



	Predicted Number of Amino	Predicted	Predicted Molecular Aass	Conserved
	Acid	pI	(kDa)	Domain
13021	212	5.58	23.2	Chloroa_b-bind
40120	236	9.09	25.5	Chloroa_b-bind
40121	236	9.33	25.7	Chloroa_b-bind
68225	207	9.57	21.7	Chloroa_b-bind
16576	94	10.39	10.2	Chloroa_b-bind
8044	94	6.71	10.4	Chloroa_b-bind

Table S1. Properties of 6 ScELIPs Unigenes.

Table S2. Sequences information for construction of the phylogenetic tree.

	Gene	Amino Acid	Accession Number
AtELIP1	ELIP1	151	U89014
AtELIP2	ELIP2	152	Z97336
Syntrichia ruralis-A	ELIPa	212	AY034890
Syntrichia ruralis-B	ELIPb	224	AY034891
Setaria italica	ELIP	181	XP_004955632
Zea mays	ELIP	192	ACG46269
Panicum miliaceum	ELIP	197	RLN34913.1
Oryza sativa	ELIP	187	BAD30330
Brachypodium distachyon	ELIP	193	XP_010228291.1
Dendrobium catenatum	ELIP	192	XP_020674324
Apostasia shenzhenica	ELIP	196	PKA64958.1
Elaeis guineensis	ELIP	189	XP_010923519.1
Phoenix dactylifera	ELIP	193	XP_008786056.1
Solanum tuberosum	ELIP	197	XP_006363471
Medicago truncatula	ELIP	197	XP_013469748.1
Gossypium raimondii	ELIP	193	XP_012487200.1
Morus notabilis	ELIP	195	XP_010107710
Capsella rubella	ELIP	196	XP_006298609.1
Brassica rapa	ELIP	191	XP_009148406.1
Selaginella moellendorffii	ELIP	197	XP_024536558
Sphagnum fallax	ELIP	253	Sphfalx0001s0155.1
Onoclea sensibilis	ELIP	230	AAB25012
Marchantia polymorpha	ELIP	227	PTQ40288
Physcomitrella patens ELIP12	ELIP12	225	A9TAX2
Physcomitrella patens ELIP8	ELIP8	325	EDQ69484
Physcomitrella patens ELIP11	ELIP11	110	A9S3S8

Int. J. Mol. Sci. 2019, 21, x FOR PEER REVIEW

Physcomitrella patens ELIP7	ELIP7	140	A9TL19
Physcomitrella patens ELIP6	ELIP6	135	A9RSF4
Physcomitrella patens ELIP10	ELIP10	220	A9SZ27
Physcomitrella patens ELIP4	ELIP4	249	A9TIL7
Physcomitrella patens ELIP9	ELIP9	225	A9T6B6
ScELIP1	ScELIP1	236	KM363766
ScELIP2	ScELIP2	207	KM363767

 Table S3. Primer information for RT-qPCR of high light treatment of plantlets.

Gene		Sequence	GeneBank Accession		
OHP2	Forward	TCTTCGACAGCTTCGTCGTCT	NM_103122	1.1	
	Reverse	GAGGCTCCCGGAGAGTAGGA		one helix protein	
ОНР	Forward	TGAGCTCGTCGCCGTTATCT	NM_120290.3	1.15	
	Reverse	GCGGCTCTGACAACGAAAGG		one helix protein	
SEP2	Forward	TGGCGATTTAGCCGAGAACGG	NP565524	stress enhanced protein 2	
	Reverse	CACCATCTCCGCCGTCCTTT			
LHCB4.2	Forward	ATCGACGCCGTTTCAGCCAT	NM_111728	PS II CP29 antenna protein	
	Reverse	GCCAAGAGTGGCGAGCATTG			
LHCA2	Forward	CTGTCTCCAGGCCAGATGCG	NM_116012	PS I antenna protein	
	Reverse	CACCAGGGAGGCTACCGTCT			
PSBS	Forward	GGGAGCCATTGGAGCTCTCG	NM_103552		
	Reverse	GAGACCGAGGGCAGATCGGA		PS II CP22 antenna protein	
PSBD	Forward	TGATGGGAGTCGCCGGTGTA	NP_051054	PS II D2 protein	
	Reverse	AAGCGGTTAGCGGTGACCAT			
ScELIP1	Forward	GGCTATGCTGGGATTCGTGT	KM363766		
	Reverse	GACGCCAGGAACCAGATCAA			
ScELIP2	Forward	GCAATGATCGGACTTGTCGC	KM363767		
	Reverse	ACGGATTGTTCACAGCAGGT			
α-TUB	Forward	GATGTACCGTGGTGATGTC			
	Reverse	GAGCCTCTGAAAATTCTCC			

 $2 \ of \ 8$

Syntrichia_caninervis_ELIP1	CAMTGGALGGIALPSRNVRTARMFAQLVPGRVVRCEALPEEKYVNPIDQATKKTITREEVLQNQAT	77
Marchantia_polymorpha	AGLRSAPLSSSLKRSSSCQSSFGIVRTPLAFGRRTSIRCEGIREAVDKTTKKEITREEILQNQEV	77
Setaria_italica	SIAFAAAGARARAGGFFVRVPASALAPRRALVVRAQAEDAEPDAEP	53
Syntrichia_ruralis_ELIPB	MALNCAALRSPSTEVLSSRTGAAAPRLFVRRS.LVRCQAGFEGLRGAVDKATKKTLTKEEIVRHQET	76
Syntrichia_ruralis_ELIPA	.ASYLGTVAGVPSLKLKFNVNTAFLGVRRNVVVYAKQTDETFLPGTKVDPEEKEDPLR	66
Glycine_max	ILANPLIRISSGSRVNCFGVPALHMRRNVGLRVRSMAKEECPSEPATPVTPPPSV	65
Dendrobium_catenatum		67
Selaginella_moellendorffii	SSAVVLKQQHLVLSRHGSSSIVSYSRIHPLVCRATKEGDSDQAAATSPVEKKVEAASP	68
Oryza sativa	AVAAAAGGAPWRAAVRFFPRREVALV.VRAQAEPEVEP.TKEETATS	53
Arabidopsis_thaliana_ELIP2	VFAAPSGVLTTRNIRNINGLFFKRIAPVGVRCMAGGDFIKEDPSVPSTSTSATPPQ	66
Gossypium raimondii	SLLLASPMTGLGSKRQMVQFYNV.KPMFRFQRKLNLQVRCLAEEGDQKEPMPAATTP	67
Onoclea_sensibilis	RLIV P TSSSSPAAPTTPPSTLRVMCSSNKAPSPPGLLSS <mark>L</mark> KENVDRSTKQELSRADIERTR <mark>P</mark> RPPQSSSLSG	88
Physcomitrella_patens_ELIP8	GAGTGAMLGGINLPCRVAGVSQAARLVNSPRLLTRRAGRVRCEVDEEGPKAFIPTSTPGVAGSFDRATKKTITKEEVLQNQAT	166
Arabidopsis_thaliana_ELIP1	VFAGGLTTRKI.NTNKLFSA.GSFFNLKRNYPVGVRCMAEGGFTNED.SSPAPSTSAAQF	67
Syntrichia caninervis ELIP2	TTTGAMSMSSVRARNVAVSSPMNIQGMRLGQMSRVSRTRCMAVEFEQSKSEVDATFVTPMATPATPAM	78
Solanum_lycopersicum	.IILGSP.LKLSQNKN.GLNQFVPS.CYLPRLHRISRVSVKCMAEEGEKESSTPSTDYSAT	65
Zea mays	PLASATPGARRAFFVRLLLQASALAFRRRALAVTVRAQSDDAEAEPKEAAAAA	63
Consensus		
Syntrichia caninervis ELIP1	NESEORSIFGERPAGSPYGRPEVERRPETGNLSPWSVFAFDGAREETINGRIALIEFVWAIIGEKTTELSVADLFSPGATE	160
Marchantia polymorpha	NESEKCSVFGAKPTSGSFYPRPEVERRPETGDKSLDSIFAFDGAPPETINGRLAMVGILWALAAKMSGLTVFDCLYTOG.TG	159
Setaria italica		115
Syntrichia ruralis ELIPB	DESECRSIFGARPTPGTPYGRPEVERRFETGDRSFLGIWSFDGAV <mark>PETVNCRIANICIVWA</mark> FFARKATCLTVIECLTAPGCTG	159
Syntrichia ruralis ELIPA	IFGGSPVEKFFRPEEERRFEDGNTSPDSLMKFDGFAFPTINSPLANICITWAFVAPIITCCSVWECVTEGR.G	138
Glycine max	EPKPCFVSAFSFKVSTKFSDVLAFSGFAFFRINGRLAMICFVAAMAVEVAKCCGVLECISNGG	128
Dendrobium catenatum		128
Selaginella moellendorffii		130
Orvza sativa		121
Arabidopsis thaliana ELIP2		129
Gossypium raimondii		129
Onoclea sensibilis	LTRFTPASTVFWPRSELDRR.LRCVTLAHYPLSCEWCFPTINGEMAN VEFVWFLVVPKMTELGVMCLFNPSTSG	163
Physcomitrella patens ELIP8	NESECRSIFGAKPTEGSVYGRPEVERREETGELSEWSVFAFDGAZEPTINGRIAN LEFVWZLYGNATELSVID VFSPGSTG	249
Arabidopsis thaliana ELIP1		131
Syntrichia caninervis ELIP2	ATPLEATESESKSKKVSTNEEDVESEAGEAEPTINGELAVICETTALGVPLETCEDLATCIGLGG	143
Solanum lycopersicum		125
Zea mays	TTPAPK SKAAAA AS FOLWLALAF SOPA FOR TNORLAN VE FU SALAWAS REGGILS CAGSOS G	126
Consensus	penranga eg g g	
Syntrichia caninervis ELIP1	LIMELASVCILSY SIVEIFNARESTDARSFGPFRAKADRUNGRAANIGFASLILTE.AIICGPLEVWFFNNARFP	235
Marchantia polymorpha	LVFYVALVPLIAYSIVEMING.ESTDARSFGPFTARASRWNGRLAMIGFISILLTE.SYIHAPVFRTFF	227
Setaria italica	LAWFAATAAVLSV <mark>A</mark> SIV <mark>E</mark> LLKG.DSAEARSGGFMSADA <mark>B</mark> I <mark>WNGRFAM</mark> LGLVALAFTEYLTGAPFINA	181
Syntrichia ruralis ELIPB	LPAFIGAVCLETYPSLIEIENG.ESTDARSFGPFTARAPRWNGRLAMLGEFSLIVTE.LERTVPVFH	224
Syntrichia ruralis ELIPA	LIWFLFVAPIIIC <mark>ATLIE</mark> MFNR.ESFDSRANGPFNACN <mark>BRWNGRAAMIGLVALLVTENIYLKGPLLGFVH</mark> SSLNL.	212
Glycine max	IPWFLGTSVVLTLASIIELFCG.VSVESKSKGFMSSIAEIWNGRFAMLGLIALAFTEYVKGSTLV	192
Dendrobium catenatum	VIWFAGAAALISV <mark>ASIVE</mark> LFRG.VDASDRSDAPMTADA <mark>B</mark> IWNGRFAMIGIVALAATEYVKGGPLV	192
Selaginella moellendorffii	SSYFVGAALLFTL <mark>SIVELFCG.VSIEKAS</mark> GGIGGVFTSKA <mark>D</mark> RWNGRAAMLGLVALGITEFVKGSPLI	197
Oryza sativa	LAWFAATATVLSAASLVELLRG.ESAEARSGGVMSADAE <mark>IWNGRFAM</mark> LGLVALAFTEFLTGSPFVNV	187
Arabidopsis thaliana ELIP2	VGWELGTTALLTL <mark>SMVEL</mark> FKG.IRAEAKSKGFMISDA <mark>B</mark> LWNGRFAMLGLVALAFTEYVTGGTLV	193
Gossypium raimondii	IPLFVGTSIVLSLASLIELFRG.ETVESRSGOFMSSDADIWNGRFAMLGLVALAFTEYVKGGTLV	193
Onoclea sensibilis	LLWFGAVVQLFTLASIIEFVNG.ESTDARRWCFFNAKAERWNGRLAMVRSFFSSLARWCARLPSSKPK	230
Physcomitrella patens ELIP8	LIWFLASVQIFTYASIVEIFNAKESTDARSFGFFTAKAERWNGRAANIGFFSIVTE.LFLOGFIIKLFANSVVPP	324
Arabidopsis thaliana ELIP1	VSWELGTTAILTLASIVELFKG.ISVESKSKGIMISDADINNGRFANLGIVALAFTEFVKGGTLV	195
Syntrichia caninervis ELIP2	VQWFIVVAAIFTCASLIEMFRG.VTVDDKSKFVFSSTR KWNGRFAN IGLVALAITEFVKGSPLV	207
Solanum lycopersicum	LLWFLGSSALLTLASLIELFQG.VIVESKSDGIMTADA IWNGRFANLGLVALAFTEYVKGAGLFQV	191
Zea mays	LAWFAATAAVLSVASIVELLRG.DSAEARSGAVMSANAEI <mark>UNDRXAM</mark> IGUVALAFTEYLTGAPFINA	192
Consensus	a p e wngram	

Figure S1. The amino acid sequences alignment of ELIPs by MEGA 7.0. *ScELIP1* and *ScELIP2* have conserved amino acids (triangular symbol) to known ELIP proteins.



Figure S2. 35S-*ScELIP1* vector construction strategy.



Figure S3. 35S-*ScELIP2* vector construction strategy.



Figure S4. Verification of transgenetic Agrobacterium by bacterium PCR. Lane 1-5 positive transgenic clones for *ScELIP1*, lane 6-10 positive transgenic clones for *ScELIP2*. Lane 1 and 6 Agrobacterium used for transforming *Atelip* mutant.



Figure S5. Hygromycin selection of transgeneic *Arabidopsis thaliana*. The plantlets in the circles are positive transgenic lines which have emergent green leaves which stay green, the negative plants have cotyledon emergence but subsequently turn yellow or white after ten days.



Figure S6. RT-PCR validation of T3 transgenic lines.



Figure S7. Quantitative real time PCR expression level analysis of *ScELIP1* and *ScELIP2* transgenic lines. Error bars represent the SD of three biological repeats. Relative expression values were obtained from $2^{-\triangle \triangle Ct}$ comparing WT and the transgenic lines with the *Atelip* mutant respectively.



Figure S8. Seed germination phenotypes for Col-0 WT, *Atelip* mutant and *35S-ScELIP* lines under different light treatments. Images, labeled a-e, depict the phenotypic response of the four genotypes to the various light treatments. Control condition (**a1**,**a2**); Red light alone (**b1**,**b2**); Blue light alone (**c1**,**c2**); UVB alone (**d1**,**d2**); High light alone (**e1**,**e2**).



Figure S9. Phenotypic response of Col-0 WT, *Atelip* mutant and *35S-ScELIP1* and *35S-ScELIP2* after seven days of exposure to different light treatments. Row 1, WT, *Atelip* mutant, *35S-ScELIP1* transgenic lines. Row 2, WT, *Atelip* mutant, *35S-ScELIP2* transgenic lines. Control conditions (**a**, **e**), Red light alone (**b**, **f**), Blue light alone (**c**, **g**), UVB alone (**d**, **h**).



Figure S10. The change of chlorophyll content of WT, *Atelip* and transgenic lines at 0 h, 3 days and 3 weeks high light stress (1000 μ mol/m²/s). Error bars represent the SD of three biological repeats. *, P < 0.05; **, P < 0.01. P-values were obtained from Dunnett's T3 test comparing WT and the transgenic lines with the *Atelip* mutant respectively.

© 2020 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under



the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/).