ORIGINAL ARTICLE

AGL6-like MADS-box Genes are Sister to AGL2-like MADS-box Genes

Sangtae Kim^{1*}, Pamela S. Soltis² and Douglas E. Soltis^{2,3*}

¹School of Biological Sciences and Chemistry, and Basic Science Institute, Sungshin University, Seoul 142-732, Korea ²Department of Biology, University of Florida, Gainesville FL 32611-7800, USA ³Florida Museum of Natural History, University of Florida, Gainesville FL 32611-7800, USA

Received: April 16, 2013 / Accepted: June 30, 2013 © Korean Society of Plant Biologists 2013

Abstract AGL6-like genes form one of the major subfamilies of MADS-box genes and are closely related to the AGL2 (Eclass) and SQUA (A-class) subfamilies. In Arabidopsis, AGL6 and AGL13 have been reported from the AGL6 subfamily, and AGL6 controls lateral organ development and flowering time. However, little is known about homologs of these genes in basal angiosperms. We identified new AGL6-like genes from several taxa from gymnosperms, basal angiosperms, monocots, and eudicots. These genes were analyzed together with previously reported AGL6-like genes. Structural analyses showed 1) a one-aa (amino acid) gap in the I-domain in all AGL6-like genes relative to AGL2-like and SQUA-like genes, 2) a seven-aa insertion in the C-domain of genes from asterids, and 3) a one-aa insertion in the C-domain of genes from gymnosperms. Broad phylogenetic analyses strongly showed that AGL6-like genes are sister to AGL2like genes, and SQUA-like genes are sister to these two groups. The phylogenetic tree of AGL6-like genes generally tracks organismal phylogeny as inferred from multigene data sets; several gene duplications were detected in angiosperms (e.g., within Magnoliales), and one duplication was detected in gymnosperms. We hypothesize that the split between AGL6-like and AGL2-like genes occurred at least 290-309.2 mya based on our phylogenetic tree and the fossil record.

Key words: AGL2, AGL6, Gene phylogeny, MADS-box, SQUA

Introduction

MADS-box genes encode transcription factors which play

important roles in developmental control in plants, animals, and fungi (for reviews, see Shore and Sharrocks 1995; Theissen et al. 1996; Riechmann and Meyerowitz 1997; Theissen et al. 2000; Ng 2001; Theissen 2001; De Bodt et al. 2003). These genes encode a highly conserved domain (MADS domain), of approximately 55 amino acids, that is involved in recognition and binding to a specific DNA region (CArG boxes) (West and Sharrocks 1999). Functions of MADS-box genes vary. In plants, some MADS-box genes are involved in the regulation of floral organ identity, predicted by the ABCDE model in Arabidopsis (AP1, AP3, PI, AG, SHP1, SHP2, STK, SEP1, SEP2, SEP3, and SEP4) (Coen and Meyerowitz 1991; Colombo et al. 1995; Pelaz et al. 2000; Theissen 2001; Ditta et al. 2004). Examples of additional known functions of plant MADS-box genes are the regulation of floral meristem identity (AP1) (Gustafsonbrown et al. 1994), the timing of flower initiation (FLC) (Michaels and Amasino 1999; Alvarez-Buylla et al. 2000), and fruit, leaf, and root development (PkMADS1, FUL, and ANR1) (Gu et al. 1998; Zhang and Forde 2000; Prakash and Kumar 2002).

The MADS-box gene family can be subdivided into two major classes termed Type I and Type II genes (Alvarez-Buylla et al. 2000). Both types of genes have been found in animals, fungi, and plants. Plant type II genes are also called MIKC-type genes (Munster et al. 1997) because these genes share a conserved structural organization: MADS, Intervening, Keratin-like, and C-terminal domains. Two different types of MIKC-type genes, MIKC^C-type and MIKC*-type, are recognized via the characterization of MADS-box genes from a club moss (Lycopodium) and a moss (Physcomitrella), respectively (Henschel et al. 2002; Kwantes et al. 2012). MIKC*-type MADS proteins have a longer I-domain region than those of MIKC^C. The presence of MIKC^C-type as well as MIKC*-type genes in both lycophytes (the sister group to all other vascular plants) and mosses suggests that a gene duplication generated these two gene groups before the divergence of mosses (and perhaps all bryophytes) and

^{*}Corresponding authors; Sangtae Kim and Douglas E. Soltis Tel: +82-2-920-7699 and +1-352-273-1963

E-mail : amborella@sungshin.ac.kr and dsoltis@ufl.edu

vascular plants (Henschel et al. 2002). Phylogenetic studies of MIKC^C-type genes recognized 14 major clades (Becker and Theissen 2003; Nam et al. 2003; Pařenicová et al. 2003; Kim et al. 2005a). Becker and Theissen (2003) suggested names for these clades (subfamilies) based on the first clade member that was identified: STMADS11, AGL17, GGM13, DEF, GLO, AG, AGL12, SQUA, AGL2, AGL6, TM8, TM3, AGL15, and FLC. In most studies, these major clades are relatively well supported whereas the relationships among the clades are poorly supported (e.g., Becker and Theissen 2003; Nam et al. 2003; Pařenicová et al. 2003; Kim et al. 2005a; Gramzow et al. 2012). In most cases, members of each clade share similar expression patterns and have closely related functions. For example, members of the DEF/GLO clade are responsible for B-function in floral organ identity, and those of the AGL2 (also referred to as SEPALLATA) clade confer E-function. Therefore, the establishment of each clade by gene duplication, diversification, and fixation probably was an important step toward the establishment of floral homeotic functions (Theissen et al. 1996).

Among the MIKC^C-type MADS-box genes, AGL6 homologs represent one of the major subfamilies and form a monophyletic group in recent phylogenetic analyses (e.g., Becker and Theissen 2003; Nam et al. 2003; Pařenicová et al. 2003; Kim et al. 2005a; Rijpkema et al. 2009; Li et al. 2010; Gramzow et al. 2012). These genes are closely related to the AGL2 (E-class) and SQUA (A-class) subfamilies of MADSbox genes. Conflicting relationships among these three groups have been reported in previous phylogenetic analyses: in some cases AGL6 is sister to AGL2 (e.g., Becker and Theissen 2003; Nam et al. 2003; Gramzow et al. 2012; Fig. 1), and in other analyses AGL6 is sister to SQUA and AGL2(e.g., Pařenicová et al. 2003; Kim et al. 2005a; Fig. 1). However, in most cases these conflicting relationships were not strongly supported, and in all previous studies these three



Fig. 1. Two different relationships among AGL2, AGL6, and SQUA subfamilies of MADS-box genes as suggested in previous studies. (A) AGL6 is sister to AGL2 (e.g., Becker and Theissen 2003; Nam et al. 2003; Gramzow et al. 2012). (B) AGL6 is sister to SQUA and AGL2 (e.g., Pařenicová et al. 2003; Kim et al. 2005). For names of subfamilies, we followed Becker and Theissen (Becker and Theissen 2003).

groups form a clade regardless of their interrelationships (e.g., Winter et al. 1999; Becker and Theissen 2003; Nam et al. 2003; Kim et al. 2005a; Kim et al. 2005b). In the *AGL6*-like genes, recent phylogenetic analyses showed the duplication history of the *AGL6*-like genes: one at the base of the core eudicots resulting in *euAGL6* and *AGL6*-like gene clades, one during basal angiosperm diversification, and two in monocot evolution (Viaene et al. 2010).

Unlike other major subgroups of MADS-box genes, AGL6 homologs have not been investigated extensively, and their functions are not completely characterized. In Arabidopsis, AGL6 (At2g45650) and AGL13 (At3g61120) have been reported from the AGL6 subfamily (Ma et al. 1991; Rounsley et al. 1995). AGL6 has recently been shown to control 1) lateral organ development and flowering time (Koo et al. 2010), 2) circadian clock (Yoo et al. 2010), and 3) negative regulation of the FLC/MAF clade genes and positive regulation of FT (Yoo et al. 2011). For AGL13, broad expression including all floral organs and leaves (especially strong expression in ovules) has been reported (Rounsley et al. 1995). In Petunia, SEPALLATA-like function of petunia AGL6 (PhAGL6) has been reported (Rijpkema et al. 2009). However, AGL6 and AGL13 homologs in basal angiosperms have rarely been reported and their functions remain obscure.

Studies of MADS-box gene protein-protein interactions in Arabidopsis (de Folter et al. 2005) showed that the AGL6 protein has an interaction pattern closely resembling that of APETALA1, suggesting that this protein plays a role in the flowering program. This hypothesis is strengthened by the fact that over-expression of OMADS1 and HoAGL6 (from Oncidium and Hyacinthus, respectively), which are included in the AGL6 subfamily, resulted in early flowering and loss of inflorescence indeterminacy in Arabidopsis (Hsu et al. 2003; Fan et al. 2007). OsMADS6, an AGL6-like gene from rice, also plays a role in the flowering program: it was strongly expressed in the floral meristem at early stages, and osmads6 mutants displayed altered palea identity, extra glume-like or mosaic organs, abnormal carpel development, and loss of floral meristem determinacy (Ohmori et al. 2009; Reinheimer and Kellogg 2009; Li et al. 2010). In core eudicots, gene expression studies showed that AGL6-like genes acquired expression in vegetative tissues, while expression of its paralog, euAGL6, remains predominantly confined to reproductive tissues (Viaene et al. 2010).

In this study, we report 13 new *AGL6*-like genes from phylogenetically pivotal taxa in angiosperm evolution, examine their structure, analyze these new sequences together with previously reported *AGL6*-like genes, and compare the results with previously reported phylogenetic trees. We consider the evolution and diversification of *AGL6*-like genes in a phylogenetic context.

Results

Sequence Structure

Thirteen new AGL6-like sequences were identified in this study from Zamia vazquezii (Za.va.AGL6.1 and Za.va.

AGL6.2), Welwitschia mirabilis (We.mi.AGL6), Nuphar advena (Nu.ad.AGL6), Illicium parviflorum (Il.pa.AGL6), Magnolia grandiflora (Ma.gr.AGL6.2; previously reported Ma.gr.AGL6 in Kim et al. (2005a) was treated as Ma.gr.AGL6.1), Liriodendron tulipifera (Li.tu.AGL6), Eupomatia bennettii (Eu.be.AGL6-1 and Eu.be.AGL6-2), Acorus americanus

Table 1. Sequences of *AGL6*-like genes used in this study. Angiosperm species are arranged by families and higher groups according to the AGP III system (APGIII 2009). Newly identified genes in this study are indicated in **bold**.

Classification	Taxa	Gene name	GenBank accession Number	n Reference
GYMNOSPERMS Cycadales				
Zamiaceae	Zamia vazquezii	Za.va.AGL6.1 Za.va.AGL6.2	KC899695 KC899696	This study. This study.
Ginkgoales				
Ginkgoaceae	Ginkgo biloba	GbMADS1 GbMADS8	AB029463 AB029470	Unpublished. Unpublished.
Gnetales				-
Gnetaceae	Gnetum gnemon	GGM9	AJ132215	Winter et al. (1999)
		GGMII	AJ132217	Winter et al. (1999)
Welwitschiaceae	Welwitschia mirabilis	GpMADS3 We.mi.AGL6	AB022665 KC899694	This study.
Coniferales Pinaceae	Picea abies	DAL1	X80902	Tandre, Albert et al. (1995)
	Pinus resinosa	MAD1	Y09611	Liu et al. (1997), Electronic Plant Gene Register PGR97-032
	Pinus radiata	PrMADS2	U42400	Mouradov et al. (1996), Electronic Plant Gene Register PGR96-124
		PrMADS3	U76726	Mouradov et al. (1997), Electronic Plant Gene Register PGR97-032
ANGIOSPERMS				
Amborellales				
Amborellaceae Nymphaeales	Amborella trichopoda	Am.tr.AGL6	AY936234	Kim et al. (2005)
Nymphaeaceae Austrobailevales	Nuphar advena	Nu.ad.AGL6	KC899697	This study.
Schisandraceae	Illicium parviflorum	Il.pa.AGL6	KC899698	This study.
MAGNOLIIDS Laurales		-		
Lauraceae	Persea americana	Pe.am.AGL6.1	DQ660395	Chanderbali et al. (2006)
		Pe.am.AGL6.2	DQ660396	Chanderbali et al. (2006)
Magnoliales				
Magnoliaceae	Magnolia grandiflora	Ma.gr.AGL6.1	AY936233	Kim et al. (2005)
	Manadia babwa	Ma.gr.AGL6.2	KC899699	I his study.
	(-M) praecocossima)	MPMAD33	AB030043	Onpublished.
	(-m. praecocossima)	MnMADS4	AB050646	Unnublished
	Michelia figo	MfAGL6A	AY306157	Litt and Irish (2003)
	interieta jugo	MfAGL6B	AY306158	Litt and Irish (2003)
	Liriodendron tulipifera	Li.tu.AGL6	KC899700	This study.
Eupomatiaceae	Eupomatia bennettii	Eu.be.AGL6-1	KC899701	This study.
*		Eu.be.AGL6-2	KC899702	This study.
Piperales				
Saururaceae MONOCOTS	Houttuynia cordata	HcAGL6	AB089160	Unpublished.
Acorales	A		V.C.900702	This study
Acoraceae	Acorus americanus	Ac.am.AGLb	KC899/03	i nis study.

318

Table 1. Continued

Classification	Таха	Gene name	GenBank accessic Number	n Reference
Asparagales				
Agapanthaceae	Agapanthus praecox	ApMADS3	AB079261	Unpublished.
Asparagaceae	Asparagus officinalis	ÂOM3	AY383559	Unpublished.
Hyacinthaceae	Hyacinthus orientalis	HoAGL6	AY591333	Unpublished.
Iridaceae	Crocus sativus	AGL6a	EF041505	Unpublished.
		AGL6b	EF041506	Unpublished.
COMMELINIDS Arecales				-
Arecaceae	Elaeis guineensis	AGL6-1	AY739701	Unpublished.
	5	mads4	AJ581469	Unpublished.
Poales				*
Poaceae	Dendrocalamus latiflorus	MADS17	AY599754	Unpublished.
		MADS18	AY599755	Unpublished.
Arecaceae Poales Poaceae	Hordeum vulgare	HvAGL6	AY541067	Unpublished.
	Lolium perenne	LpMADS4	AY198329	Petersen et al. (2004)
	Orvza sativa	OsMADS6	U78782	Unpublished.
			(=AP004178)	Unpublished.
		OsMADS17	AF109153	Moon et al. (1999)
		000000000000	(=AF095646)	Unpublished
			(=AL606688)	Feng et al. (2002)
			$(=\Delta V 551918)$	Unnublished
	Pogannua	PaMADS1	AF372840	Unpublished
	Triticum aestivum	TaMADS12	AB007505	Murai et al. (1998), Electronic Plant Gene Register PGR98-159
	Tea mays	ZAG3	I 46397	Mena et al. (1995)
	Lea mays	ZAG5	L46398	Mena et al. (1995)
Zingiberales				
Musaceae EUDICOTS Papunculales	Musa acuminata	MuaMADS2	AY941799	Unpublished.
Panaveraceae	Eschscholzia californica	Es ca AGI 6	KC800704	This study
Ranunculaceae	Rammenlus hulhosus	Rh4GI 6	AV306184	Litt and Irish (2003)
Core endicots	Kanančalas bulbosas	RUAGLO	A1500104	Ent and mish (2003)
Savifragalas				
Saxifragagaga	Dibas sanguinaum	Disa ACI 6	VC800705	This study
	Ribes sanguineum	KI.SU.AGL0	KC 899703	This study.
Vitalaa				
Vitales	1641	14.1140.02	A E272600	$\mathbf{P}_{\mathbf{a},\mathbf{a},\mathbf{a}} = \mathbf{a}_{\mathbf{a},\mathbf{a}} \left(2 0 0 2 \right)$
Villaceae	vilis vinijera	VVMAD55	AF3/3002	Boss et al. (2002)
FABIDS				
Cucurbitales			V.000070/	
Cucurbitaceae	Cucumis sativus	Cu.sa.AGL6	KC899706	This study.
Fabales	Di		12/00/1000	
Fabaceae	Pisum sativum	PEAMS	AY884289	Hecht et al. (2005)
Rosales				
Rosaceae	Malus domestica	MdMADS11	AJ000763	Yao et al. (1999)
MALVIDS				
Brassicales				
Brassicaceae	Arabidopsis thaliana	AGL6	M55554	Ma, Yanofsky et al. (1991)
		AGL13	U20183	Rounsley et al. (1995)
	Brassica oleracea	BoAGL6a	AJ508055	Unpublished.
		BoAGL6b	AJ508409	Unpublished.
ASTERIDS				
LAMIIDS				
Lamiales				
Oleaceae	Syringa vulgaris	SvAGL6	AY306188	Litt and Irish (2003)
Solanales				
Solanaceae	Solanum lycopersicon	SIMBP6	TC146409*	Hileman et al. (2006)

Table 1. Continued

Classification	Taxa	Gene name	GenBank accession Number	Reference
CAMPANULIDS Asterales	Petunia × hybrida	pMADS4	AB031035	Tsuchimoto et al. (2000)
Asteraceae	Chrysanthemum × morifolium Gerbera sp.	CDM104 grcd3	AY173062 AJ784157	Unpublished. Unpublished.

*tomato EST library number (http://tigr.org/tigr-scripts/tgi/T_index.cgi?species=tomato).

(Ac.am.AGL6), Eschscholzia californica (Es.ca.AGL6), Ribes sanguineum (Ri.sa.AGL6), and Cucumis sativus (Cu.sa.AGL6) (Table 1). Numbers following gene names indicate multiple homologs in each taxon. Because the two sequences of *E. bennettii* differ by one nucleotide, we treated them as different alleles (multiple clones were identified for each allele). Two pairs of sequences in *Z. vazquezii* and *M. grandiflora* were treated as different genes because they showed relatively high sequence differences, respectively (25% and 29% divergence in amino acid and DNA sequences between Zamia homologs and 15% and 17% sequence divergence between Magnolia homologs). Furthermore, each number of a pair was placed in a different clade in the phylogenetic tree (see phylogenetic analyses).

Aligned sequences of *AGL6-*, *AGL2-*, and *SQUA-*like genes showed that the first 20 amino acids of the I-domain were well aligned, as was the MADS-domain. In the I domain, a one-aa gap was detected in all *AGL6* sequences except a sequence from *Ranunculus* (AY306184) (Fig. 2A). In the 5' end of the K-domain region, a seven-aa insertion was found only in the *AGL6* from *Petunia*, *Lycopersicon*, *Syringa*, *Chrysanthemum*, and *Gerbera*, all asterids (APG III 2009) (Fig. 2B). In the same region, a gymnosperm-specific one-aa insertion was also detected (Fig. 2B).

Phylogenetic Analyses

In all phylogenetic analyses, AGL2-like genes were sister to AGL6-like genes, and SQUA-like sequences were sister to the clade of AGL2 + AGL6 (Fig. S1, summarized in Fig. 3). When we used TM3-like genes as the outgroup, the sistergroup relationship between AGL6-like and AGL2-like genes was supported with 71% ML bootstrap and a posterior probability of 0.94 (Fig. 3A). When we used AG/AGL12 genes as the outgroup, this relationship was weakly supported by ML bootstrap analysis, but the Bayesian posterior probability was 0.95 (Fig. 4B). In both analyses, the AGL6 + AGL2 + SQUA clade is highly supported, indicating a close relationship among these three gene groups (Fig. 3).

For intensive analyses of the *AGL6* group, various phylogenetic analyses were performed using selected *AGL2*-like genes as the outgroup (Fig. 4). Our phylogenetic tree of

AGL6 genes generally tracks organismal phylogeny as inferred from multigene molecular data sets (e.g., Soltis et al. 1999, 2000, 2011). Gymnosperm genes were sister to angiosperm genes, and these two clades were highly supported (posterior probabilities of 0.99 and 1.0, respectively). In the gymnosperm clade, two major lineages were clearly recognized, and these two clades had high posterior probability (1.0 and 0.96, respectively; Fig. 4). Each sublineage in the gymnosperm clade contains sequences from the four major gymnosperm lineages (Soltis et al. 2005): Ginkgo, cycads (Zamia), conifers (Pinus and Picea), and Gnetales (Gnetum and Welwitschia) (Soltis et al. 2005; Fig. 4), representing an ancient gene duplication in the common ancestor of gymnosperm AGL6. Although a duplication at the base of the eudicots was detected in a recent phylogenetic analysis of AGL6-like genes focused on core eudicots (Viaene et al. 2010), it is not shown in our tree because some core eudicot genes detected from recent genome studies (e.g., genes from Vitis, Populus, and Citrus) were not included in our study. Instead, localized gene duplications were detected in our tree: Magnoliales, Brassicaceae, and potentially Lauraceae (Fig. 4, large stars), respectively. Many recent duplications were also detected at the genus or species levels (Fig. 4, small stars). Our tree agrees well with that from a recent study focused on monocot MADS-box genes (Li et al. 2010). However, supporting values (posterior probabilities) for the eudicot and monocot clades in our tree are much higher: 1.0 rather than >0.5 for eudicots and 0.96 rather than >0.5 for monocots. Gaps and insertions recognized in the sequence matrix were synapomorphic characters in relevant clades (Fig. 4, gray bars on the nodes).

Discussion

Evolution of *AGL6*-like Genes in the MADS-box Gene family

Similar to previous studies (Becker and Theissen 2003; Nam et al. 2003; Pařenicová et al. 2003; Kim et al. 2005a; Gramzow et al. 2012), our phylogenetic analyses revealed a close relationship among *AGL6-*, *AGL2-* (E-class), and *SQUA-* (A-

(A)					I	
()			M	ADS-domain		I-domain
	(BoAGL6b.Brassica BoAGL6a.Brassica	MGRGRVENKRIENKINRQVTFSKRR MGRGRVENKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIVFS: NGLLKKAYELSVLCDAEVALIVFS:	SRGKLYEFGSVG SRGKLYEFGSVG	VERTIERVHRCVNCSVTNNRP
		AGL6.Arabidopsis AGL13.Arabidopsis	MGRGRVEMKRIENKINRQVTFSKRR MGRGKVEVKRIENKITROVTFSKRK	NGLLKKAYELSVLCDAEVALTIFS:	BRGKLYEFGSVG	IESTIERYNRCYNCSLSNNKP
		MdMADS11.Malus	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVGLIIFSS	SRGKLY e fasag	MSKTLERYQRCSFTPPENSI
		pMADS4.Petunia	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALTIFS: NGLLKKAYELSVLCDAEVALTIFS:	SRGKLYEFGSRG SRGKLYEFGNAG	ITKTLERYQRCCLNPQDNCG
		SIMBP6.Solanum SvAGL6.Svringa	ELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCEAEVALIIFSS NGLLKKAYELSVLCDAEVGLIIFSS	BROKLYEFOSAO Broklyefosao	ITKTLERYQRCCLNPQDNCG
		CDM104.Chrysanthemum	MORORVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVGLIIFSS	SROKLYEFGSVO	VMKTLERYQRCCFNPQDNNN
		Es.ca.AGL6.Eschscholzia	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKHYELSVLCDHEVGLIIFS: NGLLKKAYELSVLCDAEVGLIIFS:	SROKLYEFOSVO BRGKLCEFASAG	MNRTLERYQRCCFNPQDNNH
		RbAGL6.Ranunculus AGL6.1.Elaeis	MORORVELKRIENKINROVTESKRR	EMSVLCDAEVGLIIFSA	ARGKLYEFASAG	MSRTLERYHKNSFSNQDSNLAIDR-
		Ac.am.AGL6.Acorus	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIVFS	BRGKLYEFGSAG	MSKTLERYQRCSYNPQDNNA-A
AGL6		AOM3.Asparagus	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKHYELSVLCDHEVHLIVFS: NGLLKKHYELSVLCDHEVHLIIFS:	SRGKLYEFGSHG SRGKLYEFGSAG	TSKTLERYQRCCYTSQDASI-A TSKTLERYQRCCYTSQDAAI-A
		ApMADS3.Agapanthus TaMADS12.Triticum	MGRGRVELKRIENKINRQVTFSKRR MGRGRVELKRIENKINROVTFSKRR	NGLLKKAYELSVLCDAEVALIVFSS NGLLKKAYELSVLCDAEVALIIFSS	SRGKLYEFGSAG	TSKTLERYQRCCYTSQDATI-A
		HvAGL6.Hordeum	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFSS	SROKLYEFOSAO	TTKTLERYQHCCYNRQDSN-GR
		PaMADS1.Poa	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFS	BROKLYEFOSHO	TTKTLERYQHCCYNAQDSN-SA
		MADS17.Dendrocalamus MADS18.Dendrocalamus	MGRGKVELKRIENKINRQVTFSKRR MGRGNVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFSS NGLLKKAYELSVLCDAEVALIIFSS	BROKLYEFOSAG Broklyefosag	ISKTLERYQHCCYNAQD-NN-A
		ZAG5.Zea	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFS	ROKLYEFOSAG	VTKTLERYQHCCYNAQDSNNSA
		OsMADS6.Oryza	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFS	SRGKLYEFGSAG	ITKTLERYQHCCYNAQDSNN-A
		AGL6b.Crocus	MGRGRVELKRIENKINRQVTFSKRR MGRGRVELKRIENKINROVTFSKRR	NGLLKKAYELSVLCDAEVALIIFSS NGLLKKAYELSVLCDAEVALIIFSS	SRGKLYEFGSAG Broklyefgsag	INKTLEKYNSCCYNAQGSN-SA TPKTLERYORCCYTSODSTI-A
		AGL6a.Crocus Pe am AGL6 1 Persea	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFS	BROKLYEFOSAG	TPKTLERYQRCCYTSQDSTI-A
		MfAGL6B.Michelia	VQLKRMENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFS	SRGKVFEFGNHO SRGKLYEFGSAG	TNKTLERYQRCCYTPQDVVV-S
		Pe.am.AGL6.2.Persea Am.tr.AGL6.Amborella	KRIENKINRQVTFSKRR	NGLLKKAYELSILCDAEVALIIFSS	SROKLYEFOSVO	TNKTLERYQRCCYNPQDANI-S
		GGM9.Gnetum	MGRGRVQLRRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFST	TROKLYEFASSS	MSKTLERYEKCSYSMQENAS-T
		DAL1.Picea	MGRGRVQLRR I ENK I NRQVTFSKRR MGRGRVQLRR I ENK I NRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFS1 NGLLKKAYELSVLCDAEVALIIFS1	TROKLYEFASSS Troklyefasss	-MSKTLERVEKCSVSMQENAS-T -MNKTLERVEKCSVAMQDTTOVS
		PrMADS3.Pinus Za.va.AGL6.1.Zamia	MGRGRVQLRR I ENK I NRQVTFSKRR	NGLLKKAYELSVLCDAEVALTIFST	TROKLYEFASSS	MNKTLERVEKCSVRMQDTTGVS
		GbMADS1.Ginkgo	MGRGRVQLRRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIVFST	TROKLYEFASSS	MNKTLERVEKCSYRVQDTN-VS
		MAD1.Pinus	MGRGRVELKRIENKINRQVTFSKRR MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFSS NGLLKKAYELSVLCDAEVALIIFSS	SRGKLYEFGSAG Srgklyefgsag	-MLKTLERYQKCSYVLQDAT-VS MLKTLERYQKCSYVLQDAT-VS
		GbMADS8.Ginkgo GGM11.Gnetum	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALTIFS:	BRGKVYEFGSAG	MTKTLERYQKCSYVLQDVN-VS
		We.mi.AGL6.Welwitschia	MGRGRVELKRIENKINRQVTFSKRR	NGLLKKAYELSVLCDAEVALIIFS	BRGKLYEFGSVG	TLKTLERYQKCSFALQEGNTTS
	È	GRCD1.Gerbera	MGRGRVELKRIENKINROVTFSKRR MGKGRLELKRIENKINROVTFAKRR	NGLLKKAYELSVLCDAEVALIIFS: NGLLKKAYELSVLCDAEVALIVFS1	SRGKLYEFGSAG Troklyefssts:	MISKTLERYOKCSYVLODVA-IC SMLKTLERYEKCSFGPPEQR-RPA
		NsMADS3.Nicotiana Es.ca.AGL9.Eschscholzia	MORGRVELKRIENKINRQVTFAKRR	NGLLKKAYELSVLCDAEVALIIFSM NGLLKKAYELSVLCDAEVALIIFSM	ROKLYEFCSSS:	SMLKTLERYQKCNYGAPETN-IS SMFKTLERYQKSNYGAPETN-VS
AGL2		LMADS3.Lilium HcSEP1 Houtturnia	MGRGRVELKRIENKINRQVTFAKRR	NGLLKKAYELSVLCDAEVALIIFS	RGKLYEFSSTS	SMMRTLERYQKCNYGRPETN-IV
		Am.tr.AGL2.Amborella	MGRGRVELKRIENKINRQVTFAKRRI MGRGRVELKRIENKINRQVTFAKRRI	NGLMKKAFELSVLCDAEVALIVFS: NGLLKKAYELSVLCDAEVALIIFSM	RGKLYEFCSSSI RGKLYEFCSTS	GMMKTIERYQKCNYGAPEAT-VS SMVKTLERYQKCNYGALETN-VP
		BM7.Hordeum	MGRGKVELKRIENKISRQVTFAKRR MGRGKVEMBRIENKISROVTFAKRR	NGLLKKAYELSLLCDAEVALIIFS(BRORLFEFSSSS	CHYKTLERYRSCNYNSQDAR-AP CHYKTLERYRTCNSNSQEAT-PO-Y-
	l	AGL2 Arabidopsis NMADS4 Nicotiana	MGRGRVELKRIENKINRQVTFAKRR	NGLLKKAYELSVLCDAEVALIIFS	RGKLYEFCSSSI	NMLKTLDRYQKCSYGSIEVNNKP
	\geq	AP1 Arabidopsis	HORORVELKE I ENKINEQVITENKER	NGLLKKHYELSVLCDHEVHLTTFSS	SHOKLSEPCSIS	SHHOTLEKYOOCSYHSLDPH-OS
	(CI HI Circo	MGRGRVQLKRIENKINRQVTFSKRR	AGLLKKAHEISVLCDAEVALVVFSH	IKGKLFEYSTDSI	CMEKILERVERVSVAERLIAPES-DV
00114	ſ	SLM4.Silene SCM1.Solanum	MGRGRVQLKRIENKINRQVTFSKRR MGRGRVQLKNIENKINRQVTFSKRR MGRGRVQLKRIENKINROVTFSKRR	AGLLKKAHEISVLCDAEVALVVFSH SGIIKKAHEISVLCDAEVALIIFSH SGLLKKAHEISVLCDAEVGLIVFS1	IKGKLFEYSTDSI IRGKLFDFASDSI IKGKLFEYATDSI	CHEKILERVERVSYRERLIRPES-DV CHEKILERVERVCYREKQLRSNDP-D CHERLERVERVSFREKQLY-PTDHT
SQUA		SLM4.Silene SCM1.Solanum NsMADS1.Nicotiana DEFH28.Antirrhinum	MGRGRVQLKRIENKINRQVTFSKR MGRGRVQLKHIENKINRQVTFSKR MGRGRVQLKRIENKINRQVTFSKR MGRGRVQLKRIENKINRQVTFSKR	AGLLKKAHEISVLCDAEVALVVFSH SGIIKKAHEISVLCDAEVALIIFSH SGLLKKAHEISVLCDAEVGLIVFST SGLLKKAHEISVLCDAEVGLIVFST	HKGKLFEYSTDSI HRGKLFDFASDSI TKGKLFEYATDSI TKGKLFEYSTDSI	CHEKILERVERVSVAERLIAPES-DV CHEKILERVERVCVAEKQLASNOP-O CHERLLERVERVSFAEKQLV-PTOHT CHERILERVERVSVAERQLT-ATODE
SQUA		SLM4.Silene SCM1.Solanum NsMADS1.Nicotiana DEFH28.Antirrhinum AtFL.Arabidopsis	MORORVQLKRIEMKINRQVTFSKRR MororvQLKRIENKINRQVTFSKRR MororvQLKRIENKINRQVTFSKRR MororvQLKRIENKINRQVTFSKRR MororvQLKRIENKISRQVTFSKRR	AGLLKKAHE I SVLCDAEVALVVFSH SGI I IKKAHE I SVLCDAEVAL I I FSH SGLLKKAHE I SVLCDAEVGL I VFST SGLLKKAHE I SVLCDAEVGL I VFST SGLLKKAHE I SVLCDAEVAL I VFST TGLVKKAQE I SVLCDAEVAL I VFSF	HKOKLFEYSTDSI HROKLFDFASDSI TKOKLFEYATDSI TKOKLFEYSTDSI TKOKLFEYSTESI PKOKLFEYSAGSI	CHEKILERVERVSVAERLIRPES-DV CHEKILERVERVSVAEKQLASNDP-D CHERLLERVERVSVAEKQLV-PTDHT CHERILERVERVSVAERQLT-ATODE SHERILERVERVSVAERQLT-ATODE SHERILERVERSRVAEQDIFTPN-LD
SQUA		SLM4.Silene SCM1.Solanum NsMADS1.Nicotiana DEFH28.Antirrhinum AtFL.Arabidopsis MpMADS15.Magnolia OsMADS15.Oryza	MORONYOLKI JENKI INROYTSIKRA MORONYOLKI JENKI NROYTSIKRA MORONYOLKI JENKI NROYTSIKRA MORONYOLKI JENKI NROYTSIKRA MORONYOLKI JENKI RROYTSIKRA MORONYOLKI JENKI NROYTSIKRA MORONYOLKI JENKI NROYTSIKRA	AOLLIKAHE ISVLCDAEVALIVFSI SOLLIKAHE ISVLCDAEVALIIFSI SOLLIKAHE ISVLCDAEVALIIFSI SOLLIKAHE ISVLCDAEVALIVFSI SOLLIKAHE ISVLCDAEVALIVFSI TOLVIKAQE ISVLCDAEVALIVFSI AOLLIKAHE ISVLCDAEVAIVFSI	HKGKLFEYSTDSH HRGKLFDFASDSH TKGKLFEYATDS TKGKLFEYSTDSH TKGKLFEYSTGS TKGKLFEYSAGS TKGKLYEYSTDSH PKGKLYEYATDSH	CHEKILERVEYVSYAERLIAPES-DV CHEKILERVERVCYHEKQLRSNDP-D CHEKILERVERVSYAERUQLT-PTDHT CHERILERVERVSYAERUQLT-ATODE SHERILERVERVSYAERUTSO-HE SHERILDIVERSAYAQQDIPTPH-LD RHSRILERVERVSYAERULVSO-PE
SQUA		SLM4.Silene SCM1.Solanum NsMADS1.Nicotiana DEFH28.Antirrhinum AtFL.Arabidopsis MpMADS15.Magnolia OsMADS15.Oryza	MORONYQLKE EMKINGYTFSKRE MORORYQLKE EMKINGYTFSKRE MORORYQLKE EMKINGYTFSKRE MORORYQLKE EMKINGYTFSKRE MORORYQLKE EMKISGYTFSKRE MORORYQLKE EMKINGYTFSKRE MORORYQLKE EMKINGYTFSKRE MORORYQLKE EMKINGYTFSKRE	AOLLKKAHE I SVLCDAEVALVYES SOLLKKAHE I SVLCDAEVAL I I FSS SOLLKKAHE I SVLCDAEVAL I VFST SOLLKKAHE I SVLCDAEVAL I VFST TOLVKKAHE I SVLCDAEVAL I VFST HOLLKKAHE I SVLCDAEVAN I VFST	HKOKLFEYSTDSI HROKLFOFASDSI TKOKLFEYSTDSI TKOKLFEYSTDSI TKOKLFEYSTESI PKOKLFEYSTDSI PKOKLYEYSTDSI PKOKLYEYATDSI	CHERILERVERVESHERLIAPES-DV CHERILERVERVCYREKQLRSNDP-D CHERILERVERVSYREKQLV-PTOHT CHERILERVERVSYREKQLTSD-HE SHERILERVERVSYREKQLTSD-HE SHERILERVERVSYREKQLTSD-HE SHERILERVERVSYRERELVESO-PE RHDRILERVERVSYREKALISRES-E
SQUA	B	SLMA Silene SCM1 Solanum NSMADS1 Nicotiana DEFH28 Antirrhinum AFL Arabidopsis MpADS15. Magnolia OsMADS15. Oryza	HORORVQL.KR LENK I MRQYTPSKRA HORORVQL.KR LENK I MRQYTPSKRA	AGLLKRAHE I SVLCDAEVAL VYES SOLLKRAHE I SVLCDAEVAL I I FSS SOLLKRAHE I SVLCDAEVAL I I FSS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS TOLLKRAHE I SVLCDAEVAN I VFSS TOLLKRAHE I SVLCDAEVAN I VFSS	HKGKLFEYSTDS/ HRGKLFDFASDS/ TKGKLFEYATDS/ TKGKLFEYSTDS/ TKGKLFEYSTGS/ TKGKLFEYSAGS/ TKGKLFEYSAGS/ TKGKLYEYATDS/	CHERILERVERVSYRELLAPES-DV CHERILERVERVSYRENQLASNDP-D CHERILERVERVSYRENQL-PTOHT CHERILERVERVSYRENQLT-ATODE SHERILERVERVSYRENQLTSO-HE SHERILERVERVSYRENQLPTR-LD RHSRILERVERVSYRENLISAES-E HHDRILERVERVSYRENALISAES-E
SQUA ((B)	SLMA Silene SCMI Solanum NsMDS1 Nicoliana DEFH28 Antirhinum AFL Arabidopsis MpMADS15. Magnolia OsMADS15. Oryza	новолуца, на неж и парутрязкая новолуца, на неж и парутрязкая	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAN I VFSI TOLLKRAHE I SVLCDAEVAN I VFSI	HKOKLFEVSTOSH HROKLFEVSTOSH HROKLFEVSTOSH TKOKLFEVSTOSH TKOKLFEVSTOSH KOKLFEVSTOSH PKOKLVEVSTOSH PKOKLVEVSTOSH	CHER: LERVERYSYMERIL, IAPES-DV INER: LERVERYSYMERIQ, T-PTOHT CHER: LERVERYSYMERIQ, T-PTOHT CHER: LERVERYSYMERIQ, T-ATODE SHER: LERVERYSYMERIQ, T-STOS-HE SHER: LERVERYSYMERIE, VLSO-PE RHDK: LERVERYSYMERIE, VLSO-PE RHDK: LERVERYSYMERIE, VLSO-PE COMMAIN
SQUA (B)	SLMA Skene SCMI Solanum NSMADS1.Nicotiana DEFH28 Antirrhinum AFL Arabidoosis MpIADS15.Magnolia OsMADS15.Oryza BoAGL6b.Brassica	новолуоц ил енк и научтрыка новолуоц ил енк илаутрыка новолуоц ил енк илаутрыка	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI HOLLKRAHE I SVLCDAEVAL I FSI HOLLKRAHE I SVLCDAEVAN I VFSI KERQLGD I NKQLKI I KF	HKOKLPEYSTOSI HROKLPEYSTOSI HROKLPEYSTOSI TKOKLPEYSTOSI TKOKLPEYSTOSI TKOKLPEYSTOSI TKOKLVEYSTOSI PKOKLVEYSTOSI PKOKLVEYSTOSI PKOKLVEYSTOSI C- -ERGOHR	CHEFLERVERVSVÆRELLAPES-DV UNERLERVERVSVÆRELAPEND-D CHEFLERVERVSFÆRELQ-P-TOHT CHEFLERVERVSFÆRELQ-P-TOHT ENERLERVERVSVÆRELQ-FATODE SHERILERVERVSVÆRELVELTSDS-HE SHERILEVERVSVÆRELVELTSDS-HE HNDVELEVERVSVÆRELVELSS-PE HNDVELEVERVSVÆRELLISAES-E
SQUA ([В)	SLMA Skene SCMI Solanum NSMADS1.Nicotiana DEFH28 Antirrhinum AFL Arabidoosis MpMADS15.Magnolia OsMADS15.Nagnolia OsMADS15.Oryza BoAGL6b.Brassica BoAGL6b.Brassica AGL6A.rabidopsis	новолуоц ил енк и научтрыка новолуоц ил енк илауттрыка новолуоц ил енк илаутрыка новолуоц ил енк или или енк или енк новолуоц или енк или енк или енк или новолуоц или енк или новолуоц или енк или енк или новолуоц или новолуоц или енк или новолуоц или енк или новолуоц или новолуоц или енк или новолуоц или енк или новолуоц или енк или новолуоц или новолуоц или енк или новолуоц или енк или новолуоц или н	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I VFSI SOLLKRAHE I SVLCDAEVAL I VFSI HOLLKRAHE I SVLCDAEVAN I VFSI HOLLKRAHE I SVLCDAEVAN I VFSI KERQLOD I NKQLK I KF KERQLOD I NKQLK I KF	HKOKL FEYSTOSI HROKL FORSOSI HROKL FEYSTOSI TKOKL FEYSTOSI TKOKL FEYSTOSI TKOKL FEYSTOSI TKOKL FEYSTOSI TKOKL VEYSTOSI PKOKL VEYSTOSI PKOKL VEYSTOSI C- -EROOHR - EROOHR - ETEOHR	CIMERICIENVERVSVAREILIAPES-DV CIMERILEINERVSVAREUQL-P-DDHT CHERILEINERVSPAREUQL-P-TDHT CHERILEINERVSPAREUQL-P-TDHT CHERILEINERVSVAREUXLTSDS-HE SHERILEUVERVSVAREUXLTSDS-HE SHERILEUVERVSVAREUXLTSDS-HE HTDN:LEINVERVSVAREUXLUSG-PE HTDN:LEINVERVSVAREUXLISG-PE COMMAIN
SQUA (B)	SLMI Siene SCMI Solanum NSMADSI Nicotiana DEFH28 Antirthinum AFL Arabidosis MpIADS15. Nagnolia OsMADS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica AGL6A. abidopsis AGL13. Arabidopsis	Наралуация нежи інярутряхая Наралуация нежи інярутряхая Вакцая парки-тауннеемецья Анцтая парк-тауннеемецья Анцтая парк-тауннеемецья Анцтая парк-тауннеемецья Анцтая парк-тауннеемецья Анцтая парк-тауннеемецья	AGLLKKAHE I SVLCDAEVAL I FSI SOLLKKAHE I SVLCDAEVAL I FSI HOLLKKAHE I SVLCDAEVAN I FSI KERQLGD I NKQLK I KF	HCOLL PEYSTOS: IROKL FOR ADDS: IROKL FOR ADDS: IROKL FEYSTOS: IROKL FEYSTOS: IROKL FEYSTOS: IROKL VEYSTOS: IROKL VEYSTOS: IROKL VEYATDS: IROKL VEYATD	СПЕР : LEIVERVSVAEL, I APES-DV CITER : LEIVERVSVAEVQL * APBDP-D CHERLLEIVERVSPAEVQL * APDOT CHERLLEIVERVSVAERULT * ATOS-HE SHERLLEIVERVSVAERULT * ATOS-HE SHERLLEIVERVSVAERULT * ATOS-HE SHERLLEIVERVSVAERULT * ATOS-HE HIDKILEIVERVSVAERULT * ATOS-HE COMMAIN
SQUA (B)	SLM4 Silene SCM1 Solanum NstADS1 Nicotiana DEFH28 Antimhium AFL Arabidopsis MMADS15. Oryza BoAGL&b Brassica BoAGL&b Brassica AGL& Arabidopsis MdMADS11. Malus VMADS25. Vitis b	новалуоц ка некк і марутрэкля новалуоц ка некк і марутрэкля акц татараях - тоучнествоц ля акц татараях - тоучнествоц ля акц татараях - тоучнествоц ля акц татараях - тоучнествоц ля акц затараях - тоучнествоц ля	AGLLKKAHE I SVLCDAEVAL I FS3 SOLLKKAHE I SVLCDAEVAL I FS3 SOLLKKAHE I SVLCDAEVAL I FS3 SOLLKKAHE I SVLCDAEVAL I VF33 KERQLOD I NKQLK I KF	HONL PEYSTOS: IROKL PEYSTOS: IROKL PEYSTOS: IROKL PEYSTOS: IROKL PEYSTOS: IROKL VEYSTOS: IROKL PEYSTOS: IROKL PEYSTOS:	СПЕР : LEIVERVSVAEL, I APES-DV CITER I LEIVERVSVAEVQ.AFVA.RNDP-D CITER I LEIVERVSVAEVQ.T-ATODE SITER I LEIVERVSVAEVQ.T-A
SQUA (B)	SLMA Skene SCMI Solanum NsMADS1 Nicotiana DEFH28 Antimhium AFL Arabidopsis MAMDS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica BoAGL6b. Brassica AGL6 Arabidopsis MdMADS11. Malus VVMADS3. Vitis PIADD54. Petunia SIMBP6. Solanum	пололуоц ил енк и науттрыка пололуоц и пололуоц и пололуоц и пололуоц и пололуо	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI KEERQLGD I NKQLK I KF KEERQLGD I NKQLK I K	HONL PERSON HONL PERSON TROLL PERSON TROLL PERSON TROLL PERSON HONL PERSON HONL PERSON HONL VERSON HONL VERSON HONL VERSON HONL VERSON HONL VERSON HONL VERSON HONL VERSON HONL PERSON HONL PERSON HON	СПЕР I LE INVERSIVAEUL I APES-DV CITER I LE LE INVERSIVAEUL A APES-DV CITER I LE IVERVSYBEIGUT - ATODE CITER I LE IVERVSYBEIGUT - ATODE SIREI I LE IVERVSYBEIGUT - BOS-HE SIREI I LE IVERVSYBEIGUT - BOS-HE SIREI I LE IVERVSYBEIGUT - BOS-HE ANDICI I LE IVERVSYBEIGUT - BOS-HE COMMAIN
SQUA (sterids (C	SLM4 Skene SCM1 Solanum NsMADS1 Nicoliana DEFH228 Arithnium Afrabidopsis MpMADS15.Magnolia OsMADS15.Magnolia OsMADS15.Chyza BoAGL6b.Brassica BoAGL6b.Brassica BoAGL6b.Brassica AGL6 Arabidopsis MMADS1.Malus VVMADS3.Vitis pMADS4.Petunia SIMBP6.Solanum SvAGL6.Syringa	наралуац ил енк и научтрыка наралуац ил енк и научтрыка ац татарак - таучнеенер ил ац татарак - таучнеенер ил ац татарак - таучнеенер ил ац татарак - таучнеенер ил ариалуарка - таучнеенер ил ариалуа	AGLLKRAHE I SVLCDAEVAL VFS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I VFSS SOLLKRAHE I SVLCDAEVAL I VFSS HOLLKRAHE I SVLCDAEVAL I VFSS HOLLKRAHE I SVLCDAEVAN I VFSS KERQLOD I NKQLK I KF KERQLOD I NKQLK I KF KERQLOD I NKQLK I KF KERQLOD I NKQLK I K	HKOKL FEYSTOS HKOKL FEYSTOS HKOKL FEYSTOS HKOKL FEYSTOS HKOKL FEYSTOS HKOKL FEYSTOS HKOKL VEYSTOS HKOKL VEYSTOS HK	СПЕР I LE IVERYSYAE IL I PPES-DV INE I LE IVERYSYAE IL I PPES-DV CHEFL LE IVERYSYAE IL I PPES CHEFL LE IVERYSYAE IL I PAESA SHEFI I LE IVERYSYAE IL I PAESA SHEFI I LE IVERYSYAE IL I PAESA SHEFI I LE IVERYSYAE IL I SAESAE SHOW I LE IVERYSYAE I SAESAE SHOW
SQUA (Asterids (C	SLMA Skene SCMI Solanum NsMDDS1 Nicoliana DEFH28 Aniinhium Aff-Larabidopsis MpMADS15. Magnolia OsMADS15. Magnolia OsMADS15. Oryza BoAGL68. Brassica BoAGL68. Brassica AGL6. Arabidopsis AGL13. Arabidopsis MMADS4. Petunia SiMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthemum grd3. Gerbera Era ex 401 6 Escherbehter	наявачоц ка сексі накуттрізка наявачоц ка сексі накуттрізка наявача жила таража таутрізка ац. татаража таутрізка ац. татаража таутрізка ац. татаража таутнестор ац. затаража таутріства ац. татаража таутнестор ац. затаража таутнестор ац. затаража таутнестор ац. затаража таутнестор ац. затаража таутнестор ац. запаража таутнестор ац. зап	AGLLKRAHE I SVLCDAEVAL VFS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I VFSS SOLLKRAHE I SVLCDAEVAL I VFSS HOLLKRAHE I SVLCDAEVAL I VFSS HOLLKRAHE I SVLCDAEVAN I VFSS HOLLKRAHE I SVLCDAEVAN I VFSS KERQLOD I NKQLK I KF KERQLOD I NKQLK I K	икак. редуктова тикак. редуктова тикак. редуктова тикак. редуктова тикак. редуктова тикак. редуктова тикак. уедуктова тикак. уедук	CHEFLERVERVSVÆELLAPES-DV CHEFLERVERVSVÆELAPES-DV CHEFLERVERVSVÆEVALSVABPO-D CHEFLELEIVERVSVÆEVALSVABPO-D CHEFLELIVERVSVÆEVALSVABPO-D CHEFLEVERVSVÆEVALSVABPO-D CHEFLEVERVSVÆEVASVABPO-D CHEFLEVEVASVABPO-D CHEFLEVEVASVABPO-D CHEFLEVEVASVABPO-D CHEFLEVERVSVÆEVASVABPO-D CHEFLEVEVASVABPO-D CHEFLEVEVASVABPO-D CHEFLEVEVASVABPO-D CHEFLEVEVASVABPO-D CHEF
SQUA (Asterids (C	SLMA Skene SCMI Solanum NsMDS1 Nicoliana DEFH28 Antirhinum AffL Arabidopsis MpMADS15. Magnolia OsMADS15. Magnolia OsMADS15. Oryza BoAGL68. Brassica BoAGL68. Brassica AGL63. Arabidopsis MdMADS11. Malus VMADS3. Vitis PMAD54. Petunia SIMBP8. Solanum SvAGL6. Syringa CDM104. Chrysanthemum gred3. Gethera Es.ca. AGL6. Eschscholzia	новолуоц ил енк и научтрыка новолуоц ил енк и научтрыка общоторах - тоучнееноц ил общоторах - тоучнееноц и общоторах - тоучнееность	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI NOLLKRAHE I SVLCDAEVAN I FSI NOLLKRAHE I SVLCDAEVAN I FSI KERQLOD I NVQLKI KF KERQLOD I NVQLKI KF KERQLOD I NVQLKI KF KERQLOD I NVQLKI K KERRLGOLMKQLKI VSIELSSI KERHLGOLMKQLKI VSIELSSI KERBLGOHKALKI VSIELSSI KERBLGOHKALKI I VSIELSSI KERBLGOHKALKI I VSIELSSI	иконстретатово тиконс	CHEFLERVERVSVÆRELLAPES-DV CHEFLLERVERVSVÆRELLAPES-DP-D CHEFLLERVERVSVÆRELLAPEND-D CHEFLERVERVSVÆRELLAPEND-D CHEFLERVERVSVÆRELLAPEND- BIERNILEVERVSVÆRELLAPEND- BIERNILEVERVSVÆRELLAPEND- BIERNILEVERVSVÆRELLSS-PE HNDVILERVERVSVÆRELLSS-PE HNDVILERVERVSVÆRELLSS-PE HNDVILERVERVSVÆRELLSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILERVERVSVÆRELSS-PE HNDVILSS-PE LIVERSS-PE LIVERSS-PE HNDVILSS HND
SQUA (Asterids (G	SLMA Stene SCMI Solanum NEHUSS Antirrhinum AFL Azakiopsis MpIADS15. Magnolia OsMADS15. Magnolia OsMADS15. Oryza BoAGL68. Brassica BoAGL68. Brassica BoAGL68. Brassica AGL13. Arabidopsis AGL13. Arabidopsis MdMADS11. Malus VVMADS3. Vits PhADS4. Petunia SIMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthemum grcd3. Gerbera Es.ca. AGL6. Eschscholia RAGL6. Elseis AGL.6. Elseis Ac.am. AGL6. Acorus	наралуац ка ценк і інаучтрякая наралуац ка ценк і інаучтраная наралуац ка ценк і інаучтраная наралуац ка ценк і інаучтраная наралараная	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I VFSI SOLLKRAHE I SVLCDAEVAL I VFSI HOLLKRAHE I SVLCDAEVAL I VFSI HOLLKRAHE I SVLCDAEVAL I VFSI HOLLKRAHE I SVLCDAEVAL I VFSI KERQLOD I HKQLK I KF KERQLOD HKQLK I K	««««. Feynsos» «««». Feynsos» ««». Feynsos» «». Feynsos»	CITER : LEIVERSYSTERIL : I PPES-DV CITER : LEIVERSYSTERIOL - PTDHT CHER I LEIVERSYSTERIOL - PTDHT CHER I LEIVERSYSTERIOL - PTDHT CHER I LEIVERSYSTERIOL - TODE SHER I LDIVERSYMEIXL : TOD-HE SHER I LDIVERSYMEIXL : SO-HE HIDDI : LEIVERSYSTERIEL : SO-HE HIDDI : SO-HE
SQUA (Asterids (G	SLMA Stene SCMI Solanum NsKADS1 Nicotiana DEFH28 Antimhium AFL Arabidopsis MANDS15 Nagnolia OsMADS15.Oryza BoAGL6b Brassica BoAGL6b Brassica AGL6 Arabidopsis AGL6 Arabidopsis AGL61 Arabidopsis MGMADS11.Malus VMADS4 Pritris SIMBP8-Setunia SVADL6.Syringa COM140-Chrysanthemum grd03.Gethera Esc.ca AGL6.Sechscholzia RAGL6.Rannulus AGL6.Rannulus AGL6.Acorus HoAGE 6.Hyacinthus	новолодска сексі накотразка новолодска сексі накотразка накотр	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I VFSI SOLLKRAHE I SVLCDAEVAL I VFSI SOLLKRAHE I SVLCDAEVAL I VFSI HOLLKRAHE I SVLCDAEVAL I VFSI KERQLOD I MKQLKI K KERQLGOI MKQLKI K KERQLGOUNGUKI K KERQ	HKKKLFRYSTSS HKKLFRYSTSS HKKLFRYSTSSS HKKLF	CITER : LEIVERNSVAREL, I APES-DV CITER : LEIVERNSVAREN, I APES-DV CITER : LEIVERNSVAREN, I ADS-ME BIR: LEIVERNSVAREN, I ADS-ME BIR: LEIVERNSVAREN, I ADS-ME BIR: LEIVERNSVAREN, I ADS-ME BIR: LEIVERNSVAREN, I ADS-ME COMMAIN
SQUA (Asterids (G	SLMA Stene SCMI Solanum NsMADS1 Nicotiana DEFH28 Antimhium AFL Arabidopsis MADS15. Oryza OsMADS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica AGL6 Arabidopsis MMADS15. Arabidopsis MMADS15. Malus VMADS3. Vitis PMADS4. Petunia SIMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthemum grd3. Gethera Es.ca. AGL6. Eschscholzia RAGL6. Ranueulus AGL6. Eschscholzia RAGL6. Ranueulus AGL6. Arabidopsis AGL6. Eschscholzia RAGL6. Ranueulus AGL6. Ranueulus AGL6. Ranueulus AGL6. Nacinthus AMADS3. Agapanthus	Наралуация енки инаучтрыкая наралуация енки инаучтрыкая наралуация енки инаучтрыкая наралуация енки инаучтрыкая наралуация енки влаучтрыкая наралуация енки влаучтрыкая наралуация енки влаучтрыкая наралуация енки влаучтрыкая наралуация енки влаучтрыкая анд татъраки таучнеемерыя анд таралуани таучнеемерыя анд таучая таучая таучая таучая анд таучая таучая таучая таучая таучая таучая таучая таучая анд таучая тауч	AGLLKRAHE I SVLCDAEVAL VFS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I VFSS SOLLKRAHE I SVLCDAEVAL I VFSS TOLLKRAHE I SVLCDAEVAL I VFSS TOLLKRAHE I SVLCDAEVAL I VFSS TOLLKRAHE I SVLCDAEVAL I VFSS TOLLKRAHE I SVLCDAEVAL I VFSS KERQLGD I NKQLK I KF KERQLGD I NKQLK I KF KERQLGD I NKQLK I KF KERQLGD I NKQLK I K	((a), E(y)) ((a), E(y	СПЕР I LEIVERVSVAELI, I PPES-DV CITER I LEIVERVSVAEVQAEVQA. RNDP-D CHERILLEIVERVSVAEVQAEVQA. RNDP-D CHERILLEIVERVSVAERULT-ATODE SIREN LEIVERVSVAERULT-ATODE SIREN LEIVERVSVAERULT-SOS-HE SIREN LEIVERVSVAERULT-SO
SQUA (Asterids (G	SLM4 Skene SCM1 Solanum NsMDS1 Nicotiana DEFH28 Antinhium AFL Arabidopsis MpMADS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica BoAGL6b. Brassica AGL6 Arabidopsis MMADS15. Oryza CL6. Arabidopsis MMADS4. Petunia SiMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthemum grd3. Gerbera Es. ca. AGL6. Eschscholzia RAGL6. Reunuculus AGL6. Eschscholzia RAGL6. Reunuculus AGL6. Revisita RAGL6. R	Нарадуация енк і інауттрыкая нарадуация енк і інауттрыкая ала татарак - таутіветераля ала даяларак - таутіветераля ала таутарак - таутар	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FFSI TOLLKRAHE I SVLCDAEVAL I FFSI TOLLKRAHE I SVLCDAEVAL I FFSI TOLLKRAHE I SVLCDAEVAL I FFSI KERQLGD I NKQLK I K KERQLGD NKQLK K KERQ	KROKEPSTOSS KROKEPSTOSS KROKEPSTOS	СПЕР I LE IVER VSVAE IL I APES-DV CIRE I LE IVER VSVAE IL APES-DV INER I LE IVER VSVAE IL APES-DV CIRE I LE IVER VSVAE IL APES- SIRE I LE IVER VSVAE IL APES- SIRE I LE IVER VSVAE IL APES- ENDU IL E IVER VSVAE IL APES-E RHDU I LE IVER VSVAE IL APE
SQUA (Asterids (C	SLM4 Skene SCM1 Solanum NstADS1 Nicoliana DEFH28 Arithrihum Atrabidossis MpIADS15. Magnolia OsIAADS15. Magnolia OsIAADS15. Magnolia OsIAADS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica BoAGL6b. Brassica AGL6. Arabidopsis MIADS4. Petunia SMIDP6. Solanum SvAGL6. Syringa COM104. Chrysantherum grd3. Gethera Es ca AGL6. Eschscholia RbAGL6. Revisition RbAGL6.	наявачоц ка текс і падчтряская наявачоц ка текс і падчтряская акцаята одкая тексі наядчтряская акцаята одкаята с тачнівенео ная акцаята одкаята с тачнівонео ная акцаята с тачнівоне ная акцаята с тач	AGLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS HOLLKRAHE I SVLCDAEVAL I FSS KERQLOD I NKQLK I KF KERQLOD I NKQLK I K	KROLFEYSTESS KROLFEYSTESS KROLFEYSTESS KROLFEYSTESS KROLFEYSTESS KROLFEYSTESS KROLFEYSTESS KROLFEYSTESS KROLFEYSTESS KRONA	DTEFFICEINVERVESVAEELLIAPES-DV DTEFFICEINVERVESVAENULAPPO DTEFFICEINVERVESVAENULAPPO DTEFFICEINVERVESVAENULAPPO DTEFFICEINVERVESVAENULAPPO DTEFFICEINVERVESVAENULAPPO BITEFILIEUVERVSVAENULAPPO BITEFILIEU
SQUA (Asterids (G	SLMA Stene SCMI Solanum NsMDDS1 Nicoliana DEFH28 Artinhium Aff-Arabidopsis MpMADS15. Magnolia OsMADS15. Magnolia OsMADS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica BoAGL6b. Brassica AGL6 Arabidopsis MMADS1. Antional Status PMADS4. Petunia SiMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthermum grd3. Gerbera Es ca. ACL6. Eschechousia RAGL6. Eschechousia RAGL6. Branureulus AGL6. Tialexis ACL6. Arabidopsis AGL6. Branureulus AGL6. Eschechousia RAGL6. Branureulus AGL6. Hyacinthus AOM3. Agaragus HoAGL6. Hordeum HvAGL6. Hordeum LpMADS4. Lolium PaMADS1. Pod	наралуац ка текс і інауттрізка наралуац ка тексі інаутрізка наралуац ка тексі інарані наралі наралуа наралуац ка тексі інаралі наралі наралуа наралуац ка тексі інаралі наралі наралуа наралуац ка тексі інарані наралі наралуа наралуац ка тексі інарані наралі наралі наралі наралуа наралуац ка тексі інаралі наралі	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI NOLLKRAHE I SVLCDAEVAL I FSI KERQLOD I NIQLKI KF KERQLOD I NIQLKI K	KCRL FEYTERS K	DTEFLERVERVSVÆELLAPES-DV DTEFLERVERVSVÆELLAPES-DV TUFELLERVERVSVÆELLAPES-DV DTEFLLERVERVSVÆELLAPES-DE DTEFLELERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELLAPES-TATODE BITEFLERVERVSVÆELAPES-TATODE BITEFLERVERVERVERVERVERVERVERVERVERVERVERVERVE
SQUA (Asterids (G	SLMA Skene SCMI Solanum NsMDDS1 Nicoliana DEFH28 Antirhinum AtfL Arabidopsis MpMADS15. Magnolia OsMADS15. Magnolia OsMADS15. Magnolia OsMADS15. Oryza BoAGL68. Brassica BoAGL68. Brassica AGL6 Arabidopsis MMADS4. Petunia SiMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthemum grd3. Gethera Es.ca. AGL6. Eschobia RAGL6. Haleis ACM. J. Elaeis A.cam. AGL6. Acorus HoAGL6. Hordeum HAGDS1. Poid MADS1. Dendrocalamus XAGS1. Pudrocalamus MADS1. Dendrocalamus	Наралуац ка текс і інауттрізкая наралуац ка тексі інаутрізкая наралуац ка тексі інаутрізкая наралі наралуац ка тексі інаралі наралуац ка тексі інаралуац ка тексі інаралі ка тексі інаралуац ка тексі інараліац ка	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI KERQLGO I NNQLKI KF KERQLGO I NNQLKI KF KERQLGO I NNQLKI K	нконс редуктово тиски: реуктово тиски: реуктово тиски: реуктово тиски: реуктово тиски: реуктово тиски: черкатаво чиси: реуктово чиси:	DIRE I LEIVERVSVÆEL, I APES-DV DIRE I LEIVERVSVÆEU, A-PDOH TIKE I LEIVERVSVÆEU, A-PTOHT DIRE I LEIVERVSVÆEU, A-PTOHT DIRE I LEIVERVSVÆEU, A-TODOE BIER I LLOVERSVÆVEU, TODS-HE BIER I LLOVERSVÆVEU, TODS-HE DIRE I LEIVERVSVÆENEL, LSO-PE HNDI LEIVERVS HNDI LEIVERVS
SQUA (Asterids (C	SLMA Silene SCMI Solanum NsKADS1 Nicotiana DEFH28 Artinhium AFL Arabidopsis MADDS1 Nagnolia OsMADS15. Oryza BoAGL6b Brassica AGL6 Arabidopsis AGL6 Arabidopsis AGL6 Arabidopsis AGL6 Arabidopsis MRIANDS1 Sile Arabidopsis MRIANDS1 Sile Arabidopsis MRIANDS1 Sile Arabidopsis MRIANDS3 Vitis SWGL6 Syringa COM104 Chrysanthemum grd3 Serbera Esca AGL6 Resultscholzia RAGL6 Jeanus AGL6 Arabidopsis AGL6 Arabidopsis	Наралуац ка текс і інауттрізкая наралуац ка тексі інаутрізкая наралуац	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I VFSI SOLLKRAHE I SVLCDAEVAL I VFSI NOLLKRAHE I SVLCDAEVAL I VFSI NOLLKRAHE I SVLCDAEVAL I VFSI NOLLKRAHE I SVLCDAEVAL I VFSI KERQLGD I NNQLKI K	HKKKLEPHATES HKKLEPHATES HKKLEP	CITER : LEIVERYSYMEUL : I APES-DV CITER : LEIVERYSYMEUL : I APES-DV CITER : LEIVERYSYMEUL : APES-DV CITER : LEIVERYSYMEUL : TSDS-HE BIER : LEIVERYSYMEUL : TSDS-HE BIER : LEIVERYSYMEUL : SOS-HE BIER : LEIVERYSYMEUL : SOS-HE COMMINGENERYSYMEUL : SOS-HE CITER : LEIVERYSYMEUL : SOS-HE CITER : LEIVERYSYMEUL : SOS-HE CITER : SOS-FODF-H
SQUA (Asterids (C	SLMA Stene SCMI Solanum NsKADS1 Nicotiana DEFH28 Antimhium AFL Arabidopsis MADDS15. Oryza OsMADS15. Oryza OsMADS15. Oryza DAGL6a. Brassica BAGL6a. Brassica AGL6 Arabidopsis MSMADS15. Malus VMADS3. Vitis PMADS17. Vitis DAGL6. Syringa COM104. Chrysanthemum grd3. Gethera Es.ca. AGL6. Eschscholzia RAGL6. Branulus XAGL6. Eschscholzia RAGL6. Branulus AGL6. Eschscholzia RAGL6. Branulus AGL6. Branulus AGL6. Sechscholzia RAGL6. Ranuculus AGL6. Sechscholzia RAGL6. Ranuculus AGL6. Telaeis Acam. AGL6. Acadidation AGL6. Calanton DAGL6. Arabidopsis AGL6. Telaeis Acam. AGL6. Brancholzia RAGL6. Brancius AGL6. Telaeis Acam. AGL6. Acadidation AGL6. Telaeis ACAM. Asparagus AMADS3. Poca MADS17. Dendrocalamus AMDS18. Dendrocalamus ZAG5. Zea ZAG3. Zea OsMADS6. Orgza OsMADS6. Orgza	пололусция енк і інарутряская пололусция енк і інарутряская подалодих - точнівсі енсоція подалодих - точнівсі енсоція сі саралодих сі точнівсі енсоція сі саралодих сі сі сі сарасція сі саралодих сі с	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I VFSI TOLLKRAHE I SVLCDAEVAL I VFSI TOLLKRAHE I SVLCDAEVAL I VFSI TOLLKRAHE I SVLCDAEVAL I VFSI TOLLKRAHE I SVLCDAEVAL I VFSI KERGLGD I MKQLK I KF KERGLGD I MKQLK I K	HKKKLEPHATES HKKLEPHATES HKKLEP	CITER : LEIVERYSYAEIL, IAPES-DV CITER : LEIVERYSYAEIQL Y-PTOHT CITER : LEIVERYSYAEIQL Y-PTOHT CITER : LEIVERYSYAEIQL Y-PTOHT CITER : LEIVERYSYAEIQL Y-PTOHT CITER : LEIVERYSYAEIQL Y-DOE SHER : LDIVERSAWIEIX, ISS-HE SHER : LDIVERSAWIEIX, ISS
SQUA (Asterids (C	SLMA Stene SCMI Solanum NsMADS1 Nicotiana DEFH28 Artinhium AFL Arabidopsis MpMADS15 Nagnolia OsMADS15.Oryza BoAGL6b. Brassica BoAGL6b. Brassica AGL6 Arabidopsis MdMADS15.Oryza Classica AGL6 Arabidopsis MdMADS11.Malus VMADS3.Vitis PMADS4.Petunia SMBP6.Solanum SvAGL6.Syringa CDM104.Chrysanthemum grd3.Gethera Es.ca.AGL6.Eschscholzia RAGL6. Eschscholzia RAGL6. Eschscholzia RAGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Tealeris Ac.am. AGL6. Acatius AMADS1.Dendrocalamus MADS17. Dendrocalamus MADS17. Dendrocalamus ZAGS.Zea ZAG3.Zea OsMADS6.Oryza OsMADS6.Oryza OsMADS6.Oryza	пололусция енк и подутрязкая поди с подутрязкая подуторих - то и и тодутряеция подуторих - то и и тодутрешеция поди с подуторих - то и и тодутрешеция съсъяподия - то и тибориеция с	AGLLKRAHE I SVLCDAEVAL VFS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS KERQLGD I NKQLK I KF KERQLGD I NKQLK I K	(KOKLEPSTS) (KOKLEPST	CITER I LEIVERVSYAELL I APES-DV CITER I LEIVERVSYAEUL I APES-DV INFRI I LEIVERVSYAEUL I APES-DV CITER I LEIVERVSYAEUL I APES- SING I LEIVERVSYAEUL I SOS-HE SING I LEIVERVSYAEUL I SOS-HE SING I LEIVERVSYAEUL I SOS-HE SING I LEIVERVSYAEUL I SOS-SE ANDXI I LEIVERVSYAEUL I SOS I L ANDXI I LEIVERVS I LEIVERVSYAEUL I SOS I L ANDXI I LEIVERVS I LI SOS I L ANDXI I LEIVERVI I LEIVERVS I LI SOS I L ANDXI I LEIVERVS I LI
SQUA (Asterids (C	SLM4 Skene SCM1 Solanum NsMDS1 Nicotiana DEFH28 Artinhium AFL Arabidopsis MpMADS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica BoAGL6b. Brassica AGL6 Arabidopsis MMADS15. Oryza Cl. 13. Arabidopsis MMADS14. Detunia SMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthemum grd3. Gerbera Es. ca. AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Teaeis Aca. An AGL6. Acabidopsis AGL6. Arabidopsis MMADS4. Petunia SVAGL6. Syringa CDM104. Chrysanthemum grd3. Gerbera Es. ca. AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Teaeis Aca. An AGL6. Acabidopsis AMADS3. Agapanthus TAMADS4. Lolium PAMADS1. Poa MADS17. Dendrocalamus ZAG3. Zea CoMADS617. Oryza AGL6b. Crocus Pa. am AGL6. 1 Persea MAGL6. 1 Persea	наралуоц / ка енк / наруттря/ка наралуоц / ка енк / нарутря/ка наралуоц / нарутря/ка нарутря/ка наралуоц / нарутря/ка нарутря/	AGLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS KERQLGD I NKQLK I KF KERQLGD I NKQLK I KF KERQLGD I NKQLK I KF KERQLGD I NKQLK I KF KERQLGD I NKQLK I K	KROLF PATSON K	DTEF LE ELVERYSYMELL I APES-DV DTEF LE ELVERYSYMEUL I APES-DV DTEF LE LEVERYSYMEUL I APES-DV DTEF LE LEVERYSYMEUL I APES- BIEN I LE ELVERYSYMEUL I APS-TE BIEN I LE ELVERYSYMEUL I SAS-TE BIEN I LE ELVERYSYMEUL I SAS-TE BIEN I LE ELVERYSYMEUL I SAS-TE THOM I LE ELVERYSYMEUL I SAS-TE THOM I LE ELVERYSYMEUL I SAS-TE BIDD I LE ELVERYSYMEUL I SAS-TE THOM I LE ELVERYSYMEUL I SAS-TE DTEF SFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODFH FKSFODSH F
SQUA (Asterids (C	SLMA Silene SCMI Solanum NsMDDS1 Nicoliana DEFY28 Artinhium AIFL Arabidopsis MpIADS15. Chyza DefY28 Artinhium AIFL Arabidopsis MpIADS15. Chyza BoAGL6b. Brassica BoAGL6b. Brassica AGL6. Arabidopsis MIADS15. Chyza Cl. 13. Arabidopsis MIADS4. Petunia SiMBP6. Solanum SvAGL6. Syringa COM104. Chrysantherum grd3. Gerbera Es. ca. AGL6. Eschscholdza RbAGL6. Rununculus AGL6. T. Elaeis A. Cam. AGL6. Aconus HAGL6. Hyacinthus AMDS17. Dendrocalamus AMDS17. Dendrocalamus AMDS17. Dendrocalamus AGL65. Zea ZAG3. Zea CoMADS17. Dendrocalamus AGL66. Crocus AGL66. Presea MADS17. Dendrocalamus ZAGS. Zea ZAG3. Zea CoMADS6. Cryza AGL66. Crocus AGL66. Presea MAGL68. Michelia P. a. andL6. 2. Persea MIADS18. Peraeman MADS16. Persea MIADS16. 2. Persea MIADL67. Persea MIADL68. Michelia P. a. andL6. 2. Persea	INDROVOL IN LENK I INQVTFSKAR INDROVOL IN LENK I INQVTFSKAR INDROVOL IN LENK INQVTFSKAR INDROVOL INDROVOL INDROVOL INDROVOL IN LENK INDROVOL INDROVOL IN LENK INDROVOL INDROV	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI KERGLOO I NIQLK I KF KERGLOO I NIQLK I K	HIGHLERPATES HIGHLERPATES </td <td>DTEF LE ELVERYSYMELL I APES-DV DTEF LE ELVERYSYMEUL I APES-DV TOTEL LE ELVERYSYMEUL I APES-DV DTEF LE ELVERYSYMEUL I APES- BITE I LE ELVERYSYMEUL I APS-HE BITE I LE ELVERYSYMEUL I APS-HE BITE I LE ELVERYSYMEUEL VL SO-PE BITE I LE ELVERYSYMEUEL VL SO-PE BITORI LE ELVERYSYMEUEL LE SO BITORI LE ELVERYSYMEUEL VL SO-PE BITORI LE ELVERYSYMEUEL VL SO BITORI LE ELVERYSY</td>	DTEF LE ELVERYSYMELL I APES-DV DTEF LE ELVERYSYMEUL I APES-DV TOTEL LE ELVERYSYMEUL I APES-DV DTEF LE ELVERYSYMEUL I APES- BITE I LE ELVERYSYMEUL I APS-HE BITE I LE ELVERYSYMEUL I APS-HE BITE I LE ELVERYSYMEUEL VL SO-PE BITE I LE ELVERYSYMEUEL VL SO-PE BITORI LE ELVERYSYMEUEL LE SO BITORI LE ELVERYSYMEUEL VL SO-PE BITORI LE ELVERYSYMEUEL VL SO BITORI LE ELVERYSY
SQUA (Asterids (C	SLMA Stene SCMI Solanum NsMADS1 Nicoliana DEFH28 Arithihum Atrabidossis MpMADS15. Magnolia OsMADS15. Magnolia OsMADS15. Magnolia OsMADS15. Oryza BoAGL6b. Brassica BoAGL6b. Brassica BoAGL6b. Brassica AGL6. Arabidopsis MMADS15. Malus VMADS3. Vitis pMADS4. Petunia SIMBP6. Solanum SvAGL6. Syringa CDM104. Chrysantherum grd3. Gerbera Es ca AGL6. Eschschobia RbAGL6. Rounceluba RbAGL6. Rounceluba RbAGL6. Revision RbAGL6. Revision RbAGL7. Revision RbAGL6. Revision RbAGL7. Revision RbAGL	наралуац ил енк и наруттракар наралуац ил енк и нарутракар наралуац и или или или или или или или наралуац и или или или или или или или или или наралуац и или или или или или или или или или	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI NOLLKRAHE I SVLCDAEVAL I FSI NOLLKRAHE I SVLCDAEVAL I FSI KERQLOO I NIQLK I KF KERQLOO I NIQLK I KF KERQLOO I NIQLK I KF KERQLOO I NIQLK I K	KICALF (1975) KICALF	DTEFICIENVENSIONELLAPES-DV DTEFICIENVENSIONELLAPES-DV TOTELLENVENSIONEDULT-BND-D DTEFICIENVENSIONEDULT-BND-D DTEFICIENVENSIONEDULT-BND-H BND DTEFICIENVENSIONEDULT-BND-HE BND DTEFICSONEDULT-BND-HE BND DTEFICSONEDULT-BND BND DTEFICSONEDULT-BND BND DTEFICSONEDULT-BND BND DTEFICSONEDULT-BND BND
SQUA (subjosperms	Asterids (C	SLMA Stene SCMI Solanum NsKADS1 Nicotiana DEFH28 Artinhium AFL Arabidopsis MADDS1 Nicotiana DEFH28 Artinhium AFL Arabidopsis OsMADS15.Oryza BoAGL6b Brassica BoAGL6b Brassica AGL6 Arabidopsis AGL13 Arabidopsis AGL13 Arabidopsis AGL13 Arabidopsis MdHADS11 Mahus VMADS3 Vitis PMAD54 Petunia SIMBP6 Solanum SMGL6 Syringa CDM104 Chrysanthemum grd3 Gethera E s.ca AGL6 Eschechobia RDAGL6 Leschechobia RDAGL6 Loium PAMD51 Poa MADS18 Dendrocalamus AGL6 Acorus HaAGL6 Hordeum LMADS1 Loium PAMD518 Dendrocalamus MADS18 Dendrocalamus AGL6 J. Flees Dendrocalamus AGL6 J. Flees Dendrocalamus AGL6 J. Flees ADM3518 Dendrocalamus AGL6 J. Flees ZAG3 Zea ZAG3 Zea ZAG3 Zea ZAG3 Zea ZAG3 Zea ZAGB Crocus Pa am AGL6 J. Persea ZAGB Crocus Pa am AGL6 J. Persea AGL6 J. Persea	наралуац ка текс і інауттрізка наралуац ка тексі інаутрізка наралуац ка тексі інаралі ка тексі іна	AGLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS HOLLKRAHE I SVLCDAEVAL I FSS HOLLKRAHE I SVLCDAEVAL I FSS HOLLKRAHE I SVLCDAEVAL I FSS HOLLKRAHE I SVLCDAEVAL I FSS KERQLOO I NIQLKI K	HKKKLEPKATES HKKLEPKATES HKKLEP	CHEFLENVERVSVÆELLAPES-DV CHEFLENVERVSVÆELAPES-DV CHEFLENVERVSVÆELAP-DD CHEFLENVERVSVÆELA-TADDE SHEFLENVERVSVÆELA-TADDE SHEFLENVERVSVÆELA-TADDE SHEFLENVERVSVÆELA-TADDE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELALTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEFLENVERVSVÆELATTSDS-HE SHEVREN-HOORS-HE
SQUA (Asterids (C	SLMA Stene SCMI Solanum NsKADS1 Nicotiana DEFH28 Antimhium AFL Arabidopsis MADS15 Nicotiana OsMADS15 Oryza OsMADS15 Oryza OsMADS15 Oryza OsMADS15 Oryza OsMADS15 Oryza OsMADS2 Nitis StMBPB Solanum SvAGL6 Syringa COM104 Chrysanthemum grd3 Gethera Esca AGL6 Eschschobia RAGL6 Ranunulus AGL6 Stringa CoM104 Chrysanthemum grd3 Gethera Esca AGL6 Eschschobia RAGL6 Ranunulus AGL6 Syringa COM104 Chrysanthemum grd3 Gethera Esca AGL6 Sechschobia RAGL6 Ranunulus AGL6 Syringa CoM104 Chrysanthemum grd3 Gethera Esca AGL6 Ranunulus AGL6 Syringa CoM104 Chrysanthemum grd3 Sethera Esca AGL6 Beschschobia RAGL6 Ranunulus AGL6 Syringa CoM105 Chrysanthus AMADS17 Dendrocalamus MADS17 Dendrocalamus ZM35 Zea ZM35 Z	INDROVOLINE EMKI IMQVTFSIKA INDROVOLINE EMKI	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I VFSI TOLLKRAHE I SVLCDAEVAL I VFSI TOLLKRAHE I SVLCDAEVAL I VFSI TOLLKRAHE I SVLCDAEVAL I VFSI KERQLGD I MKQLK I KF KERQLGD I MKQLK I KF KERQLGD I MKQLK I KF KERQLGD I MKQLK I KF KERQLGD I MKQLK I K	HIGHLERPISTES	DIRE I LEIVERVSVÆRLI APES-DV DIRE I LEIVERVSVÆRUL APED DIRE I LEIVERVSVÆRUL APD-D DIRE I LEIVERVSVÆRUL AFDD-D DIRE I LEIVERVSVÆRUL AFDD-H BIR I LUDVERSAVHOUD (JPTPH-LD BIR I LUDVERSAVHOUD (JPTPH-LD DIS I LEIVENVSYMEREL (JSACS-RE FIC) - FOODH -FRA1005-H -FRA1
SQUA (Asterids (C	SLMA Stene SCMI Solanum NsMADS1 Nicotiana DEFH28 Archinhium AFL Arabidopsis MMADS1 Nicotiana DEFH28 Archinhium AFL Arabidopsis MADS15. Oryza OsMADS15. Oryza Col. 13. Arabidopsis MMADS15. Majos ptAD024. Petunia SIMBP6. Solanum SvAGL6. Syringa COM104. Chrysanthemum grd3. Gethera Es. ca. AGL6. Eschscholzia RbAGL6. Ranunulus AGL6. Eschscholzia RbAGL6. Ranunulus AGL6. Eschscholzia RbAGL6. Ranunulus AGL6. Eschscholzia RbAGL6. Ranunulus AGL6. State State Acam. AGL6. Acabide RbAGL6. Arabidopsis MMADS1. Pica RbAGL6. State RbAGL6. Arabidopsis AGL6. Tealenis Acam. AGL6. Schscholzia RbAGL6. Sagapanthus AMADS3. Horderum LpMADS1. Pica MADS1. Pica MADS1. Pica MADS1. Pica MADS1. Pica MADS1. Pica MADS1. Pica MADS1. Crocus P.a. m. AGL6. Amborella Persea MAGL6. Amborella Persea MAGL6. Amborella Persea MAGL6. Amborella Persea MAGL6. Amborella Persea MAGL6. Amborella Persea MAGL6. S. Persea MAGL6. Amborella Persea MAGL6. S. Picos P.a. MaGL6. 2. Persea PMADS3. Pinus Zava. AGL6. 1. Zamia GMMADS1. Jinkpo	INDROVOLINE EMKI IMQYTPSIAR INDROVOLINE EMKI	AGLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS KERQLGO I NKQLK I KF KERQLGO I NKQLK I KF KERQLGO I NKQLK I K	(KOLL FUNTOS) (KOLL F	DIRE I LEIVERVSVAELI I APES-DV DIRE I LEIVERVSVAEUL I APES-DV INE I LEIVERVSVAEUL I APES-DV DIRE I LEIVERVSVAEUL I APES- BIER I LEIVERVSVAEUL I SOS-HE BIER I LEIVERVSVAEUL I SOS-HE BIER I LEIVERVSVAEUL I SOS-HE INE I LEIVERVSVAEUL I SOS HE INE I LEIVERVAEUL I SOS HE
SQUA (Asterids	SLMA Stene SCMI Solanum NsMADS1 Nicotiana DEFH28 Archinhum AFL Arabidopsis MoMADS15. Oryza DeFH28 Archinhum AFL Arabidopsis MoMADS15. Oryza DeAGL68. Brassica AGL6. Arabidopsis MoMADS15. Oryza Classical Scheman SvAGL68. Syringa CDM104. Chrysanthemum grd3. Gethera Es. ca. AGL6. Eschscholzia RbAGL6. Ranuerulus AGL6. Eschscholzia RbAGL6. Reschendla RbAGL6. Rauerulus AGL6. Eschscholzia RbAGL6. Rauerulus AGL6. Eschscholzia RbAGL6. Rauerulus AGL6. Eschscholzia RbAGL6. Rauerulus AGL6. Eschscholzia RbAGL6. Rauerulus AGL6. Tealeris Ac. am. AGL6. Acabide Acam. AGL6. Arabide MADS17. Dendrocalamus MADS17. Dendrocalamus MADS17. Dendrocalamus ZAGS. Zea CMADS17. Oryza AGL68. Crocus P.a. am. AGL6. Amborella GMMS Gnetum GMADS3. Pinus Zav. AGL6. 1. Zamia GMADS3. Pinus	INDROVQLIA LENK I MQYTFSIAR INDROVQLIA LENK I MQYTFSIAR INDROVQLIA LENK I MQYTFSIAR INDROVQLIA LENK INQYTFSIAR INDROVQLIA LENK INDROVCLIA INDROVQLIA LENK INDROVCLIA	AGLLKRAHE I SVLCDAEVAL I FSS SOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS MOLLKRAHE I SVLCDAEVAL I FSS KERQLGO I NKQLK I KF KERQLGO I NKQLK I K	(KOKLEP(1)) (KOKLEP(1	СПЕР I LEIVERVSVÆELL I APES-DV CIER I LEIVERVSVÆEULA SNP-D CIER I LEIVERVSVÆEULA - PTOHT CIER I LEIVERVSVÆEULA - TATODE SINEN I LEIVERVSVÆEULA - SOS-HE SINEN - GODF-H - FKSFODF-H - FKSFODH - SINEN - HOSS-H - FKSGOS-H - FKRHOSS-H - SINEN - HOSS-H - SINEN - HOS
SQUA (Angiosperms	Asterida	SLMA Siene SCMI Solanum NsMADS1 Nicotiana DEFH28 Arithihum AFL Arabidopsis MpMADS1 Nicotiana DEFH28 Arithihum AFL Arabidopsis MpMADS15. Oryza DeMADS15. Oryza DeMADS16. Arabidopsis MdMADS11. Malus VMADS3. Nitis DMADS4. Petunia SiMBP6. Solanum SvAGL6. Syringa CDM104. Chrysanthemum grd3. Gerbera Es. ca AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Eschscholzia RAGL6. Ranunculus AGL6. Teaeis A.c. am. AGL6. Acabidopsis MADS17. Dendrocalamus MADS17. Dendrocalamus ZAG3. Zea CMADS17. Oryza AGL66. Crocus Pa. am. AGL6. 1 Persea MADS6. Dendrocalamus PMADS5. Pinus ZAG3. Zea CMADS17. Oryza AGL66. Crocus Pa. am. AGL6. 1 Persea MAGL6. Amborella GMADS3. Pinus Zava. AGL6. 1 Zamia GMADS3. Pinus Zava. AGL6. 1 Zamia GMADS3. Pinus Zava. AGL6. 1 Zamia GMADS3. Pinus	INDROVOL IN ENK INNOVTESIAN INDROVOL IN ENK INNOVE INDROVOL IN ENK INNOVE INDROVOL IN ENK INNOVE INDROVOL IN ENK INNOVE INDROVOL INNOVE INDROVOL INTERES INDROVOL I	AGLLKRAHE I SVLCDAEVAL I I FSI SOLLKRAHE I SVLCDAEVAL I FSI TOLLKRAHE I SVLCDAEVAL I FSI KERQLGD I NKQLK I K KERQLGD NKQLK K KERQLGD NKQLK K KERQLGD NKQLK K KERQLGD NKQLK K KERQLGO NKQLK K KERQLGO NKQLK K KERQLGO NKQLK	HIGHLERPATES HIGHLERPATES </td <td>DIRE I LEIVERVSVÆELL I APES-DV DIRE I LEIVERVSVÆELL APES-DV INE I LEIVERVSVÆELL APES-DV DIRE I LEIVERVSVÆELL APES- BIR I LEIVERVSVÆELL AF ADS-HE SIKE I LEIVERVSVÆEVEL TSDS-HE SIKE I LEIVERVSVÆEVEL TSDS-HE SIKE I LEIVERVSVÆEVEL TSDS-HE SIKE I LEIVERVSVÆEVEL I SAES-E INDX I LEIVERVERVEL I SAES-E I LI SAES I LI SAES-E I LI SAES I LI SAES-E I LI SAES I LI SAES I</td>	DIRE I LEIVERVSVÆELL I APES-DV DIRE I LEIVERVSVÆELL APES-DV INE I LEIVERVSVÆELL APES-DV DIRE I LEIVERVSVÆELL APES- BIR I LEIVERVSVÆELL AF ADS-HE SIKE I LEIVERVSVÆEVEL TSDS-HE SIKE I LEIVERVSVÆEVEL TSDS-HE SIKE I LEIVERVSVÆEVEL TSDS-HE SIKE I LEIVERVSVÆEVEL I SAES-E INDX I LEIVERVERVEL I SAES-E I LI SAES I LI SAES-E I LI SAES I LI SAES-E I LI SAES I

Fig. 2. A part of the alignment of the *AGL6*, *AGL2*, and *SQUA* genes. (A) *AGL6* genes have a one-amino acid deletion in the I-domain (arrow). (B) Gymnosperm-specific one-amino acid insertion (arrowhead) and asterid-specific seven-amino acid insertion were detected in the C-domain (arrow).

 $\underline{\mathscr{D}}$ Springer



Fig. 3. Summary of phylogenetic analyses of *AGL6-*, *AGL2-*, and *SQUA-*like genes with *TM3-*like genes as outgroup (A) or *AG-*like plus *AGL12-*like genes as outgroup (B). Values above the nodes indicate bootstrap values in maximum likelihood analyses and posterior probability (X 100) in the Bayesian analyses of DNA analyses. "–" indicates value less than 50.



Fig. 4. Maximum likelihood tree of 63 *AGL6* genes and 25 representatives of *AGL2* genes as outgroup. Large stars indicate recent duplications at the genus or species level and small stars indicate duplications at the higher level. Three numbers above each node indicate bootstrap values from parsimony and maximum likelihood analyses and posterior probability from Bayesian analysis (X100). "–" indicates value less than 50.



Fig. 5. A hypothesis for the evolutionary history of *AGL6-*, *AGL2-*, and *SQUA-*like genes based on the phylogenetic analyses with *TM3-*like genes as outgroup (Fig. 3A). A duplication between *AGL2-* and *AGL6-*like genes occurred before the divergence of angiosperms and gymnosperms (star). *SQUA* and *AGL2* genes have not been detected in gymnosperms (asterisks).

class) like genes. Furthermore, our phylogenetic analyses strongly demonstrated a sister relationship between AGL6like genes and AGL2-like genes. MADS-box genes have diverged into many sublineages via several duplication events (Becker and Theissen 2003; Nam et al. 2003). We can estimate an approximate divergence time of clades by comparison with the organisms from which the genes derive, as long as this group forms a well-supported clade in the phylogenetic tree. For example, it is clear that the AGL6 + AGL2 + SQUA clade (L6L2SQ) diverged from other lineages of MADS-box genes before the split of angiosperms and extant gymnosperms because the L6L2SQ clade contains both angiosperm and gymnosperm genes (Fig. 5). However, of the three subclades found in the L6L2SQ clade, only the AGL6 clade contains gymnosperm genes. SQUA- and AGL2like genes have not been reported in gymnosperms. Although one AGL2-like gene from a gymnosperm, Pinus radiata (PrMADS1; U42399), has been published, this sequence grouped with other angiosperm AGL2-like genes in phylogenetic analyses (and was most closely related to a Eucalyptus sequence) (Zahn et al. 2005): the identity of this sequence is therefore in question, and it was excluded in the previous phylogenetic study of AGL2-like genes (Zahn et al. 2005).

The sister group of the L6L2SQ clade varies among the previous phylogenetic analyses of MADS-box genes (e.g., Winter et al. 1999; Becker and Theissen 2003; Nam et al. 2003). However, previous broad analyses, which contain all *Arabidopsis* and rice MIKC-type MADS-box sequences, suggest that *TM3*-like genes (Nam et al. 2003) or *AG*- plus *AGL12*-like genes (Becker and Theissen 2003) are the best candidate for the sister group of the L6L2SQ clade. Fig. 5 shows the possible evolutionary history of *AGL6*-like genes

when the TM3-like genes are sister to the L6L2SQ clade. In this case, a duplication to produce AGL6-like and AGL2-like genes predates the divergence of angiosperms and extant gymnosperms because both the TM3 and L6L2SQ clades contain gymnosperm and angiosperm sequences. We can explain gymnosperm-less SQUA and AGL2 lineages by the losses of these genes in gymnosperms after the SQUA and AGL2 lineages diverged from the common ancestor of the L6L2SQ clade (Fig. 5 asterisks). Alternatively, it is possible that gymnosperm SQUA- and AGL2-like genes have not yet been found. However, the former is more likely because these genes were not detected in the intensive screening of expressed genes conducted in reproductive organs of a cycad (ESTs of Zamia vazquezii in the Floral Genome Project; see below) or in the genome sequence of a conifer (*Picea abies*; Nystedt et al. 2013).

Extant seed plants originated approximately 290-309.2 mya (Mapes and Rothwell 1984; Mapes and Rothwell 1991), and most evidence indicates a very early split between the living gymnosperms and the line leading to angiosperms (Soltis *et al.* 2002; Donoghue 2010; Magallon 2010; Doyle 2012). Therefore, we hypothesize that the split between AGL6-like and AGL2-like genes occurred at least 290-309.2 mya based on the above assumptions. This scenario is the same when AG/AGL12 is the outgroup because gymnosperm genes have also been reported in both AG and AGL12 lineages.

The function of many *AGL2*-like and *SQUA*-like genes is now well characterized and includes the formation of each floral whorl in *Arabidopsis* and *Petunia* (Coen and Meyerowitz 1991; Kotilainen et al. 2000; Ditta et al. 2004). In contrast, the function of *AGL6*-like genes has only been characterized in a few cases (e.g., Rijpkema et al. 2009). Our phylogenetic analyses showed that *AGL6*-like genes are sister to *AGL2*like genes, and *SQUA*-like genes are sister to these two groups. Recognizing phylogenetic relationships among these orthologous gene groups and their approximate divergence time, when combined with detailed investigation of their expression patterns, will provide a better understanding of the evolutionary history of the genetic control mechanisms of flowers.

Materials and Methods

Data Collection

We collected 62 *AGL6*-like sequences, including 13 newly identified sequences (Table 1). We searched for *AGL6*-like genes using amino acid BLAST (BLASTN) in GenBank with the *Arabidopsis AGL6* protein sequence as the seed and an e^{-5} cut-off level. Some sequences resulting from this search were members of the *AGL2* or *SQUA* subfamilies, but we were easily able to identify members of the *AGL6* subfamily, based on the result of initial phylogenetic analyses and sequence structure analyses (see Results). Through this search, we

identified 48 previously reported angiosperm and gymnosperm *AGL6*-like sequences from GenBank. We also blasted *AGL6* against the expressed sequence tag (EST) collection of the Floral Genome Project (FGP; http://www.floralgenome.org) (cut-off level was e⁻⁵). After phylogenetic analysis of these sequences with 108 previously reported *Arabidopsis* MADS-box genes (Pařenicová et al. 2003), we identified 10 *AGL6*-like sequences (phylogenetic analysis not shown) from the FGP EST collections. Genes detected from EST libraries were completed by additional sequencing of identified clones using universal primers included in the library vector. We also added a sequence from the tomato EST library (http://tigr.org/tigr-scripts/tgi/T index.cgi?species=tomato).

In the case of sequences of *Eupomatia bennettii* and *Ribes sanguineum*, we screened MADS-box genes from cDNAs of young flowering buds (vouchers are *Endress 5197* and *S. Kim 1143*, respectively) using a MADS-box-specific degenerate primer (5'-GGGGTACCAAYMGI-CARGTIACITAYTCIAAGMGIMG-3'; Kramer et al. 1999). For RNA extraction, reverse-transcription, PCR, cloning, and sequencing, we followed the methods described in Kim et al. (2005b). We distinguished sequences of *AGL6*-like genes from other MADS-box genes using the same phylogenetic analysis approach described above.

Alignment and Phylogenetic Analysis

To clarify the phylogenetic position of AGL6-like genes in the MADS-box gene family, we constructed a DNA matrix containing AGL6-like genes (62 sequences), along with AGL2-like (107 sequences) and SQUA-like (91 sequences) genes, which were potential sister groups to AGL6-like genes in previous broad phylogenetic analyses (Becker and Theissen 2003; Nam et al. 2003; Pařenicová et al. 2003; Kim et al. 2005a; Gramzow et al. 2012). Then we added either representatives of TM3-like genes or AGAMOUS (AG)-like plus AGL12-like genes as the outgroup independently to test the effect of outgroup.

First, we translated these gene sequences to amino acid sequences using Se-Al (http://tree.bio.ed.ac.uk/software/seal/) and aligned the amino acid sequences of AGL6-like genes using CLUSTALX (version 1.83) (Thompson et al. 1997) with default options. Then alignments of 107 AGL2-like and 91 SQUA-like sequences used in the studies of Becker and Theissen (2003) and Zahn et al. (2005) (authors of these studies kindly provided their alignments) were combined with the AGL6 matrix using the "profile alignment" method in CLUSTALX (file-to-file alignment). Because TM3-like genes or AGAMOUS (AG)-like plus AGL12-like genes were sister to the AGL6 + AGL2 + SQUA clade in the previous phylogenetic analyses (Becker and Theissen 2003; Nam et al. 2003), we included these two groups independently in our matrix to test the effect of outgroup. The alignment of amino acid sequences was converted into an alignment of DNA sequences using the program AA2DNA (http:/ /www.mybiosoftware.com/alignment/5250) for DNA analyses.

Phylogenetic analyses were carried out on the nucleotide sequences using maximum-likelihood (ML) (Felsenstein 1981) and Bayesian inference (Huelsenbeck and Ronquist 2001) in PHYML (version 2.4) (Guindon and Gascuel 2003) and MrBayes (version 3.0b4) (Huelsenbeck and Ronquist 2001), respectively. Prior to these analyses, we selected the best model of molecular evolution using MODELTEST (version 3.06) (Posada and Crandall 1998). The GTR + I + Γ model of nucleotide substitution, which assumes general time reversibility (GTR), a certain proportion of invariant sites (I), and a gamma distribution to accommodate rate variation among sites (Å), was selected for both matrices. For ML analysis, ML parameter values were optimized with a BIONJ tree as a starting point (Gascuel 1997). Support values for nodes on the ML tree were estimated with 250 bootstrap replicates (Felsenstein 1985). For Bayesian analyses, we ran four chains, sampling one tree every 1,000 generations for 10,000,000 generations (starting with a random tree). When we plot log likelihood values to trees from every 1,000 generations, stationarity was reached at approximately 150,000 generations in both analyses; thus, the first 150 trees were considered the "burn in" of the chain, and phylogenetic inferences were based on those trees sampled after 150,000 generations.

For intensive analyses of the *AGL6* group, a reduced data set, which contains *AGL6*-like genes and 25 selected representatives of *AGL2*-like genes as outgroup, was analyzed: for the *AGL2*-like genes, we selected one or two genes from major lineages of angiosperms for the *AGL9* and *AGL2/3/4* sublineages (see Fig 4). In addition to ML and Bayesian analyses (same conditions as full matrix), maximum parsimony (MP) analysis was also conducted for the reduced data set using PAUP* (version 4.0b10) (Swofford 2001): the heuristic search strategy involved 100 random addition replicates with TREE bisection-reconnection (TBR) branch swapping, saving all optimal trees. Bootstrap analyses (Felsenstein 1985) were performed using 500 re-samplings and 10 random addition replicates with TBR branch swapping, saving all optimal trees.

Supporting Information

Additional Supporting Information is in the online version of this article: **Fig. S1.** Maximum likelihood tree of *AGL2*-like, *AGL6*-like, and *SQUA*-like genes with outgroup of *TM3*-like genes (A) and *AG*-like/*AGL12*-like genes (B), respectively.

Acknowledgments

This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF 2010-0008996) and by the National Science Foundation of USA (grants PRG-0115684 and IOS-0922742). We thank Annette Becker and Günter Theissen for sharing sequence alignments for *AGL2* genes, Eunsook Roh for figure drawing, and Junggi Park for technical advice in phylogenetic analyses.

Author's Contributions

SK carried out sequence analysis, phylogenetic analyses, interpreted the results, and drafted the manuscript. PSS and DES jointly contributed to the conception and coordination of the study, were involved in revising the manuscript. All authors agreed on the contents of the paper and post no conflicting interest.

References

- Alvarez-Buylla ER, Liljegren SJ, Pelaz S, Gold SE, Burgeff C, Ditta GS, Vergara-Silva F, Yanofsky MF (2000) MADS-box gene evolution beyond flowers: expression in pollen, endosperm, guard cells, roots and trichomes. Plant J 24:457–466
- APGIII (2009) An update of the Angiosperm Phylogeny Group classification for the orders and families of flowering plants: APG III. Bot J Linn Soc 161:105–121
- Becker A, Theissen G (2003) The major clades of MADS-box genes and their role in the development and evolution of flowering plants. Mol Phylogenet Evol 29:464-489
- Boss PK, Sensi E, Hua C, Davies C, Thomas MR (2002) Cloning and

characterisation of grapevine (*Vitis vinifera* L.) MADS-box genes expressed during inflorescence and berry development. Plant Science 162:887–895

- Chanderbali AS, Kim S, Buzgo M, Zheng Z, Oppenheimer DG, Soltis DE, Soltist PS (2006) Genetic footprints of stamen ancestors guide perianth evolution in *Persea* (Lauraceae). Int J Plant Sci 167:1075–1089
- Coen ES, Meyerowitz EM (1991) The war of the whorls genetic interactions controlling flower development. Nature 353:31–37
- Colombo L, Franken J, Koetje E, Vanwent J, Dons HJM, Angenent GC, Vantunen AJ (1995) The *Petunia* MADS box gene *FBP11* determines ovule identity. Plant Cell 7:1859–1868
- De Bodt S, Raes J, Van de Peer YV, Theissen G (2003) And then there were many: MADS goes genomic. Trends Plant Sci 8:475–483
- de Folter S, Immink RGH, Kieffer M, Pařenicová L, Henz SR, Weigel D, Busscher M, Kooiker M, Colombo L, Kater MM, Davies B, Angenent GC (2005) Comprehensive interaction map of the *Arabidopsis* MADS box transcription factors. Plant Cell 17:1424–1433
- Ditta G, Pinyopich A, Robles P, Pelaz S, Yanofsky MF (2004) The *SEP4* gene of *Arabidopsis thaliana* functions in floral organ and meristem identity. Curr Biol 14:1935–1940
- Donoghue MJ (2010) An uncorrelated relaxed-clock analysis suggests an earlier origin for flowering plants. Proc Natl Acad Sci USA 107:5897–5902
- Doyle JA (2012) Molecular and fossil evidence on the origin of angiosperms. Annu Rev Earth Planet Sci 40:301–326
- Fan J, Li W, Dong X, Guo W, Shu H (2007) Ectopic expression of a hyacinth AGL6 homolog caused earlier flowering and homeotic conversion in Arabidopsis. Sci China C Life Sci 50:676–689
- Felsenstein J (1981) Evolutionary trees from DNA-sequences: a maximum-likelihood approach. J Mol Evol 17:368–376
- Felsenstein J (1985) Confidence limits on phylogenies an approach using the bootstrap. Evolution 39:783–791
- Feng Q, Zhang Y, Hao P, Wang S, Fu G, Huang Y, Li Y, Zhu J, Liu Y, Hu X, Jia P, Zhao Q, Ying K, Yu S, Tang Y, Weng Q, Zhang L, Lu Y, Mu J, Zhang LS, Yu Z, Fan D, Liu X, Lu T, Li C, Wu Y, Sun T, Lei H, Li T, Hu H, Guan J, Wu M, Zhang R, Zhou B, Chen Z, Chen L, Jin Z, Wang R, Yin H, Cai Z, Ren S, Lv G, Gu W, Zhu G, Tu Y, Jia J, Chen J, Kang H, Chen X, Shao C, Sun Y, Hu Q, Zhang X, Zhang W, Wang L, Ding C, Sheng H, Gu J, Chen S, Ni L, Zhu F, Chen W, Lan L, Lai Y, Cheng Z, Gu M, Jiang J, Li J, Hong G, Xue Y, Han B (2002) Sequence and analysis of rice chromosome 4. Nature 420:316–320
- Gascuel O (1997) BIONJ: An improved version of the NJ algorithm based on a simple model of sequence data. Mol Biol Evol 14:685-695
- Gramzow L, Barker E, Schulz C, Ambrose B, Ashton N, Theissen G, Litt A (2012) *Selaginella* genome analysis - entering the "homoplasy heaven" of the MADS world. Front Plant Sci 3:214
- Gu Q, Ferrandiz C, Yanofsky MF, Martienssen R (1998) The FRUITFULL MADS-box gene mediates cell differentiation during Arabidopsis fruit development. Development 125:1509–1517
- Guindon S, Gascuel O (2003) A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. Syst Biol 52:696–704
- Gustafsonbrown C, Savidge B, Yanofsky MF (1994) Regulation of the *Arabidopsis* floral homeotic gene *APETALA1*. Cell 76:131– 143
- Hecht V, Foucher F, Ferrandiz C, Macknight R, Navarro C, Morin J, Vardy ME, Ellis N, Beltran JP, Rameau C, Weller JL (2005) Conservation of *Arabidopsis* flowering genes in model legumes. Plant Physiol 137:1420–1434
- Henschel K, Kofuji R, Hasebe M, Saedler H, Munster T, Theissen G (2002) Two ancient classes of MIKC-type MADS-box genes are present in the moss *Physcomitrella patens*. Mol Biol Evol

19:801-814

- Hileman LC, Sundstrom JF, Litt A, Chen M, Shumba T, Irish VF (2006) Molecular and phylogenetic analyses of the MADS-box gene family in tomato. Mol Biol Evol 23:2245–2258
- Hsu HF, Huang CH, Chou LT, Yang CH (2003) Ectopic expression of an orchid (*Oncidium* Gower Ramsey) *AGL6*-like gene promotes flowering by activating flowering time genes in *Arabidopsis thaliana*. Plant Cell Physiol 44:783–794
- Huelsenbeck JP, Ronquist F (2001) MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17:754–755
- Kim S, Koh J, Yoo MJ, Kong HZ, Hu Y, Ma H, Soltis PS, Soltis DE (2005a) Expression of floral MADS-box genes in basal angiosperms: implications for the evolution of floral regulators. Plant J 43:724–744
- Kim S, Koh J, Ma H, Hu Y, Endress PK, Hauser BA, Buzgo M, Soltis PS, Soltis DE (2005b) Sequence and expression studies of A-, B-, and E-class MADS-box homologues in *Eupomatia* (Eupomatiaceae): support for the bracteate origin of the calyptra. Intl J Plant Sci 166:185–198
- Koo SC, Bracko O, Park MS, Schwab R, Chun HJ, Park KM, Seo JS, Grbic V, Balasubramanian S, Schmid M, Godard F, Yun DJ, Lee SY, Cho MJ, Weigel D, Kim MC (2010) Control of lateral organ development and flowering time by the *Arabidopsis thaliana* MADS-box gene *AGAMOUS-LIKE6*. Plant J 62:807–816
- Kotilainen M, Elomaa P, Uimari A, Albert VA, Yu D, Teeri TH (2000) *GRCD1*, an *AGL2*-like MADS box gene, participates in the C function during stamen development in *Gerbera hybrida*. Plant Cell 12:1893–1902
- Kramer EM, Dorit RL, Irish VF (1999) Molecular evolution of genes controlling petal and stamen development: duplication and divergence within the *APETALA3* and *PISTILLATA* MADS-box gene lineages. Genetics 151:915–915
- Kwantes M, Liebsch D, Verelst W (2012) How MIKC* MADS-box genes originated and evidence for their conserved function throughout the evolution of vascular plant gametophytes. Mol Biol Evol 29:293–302
- Li H, Liang W, Jia R, Yin C, Zong J, Kong H, Zhang D (2010) The *AGL6*-like gene *OsMADS6* regulates floral organ and meristem identities in rice. Cell Res 20:299-313
- Litt A, Irish VF (2003) Duplication and diversification in the *APETALA1/FRUITFULL* floral homeotic gene lineage: Implications for the evolution of floral development. Genetics 165:821–833
- Ma H, Yanofsky MF, Meyerowitz EM (1991) *AGL1-AGL6*, an *Arabidopsis* gene family with similarity to floral homeotic and transcription factor genes. Genes Dev 5:484–495
- Magallon S (2010) Using fossils to break long branches in molecular dating: a comparison of relaxed clocks applied to the origin of angiosperms. Syst Biol 59:384–399
- Mapes G, Rothwell GW (1984) Premineralized ovulate cones of *Lebachia* from the late Palaeozoic limestones of Kansas. Paleontology 27:69–94
- Mapes G, Rothwell GW (1991) Structure and relationships of primitive conifers. Neues Jahrbuch für Geologie and Paläontologie-Abhandulungen 183:269–287
- Mena M, Mandel MA, Lerner DR, Yanofsky MF, Schmidt RJ (1995) A characterization of the MADS-box gene family in maize. Plant J 8:845–854
- Michaels SD, Amasino RM (1999) *FLOWERING LOCUS C* encodes a novel MADS domain protein that acts as a repressor of flowering. Plant Cell 11:949–956
- Moon YH, Kang HG, Jung JY, Jeon JS, Sung SK, An G (1999) Determination of the motif responsible for interaction between the rice *APETALA1/AGAMOUS-LIKE9* family proteins using a yeast two-hybrid system. Plant Physiol 120:1193–1204
- Munster T, Pahnke J, DiRosa A, Kim JT, Martin W, Saedler H, Theissen G (1997) Floral homeotic genes were recruited from

homologous MADS-box genes preexisting in the common ancestor of ferns and seed plants. Proc Natl Acad Sci USA 94:2415-2420

- Nam J, dePamphilis CW, Ma H, Nei M (2003) Antiquity and evolution of the MADS-box gene family controlling flower development in plants. Mol Biol Evol 20:1435–1447
- Ng M, Yanofsky MF (2001) Function and evolution of the plant MADS-box gene family. Nat Rev Genet 2:186–195
- Nystedt B, Street NR, Wetterbom A, Zuccolo A, Lin YC, Scofield DG, Vezzi F, Delhomme N, Giacomello S, Alexeyenko A, Vicedomini R, Sahlin K, Sherwood E, Elfstrand M, Gramzow L, Holmberg K, Hallman J, Keech O, Klasson L, Koriabine M, Kucukoglu M, Kaller M, Luthman J, Lysholm F, Niittyla T, Olson A, Rilakovic N, Ritland C, Rossello JA, Sena J, Svensson T, Talavera-Lopez C, Theissen G, Tuominen H, Vanneste K, Wu ZQ, Zhang B, Zerbe P, Arvestad L, Bhalerao R, Bohlmann J, Bousquet J, Garcia Gil R, Hvidsten TR, de Jong P, MacKay J, Morgante M, Ritland K, Sundberg B, Thompson SL, Van de Peer Y, Andersson B, Nilsson O, Ingvarsson PK, Lundeberg J, Jansson S (2013) The Norway spruce genome sequence and conifer genome evolution. Nature 497:579–584
- Ohmori S, Kimizu M, Sugita M, Miyao A, Hirochika H, Uchida E, Nagato Y, Yoshida H (2009) *MOSAIC FLORAL ORGANS1*, an *AGL6*-like MADS box gene, regulates floral organ identity and meristem fate in rice. Plant Cell 21:3008–3025
- Pařenicová L, de Folter S, Kieffer M, Horner DS, Favalli C, Busscher J, Cook HE, Ingram RM, Kater MM, Davies B, Angenent GC, Colombo L (2003) Molecular and phylogenetic analyses of the complete MADS-box transcription factor family in *Arabidopsis*: new openings to the MADS world. Plant Cell 15:1538–1551
- Pelaz S, Ditta GS, Baumann E, Wisman E, Yanofsky MF (2000) B and C floral organ identity functions require SEPALLATA MADS-box genes. Nature 405:200–203
- Petersen K, Didion T, Andersen CH, Nielsen KK (2004) MADS-box genes from perennial ryegrass differentially expressed during transition from vegetative to reproductive growth. J Plant Physiol 161:439–447
- Posada D, Crandall KA (1998) MODELTEST: testing the model of DNA substitution. Bioinformatics 14:817–818
- Prakash AP, Kumar PP (2002) *PkMADS1* is a novel MADS box gene regulating adventitious shoot induction and vegetative shoot development in *Paulownia kawakamii*. Plant J 29:141–151
- Reinheimer R, Kellogg EA (2009) Evolution of *AGL6*-like MADS box genes in grasses (Poaceae): ovule expression is ancient and palea expression is new. Plant Cell 21:2591–2605
- Riechmann JL, Meyerowitz EM (1997) Determination of floral organ identity by *Arabidopsis* MADS domain homeotic proteins *AP1*, *AP3*, *PI*, and *AG* is independent of their DNA-binding specificity. Mol Biol Cell 8:1243–1259
- Rijpkema AS, Zethof J, Gerats T, Vandenbussche M (2009) The petunia *AGL6* gene has a *SEPALLATA*-like function in floral patterning. Plant J 60:1–9
- Rounsley SD, Ditta GS, Yanofsky MF (1995) Diverse roles for MADS box genes in *Arabidopsis* development. Plant Cell 7:1259–1269
- Shindo S, Ito M, Ueda K, Kato M, Hasebe M (1999) Characterization of MADS genes in the gymnosperm *Gnetum parvifolium* and its implication on the evolution of reproductive organs in seed plants. Evol Dev 1:180–190
- Shore P, Sharrocks AD (1995) The MADS-Box family of transcription factors. Eur J Biochem 229:1–13

- Soltis DE, Soltis PS, Chase MW, Mort ME, Albach DC, Zanis M, Savolainen V, Hahn WH, Hoot SB, Fay MF, Axtell M, Swensen SM, Prince LM, Kress WJ, Nixon KC, Farris JS (2000) Angiosperm phylogeny inferred from 18S rDNA, *rbcL*, and *atpB* sequences. Bot J Linn Soc 133:381–461
- Soltis DE, Soltis PS, Endress P, K., Chase MW (2005) Phylogeny and evolution of angiosperms, Sinauer, Sunderland
- Soltis PS, Soltis DE, Chase MW (1999) Angiosperm phylogeny inferred from multiple genes as a tool for comparative biology. Nature 402:402–404
- Swofford DL (2001) PAUP* 4.0b10: phylogenetic analysis using parsimony (*and other methods), Sinauer, Sunderland
- Tandre K, Albert VA, Sundas A, Engstrom P (1995) Conifer homologues to genes that control floral development in angiosperms. Plant Mol Biol 27:69–78
- Theissen G (2001) Development of floral organ identity: stories from the MADS house. Curr Opin Plant Biol 4:75–85
- Theissen G, Becker A, Di Rosa A, Kanno A, Kim JT, Munster T, Winter KU, Saedler H (2000) A short history of MADS-box genes in plants. Plant Mol Biol 42:115–149
- Theissen G, Kim JT, Saedler H (1996) Classification and phylogeny of the MADS-box multigene family suggest defined roles of MADS-box gene subfamilies in the morphological evolution of eukaryotes. J Mol Evol 43:484–516
- Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG (1997) The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 25:4876–4882
- Tsuchimoto S, Mayama T, van der Krol A, Ohtsubo E (2000) The whorl-specific action of a petunia class B floral homeotic gene. Genes Cells 5:89–99
- Viaene T, Vekemans D, Becker A, Melzer S, Geuten K (2010) Expression divergence of the AGL6 MADS domain transcription factor lineage after a core eudicot duplication suggests functional diversification. BMC Plant Biol 10:148
- West AG, Sharrocks AD (1999) MADS-box transcription factors adopt alternative mechanisms for bending DNA. J Mol Biol 286:1311–1323
- Winter KU, Becker A, Munster T, Kim JT, Saedler H, Theissen G (1999) MADS-box genes reveal that gnetophytes are more closely related to conifers than to flowering plants. Proc Natl Acad Sci USA 96:7342–7347
- Yao J-L, Dong Y-H, Kvarnheden A, Morris B (1999) Seven MADSbox genes in apple areexpressed in different parts of the fruit. J Am Soc Hortic Sci 124:8–13
- Yoo SK, Hong SM, Lee JS, Ahn JH (2011) A genetic screen for leaf movement mutants identifies a potential role for AGAMOUS-LIKE 6 (AGL6) in circadian-clock control. Mol Cells 31:281– 287
- Yoo SK, Wu X, Lee JS, Ahn JH (2011) AGAMOUS-LIKE 6 is a floral promoter that negatively regulates the FLC/MAF clade genes and positively regulates FT in Arabidopsis. Plant J 65:62–76
- Zahn LM, King HZ, Leebens-Mack JH, Kim S, Soltis PS, Landherr LL, Soltis DE, dePamphilis CW, Ma H (2005) The evolution of the *SEPALLATA* subfamily of MADS-Box genes: a preangiosperm origin with multiple duplications throughout angiosperm history. Genetics 169:2209–2223
- Zhang HM, Forde BG (2000) Regulation of *Arabidopsis* root development by nitrate availability. J Exp Bot 51:51–59