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Supplemental information

Environmental control of rice flowering time

Giulio Vicentini, Marco Biancucci, Lorenzo Mineri, Daniele Chirivì, Francesca Giaume, Yiling Miao, Junko Kyozuka, Vittoria Brambilla, Camilla Betti, and Fabio Fornara

Supplementary Table 1. List of rice flowering time genes. The list includes a brief description of the function of genes not discussed in the main text. References used to elaborate the description are also indicated. Genes are listed in alphabetical order.

Name	Description	Source
Ehd2/RID1/OsID1 - Os10g0419200 SID1/OsIDD4 - Os02g0672100	Ehd2 is an IDD domain containing transcription factor. *SID1* encodes for a zinc finger transcription factor. *Ehd2* promotes flowering through *Ehd1* both in LD and SD. Knockout mutants of *Ehd2* never flower, but if *SID1* is overexpressed, then flowering is recovered. However, overexpression of *Ehd1* in the *ehd2* mutant background does not restore the never-flowering phenotype. In a WT background *SID1* overexpressors show no phenotypes. Both Ehd2 and SID1 can bind to the same location in florigens promoters.	(Matsubara et al., 2008; Park et al., 2008; Cai et al., 2014; Deng et al., 2017)
Ehd3 - Os08g0105000	PHD finger motifs containing protein expressed in developing leaves and in the shoot apex. It promotes flowering both in SD and LD. In SD, it promotes *Ehd1* expression while in LD it is a key repressor of *Ghd7*. Knockout of *Ehd3* prevents flowering in LD due to constitutive high levels of *Ghd7*.	(Matsubara et al., 2011)
Ehd4 - Os03g0112700	CCCH-type zinc finger protein. Its knockout mutant is late flowering both in LD and SD, with null expression of *Ehd1* and the florigens. The effect of Ehd4 on *Ehd1* transcription is indirect.	(Gao et al., 2013)
EL1/CK1 - Os03g0793500	The *el1* loss of function mutant is early flowering only in LD. It represses *Ehd1* possibly by activating Ghd7 protein and maybe other flowering repressors via phosphorylation.	(Hori et al., 2013)
HGW - Os06g0160400	UBA domain protein involved in ubiquitination. It promotes flowering under field conditions by promoting *OsGI*, *Hd1* and *Hd3a* expression.	(Li et al., 2012)
OsCONSTANS-like genes	Many CONSTANS-like genes have been characterized having effects on flowering time and including *OsCO3*, *OsCOL10*, *OsCOL13*, *OsCOL15* and *OsCOL16*. All have been shown to delay flowering when overexpressed both in LD and SD by repressing *Ehd1*. Frequently, knockout mutants don't have phenotypes, possibly because of redundancy among them. The *oscol4* knockout shows early flowering in both LD and SD and increased levels of *Ehd1* transcription. Expression of *OsCOL4* is high during vegetative growth but it progressively reduces over time, permitting *Ehd1* mRNA levels to rise. *OsCOL4* overexpression leads to late flowering in both photoperiods.	(Kim et al., 2008; Lee et al., 2016; Lee et al., 2010; Tan et al., 2016; Sheng et al., 2016; Tan et al., 2017; Wu et al., 2017; Wu et al., 2018)
OsDOF12 - Os03g0169600	*OsDOF12* encodes for a zinc finger transcriptional activator. Its overexpression leads to higher *Hd3a* levels in LD, causing early flowering.	(Li et al., 2009)
OsELF3 - Os01g0566100	Knockout mutants are late flowering under LD. Its overexpressor are early flowering in LD but late flowering in SD. It acts by inhibiting *OsGI*, that in turn results in higher amounts of *Hd1* in the *oself3* mutant. OsELF3 can also inhibit the red light-induced expression of Ghd7.	(Saito et al., 2012; Zhao et al., 2012; Yang et al., 2013a)
OsEMF2b - Os09g0306800	*OsEMF2b* encodes for a zinc finger protein homolog of Arabidopsis EMF2, which is part of a polycomb complex acting to silence gene expression by histone methylation. The *OsEMF2b* loss of function mutant is late flowering both in LD	(Xie et al., 2015)

	and SD. OsEMF2b is responsible for methylating OsLFL1, leading to its silencing and thus promoting flowering.	
OsFKF1 - Os11g0547000	Homolog of FKF1 and encoding for a blue light photoreceptor with F-box domain typical of E3 ubiquitin ligase. The knockout is late flowering both in LD and SD. OsFKF1 promotes flowering by inducing *Ehd2* expression, that results in *Ghd7* inhibition and finally an activation of the *Ehd1* pathway.	(Han et al., 2015)
OsLFL1 - Os01g0713600	The overexpressor is late flowering because OsLFL1 can bind to the *Ehd1* promoter to prevent its expression. It can also bind to the *OsMFT1* promoter to activate its expression.	(Peng et al., 2007; Peng et al., 2008; Song et al., 2018)
OsMADS50 – Os03g0122600 **OsMADS56 – Os10g0536100**	Knockout mutants of *OsMADS50* are late flowering only in LD while knockout mutants of *OsMADS56* have no phenotype; however, *OsMADS56* overexpressors are late flowering only in LD. So OsMADS50 and OsMADS56 are specific LD flowering promoter and repressor respectively. Both *osmads50* mutant and *OsMADS56* overexpressor show upregulation of *LFL1*, explaining their phenotype. They can form homodimers or heterodimers between each other.	(Ryu et al., 2009)
OsMADS51 - Os01g0922800	Acts as a flowering promoter in SD by activating the *Ehd1* pathway. *OsMADS51* expression is promoted by *OsGI*.	(Kim et al., 2007)
OsMFT1 - Os06g0498800	Belongs to the family of phosphatidylethanolamine-binding proteins. In LD the overexpressor is late flowering while the knockout mutant is slightly early. Its expression is positively affected by *Ghd7*, and OsMFT1 acts by reducing *Ehd1* expression.	(Song et al., 2018)
OsNF-YB9 - Os06g0285200 **OsNF-YC12 - Os05g0304800**	OsNF-YB9 and OsNF-YC12 are subunit of a heterotrimeric transcription factor. These 2 subunits interact together and each one is also able to bind OsGI. Their overexpressors are late flowering.	(Das et al., 2019)
OsVIL2 - Os02g0152500	The knockout mutant is late flowering in both LD and SD. OsVIL2 seems to positively regulate *Ehd1* expression by reducing transcription of the flowering inhibitor *OsLFL1*.	(Yang et al., 2013b)
OsVIL3 - Os05g0145400	The *osvil3* mutant is late flowering only in SD. OsVIL3 can bind to the promoter of OsLF (a minor flowering repressor) to reduce its expression.	(Wang et al., 2013)
RCN1 - Os03g0281900 **RCN2 - Os02g0531600**	Transcription factors homologs of TFL1/CEN. *RCN1* is expressed in developing panicles; *RCN2* both in vegetative and reproductive meristems. Overexpressors show delayed heading and altered panicle morphology, sometimes plants are incapable of concluding panicle development.	(Nakagawa et al., 2002)
RFL - Os04g0598300	Transcription factor homolog to LFY. It promotes flowering by increasing *OsMADS50* expression. It is also fundamental for a correct panicle architecture.	(Rao et al., 2008)
SDG724 – Os09g0307800	*SDG724* encodes for a histone methyltransferase which promotes flowering in LD. The loss-of-function mutant flowers late in LD and with only a slight flowering delay in SD. SDG724 promotes H3K36me2/3 methylation of *OsMADS50* and *RFT1*, and enhances the expression of both florigens.	(Sun et al., 2012)
SDG725 - Os02g0554000 **MRG702 – Os11g0545600**	*SDG725* encodes for a histone methyltransferase. Knockdown plants show brassinosteroid-deficiency phenotypes, and are late flowering both in LD and SD due to altered methylation in many flowering related genes which leads to increased	(Sui et al., 2012; Sui et al., 2013; Jin et al., 2015)

	expression of the florigens. MRG702 encodes for a reader protein of H3K4me3 and H3K36me3. Knock-down plants show brassinosteroids-deficiency phenotypes and late flowering phenotypes, just as *SDG725* knock-downs. Indeed, MRG702 is able to bind DNA methylated by SDG725 and promote expression of flowering promoters, even though the precise mechanism is still unclear.	
Se14 - Os03g0151300	It encodes an H3K4 demethylase. It represses flowering in LD by inhibiting *Ehd1* and *RFT1* expression. The effect on *RFT1* is due to the demethylation activity on the *RFT1* promoter and gene, while the effect on *Ehd1* is indirect.	(Yokoo et al., 2014)
miR172 **SNB - Os07g0235800** **OsIDS1 - Os03g0818800**	*miR172* is a flowering promoter inhibited by PHYB. It targets the two *AP2*-like genes *SNB* and *OsIDS1*. These genes are flowering repressors positively regulated by *Hd1* and *OsCOL4*. Overexpressors of *SNB* and *OsIDS1* have decreased *Ehd1* expression both in LD and SD. Expression of *miR172* increase with the age of the plant, facilitating the repression of *SNB* and *OsIDS1* with aging.	(Lee et al., 2014)
SPIN1 - Os03g0815700 **SPL11 - Os12g0570000**	SPIN1 is an E3-ubiquitin ligase involved in the degradation of the flowering inhibitor SPL11, which suppress *Hd3a* expression.	(Vega-Sánchez et al., 2008)
OsTrx1 - Os09g0134500 **SIP1 - Os09g0560900**	OsTrx1 is a histone methyltransferase expressed mainly in leaf blades. It promotes flowering in LD by promoting *Ehd1* expression. SIP1 is a C2H2 zinc finger transctiption factor which can bind to OsTrx1 and to the *Ehd1* promoter, effectively directing the action of OsTrx1 to the *Ehd1* locus.	(Choi et al., 2014; Jiang et al., 2018)

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