Complex Regulatory Networks of Flowering Time in Rice

Yang-Seok Lee and Gynheung An*

Crop Biotech Institute & Graduate School of Biotechnology, Kyung Hee University, Yongin 446-701, Korea

Abstract

Rice flowering is inhibited when days are long during Spring and early Summer. This phenomenon is mediated by several independent pathways. Several genes are preferentially expressed under such conditions, including Grain yield and heading date 7 (Ghd7), Heading date 1 (Hd1), Heading date 5 (Hd5), and Heading date 6 (Hd6). By contrast, *Oryza sativa* Constans-like 4 (OsCOL4) deters flowering regardless of day length. The AP2-like genes Supernumerary Bract (SNB) and *Oryza sativa* Indeterminate Spikelet1 (OsIDS1) constitutively inhibit flowering. However, as days become shorter in late Summer, flowering is induced. Although Hd1 protein functions as a repressor under long days, it becomes a promoter under short days (SD). Both OsMADS50 and OsDof12 induce flowering specifically under LD, while *Oryza sativa* Indeterminate 1 (OsId1) causes flowering regardless of day length. Levels of expression by the repressors decrease as plants mature. For example, Ghd7 transcripts are more abundant in young plants. Transcripts of SNB and OsIDS1 are degraded by miR172, which is induced in older plants. Most of the upstream signals are transferred to Early heading date 1 (Ehd1), an immediate upstream regulator of the florigen genes Heading date 3a (Hd3a) and Rice FT 1 (RFT1). However, some signals directly turn on the florigens that are transferred to the shoot apical meristem, where the reproductive transition occurs.

Keywords: Day length; Florigens; Flowering time; Regulatory genes

Introduction

Plant yields are maximized and the exchange of genetic information among individuals is enhanced when flowering occurs at the optimal time. This phenomenon is modulated by environmental factors such as day length as well as by endogenous cues, e.g., developmental age. Rice (*Oryza sativa*) is a facultative short-day (SD) plant that flowers earlier under SD conditions. Photoreceptors and circadian clock genes play roles in modulating the expression of genes that regulate this timing. Flowering is inhibited during the early stage of development to allow sufficient vegetative growth. Various transcription factors (TFs) modulate flowering time by several independent pathways. Chromatin remodeling factors and microRNAs also control that activity. Signals are merged to Ehd1 or directly to florigens that induce flowering when an adequate amount has accumulated. Summaries of rice research have covered photoperiodic flowering [1-4] comparative biology [5-7], and the florigen mechanism [2]. Other reviews have focused on the relationships among photoperiod, epigenetic regulation [8] (Sun et al.), and temperature [9]. Here, we review integrations among various flowering pathways.

Review

Several rice cultivars have been domesticated for cultivation in a range of growing regions. Flowering time, often defined by heading date, is one of the most important agronomic traits that can be adapted to a new environment to increase yields. Genes that influence flowering time have been identified through analyses of Quantitative Trait Loci (QTL) from cultivars growing in different geographical locations [10]. Genes that control this regulatory network have also been found by studying either naturally occurring mutants or those that are generated through T-DNA or Tos17 insertions [11-13].

Table 1 summarizes those genes and roles.

Florigens

Heading date 3a (Hd3a) protein is a florigen in rice. Generated in the leaf phloem and transferred to the shoot apical meristem (SAM), this protein induces reproductive development when a plant reaches a certain growth stage [14]. Hd3a was initially identified by QTL mapping that utilized a population derived from a cross between the photoperiod-sensitive cultivar ‘Nipponbare’ and the photoperiod-insensitive cultivar ‘Kasalath’ [15]. Through high-resolution mapping, the candidate gene was located within an approximately 20-kb region that includes four genes [16]. One of those is highly homologous to Arabidopsis Flowering Locus T (FT), which prompts flowering. A genomic DNA fragment containing the gene from ‘Kasalath’ causes early flowering when introduced to ‘Nipponbare’, indicating that the FT-homologous gene is Hd3a [17].

Among the 13 rice proteins homologous to FT, RFT1 also functions as a florigen [18,19]. RFT1 is adjacent to Hd3a, separated by 11.5 kb on Chromosome 6, suggesting that the two arose through tandem duplication [18-20]. The RFT1 amino acid sequence shares 91% identity with Hd3a [16,18,21,22] (Chardon and Damerval). Transgenic plants expressing RNAi of both Hd3a and RFT1 do not flower until 300 days after sowing (DAS) [23]. Overexpression of Hd3a and RFT1 causes flowering at the callus induction stage [17,24,25]. These results are evidence that Hd3a and RFT1 are essential for flowering in rice [25]. Overexpression of FTL1, another FT-like gene in rice, also induces early flowering at the callus stage [22].

Hd3a is preferentially functional under SD whereas RFT1 has an LD role [19,23,25]. During short photoperiods, flowering of Hd3a RNAi plants is delayed by approximately one month, whereas timing for RFT1 RNAi plants is similar to that for the wild type, or WT [19,23,25]. By contrast, under LD conditions, RFT1 RNAi plants bolt later while the flowering time for Hd3a RNAi plants is similar to the WT [19]. Although temporal expression of both Hd3a and RFT1

*Corresponding author: Gynheung An, Crop Biotech Institute & Graduate School of Biotechnology, Kyung Hee University, Yongin 446-701, Korea, Tel: +82 51 6272 9029; E-mail: genean@khu.ac.kr

Received March 19, 2015; Accepted April 22, 2015; Published April 26, 2015

Citation: Lee YS, An G (2015) Complex Regulatory Networks of Flowering Time in Rice. J Rice Res 3: 141. doi:10.4172/2375-4338.1000141

Copyright: © 2015 Lee YS, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.
peaks at 35 DAS under SD conditions, transcript levels are higher for the former [23]. Because RFT1 transcripts are more abundant at later developmental stages in Hd3a RNAi plants under SD [23], RFT1 appears to function as a florigen when Hd3a is suppressed. In temperate regions, rice is grown under LD conditions, where RFT1 is preferentially functional as a florigen. An indica cultivar, 'Nona Bokra', flowers extremely late (about 200 DAS) in its natural habitat in Tsukuba, Japan (36˚N) but bolts at about 60 DAS under SD conditions.

Table 1: Flowering regulators in rice.

| Gene name | TIGR locus ID | Function | Note | Elucidation method | Pathways |
|-----------|---------------|----------|------|--------------------|----------|
| Hd3a      | LOC_Os06g06320 | Florigen | Phosphatidylethanolamine-binding protein (PEBP) | QTL/Overexpression/RNAi |          |
| RFT1      | LOC_Os06g06300 | Florigen | Phosphatidylethanolamine-binding protein (PEBP) | RNA/Overexpression |          |
| OsMADS14  | LOC_Os03g54160 | Floral transition | AP1 homolog | Overexpression |          |
| OsMADS15  | LOC_Os07g01820 | Floral transition | AP1 homolog | Overexpression |          |
| Hdt1/Se1  | LOC_Os06g16370 | SD activator/LD repressor | Constans-like (COL) | QTL/Tos17/T-DNA/Overexpression | Hdt1 |
| Ehd1      | LOC_Os10g32600 | Signal integrator | B-type response regulator | QTL/RNAi/Overexpression | Hdt1 |
| Hdt4/Hgi7/Lhd4 | LOC_Os07g15770 | LD repressor | Constans-like (COL) | QTL/Overexpression | Ehd1 |
| Hdt5/DTB8/Ghd8/LHD1/Dos9 | LOC_Os08g07740 | SD activator/LD repressor | HAP3 subunit | QTL/Ds | Hdt1,Ehd1 |
| Hill/CK2a | LOC_Os03g55389 | LD repressor | Casein kinase 2a | QTL | Hdt1, Hdt3a |
| Hid16/EL1/CK1 | LOC_Os03g57940 | LD repressor | Casein kinase 1 | QTL/T-DNA | Ghd7 |
| OsMADS50  | LOC_Os03g53100 | LD activator | SOC1 homolog | Overexpression | OsLFL1 |
| OsMADS56  | LOC_Os10g39130 | LD repressor | SOC1 homolog | Overexpression | OsLFL1 |
| OsDof12   | LOC_Os03g73600 | LD activator | DNA-binding with one zinc finger protein | Overexpression | Hdt3a |
| OsMADS51  | LOC_Os06g08500 | LD activator | Type 1 MADS-box protein | T-DNA/Overexpression | OsGI,Ehd1 |
| OsCo3     | LOC_Os09g06464 | LD repressor | CONSTANS-like (COL) | Overexpression | Hdt3a |
| Ehd2/Osd1/Rid1 | LOC_Os10g28330 | Constitutive activator | C2H2-type zinc finger protein | QTL/T-DNA/RNAi | Ehd1 |
| Ehd4      | LOC_Os03g02160 | Constitutive activator | C2H2-type zinc finger protein | QTL | Ehd1 |
| OsCo1     | LOC_Os02g39710 | Constitutive repressor | CONSTANS-like (COL) | T-DNA/Overexpression | Ehd1 |
| OsLF      | LOC_Os05g46370 | Constitutive repressor | Atypical HLH protein | Activation tagging by T-DNA | OsGI |
| SNB       | LOC_Os07g13170 | Constitutive repressor | AP2-like | Overexpression | miR172,Ehd1 |
| OsID51    | LOC_Os03g04330 | Constitutive repressor | AP2-like | Overexpression | miR172,Ehd1 |
| OsLFL1    | LOC_Os01g51610 | Constitutive repressor | B3 domain transcription factor | Overexpression | Ehd1 |
| OsGI      | LOC_Os01g08700 | Constitutive activator | C2H2-type zinc finger protein | Overexpression | Ehd1 |
| Hid2/Orpr37 | LOC_Os07g49460 | Circadian rhythm/LD activator | GIGANTEA ortholog | γ-ray radiation/RNAi/T-DNA | Hid3a |
| Hid3b/Hid17/Eift/OsELF3 | LOC_Os06g05060 | Circadian rhythm/LD activator | ELF3 homolog | QTL/T-DNA/RNAi | Hid1,Ghd7,OsGI |
| OsEF3     | LOC_Os01g38530 | Circadian rhythm/LD activator | ELF3 homolog | T-DNA |          |
| OsPhyA    | LOC_Os03g51030 | SD activator/LD repressor | Phytochrome | Tos17/T-DNA |          |
| OsPhyB    | LOC_Os03g19590 | Constitutive repressor | Phytochrome | γ-ray radiation/T-DNA |          |
| OsPhyC    | LOC_Os03g54084 | LD repressor | Phytochrome | Tos17/T-DNA |          |
| SE5       | LOC_Os06g40080 | SD activator/LD repressor | Heme oxygenase | γ-ray radiation |          |
| OsCRY2    | LOC_Os02g11550 | Constitutive activator | Cryptochrome | antisense |          |
| OsVIL1/OsVIL2 | LOC_Os12g34850 | Flowering activator | VIN3-like (PRC2 complex) | RNAi | OsLF |
| OsVIL2/C2/OsVIL3 | LOC_Os02g5840 | Flowering activator | VIN3-like (PRC2 complex) | T-DNA | OsLFL1 |
| OsEMF2b   | LOC_Os04g08037 | Flowering activator | Su(z)2-12-like (PRC2 complex) | T-DNA/RNAi/Overexpression | OsLFL1 |
| OsTnx1    | LOC_Os09g04890 | LD activator | TnxG | T-DNA | Ghd7 |
| Ehd3      | LOC_Os08g01420 | Flowering activator | Plant Homeodomain (PHD) | Overexpression | Ghd7 |
| SDG724/LVP1 | LOC_Os09g13740 | LD activator | SET domain | Somaclonal variation by tissue culture | OsMADS50 |
| SDG711    | LOC_Os06g16390 | LD repressor | SET domain | RNAi | Overexpression |
| SDG718    | LOC_Os03g19480 | SD activator | SET domain | RNAi | Overexpression |
Overexpression of the RFT1 allele from 'Nipponbare' or 'Kasalath' induces extremely early flowering while overexpression of that allele from 'Nona Bokra' does not [27] possibly because an amino acid substitution of E to K at the 150th position of RFT1 causes a functional defect in that cultivar. In addition, polymorphisms in the RFT1 promoter region reduce this expression in 'Nona Bokra' [27].

Florigens are produced in leaves and transported to the SAM where they induce reproductive developments [14,19]. After their arrival, they bind to the 14-3-3 proteins GF14b and GF14c [28,29], and the complex interacts with OsFD1 [2]. Crystalllographic analyses have also shown that these three proteins form a florigen activation complex [2] that is composed of two Hd3a molecules, the GF14c (14-3-3 protein) dimer, and two OsFD1s. That complex binds to the promoter of OsMADS15 to induce expression of the target gene [2]. Expression of OsMADS14 and OsMADS15 is decreased in the SAM of Hd3a RNAi or RFT1 RNAi plants [19,23,25]. Whereas overexpression of OsMADS14 causes extremely early flowering at the callus induction stage [30], flowering by GF14c overexpression (OX) plants is delayed approximately 20 d. The GF14c/GF14c heterozygous mutants bolt early, by about 14 d under SD [28]. These findings suggest that, although GF14c alone functions as an inhibitor, it becomes an activator when it forms that complex with Hd3a and OsFD1.

**Hd1 and Ehd1**

Hd3a is controlled by Hd1, which binds to the Hd3a promoter [31]. Hd1 is a rice ortholog of Arabidopsis Constans (CO) [32]. First identified by QTL mapping of a cross between 'Nipponbare' and 'Kasalath' [15,32], Hd1 is allelic to SE1 (Photoperiodic Sensitivity 1), a major QTL controlling photoperiodic sensitivity [33]. The se1 mutant has been induced by γ-ray irradiation of seeds from the japaonica cultivar "Gimbozu". It flowers early under LD conditions [33]. Nonfunctional Hd1 causes late flowering under SD but early flowering under LD [32], indicating that Hd1 can be either a flowering activator or repressor, depending upon light conditions. This behavior is contradictory to that of Arabidopsis CO, which is a constitutive flowering activator under both SD and LD [34]. The hd1-1 mutants generated by Tosi17 insertion also show flowering phenotypes similar to se1 [35]. Transcript levels of Hd3a and RFT1 are decreased in hd1 mutants under SD conditions, but increased under LD [28,35]. How Hd1 functions differently between SD and LD is unknown. Overexpression of Hd1 causes late flowering, but the phenotype is not observed in the osphyB mutant background [36], thereby demonstrating that OsPhyB is necessary for the suppressive functioning of Hd1. As a member of the family of CO-like proteins, Hd1 contains conserves B-box zinc fingers and CCAAT domains [37,38].

Expression of Hd3a is also controlled by Ehd1, as first revealed by QTL mapping of a cross between 'Taichung 65' and *Oryza glaberrima* [21]. Introggression of the Ehd1 allele from *O. glaberrima* causes early flowering in 'Taichung 65' under both SD and LD [39]. Ehd1 protein is a member of the B-type response regulators, which have a receiver domain and a GARP domain [39]. The latter functions to bind DNA; an alteration of Gly in the domain to Arg greatly reduces this binding capacity in 'Taichung 65' [39]. In that cultivar, a single amino acid substitution in the GARP domain disrupts binding to the target DNA [39]. Ehd1 induces transcript levels for Hd3a, RFT1, OsMADS14, and OsMADS15 [39]. Ehd1 RNAi plants flower later, by 7 d under SD [40] and by 10 d under LD [41]. All of these observations indicate that Ehd1 is a flowering activator.

**LD-preferential regulatory elements**

In temperate zones, rice is grown under LD conditions. When plants are young, flowering is inhibited to allow for sufficient vegetative growth and tillering. After a certain period, a flowering signal is induced to initiate the formation of reproductive organs.

Grain yield and heading date 7 (Ghd7)/Late Heading Date 4 (Lhd4) is an LD-specific repressor identified through QTL mapping of plant height and grain yield traits [42,43]. Introgressing a functional allele of Ghd7 from 'Minghui 63' to 'Zhenshan 97' can cause pleiotropic phenotypes such as late flowering and increases in height, stem diameter, and yield [42,43]. Ghd7 encodes a CO-like protein containing the B-box and CCT domains [38,43]. This gene suppresses flowering by inhibiting the expression of Ehd1 [43]. Ghd7 is strongly expressed in the vascular bundle where Ehd1 is expressed, providing evidence that Ghd7 functions upstream of Ehd1 [43]. Ghd7 is phosphorylated by HEADING DATE 16 (Hd16), a casein kinase-1 protein [24]. It expression is very low under SD but significantly higher under LD [43,44]. Natural variations include Ghd7-1, Ghd7-4, Ghd7-3, Ghd7-0, and Ghd7-0a. Among them, Ghd7-0 and Ghd7-0a are nonfunctional alleles mainly observed in high-latitude cultivars that are grown during shorter seasons [43]. The rest of the alleles are functional and found in low-latitude cultivars [43] (Xue et al.). Therefore, these reports indicate that Ghd7 alleles have played an important role during the progression of rice domestication.

Heading date 5 (Hd5)/QTL for days to heading on chromosome 8 (DTH8)/Grain yield and heading date 8 (Ghd8)/Late Heading Date 1 (LHD1) encodes a putative HAP3 subunit of the CCAAT-box-binding TF [45]. The HAP proteins have three subunits – HAP2, HAP3, and HAP5 – that form trimeric complexes [46,47]. Introgression of the functional Hd5 allele causes late flowering under LD by suppressing expression of Ehd1, Hd3a, and RFT1 [45,48-50]. However, under SD conditions, expression by those genes is not affected by Hd5. Flowering inhibition is independent of activity by Ghd7 and Hd1 [45]. By contrast, the ds9 mutant, another allelic mutant for Hd5, shows an early-flowering phenotype under LD but a late-flowering phenotype under SD [51]. Those flowering patterns are similar to the phenotype of the hd1 mutant [52]. Because the HAP complex forms a trimeric complex with CO protein in Arabidopsis, Hd5 cooperates with Hd1 through protein–protein interactions. The former also controls plant architecture, e.g., height, yield, grain dry weight, and the number of tillers.

Heading date 6 (Hd6) encodes a CK2 α-subunit and was identified by crossing 'Nipponbare' and 'Kasalath' [15,53]. The Hd6 allele from 'Nipponbare' is nonfunctional due to an early stop in the coding region. Introgression of the functional Hd6 allele from 'Kasalath' to 'Nipponbare' results in late flowering [53]. Hd6 functions as a flowering repressor of Hd3a and RFT1 under LD [10]. Although Hd6 has a late-flowering phenotype when functional Hd1 allele is present, it does not phosphorylate Hd1 [10].

Heading date 16 (Hd16)/Early flowering 1 (EL1) is another flowering repressor [50,54]. This gene was identified from a cross between the japaonica rice 'Nipponbare' and 'Koshihikari' [55] (Matsubara et al.). 'Koshihikari' flowers later than 'Nipponbare' under SD but earlier under LD [55]. Introggression of a deficient allele of Hd16 from 'Koshihikari' into 'Nipponbare' weakens photoperiodic sensitivity and increases expression of floral activators Ehd1, Hd3a, and RFT1 under LD [24]. Hd16 encodes a casein kinase 1 that phosphorylates the rice DELLA protein SLR1 [50] and Ghd7 protein [24,50,56]. Therefore, Hd16 might possibly act as a mediator between floral transition and other developmental processes such as gibberellin signaling and tillering.

---

**Citation:** Lee YS, An G (2015) Complex Regulatory Networks of Flowering Time in Rice. J Rice Res 3: 141. doi:10.4172/2375-4338.1000141
OsMADS50 is an LD-specific promoter of flowering [57]. Mutation induced by T-DNA causes a flowering delay of more than one month under LD, but has no such effect under SD [57]. OsMADS50 is an ortholog of Suppressor of Overexpression of CO 1 (SOC1), a flowering activator in Arabidopsis [58]. OsMADS50 suppresses expression of OsLF1 [41] which inhibits Ehd1 by binding to the promoter region [59,60]. Transcript levels of OsMADS50 increase continuously until five weeks after germination [41]. This expression pattern is opposite to that of Ghd7, supporting the idea that OsMADS50 is a floral inducer. OsMADS56, the most homologous to OsMADS50, functions antagonistically when it binds to OsMADS50 [41]. Plants that over-express OsMADS56 flower later, by more than a month, under LD because expression of Ehd1, Hd3a, and RFT1 is repressed [41]. Both OsMADS50 and OsMADS56 are MADS-box TFs that contain a highly conserved MADS-box domain and K domain. The MADS-box domains function in DNA binding and dimerization while the K domains are involved in dimerization. The C domain is the least-conserved in both length and sequence. In some cases, it either possesses transactivation capability or contributes to the formation of multimeric complexes among MADS proteins [61,62]. The C region is shorter in OsMADS56 than in OsMADS50 and their sequences are diverse, suggesting that the former inhibits the latter.

Overexpression of OsDof12 causes early flowering under LD but not under SD [63] (Li et al.). In OsDof12 OX plants, transcript levels of Hd3a and OsMADS14 are increased under LD while those of Hd1, OsMADS51, Ehd1, and OsGI are not changed [63]. These results suggest that OsDof12 induces flowering by a pathway that does not go through Ehd1.

**SD-preferential regulatory elements**

In addition to the inducer Hd1, several regulatory elements control flowering time under SD. They include OsMADS51, a Type I MADS-box protein [40]. The osmads51 mutant flowers approximately two weeks later under SD, but its timing is unaltered under LD. The OsMADS51 OX plants bolt early, by about 10 d, under SD because expression by Ehd1, H3d3a, and OsMADS14 is enhanced [40]. However, flowering time is not changed under LD. This implies that OsMADS51 induces flowering only under SD, probably because it generates a product that functions preferentially under such conditions. Alternatively, the protein either inhibits an SD-specific repressor or enhances an SD-specific inducer.

Another SD-specific suppressor, OsCO3, is a member of the CO-like proteins and is similar to HvCO3 in barley [38,64]. Transcript levels are high during the daytime and low at night [64]. OsCO3 OX plants show SD-preferential flowering that is delayed by approximately 40 d because Hd3a, FTL, and OsMADS14 are suppressed [65].

**Constitutive regulators**

OsIndeterminate 1 (OsInd1), Early heading date 2 (Ehd2)/Rice Indeterminate 1 (RID1) is a constitutive activator. RNAi plants of OsInd1 have significantly delayed flowering under both SD and LD [65] and knock-out mutants do not flower for more than 365 d [66,67]. This indicates that OsInd1 is required for promoting a flowering signal regardless of light conditions. However, no research has shown that overexpression of OsInd1 causes early flowering. Therefore, it is possible that OsInd1 must form an activation complex with another protein. OsInd1 regulates the expression of Ehd1 and its downstream genes Hd3a and RFT1. Transcription of other regulators is not affected in osid1 mutants, suggesting that OsInd1 may directly induce Ehd1 expression. OsInd1 is the rice ortholog of maize Indeterminate 1 (Id1), which encodes a TF with an indeterminate domain [65]. Because id1 mutants show phenotypes of prolonged vegetative growth [68], it has been suggested that Id1 is involved in the synthesis of a florigen [69,70]. The presence of Ehd1 homologs in maize implies that the Id1–Ehd1 pathway is conserved among grass species.

**Early heading date 4 (Ehd4)** is another constitutive activator that encodes a CCCH-type zinc finger protein. The ehd4 mutant was identified as a somaclonal variant in Kitaake [71]. The ehd4 mutant flowered later under both SD and LD [71]. In the mutant, transcript levels of Ehd1, Hd3a and RFT1 are decreased, suggesting that Ehd4 prompts flowering time via Ehd1.

**OsCOL4** functions as a constitutive flowering repressor [72]. The oscol4 mutants flower earlier, by approximately two weeks under SD and approximately three weeks under LD because Ehd1 expression is enhanced. Overexpression of OsCOL4 delays flowering by approximately three weeks under SD and approximately six weeks under LD conditions when transcript levels of Ehd1 are suppressed [72]. Expression of OsCOL4 is decreased in osphyB mutants and flowering time is similar between osphyB oscol4 double mutants and osphyB single mutants, indicating that OsCOL4 is positively controlled by OsPhyB [72]. Whereas OsPhyB is involved in the night break (NB) effect [35], OsCOL4 is NB-insensitive, demonstrating that the former controls flowering time through an alternative pathway.

OsLF encodes an atypical BHLH TF that is a constitutive flowering repressor. Overexpression of OsLF causes late flowering regardless of photoperiod length [73]. Under SD, expression by OsGI and Hd1 is partially decreased in BX5 lines [73].

As a flowering activator, mir172 suppresses AP2-like genes in Arabidopsis [74]. Similarly, mir172a and mir172d induce flowering in rice [75]. Transcripts of the AP2-like genes Supernumerary Bract (SNB) and *Oryza sativa* Indeterminate Spikelet 1 (OsdS1) are targeted by mir172s. Their overexpression delays flowering by suppressing the expression of Ehd1 [75]. Phytochromes inhibit mir172, thereby increasing the expression of those AP2-like genes (Lee et al.). This indicates that the phytochrome–mir172–AP2–Ehd1 pathway also plays a role in controlling flowering time.

**Circadian rhythm**

GIGANTEA (GI) controls CO, a positive regulator of FT in Arabidopsis [76]. The GI–CO–FT pathway is conserved in rice [31]. Knockout mutants and RNAi-suppressed plants of OsGI flower late under SD but early under LD, exhibiting reduced photoperiodic sensitivity [31,77]. OsGI positively controls Hd1 expression, with the latter being reduced in OsGI RNAi plants but increased in BX plants [31]. Transcriptome analyses between WT and osgi mutants have revealed that numerous rhythmic genes are affected [77]. In particular, expression by Ehd1, H3d3a, and Ghd7 is diminished in those mutants [44]. That of OsMADS51 is also decreased in OsGI antisense plants [40], indicating that OsGI controls flowering time via several independent pathways. An osgi knockout mutant generated by T-DNA insertion flowers late by 36 d under SD and by 9 d under LD conditions [78]. This SD-preferential phenotype is similar to that of the mutant by gamma irradiation [79]. Under SD, transcript levels of floral activators such as H3d3a, RFT1, Ehd1, H1d, OsMADS51 and OsInd1 are decreased in the osgi, demonstrating that the delayed flowering is due to decreased expression by the flowering activators [78]. However, under LD, transcript level of OsGI is reduced to a low level at later stage of development when the flowering signals are generated. Consequently,
effect of OsGI on controlling flowering time under LD conditions is minimal.

Heading date 2 (Hd2) was identified by QTL mapping using crossed progenies between ‘Nipponbare’ and ‘Kasalath’ [15]. Introgenressing the Hd2 allele of ‘Kasalath’ to ‘Nipponbare’ causes late flowering under SD but early flowering under LD [32]. This is evidence that Hd2 is involved in photoperiodic sensitivity. Hd2 is closely linked to Osrya sativa Pseudo Response Regulator 37 (OsPRR37), which encodes a pseudo-response regulator that functions as a major component of the circadian clock [80-83]. In two early-flowering Hokkaido cultivars, ‘Kitaake’ and ‘H143’, OsPRR37 is defective [84,85].

QTL mapping has shown that Heading date 3b (Hdb3b)/Heading date 17 (Hd17)/Early flowering 7 (Ef7)/Oryza sativa Early flowering 3 (OsELF3) is a flowering inducer [16]. Hdb3a encodes a homolog of Arabidopsis, EARLY FLOWERING 3 (ELF3), which has crucial roles in maintaining circadian rhythms [16,86-90]. In Arabidopsis, ELF3 modulates re-setting of the circadian clock [91,92]. A mutation in that gene leads to an early and photoperiod-insensitive flowering phenotype in Arabidopsis [93]. Hd17, an allele of the circadian clock gene, has also been identified by QTL mapping of a cross between ‘Nipponbare’ and ‘Koshikihari’ [94]. Introgenression of the Hd17 allele from ‘Koshikihari’ to ‘Nipponbare’ causes late flowering because of enhanced expression by Ghd7. The ef7 mutant, another allelic mutant for Hdb3b, was developed via γ-irradiation of seeds from the japonica cultivar ‘Gimbozu’ [88]. Double-mutant analyses suggest that Hdb3b functions as a floral activator by suppressing Ghd7 and Hd1. Hdb3b is preferentially expressed in the mesophyll cells of the leaf blade, and also weakly in floral organs such as the lemma, palea, stamen, and pistil [88]. Because Ghd7 is preferentially expressed in the vascular tissue [43] (Xue et al.), further study is needed to determine how the mesophyll differentially expresses Hdb3b controls Ghd7. Toss1 and T-DNA insertions cause late flowering by enhancing Ghd7 [89,90]. Various circadian clock components, e.g., OsLHY, OsPRR1, -37, -73, -95, and OsGI are changed in the ef7 mutants [89,90]. Therefore, one might conclude that, similar to Arabidopsis ELF3, Hdb3b is involved in circadian clock control. In the rice genome, OsEF3 is also highly homologous to ELF3. Mutations in the rice gene cause pleiotropic effects, including late flowering [95].

Photoreception

Photoreception is one of the most important processes by which plants determine flowering time. In rice, day length is recognized by three phytochromes, OsPhyA, OsPhyB, and OsPhyC. Mutations in OsPhyB or OsPhyC result in early flowering, indicating that function as flowering repressors [96]. OsPhyB suppresses flowering by activating OsCOL4 [35,72] and is also involved in the NB effect, as observed in SD plants [97,98]. Flowering in rice is inhibited by night breaks because of decreased Hd3a expression [35]. However, the NB effect is not seen in the osphyB mutant, and Hd3a transcript levels are not altered there [35].

The flowering time of osphyB osphyC double mutants is similar to that of osphyB single mutants, probably due to the post-translational process of OsPhyC in osphyB mutants, where the amount of protein is significantly lower [79]. In Arabidopsis, PhyC protein levels are also reduced in phyB mutants [99,100]. In addition, phyB and phyC mutants show early flowering phenotypes under SD, and flowering time is similar between phyB and the phyB phyC double mutants [100]. This phenomenon is also found in rice [96,100]. It has been reported that PhyB interacts with PhyC in Arabidopsis [101], suggesting that OsPhyB and OsPhyC function as flowering repressors by forming a heterodimer, whereas OsPhyB or OsPhyC alone is unstable.

Although mutation of OsPhyA by itself does not affect flowering time, the double mutants osphyA osphyB and osphyA osphyC flower earlier under SD and later under LD when compared with osphyB or osphyC alone [96]. This demonstrates that OsPhyA cooperates with other phytochromes to modulate the expression of flowering regulators [3]. Ghd7 expression is increased in osphyB and osphyB osphyC mutants but decreased in osphyA osphyC and osphyA osphyB, indicating that OsPhyA positively controls Ghd7 expression while OsPhyB and OsphyC have the opposite effect [79]. Interestingly, Ehd1 expression is not changed despite Ghd7 expression being elevated in the osphyB osphyC mutants. This suggests that OsPhyA controls flowering time through an alternative pathway [79]. In Arabidopsis, PhyA prompts floral induction by stabilizing CO protein whereas Phyb suppresses flowering via CO degradation [102]. In rice, Hd1 protein levels are similar between light and dark conditions in 35S::Hd1::myc plants [36]. This implies that, unlike CO in Arabidopsis, Hd1 protein is not degraded by light in rice.

SE5 encodes a heme oxygenase that is highly homologous to Arabidopsis HY1, which is involved in the biosynthesis of phytochrome chromophore [77,103] (Izawa et al.; Andrés et al.). The se5 mutants exhibit an extremely early flowering phenotype under both SD and LD [103,104] flowering at 44 d after germination, regardless of day length, because of elevated transcript levels of Ehd1 and Hd1 [104]. This phenotype is similar to that of osphyA osphyB mutants [3,77,35,103].

Flowering time is also controlled by a blue light receptor cryptochrome (CRY) in Arabidopsis [102,105-107]. The rice genome has three CRY genes, OsCRY1a, OsCRY1b, and OsCRY2 [108,109]. While OsCRY1a and OsCRY1b are responsible for regulating blue light-mediated de-etiolation [108,109], OsCRY2 functions in controlling flowering time [108,109]. OsCRY2 antisense plants flower late under both SD and LD [108] indicating that OsCRY2 is a flowering activator. In Arabidopsis, CRY2 activates flowering by stabilizing CO protein [102]. However, the molecular mechanism for OsCRY2 is not yet known in rice.

In Arabidopsis, GI interacts with several blue light receptors, e.g., Zeitluppe (ZTL) and Flavin-Binding Kelch Repeat F-Box 1 (FKF1) [110,111]. The protein complexes are more stable under blue light treatment, but this activation is diminished in osgi mutants, suggesting that OsGI is involved in blue light signaling [3].

Epigenetic regulation

Expression by some flowering time genes is developmentally regulated. For example, transcripts of OsLFL1 are maintained at a high level for the first four weeks but gradually decrease as plants mature. By comparison, transcripts of OsVIL2 (Oryza sativa VIN3-like 2)/LC2 (Leaf inclination 2)/OsVIL3 (Oryza sativa VIN3-like 3) remain at a low level but increase rapidly as OsLFL1 expression declines. Whereas overexpression of OsLFL1 causes late flowering [59,60] knockout mutations of OsVIL2 delay flowering under both SD and LD [112]. However, a knockout mutation of LC2, an allelic mutation of OsVIL2, causes late flowering only under SD [54,113]. The difference in results reported by those two research groups may be related to the day length that was tested. Whereas experiments by the former group entailed a 14.5-h photoperiod, plants used by the latter group were exposed to 14 h of light.
OsVIL2 protein binds to histone H3 and OsLFL1 chromatin (Yang et al.). Histone H3 lysine 27 trimethyl (H3K27me3) levels of OsLFL1 chromatin are reduced in osv12 mutants (Yang et al.). This indicates that OsVIL2 suppresses expression of OsLFL1 by mediating the methylation of lysine 27 residue of histone H3. OsVIL2 binds to O. sativa Embryonic Flower 2b (OsEMF2b), a core component of the polycomb repressive complex 2 (PRC2) that represses the expression of target genes by condensing their chromatin [112]. The osem2b mutants also show late flowering phenotypes [112,114]. Emf2b promotes flowering by directly suppressing the expression of OsLFL1 [115]. OsVIL1–RNAi plants flower later under SD conditions [113]. OsVIL1 engages with OsVIL2, suggesting that the two cooperate as flowering activators through protein–protein interactions.

Transcription of Ghd7 is epigenetically regulated by OsTrx1 (Oryza sativa Trithorax 1), which encodes a histone methyltransferase [75]. OsTrx1 belongs to a Trithorax group (TrxG) of proteins that enhance the expression of target genes by loosening their chromatin. The ostrx1 mutants show significantly delayed flowering that is preferential under LD [75]. In those mutants, Ghd7 transcripts are more abundant under LD [75].

OsTrx1 protein interacts with Early heading date 3 (Ehd3) protein in Plant Homeodomain (PHD) finger regions [75]. The ehd3 mutant was identified as a late-flowering variant of M2 plants from a γ-ray-mutagenized line of O. sativa ssp. japonica 'Tohoku IL9' [116]. Those transcripts are increased in ehd3 mutants, all evidence that OsTrx1 and Ehd3 cooperatively suppress Ghd7.

The rice genome has at least 37 SET domain group (SDG) proteins that may be involved in chromatin remodeling via histone demethylation [117]. For example, SDG724/Long Vegetative Phase 1 (LVPI), which has histone methyltransferase activity, preferentially functions as a flowering activator under LD [118]. In the lvp1 mutant, expression by activators OsMADS50, Hd3a, RFT1, and Ehd1 is significantly decreased under LD [118]. These findings confirm that SDG724 serves as an LD-preferential activator by inducing OsMADS50. Both SDG711 and SDG718 encode the rice enhancer of zeste [E(z)], a subunit of PRC2 [119]. SDG711 is a flowering repressor under LD, as demonstrated by the late flowering phenotype of OX plants, whereas SDG711 RNAi plants display early flowering phenotypes under LD [119]. In the SDG711 OX plants, expression is reduced for Ehd1, Hd3a, RFT1, OsMADS14, OsMADS15, and OsLF while transcript levels of Hd1 are increased under LD [119]. By contrast, in the SDG711 RNAi plants, expression is preferentially increased for OsMADS14 and OsLF but decreased for Hd1 under LD [119]. Those results demonstrate that SDG711 functions as an LD-preferential flowering repressor by inhibiting OsLF. Furthermore, SDG718 RNAi plants flower late preferentially under SD, with expression being decreased for OsMADS14, RFT1, Hd3a, and Hd1 but increased for OsLF [119]. Therefore, SDG718 functions as an SD-preferential flowering activator by suppressing OsLF.

Conclusions

In addition to the conserved GI–Hd1–Hd3a pathway present in all plant species, rice has several other pathways that control flowering time. Most of them are merged to Ehd1 or, occasionally, directly to florigens. The Ghd7 pathway is the major route that functions under LD. Several upstream elements, e.g., phytochromes, GI, and chromatin remodeling factors, modulate Ghd7 expression. The OsMADS50 pathway induces flowering preferentially under LD. By contrast, the OsMADS51 pathway enhances flowering specifically under SD while OsCO3 inhibits flowering only under SD. OsID1 is a constitutive activator that is essential for flowering. The constitutive repressor OsCOL4 is controlled by OsPhyB. Flowering is induced by the miR172 pathway through the degradation of mRNA from AP2 family genes. Although several regulatory genes that control flowering time have been identified, their relationships and the way in which their proteins function are not well understood and must still be addressed. Moreover, the regulatory mechanisms for plant responses to environmental stimuli such as temperature extremes, nutrient deficiencies, and various stresses require further exploration.

Acknowledgements

We thank the members of the Crop Biotech Center at Kyung Hee University for their participation in discussions. We also thank Priscilla Licht for critical proofreading of the manuscript. This work was supported in part by grants from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center, No. PJ01108001), Rural Development Administration, Republic of Korea; the Basic Research Promotion Fund, Republic of Korea (NRF-2007-0093862); and Kyung Hee University (20130214).

References

1. Izawa T (2007) Adaptation of flowering-time by natural and artificial selection in Arabidopsis and rice. J Exp Bot 58: 3091-3097.
2. Tsuji H, Taoka K, Shimamoto K (2011) Regulation of flowering in rice: Two florigen genes, a complex gene network, and natural variation. Curr Opin Plant Biol 14: 45-52.
3. Itoh H, Izawa T (2013) The coincidence of critical day length recognition for florigen gene expression and floral transition under long-day conditions in rice. Mol Plant 6: 635-649.
4. Yeang HY (2013) Solar rhythm in the regulation of photoperiodic flowering of long-day and short-day plants. J Exp Bot 64: 2643-2652.
5. Hayama R, Coupland G (2004) The molecular basis of diversity in the photoperiodic flowering responses of Arabidopsis and rice. Plant Physiol 135: 677-684.
6. Greenup A, Peacock WJ, Dennis ES, Trevaskis B (2009) The molecular biology of seasonal flowering-responses in Arabidopsis and the cereals. Annu Bot 103: 1165-1172.
7. Song YH, Ito S, Imaizumi T (2010) Similarities in the circadian clock and photoperiodism in plants. Curr Opin Plant Biol 13: 594-603.
8. Sun C, Chen D, Fang J, Wang P, Deng X, Chiu C (2014) Understanding the genetic and epigenetic architecture in complex network of rice flowering pathways. Protein Cell 5: 889-898.
9. Song YL, Luan WJ (2012) Molecular regulatory network of flowering by photoperiod and temperature in rice. Rice Sci 19: 169-176.
10. Ogiso E, Takahashi Y, Sasaki T, Yano M, Izawa T (2010) The role of casein kinase II in flowering time regulation has diversified during evolution. Plant Physiol 152: 808-820.
11. Jeon JS, Lee S, Jung KH, Jun SH, Jeong DH, et al. (2000a) T-DNAinsertional mutagenesis for functional genomics in rice. Plant Mol Biol 42: 561-570.
12. An S, Park S, Jeong DH, Lee DY, Kang HG, et al. (2003) Generation and analysis of end sequence database for T-DNA tagging lines in rice. Plant Physiol 133: 2040-2047.
13. Hirochika H, Guiderdoni E, An G, Hsing YI, Eun MY, Han CD, et al. (2004) Rice mutant resources for gene discovery. Plant Mol Biol 54: 325-334.
14. Tamaki S, Matsu S, Wong HL, Yokoi S, Shimamoto K (2007) Hd3a protein is a mobile flowering signal in rice. Science 316: 1033-1036.
15. Yano M, Sasaki T (1997) Genetic and molecular dissection of quantitative traits in rice. Plant Mol Biol 35: 145-153.
16. Kojima S, Takahashi Y, Kobayashi Y, Monna L, Sasaki T, et al. (2002) Hd3a, a rice ortholog of the Arabidopsis FT gene, promotes transition to flowering downstream of Hd1 under short-day conditions. Plant Cell Physiol 43: 1096-1105.
17. Monna L, Lin X, Kojima S, Sasaki T, Yano M (2002) Genetic dissection of a genomic region for a quantitative trait locus, Hd3, into two loci, Hd3a and Hd3b, controlling heading date in rice. Theor Appl Genet 104: 772-778.

18. Chardon F, Damerval C (2005) Phylogenetic analysis of the PEBP gene family in cereals. J Mol Evol 61: 579-590.

19. Komiyama R, Yokoi S, Shimamoto K (2009) A gene network for long-day flowering activates RFT1 encoding a mobile flowering signal in rice. Development 136: 3443-3450.

20. Hagiwara WE, Uwatoko A, Sasaki A, Matsubara K, Nagano H, et al. (2009) Diversification in flowering time due to tandem FT-like gene duplication, generating novel Mendelian factors in wild and cultivated rice. Mol Ecol 18: 1537-1549.

21. Doi K, Izawa T, Fusse T, Yamanouchi U, Kubo T, et al. (2004) Ehd1, a B-type response regulator in rice, confers short-day promotion of flowering and controls FT-like gene expression independently of Hd1. Genes Dev 18: 928-936.

22. Izawa T, Oikawa T, Sugiyama N, Tanisaka T, Yano M, Shimamoto K (2002) Phytochrome mediates the external light signal to repress FT orthologs in photoperiodic flowering of rice. Genes Dev 16: 2006-2020.

23. Komiyama R, Iegami A, Tamaki S, Yokoi S, Shimamoto K (2008) Hd3a and RFT1 are essential for flowering in rice. Development 135: 767-774.

24. Hori K, Ogiso-Tanaka E, Matsubara K, Yamanouchi U, Ebana K, et al. (2013) Hd16, a gene for casein kinase I, is involved in the control of rice flowering time by modulating the day-length response. Plant J 76: 36-46.

25. Tsuchi H, Tamaki S, Komiyama R, Shimamoto K (2008) Floreign and the photoperiodic control of flowering in rice. Rice 1: 25-35.

26. Uga Y, Nonoue Y, Liang WZ, Lin HY, Yamanouchi U, et al. (2007) Accumulation of additive effects generates a strong photoperiod sensitivity in the extremely late-heading rice cultivar 'Nona Bokra'. Theor Appl Genet 114: 1457-1466.

27. Ogiso-Tanaka E, Matsubara K, Yamanouchi U, Ichimura E, etc. (2008) Natural variation of the RICE FLOWERING LOCUS T contributes to flowering time divergence in rice. PLoS One 3: e75995.

28. PurwesriYA, Ogaki Y, Tamaki S, Tsuji H, Shimamoto K (2009) The 14-3-3 protein GF14c acts as a negative regulator of flowering in rice by interacting with the florigen Hd3a. Plant Cell Physiol 50: 429-438.

29. Taoka K-I, Ohki I, Tsuji H, Funakita K, Hayashita K, et al. (2011) 14-3-3 proteins act as intracellular receptors for rice Hd3a florigen. Nature 476: 332-335.

30. Jeon J-S, Lee S, Jung K-H, Yang W-S, Yi G-H, et al. (2013) Natural variation of the RICE FLOWERING LOCUS T contributes to flowering time divergence in rice. PLoS One 8: e57995.

31. Dey S, Sreenivasulu N, et al. (2009) OsMADS50 and OsMADS56 function antagonistically in regulating long-day flowering in rice. Plant J 76: 36-46.

32. Lin H, Liang Z-W, Sasaki T, Yano M (2003) Fine mapping and characterization of quantitative trait loci Hd4 and Hd5 controlling heading date in rice. Breed Sci 53: 51-59.

33. Yan WH, Wang P, Chen HX, Zhou HU, Li QP, et al. (2011) A major QTL, Ghd8, plays pleiotropic roles in regulating grain productivity, plant height, and heading date in rice. Plant J 74: 319-330.

34. Dai C, Xue HW (2010) Rice early flowering1, a CKI, phosphorylates DELLA protein SLR1 to negatively regulate gibberellin signalling. EMBO J: 29: 1961-1972.

35. Lee YS, An G (2015) Complex Regulatory Networks of Flowering Time in Rice. J Rice Res 3: 141. doi:10.4172/2375-4338.1000141

36. Ishikawa R, Aoki M, Kurotani K, Yokoi S, Shinomura T, et al. (2011) An early-heading mutant gene of Oryza sativa L. was isolated encoding OsHAP3H and its C-terminus was required for interaction with HDAP2 and HAP5. J Plant Biol 58: 26-37.

37. Yano M, Katayose Y, Ashikari M, Yamanouchi U, etc. (2000) Hd1, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the arabidopsis flowering time gene CONSTANS. Plant Cell 12: 2473-2483.

38. Takahashi Y, Shomura A, Sasaki T, Yano M (2001) Hd1, a quantitative trait locus involved in photoperiod sensitivity, encodes the alpha subunit of protein kinase CK2. Proc Natl Acad Sci USA 98: 7922-7927.

39. Dai C, Xue HW (2010) Rice early flowering1, a CKI, phosphorylates DELLA protein SLR1 to negatively regulate gibberellin signalling. EMBO J: 29: 1961-1972.

40. Meng Q, Zhang Z, Zhou X, Chen X, Guo Z (2015) Ds9 was isolated encoding as OsHAP3H and its C-terminus was required for interaction with HAP2 and HAP5. J Plant Biol 58: 26-37.

41. Yano M, Katayose Y, Ashikari M, Yamanouchi U, etc. (2000) Hd1, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the arabidopsis flowering time gene CONSTANS. Plant Cell 12: 2473-2483.

42. Takahashi Y, Shomura A, Sasaki T, Yano M (2001) Hd1, a quantitative trait locus involved in photoperiod sensitivity, encodes the alpha subunit of protein kinase CK2. Proc Natl Acad Sci USA 98: 7922-7927.

43. Zhao SQ, Hu J, Guo LB, Qian Q, Xue HW (2010) Rice leaf inclination 2, a VIN3-LIKE protein, regulates leaf angle through modulating cell division of the collar. Cell Res 20: 935-947.

44. Matsuura K, Kono I, Hori K, Nonoue Y, Ono N, et al. (2008a) Novel QTLs for photoperiodic flowering revealed by using reciprocal backcross inbred lines crosses from between japonica rice cultivars. Theor Appl Genet 117: 935-945.

45. Kwon CT, Yoo SC, Koo BH, Cho SH, Park JW, et al. (2014) Natural variation in Early flowering 1 contributes to early flowering in japonica rice under long days. Plant Cell Environ 37: 101-112.

46. Lee S, Kim JH, Lee BJ, et al. (2004) Functional analyses of the flowering time gene OsMAF555, the putative SUPPRESSOR OF OVEREXPRESSION OF CO 1/AGAMOUS-LIKE 20 (SOC1/AGL20) ortholog in rice. Plant J 38: 754-764.

47. Lee H, Suh HS, Park E, Cho E, Ahn JH, et al. (2000) The AGAMOUS-LIKE 20 MADS domain protein integrates floral inductive pathways in Arabidopsis. Genes Dev 14: 2366-2376.

48. Peng LT, Shi ZY, Li L, Shen GZ, Zhang JL (2007) Ecopic expression of OsLFL1 in rice represses Ehd1 by binding on its promoter. Biochem Biophys Res Commun 360: 251-256.

49. Peng LT, Shi ZY, Li L, Shen GZ, Zhang JL (2008) Overexpression of transcription factor OsLFL1 delays flowering time in Oryza sativa. J Plant Physiol 165: 876-885.
61. Cho S, Jang S, Chae S, Chung KM, Moon YH, et al. (1999) Analysis of the C-terminal region of Arabidopsis thaliana APETALA1 as a transcription activation domain. Plant Mol Biol 40: 419-429.

62. Lim J, Moon YH, An G, Jang SK (2000) Two rice MADS domain proteins interact with OsMADS1. Plant Mol Biol 44: 513-527.

63. Li D, Yang C, Li X, Gan Q, Zhao X, Zhu L (2009) Functional characterization of rice OsDof12. Planta 229: 1159-1169.

64. Kim S-K, Yun C-H, Lee JH, Jang YH, Park H-Y, et al. (2008) OsCO3, a CONSTANS-LIKE gene, controls flowering by negatively regulating the expression of FT-like genes under SD conditions in rice. Planta 228: 355-365.

65. Park SJ, Kim SL, Lee S, Je BI, Piao HL, et al. (2008) Rice Indeterminate 1 (Osd1) is necessary for the expression of Ehd1 (Early heading date 1) regardless of photoperiod. Plant J 56: 1018-1029.

66. Matsubara K, Yamanouchi K, Wang ZX, Minobe Y, Izawa T, et al. (2006b) Eff7, a rice ortholog of the maize INDETERMINATE1 gene, promotes flowering by up-regulating Ehd1. Plant Physiol 148: 1425-1435.

67. Wu CY, You CJ, Li CS, Long T, Chen GX, et al. (2006) RID1, encoding a Cys2/His2-type zinc finger transcription factor, acts as a master switch from vegetative to floral development in rice. Proc Natl Acad Sci USA 103: 12915-12920.

68. Galinant WC, Naylor AW (1951) Relation of photoperiod to inflorescence proliferation in Zea mays L. Am J Bot 38: 38-47.

69. Colasanti J, Yuan Z, Sundaresan V (1998) OsGIGANTEA, a circadian clock-controlled gene of Arabidopsis, regulates photoperiodic flowering in rice. PLoS Genet 9: e1000326.

70. Lee YS, Jeong DH, Lee DY, Yi J, Ryu CH, et al. (2010) OsCOL4 is a constitutive flowering repressor upstream of Ehd1 and downstream of OsphyB. Plant J 63: 18-30.

71. Zhao XL, Shi ZY, Peng LT, Shen GZ, Zhang JL (2011) An atypical HLH protein OsELF in rice regulates flowering time and interacts with OsPIL13 and OsPIL15. Nat Biotechnol 28: 788-797.

72. Aukerman MJ, Sakai H (2003) Regulation of flowering time and floral organ identity by a MicroRNA and its APETALA2-like target genes. Plant Cell 15: 2730-2741.

73. Choi SC, Lee S, Kim SR, Lee YS, Liu C, et al. (2014) Trithorax group protein OsTrx1 controls flowering time in rice via interaction with Ehd3. Plant Physiol 164: 1326-1337.

74. Fowler S, Lee K, Onouchi H, Samach A, Richardson K, et al. (1999) Gigantea: A circadian clock-controlled gene that regulates photoperiodic flowering in Arabidopsis and encodes a protein with several possible membrane spanning domains. EMBO J 18: 4679-4688.

75. Izawa T, Mihara M, Suzuki Y, Gupta M, Itoh H, et al. (2011) OsLF in rice regulates flowering time and interacts with OsPIL13 and OsPIL15. Aukerman MJ, Sakai H (2003) Regulation of flowering time and floral organ identity by a MicroRNA and its APETALA2-like target genes. Plant Cell 15: 2730-2741.

76. Fowler S, Lee K, Onouchi H, Samach A, Richardson K, et al. (1999) Gigantea: A circadian clock-controlled gene that regulates photoperiodic flowering in Arabidopsis and encodes a protein with several possible membrane spanning domains. EMBO J 18: 4679-4688.

77. Fowler S, Lee K, Onouchi H, Samach A, Richardson K, et al. (1999) Gigantea: A circadian clock-controlled gene that regulates photoperiodic flowering in Arabidopsis and encodes a protein with several possible membrane spanning domains. EMBO J 18: 4679-4688.

78. Izawa T, Mihara M, Suzuki Y, Gupta M, Itoh H, et al. (2011) OsLF in rice regulates flowering time and interacts with OsPIL13 and OsPIL15. Aukerman MJ, Sakai H (2003) Regulation of flowering time and floral organ identity by a MicroRNA and its APETALA2-like target genes. Plant Cell 15: 2730-2741.

79. Lee YS, Jeong DH, Lee DY, Yi J, Ryu CH, et al. (2010) OsCOL4 is a constitutive flowering repressor upstream of Ehd1 and downstream of OsphyB. Plant J 63: 18-30.

80. Zhao XL, Shi ZY, Peng LT, Shen GZ, Zhang JL (2011) An atypical HLH protein OsELF in rice regulates flowering time and interacts with OsPIL13 and OsPIL15. Nat Biotechnol 28: 788-797.

81. Aukerman MJ, Sakai H (2003) Regulation of flowering time and floral organ identity by a MicroRNA and its APETALA2-like target genes. Plant Cell 15: 2730-2741.

82. Choi SC, Lee S, Kim SR, Lee YS, Liu C, et al. (2014) Trithorax group protein OsTrx1 controls flowering time in rice via interaction with Ehd3. Plant Physiol 164: 1326-1337.

83. Hirschi KD, Jacobs CI, Young JC, Hungarter RP, et al. (1996) The Arabidopsis ELF3 gene regulates vegetative photomorphogenesis and the photoperiodic induction of flowering. Plant J 10: 691-702.

84. Matsubara K, Ogiso-Tanaka E, Hori K, Ebana K, Ando T, Yano M (2012) Natural variation in Hdt17, a homolog of Arabidopsis ELF3 that is involved in rice photoperiodic flowering. Plant Cell Physiol 53: 709-716.

85. Fu C, Yang XO, Chen X, Chen W, Ma Y, et al. (2009) OsELF3, a homologous gene of Arabidopsis ELF3, has pleiotropic effects in rice. Plant Biol 11: 751-757.

86. Takano M, Inagaki N, Xie X, Yuzurithara N, Hihara F, et al. (2005) Distinct and cooperative functions of phytochromes A, B, and C in the control of deetiolation and flowering in rice. Plant Cell 17: 3311-3325.

87. Hamner KC, Bonner J (1938) Photoperiodism in relation to hormones as factors in floral initiation and development. Bot Gaz 100: 388-431.

88. Thomas B, Vince-Prue D (1997) Photoperiodism in Plants. (London: Academic Press).

89. Hirschfeld M, Tepperman JM, Clark T, Quail PH, Sharrock RA (1998) Coordination of phytochrome levels in phyB mutants of Arabidopsis as revealed by apoprotein-specific monoclonal antibodies. Genetics 149: 523-535.

90. Monte E, Alonso JM, Ecker JR, Zhang Y, Li X, et al. (2003) Isolation and characterization of phyC mutants in Arabidopsis reveals complex crosstalk between phytochrome signaling pathways. Plant Cell 15: 1962-1980.

91. Shinozuka K, Okada Y, Seki M, Mochida K, et al. (2000) The transcription factor DREB2A acts as a master regulator of the cold- and drought-stress-responsive gene expression pathway in Arabidopsis. Plant Cell 12: 2311-2328.

92. Valverde F, Mouradov A, Soppe W, Ravenscroft D, Samach A, et al. (2004) Photoreceptor regulation of CONSTANS protein in photoperiodic flowering. Science 303: 1003-1006.

93. Andrus F, Galbraith DW, Talon M, Domino M (2009) Analysis of photoperiod sensitivity5 sheds light on the role of phytochromes in photoperiodic flowering in rice. Plant Physiol 151: 681-690.

94. Izawa T, Oikawa T, Tokumori S, Okuno K, Shimamoto K (2000) Phytochromes...
confer the photoperiodic control of flowering in rice (a short-day plant). Plant J 22: 391-399.

105. Guo HW, Yang WY, Mockler TC, Lin CT (1998) Regulation of flowering time by Arabidopsis photoreceptors. Science 279: 1360-1363.

106. Cashmore AR, Jarillo JA, Wu YJ, Liu D (1999) Cryptochromes: Blue light receptors for plants and animals. Science 284: 760-765.

107. Lin C (2002) Blue light receptors and signal transduction. Plant Cell 14: S207-S225.

108. Hirose F, Shinomura T, Tanabata T, Shimada H, Takano M (2006) Involvement of rice cryptochromes in de-etiolation responses and flowering. Plant Cell Physiol 47: 915-925.

109. Zhang YC, Gong SF, Li QH, Sang Y, Yang HQ (2006) Functional and signaling mechanism analysis of rice cryptochrome. Plant J 46: 971-983.

110. Kim WY, Fujiwara S, Suh SS, Kim J, Kim Y, et al. (2007b) ZEITLUPE is a circadian photoreceptor stabilized by GIGANTEA in blue light. Nature 449: 356-360.

111. Sawa M, Nusinow DA, Kay SA, Imaizumi T (2007) FKF1 and GIGANTEA complex formation is required for day-length measurement in Arabidopsis. Science 318: 261-265.

112. Yang J, Lee S, Hang R, Kim SR, Lee YS, et al. (2013a) OsVIL2 functions with PRC2 to induce flowering by repressing OsLFL1 in rice. Plant J 73: 566-578.

113. Wang J, Hu J, Qian Q, Xue HW (2013) LC2 and OsVIL2 promote rice flowering by photoperiod-induced epigenetic silencing of OsLFL. Mol Plant 6: 514-527.

114. Conrad L, Khanday I, Johnson C, Guiderdoni E, An G, et al. (2014) The polycomb group gene EMF2B is essential for maintenance of floral meristem determinacy in rice. Plant J 80: 883-894.

115. Xie S, Chen M, Pei R, Quyang Y, Yao J (2015) OsEMF2b acts as a regulator of flowering transition and floral organ identity by mediating H3K27me3 deposition at OsLFL1 and OsMADS4 in rice. Plant Mol Biol Rep 33: 121-132.

116. Matsubara K, Yamanouchi U, Nonoue Y, Sugimoto K, Wang ZX, et al. (2011) Ehd3, encoding a plant homeodomain finger-containing protein, is a critical promoter of rice flowering. Plant J 66: 603-612.

117. Ng DW, Wang T, Chandrasekharan MB, Aramayo R, Kerbundit S, et al. (2007) Plant SET domain-containing proteins: Structure, function and regulation. Biochim Biophys Acta 1769: 316-329.

118. Sun C, Fang J, Zhao T, Xu B, Zhang F, et al. (2012) The histone methyltransferase SDG724 mediates H3K36me2/3 deposition at MADS50 and RFT1 and promotes flowering in rice. Plant Cell 24: 3235-3247.

119. Liu X, Zhou C, Zhao Y, Zhou S, Wang W, et al. (2014) The rice enhancer of zeste [E(z)] genes SDG711 and SDG718 are respectively involved in long day and short day signaling to mediate the accurate photoperiod control of flowering time. Front Plant Sci 5: 591.