Supplemental Figure 1. Differences in amino acid composition between the paralogous copies Os *MADS17* and Os *MADS6*.
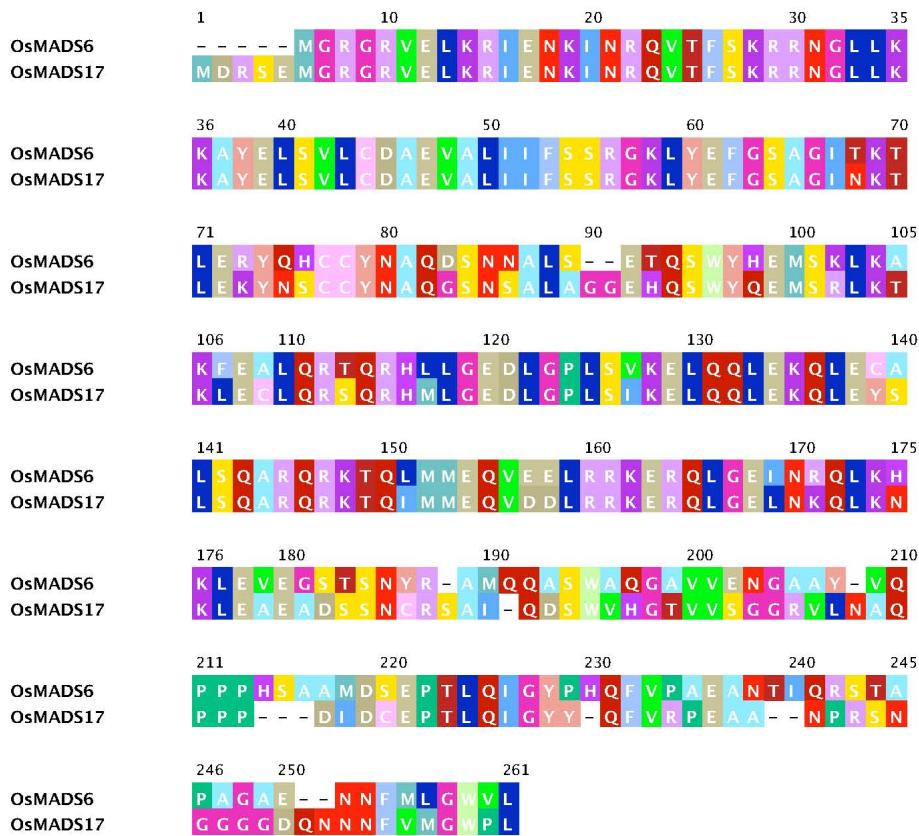
Supplemental Figure 2. Alignment of the predicted amino acid sequences of *AGL6-like* genes included in this study (only the IKC-terminus domains are shown). The black arrow indicates the single amino acid in the K-domain changed before the divergence of *Pharus*, which correlates with the origin of the grass spikelet.
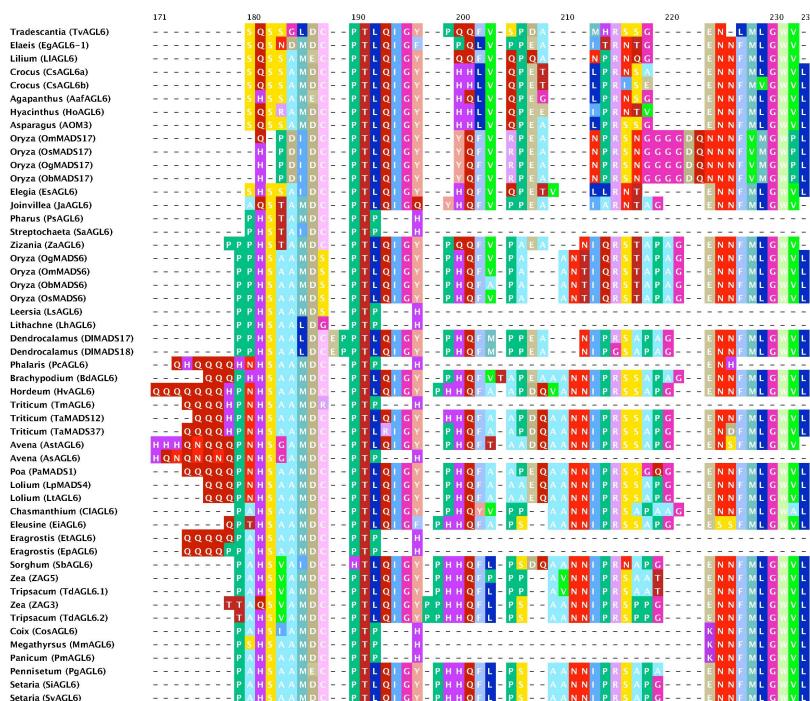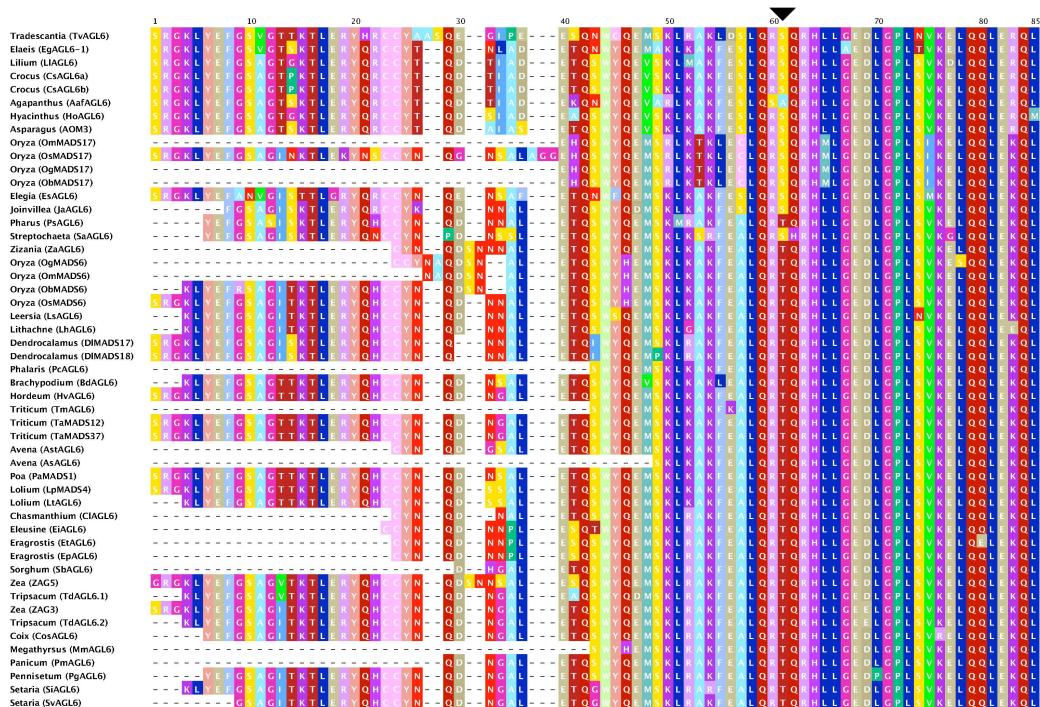
Supplemental Figure 3. *AGL6-like* RT-PCR products from RNA of roots (**R**), stems (**S**), leaves (**L**), and inflorescence (**I**) in *Agapanthus africanus* and grasses, and outer tepals (**OT**), inner tepals (**IT**), stamens (**ST**) and carpels (**CA**) in *Agapanthus africanus*. *ACTIN* was used as a positive control. The question mark indicates missing data.
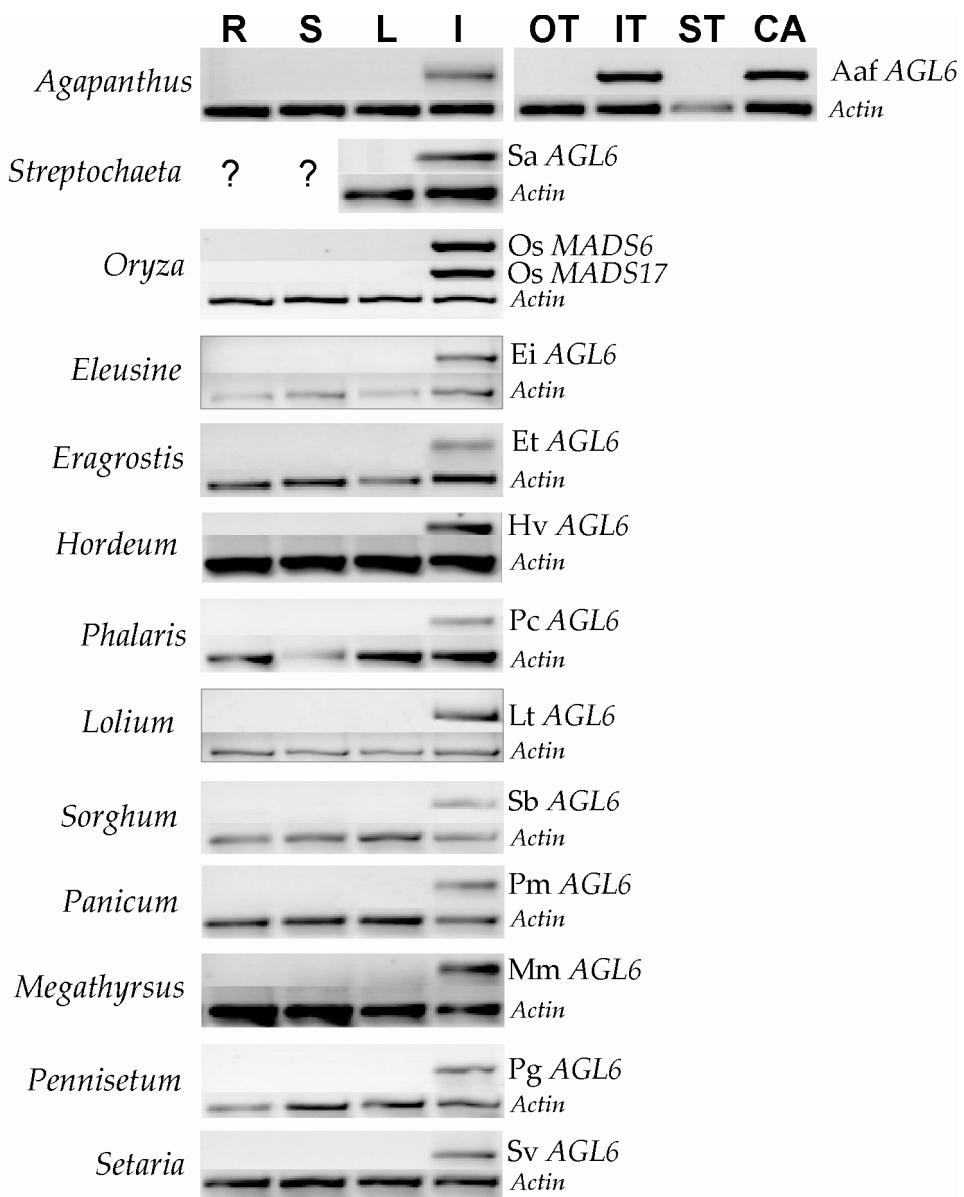
Supplemental Figure 4. *AGL6-like* expression in floral meristems of *Streptochaeta angustifolia* (Anomochlooideae), and *Triticum monoccocum* (Pooideae). **(A)** Sa AGL6 in *S. angustifolia*. **(B)** Tm *AGL6* in *T. monococcum*. The arrowhead indicates the floral meristem. Bar = 100μm.
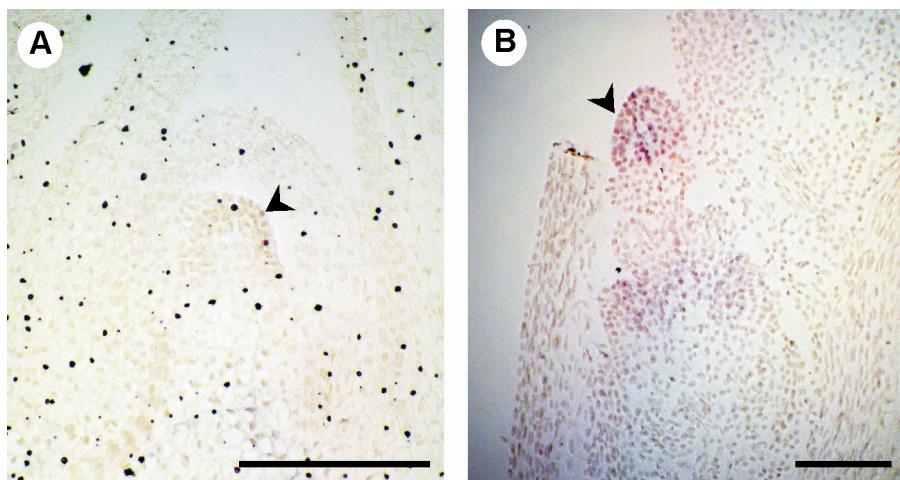
Supplemental Table 1. Expression patterns reported for *AGL6-like* homologs in gymnosperm species. Abbreviations: IH, in situ hybridization; RT-PCR, Reverse transcriptase, polymerase chain reaction.

Species	Gene	Expression				Technique	References
		Female cones	Male cones	Leaves	Vegetative shoot		
Gnetum gnemon	GMM9	+	+	-	?	RNA gel blot	Winter et al. (1999) Becker et al. (2003)
	GMM11	+	+	-	?	IH	
Picea abies	DAL1	+	+	?	+	RNA gel blot	Tandre et al. (1995)
Pinus radiata	PrMADS2	+	+	?	-	RNA gel blot, IH	Mouradov et al. (1998)
	PrMADS3	+	+	?	+		
Pinus resinosa	PMADS1	+	+	?	?	RNA gel blot	Liu and Podila (1997)

Supplemental Table 2. *AGL6-like* gene expression patterns reported in eudicots and monocots. Abbreviations: IH, in situ hybridization; MA, microarrays; RQ RT-PCR, Relative Quantitative RT-PCR; RT-PCR, Reverse transcriptase - polymerase chain reaction; DNA gel blot; Veg., vegetative tissues; W1, first whorl or sepals in eudicots, outer tepals in non-grass monocots, and lemma and palea in Grasses; W2, second whorl or petals in eudicots, inner tepals in Non-grasses monocots and lodicules in grasses; W3, third whorl or stamens; W4, fourth whorl or carpels.

Species	Gene	Expression						Technique	References
		W1	W2	W3	W4	Fruit	Veg. tissues		
Dicots									
Arabidopsis	*AGL6*	+	+	+	+	-	+	RNA gel blot	Ma et al. (1990)
	AGL13	-	-	+	+	-	+	RNA gel blot, IH	Rounsley et al. (1995)
Vitis vinifera	*VvMADS3*	-	+	+	+	+	-	RNA gel blot	Boss et al. (2002)
Petunia	*pMADS4*	+	+	-	+	?	?	RNA gel blot	Tsuchimoto et al. (2000)
Amborellales									
Amborella trichopoda	*Am.tr.AGL6*	+	+	+	+	?	-	RQ RT-PCR	Kim et al. (2005)
Magnoliales									
Magnolia grandiflora	*Ma.gr.AGL6*	+	+	-	-	?	-	RQ RT-PCR	Kim et al. (2005)
Persea americana	*AGL6.1*	+	+	-	-	?	-	RQ RT-PCR	Chanderbali et al. (2006)
Persea borbonia	*AGL6.2*	+	+	-	-	?	-		
Non-grass monocots									
Asparagus officinalis	*AOM3*	+	+	+	+	?	-	RNA gel blot, IH	Losa et al. (2004)

Species	Gene							Method	Reference
Oncidium Gower Ramsey	O *MADS1*	-	+	-	+	?	-	RT-PCR, DNA gel blot	Hsu et al. (2003)
Hyacinthus orientalis	Ho *AGL6*	+	+	-	+	?	-	RNA gel blot	Fan et al. (2007)
Grasses									
Oryza sativa	Os *MADS6*	+	+	-	+	?	-	RNA gel blot IH	Moon et al. (1999) Pelucchi et al. (2002)
		-	-	-	+	?	?		
	Os *MADS17*	?	?	?	?	?	-	MA	Arora et al. (2007)
Lolium perenne	Lp *MADS4*	-	?	?	?	?	-	RQ RT-PCR	Petersen et al. (2004)
Triticum aestivum	Ta *MADS37*	?	?	?	?	+	-	RT-PCR	Zhao et al. (2006)
Poa annua	Pa *MADS1*	-	?	?	?	?	-	RNA gel blot	Aiguo and Griffin (2002)
Zea mays	*zag3*	+	+	-	+	?	-	RNA gel blot IH	Mena et al. (1995) Thompson et al (submitted)
		+	+	-	+	?	?		
	zag5	-	-	-	+	?	-	RNA gel blot	Mena et al. (1995)

Supplemental Table 3. *AGL6* homologs included in this study

Species	Family/Subfamily	Gene	Accession no
Crocus sativus	Iridaceae/—	Cs *AGL6a*	EF041505
		Cs *AGL6b*	EF041506
Lilium lancifolium	Liliaceae/—	Ll *AGL6*	GQ496626
Hyacinthus orientalis	Hyacinthaceae/—	Ho *AGL6*	AY591333
Asparagus officinalis	Asparagaceae/—	Ao *M3*	AY383559.1
Agapanthus africanus	Agapanthaceae/—	Aaf *AGL6*	GQ496627
Elaeis guineensis	Arecaceae/—	Eg *AGL6-1*	AY739701
Tradescantia virginiana	Commelinaceae/—	Tv *AGL6*	GQ496625
Elegia sp	Restionaceae/—	Es *AGL6*	Malcomber and Christensen (unpublished)
Joinvillea ascendens	Joinvilleaceae/—	Ja *AGL6*	GQ496631
Streptochaeta angustifolia	Poaceae/Anomochlooideae	Sa *AGL6*	GQ496633
Pharus sp.	Poaceae/Pharoideae	Ps *AGL6*	GQ496632
Dendrocalamus latiflorus	Poaceae/Bambusoideae	Dl *MADS17*	AY599754.1
		Dl *MADS18*	AY599755.1
Lithachne humilis	Poaceae/Bambusoideae	Lh *AGL6*	GQ496639
Oryza sativa	Poaceae/Ehrhartoideae	Os *MADS6*	U78782.1
		Os *MADS17*	AF109153.1
Oryza barthii	Poaceae/Ehrhartoideae	Ob *MADS6*	GQ496637
		Ob *MADS17*	GQ496630
Oryza glaberrima	Poaceae/Ehrhartoideae	Og *MADS6*	GQ496635
		Og *MADS17*	GQ496629
Oryza meridionalis	Poaceae/Ehrhartoideae	Om *MADS6*	GQ496636
		Om *MADS17*	GQ496628
Leersia sp.	Poaceae/Ehrhartoideae	Ls *AGL6*	GQ496638
Zizania aquatica	Poaceae/Ehrhartoideae	Za *AGL6*	GQ496634
Brachypodium distachyon	Poaceae/Pooideae	Bd *AGL6*	GQ496641
Triticum aestivum	Poaceae/Pooideae	Ta *MADS37*	DQ512353.1
		Ta *MADS12*	AB007505.1

Triticum monococcum	Poaceae/Pooideae	Tm *AGL6*	GQ496643
Hordeum vulgare	Poaceae/Pooideae	Hv *AGL6*	GQ496642
Lolium temulentum	Poaceae/Pooideae	Lt *AGL6*	GQ496646
Lolium perenne	Poaceae/Pooideae	Lp *MADS4*	AY198329.1
Phalaris canariensis	Poaceae/Pooideae	Pc *AGL6*	GQ496640
Avena strigosa	Poaceae/Pooideae	Ast *AGL6*	GQ496644
Avena sativa	Poaceae/Pooideae	As *AGL6*	GQ496645
Poa annua	Poaceae/Pooideae	Pa *MADS1*	AF372840.1
Eleusine indica	Poaceae/Chloridoideae	Ei *AGL6*	GQ496648
Eragrostis pilosa	Poaceae/Chloridoideae	Ep *AGL6*	GQ496650
Eragrostis tef	Poaceae/Chloridoideae	Et *AGL6*	GQ496649
Chasmanthium latifolium	Poaceae/Centothecoideae	Cl *AGL6*	GQ496647
Setaria viridis	Poaceae/Panicoideae	Sv *AGL6*	GQ496659
Setaria italica	Poaceae/Panicoideae	Si *AGL6*	GQ496658
Pennisetum glaucum	Poaceae/Panicoideae	Pg *AGL6*	GQ496657
Megathyrsus maximus	Poaceae/Panicoideae	Mm *AGL6*	GQ496655
Panicum miliaceum	Poaceae/Panicoideae	Pm *AGL6*	GQ496656
Sorghum bicolor	Poaceae/Panicoideae	Sb *AGL6*	GQ496651
Zea mays	Poaceae/Panicoideae	*ZAG3*	NM_001111862.1
		ZAG5	NM_001112222.1
Tripsacum dactyloides	Poaceae/Panicoideae	Td *AGL6.1*	GQ496652
		Td *AGL6.2*	GQ496653
Coix sp.	Poaceae/Panicoideae	Cos *AGL6*	GQ496654

Voucher information for each sequence is included in GenBank. Newly generated sequences are underlined.

Supplemental Table 4. Primers used for isolation of Os *MADS6*-like sequences and Os *MADS17*-like sequences, and expression analysis in Poaceae and other monocots**.**

Method	*Species*	Primer	Primer sequence
Isolation of Os *MADS6*-like genes			
	Lilium lancifolium	147F	SAG CCG HGG CAA RCT CTA
	Agapanthus africanus	147F	SAG CCG HGG CAA RCT CTA
	Tradescantia virginiana	147F	SAG CCG HGG CAA RCT CTA
	Xyris sp.	147F	SAG CCG HGG CAA RCT CTA
	Joinvillea ascendens	163F	TAC GAR TTC GGY AGC GCC
	Streptochaeta angustifolia	163F	TAC GAR TTC GGY AGC GCC
	Pharus sp.	163F	TAC GAR TTC GGY AGC GCC
	Oryza barthii	157F	AAG CTS TAC GAR TTC GGY AG
	Oryza glaberrima	215F	GYT GCT AYA ATG CTC AAG ATT CC
	Oryza meridionalis	215F	GYT GCT AYA ATG CTC AAG ATT CC
	Lithachne humilis	157F	AAG CTS TAC GAR TTC GGY AG
	Leersia sp.	157F	AAG CTS TAC GAR TTC GGY AG
	Zizania aquatica	157F	AAG CTS TAC GAR TTC GGY AG
	Brachypodium distachyon	157F	AAG CTS TAC GAR TTC GGY AG
	Triticum monococcum	270F	GAG YTG GTA CCA KGA AAT GTC AAA
	Lolium temulentum	157F	AAG CTS TAC GAR TTC GGY AG
	Phalaris canariensis	270F	GAG YTG GTA CCA KGA AAT GTC AAA
	Avena strigosa	215F	GYT GCT AYA ATG CTC AAG ATT CC
	Avena sativa	270F	GAG YTG GTA CCA KGA AAT GTC AAA
	Eleusine indica	215F	GYT GCT AYA ATG CTC AAG ATT CC
	Eragrostis pilosa	215F	GYT GCT AYA ATG CTC AAG ATT CC
	Eragrostis tef	215F	GYT GCT AYA ATG CTC AAG ATT CC
	Chasmanthium latifolium	215F	GYT GCT AYA ATG CTC AAG ATT CC
	Setaria viridis	157F	AAG CTS TAC GAR TTC GGY AG
	Setaria italica	157F	AAG CTS TAC GAR TTC GGY AG
	Pennisetum glaucum	163F	TAC GAR TTC GGY AGC GCC
	Megathyrsus maximus	270F	GAG YTG GTA CCA KGA AAT GTC AAA
	Panicum miliaceum	270F	GAG YTG GTA CCA KGA AAT GTC AAA
	Sorghum bicolor	270F	GAG YTG GTA CCA KGA AAT GTC AAA
	Tripsacum dactyloides	157F	AAG CTS TAC GAR TTC GGY AG
	Coix sp.	163F	TAC GAR TTC GGY AGC GCC
Isolation of Os *MADS17*-like sequences			
		150F	CCG TGG CAA ACT GTA TGA ATT
		177F	CGC GGG CAT TAA CAA AAC
		192F	AAC CCT GGA AAA ATA TAA CAG CTG
		257F	GCG AAC ATC AGA GCT GGT ATC
		157F	AAG CTS TAC GAR TTC GGY AG
		163F	TAC GAR TTC GGY AGC GCC
		650R	CGC ACA AAC TGA TAA TAG CCA A
		711R	ATC ACA AAG TTG TTG TTC TGA TCG
		714R	TCA GAA CAA CAA CTT TGT GAT GG
		725R	ACT TTG TGA TGG GCT GGC
		polyT	CCG GAT CCT CTA GAG CGG CCG CTT TTT TTT TTT TTT
Q-PCR			
		ACTIN591F	GAG RGG TTA CTC CTT CAC VAC
		764R	GGA CCT CGG GGC ACC TGA ACC TCT
	Streptochaeta angustifolia	StrepAGL6_1F	TGC TAT TCT ATA CCT AAG TCG TTG GA
		Strep_3UTR	TTA TAC CCA CCT TGG ATG TCG
	Oryza sativa	OsMADS6_2F	TCT GTA GTT GCT GGT GGA ACC
		OSMADS6_5CT113	ATT ATT AGC CCC AAC TTC TGA CAG
		OsMADS17_1F	CGT GCT ATA ATA TAT AGT TCG GCA AA
		OSMADS17_3UTR451	CAA ACA TAC ACT CAT AGG TAC GTG C
	Eleusine indica	EiAGL6_2F	TTT GAC CTA CAG ATC CAT CCG
		Ei3UTR	ACG ACC ACA CAA TCA CGG T

	Lolium temulentum	LtAGL6_1F	CTA ATA AAA TGC GTG TTC TGC TTC T
		Lt3UTR	TTC AAA TAA TCA AAA CGT AGA AGT GG
	Setaria italica	SiAGL6_1F	TTC TAT GTG ATT GTA TTG TGG CAC TT
		Seta3UTR	ATA CGT ACC GGT AGA GAT AAT TTT GG
	Sorghum bicolor	SbAGL6_2F	GTG GTG TGG CAC TTC TAT GTT TT
		Sb3UTR	ATA AGT ACC GTT GCA GAT AAT TTT GG
	Triticum monoccocum	TmAGL6_1F	TCG TTA TTT GTG CGT GTA AGA AGTA
		Tri_3UTR	GCA TGC ATG GAT AGC TTG G
RT-PCR and in situ hybridization			
	Agapanthus africanus	147F	SAG CCG HGG CAA RCT CTA
		559r	CCC AGC CCA GCA TAA AGT T
	Joinvillea ascendens	JO_5CT158	CTC TGC AAA TTG GGC AGT ATC
		JO23_3UTR	AGA GCT TAA ATT TTA CAA GGT CC
		Jo5CT	GGA GAA ATT AAC AAA CAA CTC AAA AAC
		JO32_3UTR	TTT TTG GCA GTC AAG GGA ATA
	Streptochaeta angustifolia	Strep_5CT270	CGT AGA CTG AGT TTA TCT GCC TAG C
		Strep_5CT	TAA CAG GCA GCT CAA AAA CAA G
		Strep_3UTR	TTA TAC CCA CCT TGG ATG TCG
	Lithachne humilis	LITHA_5CT316	GTG GGT TCT TTA AGC TTG CTT G
		Litha_181_3UTR	TTT GAG TTG CTA GGG AAT TTG AA
	Oryza sativa	OsMADS6_5CT	CTG GGT GAA ATT AAT AGG CAA CTC
		OSMADS6_5CT113	ATT ATT AGC CCC AAC TTC TGA CAG
		OsMADS6_3UTR	CAG CTA GCA GTA GCT TAC ACA CAA A
		OSMADS17_5CT100	AAG CTA GAA GCT GAA GCC GAT A
		OSMADS17_3UTR451	CAA ACA TAC ACT CAT AGG TAC GTG C
		OsMADS17_5CT	CAG GCT CGA CAA CGA AAG A
		OsMADS17_3UTR	ACC GGA TAG GGG AGA AAT ATA CA
	Leersia sp.	LE_5CT202	CGG CCA TGG ACT CTG AAC
		Le_3UTR	AAA CAC AGC CAC GTA CGT AGA AC
	Hordeum vulgare	Hv5CT	GCG TCA GCT GGG AGA CAT
		Hv3UTR	AAT TGT CCA GAA ATT ATG GTT GTA CT
	Triticum monococcum	Tri_5CT	GGC AGC AAC AGC AAC AAC TA
		Tri_3UTR	GCA TGC ATG GAT AGC TTG G
	Lolium temulentum	Lt5CT	CAG CAG CAG CCA AAT CAC T
		Lt3UTR	TTC AAA TAA TCA AAA CGT AGA AGT GG
	Phalaris canariensis	270F	GAG YTG GTA CCA KGA AAT GTC AAA
		805R	TTC ATG CTG GGR TGG GTT
	Eleusine indica	Ei5CT	TGG GAG AAA TGA ACA GGC A
		Ei3UTR	ACG ACC ACA CAA TCA CGG T
	Eragrostis tef	270F	GAG YTG GTA CCA KGA AAT GTC AAA
		805R	TTC ATG CTG GGR TGG GTT
	Setaria viridis	Seta5CT	GAG AAA TGA ACA GGC AAC TCA AG
		Seta3UTR	ATA CGT ACC GGT AGA GAT AAT TTT GG
	Setaria italica	Seta5CT	GAG AAA TGA ACA GGC AAC TCA AG
		Seta3UTR	ATA CGT ACC GGT AGA GAT AAT TTT GG
	Pennisetum glaucum	Pg5CT	GTC ACC TGG GAG AAA TGA ACA
		Pg3UTR	CGG CAG CAT AGA AGT ATT TTT ACA
	Megathyrsus maximus	270F	GAG YTG GTA CCA KGA AAT GTC AAA
		805R	TTC ATG CTG GGR TGG GTT
	Sorghum bicolor	Sb5CT	GAA CAG GCA ACT CAA ACA CAA G
		Sb3UTR	ATA AGT ACC GTT GCA GAT AAT TTT GG

Statistical tests

Statistical tests of nucleotide sequences (tabulated results at Supplemental Table 5 bellow)

We performed a Shimodaira–Hasegawa (SH) test (Goldman et al. 2000) to test whether we could statistically reject alternative hypotheses for the timing of the *AGL6/*Os *MADS6/*Os *MADS17* duplication and the *zag3/zag5* duplication.

We tested whether the duplication could have taken place at the base of the grasses after the divergence of Joinvilleaceae. Also, we explored alternative hypothesis for the Os *MADS6/*Os *MADS17* duplications based on previous studies that suggested that the two copies are the result of rice genome duplication event (Arora et al., 2007). Each topology differed in the placement of *Oryza MADS17* sequences as follows: (1) *Oryza MADS17-like* sequences sister to the *Oryza MADS6* clade (testing whether the duplication could have occurred just prior to the origin of the genus *Oryza*), (2) *Oryza MADS17-like* sequences sister to the Oryzeae clade sequences (testing whether the duplication could have occurred just prior to the origin of the tribe Oryzeae), (3) *Oryza MADS17-like* sequences sister to the Ehrhartoideae (testing whether the duplication could have occurred just prior to the origin of the subfamily Ehrhartoideae), (4) *Oryza MADS17-like* sequences sister to the grass family (testing whether the duplication could have occurred just prior to the origin of the grasses), (5) *Oryza MADS17-like* sequences sister to the BEP clade (testing whether the duplication could have occurred just prior to the common ancestor of Bambusoideae, Ehrhartoideae, and Pooideae).

In addition, phylogenetic analysis could not determine precisely when the duplication of *zag3/*Td *AGL6.2* and *zag5/*Td *AGL6.1* happened. We tested whether *zag3/*Td *AGL6.1* and *zag5/*Td *AGL6.2* genes are sister taxa, meaning that the duplication occurred prior the divergence of maize and *Tripsacum*.

A priori constraint trees were created in MacClade (Maddison and Maddison 2003). Each constraint tree was tested against the unconstrained ML phylogeny using PAUP* version 4.0b10 (Swofford 2001). The SH test was performed using 1000 bootstrap replicates and the RELL (resampling estimated log likelihoods) option.

Tests for positive selection (tabulated results at Supplemental Tables 6-9 bellow)
The tests are based on estimates of the ratio of non-synonymous to synonymous substitutions (dN/dS, or ω). If this ratio is appreciably less than 1, then we infer that the

protein has been subject to purifying selection, such that mutations causing amino acid changes have been selectively eliminated. If the ratio is near 1, we infer that selection pressures are relaxed, and if the ratio is greater than 1, we infer that there has been selection for diversification (positive selection).

The best-supported tree obtained from Bayesian inference analysis was pruned to include only full-length sequences, and likelihood scores were calculated and statistically compared using the program codeml from the PAML package, version 4 (Yang, 2007). PAML calculates the likelihood of the data given the tree under a set of increasingly complex models of evolution. We began with the simplest model (M_0), which calculates a single ω ratio averaged over the entire tree (Yang et al., 1998). We compared this to a set of models that allow the ω ratio to vary among sites (among codons or amino acids in the protein) (Nielsen and Yang 1998; Yang et al. 2000). Model 1a assumes two site classes with $0 < \omega_0 < 1$ and $\omega_1 = 1$, Model 2a is like 1a but also assumes positive selection, Model 3 uses three site classes, Model 7 assumes variable selection among sites, and Model 8 is like Model 7, but with the addition of positive selection. We repeated this set of tests on an alignment including all sequences but excluding the MADS box, and on another alignment including only the C terminus of all sequences.

We also wanted to test for positive selection on particular branches of the *AGL6-like* gene tree. In particular, we were interested in testing for positive selection along all branches subsequent the *AGL6*/Os *MADS6* and Os *MADS17*. For this test we used the following models that incorporate heterogeneity over sites and branches: Model A (assumes $0 < \omega_0 < 1$ estimated from the data and $\omega_1 = 1$) and Model B (determines ω_0 and ω_1 as free parameters estimated from the data). We tested the data set that included only the IKC regions and excluded the MADS-box, which we had shown to be largely invariant.

Models were compared using the likelihood ratio test statistic ($2\Delta \ln L$).

Tajima's relative rate test (tabulated results at Supplemental Tables 10 bellow)

To test whether Os *MADS17/*Os *MADS6,* as well as *zag5/zag3* duplicates show differences in evolutionary rates, we used the test proposed by Tajima (1993) using MEGA4 (Tamura et al., 2007). This method compares three sequences, where one of them is an outgroup sequence. The test compares the identical sites in all three

sequences (m_{iii}), the divergent sites in all three sequences (m_{ijk}), the unique differences in sequence A (m_{ijj}), the unique differences in sequence B and the unique differences in the outgroup sequence. Statistical significance among these is assessed under the χ^2 distribution. We compared the evolutionary rate between Os *MADS17* vs. Os *MADS6* and *zag5* vs. *zag3* using Es *AGL6* and Os *MADS6* as outgroups, respectively.

Supplemental Table 5. Results of the Shimodaira-Hasegawa test preformed to evaluate whether we could statistically reject alternative hypotheses for the timing of the Os *MADS6/*Os *MADS17* duplication and *ZAG3/ZAG5* duplication. Statistically worse trees as compared to the best tree are marked with an asterisk (*), and *P* values < 0.05.

Tree	-ln Likelihood	Difference from best tree (-ln *L*)	*P* value
Likelihood tree (GTR+I+G)	8550.63754	(best)	
Oryza MADS17-like sequences sister to *Oryza MADS6* clade	8586.81569	36.17815	0.000*
Oryza MADS17-like sequences sister to the Oryzeae clade sequences	8579.31828	28.68074	0.004*
Oryza MADS17-like sequences sister to the Ehrhartoideae subfamily	8572.32382	21.68628	0.020*
Oryza MADS17-like sequences sister to the grass family	8551.18172	0.54418	0.691
Oryza MADS17-like sequences sister to the BEP clade	8572.40916	21.77162	0.020*
*zag3/*Td *AGL6.1* and *zag5/*Td *AGL6.2* are sister taxa	8551.78152	1.14398	0.327

Supplemental Table 6. Likelihoods and estimated parameters under different site models of codon substitution using the pruned data set with sequences that expand the MIKC regions. Abbreviations: -ln L, log likelihood, p, parameter; Kappa (ts/tv), transition/transversion ratio; NA, non applicable; ω, dN/dS value calculated under each model and applied to all branches in the phylogeny. Parameters in parenthesis are not free parameters.

Model	p	-ln L	Kappa (ts/tv)	ω	Additional Parameters Calculated
0	1	-4129.210037	2.72999	0.0954	NA
1a (neutral)	2	-4245.967313	2.69268	0.4632	$p_0 = 0.53680$, ($p_1 = 0.46320$)
2a (positive)	4	-4245.967313	2.69267	0.4632	$p_0 = 0.53682$, $p_1 = 0.46318$, ($p_2 = 0.00000$) $\omega = \infty$
3 (discrete)	3	-4015.407265	1.81912	0.1158	$p_0 = 0.54898$, ($p_1 = 0.35404$), $p_2 = 0.09698$ $\omega_0 = 0.01390$, $\omega_1 = 0.13578$, $\omega_2 = 0.61991$
7 (β)	2	-4054.198096	1.80986	0.1162	$p = 0.33480$, $q = 2.45264$
8 (B + ω)	4	-4054.328221	1.79949	0.5511	$p_0 = 0.99940$, $p = 0.33622$, $q = 2.45648$, ($p_1 = 0.00060$), $\omega = 724.93092$

Supplemental Table 7. Likelihoods and estimated parameters under different site models of codon substitution using the data set excluding the MADS-box. Abbreviations: -ln L, log likelihood, p, parameter; Kappa (ts/tv), transition/transversion ratio; NA, non applicable; ω, dN/dS value calculated under each model and applied to all branches in the phylogeny. Parameters in parenthesis are not free parameters.

Site Model	p	-ln L	Kappa (ts/tv)	ω	Additional Parameters Calculated
0	1	-3842.679439	2.09356	0.1317	NA
1a (neutral)	2	-3784.514745	2.15909	0.1977	$p_0 = 0.88116$, $(p_1 = 0.11884)$
2a (positive)	4	-3784.514745	2.15909	0.1977	$p_0 = 0.88116$, $p_1 = 0.11884$, $(p_2 = 0.00000)$ $\omega = \infty$
3 (discrete)	3	-3770.470138	2.01294	0.1590	$p_0 = 0.61960$, $(p_1 = 0.27508)$, $p_2 = 0.10532$ $\omega_0 = 0.04262$, $\omega_1 = 0.20315$, $\omega_2 = 0.72797$
7 (β)	2	-3777.500304	1.99916	0.1636	$p = 0.54167$, $q = 2.70239$
8 (B + ω)	4	-3777.500402	1.99916	0.1636	$p_0 = 1.00000$, $p = 0.54167$, $q = 2.70239$ $(p_1 = 0.00000)$, $\omega = 6.48257$

Supplemental Table 8. Likelihoods and estimated parameters under different site models of codon substitution using only the C-terminus. Abbreviations: -ln L, log likelihood, p, parameter; Kappa (ts/tv), transition/transversion ratio; NA, non applicable; ω, dN/dS value calculated under each model and applied to all branches in the phylogeny. Parameters in parenthesis are not free parameters.

Site Model	p	-ln L	Kappa (ts/tv)	ω	Additional Parameters Calculated
0	1	-1640.637362	2.15397	0.1994	NA
1a (neutral)	2	-1690.315486	3.46592	0.7867	$p_0 = 0.21335$, $(p_1 = 0.78665)$
2a (positive)	4	-1690.318441	3.46590	0.7866	$p_0 = 0.21337$, $p_1 = 0.78663$, $(p_2 = 0.00000)$ $\omega = \infty$
3 (discrete)	3	-1618.117196	2.03426	0.2106	$p_0 = 0.70167$, $(p_1 = 0.29833)$, $p_2 = 0.000000$ $\omega_0 = 0.10034$, $\omega_1 = 0.46658$, $\omega_2 = 999.000$
7 (β)	2	-1614.406920	2.06628	0.2117	$p = 0.76756$, $q = 2.81030$
8 (B + ω)	4	-1614.497092	2.06632	2.1553	$p_0 = 0.99758$, $p = 0.76772$, $q = 2.81123$, $(p1 = 0.00242)$, $\omega = 804.09372$

Supplemental Table 9. Hypothesis tested using likelihood ratio tests. Abbreviations: $2\Delta \ln L$, the likelihood ratio statistic; df, degrees of freedom (is the difference in the number of parameters calculated under the models being compared).

Model	Data set	H$_0$(null)	H$_1$ (alternate)	$2\Delta \ln L$	df	P value ($\chi 2$)
Site Models						
	MIKC					
		0	3	227.60	4	0.000
		1a	2a	0.00	2	1.000
		7	8	-0.26	2	1.000
	IKC					
		0	3	144.41	4	0.000
		1a	2a	0.00	2	1.000
		7	8	0.00	2	1.000
	C-terminus					
		0	3	45.04	4	0.000
		1a	2a	0.00	2	1
		7	8	-0.18	2	1
Branch site Models						
	IKC	**Os *MADS17***				
		Model A null	A	-12.46	2	1.000
		Model B null	B	-14.42	1	1.000
		AGL6/*Os *MADS6				
		Model A null	A	-11.42	2	1.000
		Model B null	B	-14.42	1	1.000
		Gain of palea expression				
		Model A null	A	-10.19	2	1.000
		Model B null	B	-8.87	1	1.000

Supplemental Table 10. Results from Tajima's relative rates test. The asterisk indicates *P* values less than 0.05 is often used to reject the null hypothesis of equal rates between lineages. dN/dS ratio was estimated using codeml as implemented in PAML 3.14 package (Yang 1997).

Test	Gene	dN/dS = ω	Unique sites	*P* value
ZAG5 vs *ZAG3*	*ZAG5*	0.09049	7	0.36571
	ZAG3	0.08171	4	
Os *MADS17* vs Os *MADS6*	Os *MADS17*	0.57442	25	0.01963*
	Os *MADS6*	0.21785	11	

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