.

### Histochemical GUS analyses

Plant samples (seedlings, roots, leaves, inflorescences, and siliques) were vacuum infiltrated for 10 min in a solution containing 500 mM Na<sub>2</sub>PO<sub>4</sub>, 1mM EDTA pH 8, 0.5 mM potassium ferrocyanide, 0.5 mM potassium ferricyanide, 0.5% (v/v) Triton X-100, 0.5% (v/v) N, N-dimethylformamide, and 1mM X-Gluc and incubated at 37 °C for 24 h. The substrate 5-bromo-4-chloro-3-indolyl-β-D-glucuronic acid cyclohexylammonium salt (X-Gluc), used for histochemical GUS staining, was purchased from X-Gluc DIRECT. Following staining, chlorophyll was removed by immersion in 70% ethanol. Plants were then analyzed and photographed using a ZEISS Stemi 2000-C stereomicroscope coupled to a digital camera.

### Data availability

The promotor sequences analyzed in this study were retrieved from the publicly available Sorghum bicolor genome (NCBI BioProject ID: PRJNA1387). Detailed information on the genes and their promoter regions is provided in the manuscript.

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## Author contributions

AMZ conceived and supervised research. LAC, AEM and LM designed and performed the experiments. LAC, AEM and LM analyzed the in silico data. AMZ, AEM and LM wrote the manuscript. AMZ, LAC, LM, AEM and GES reviewed and revised the manuscript. All authors contributed to the article and approved the submitted version.

## Declarations

## Competing interests

The authors declare no competing interests.

## Additional information

**Supplementary Information** The online version contains supplementary material available at <https://doi.org/10.1038/s41598-025-08625-8>.

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