

Long-Day Flowering Regulation Network in Rice by *RFT1* Gene: A Review

Sulaiman Mohammed^{1,3}, Azman Abd Samad¹ and Zaidah Rahmat^{1,2*}

¹Department of Biotechnology and Medical Engineering, Faculty of Biosciences and Medical Engineering, Universiti Teknologi Malaysia, 81310, Johor-Bahru, Johor, Malaysia

²Innovation Center in Agrotechnology for Advance Bioprocessing (ICA), Universiti Teknologi Malaysia, 81310, Johor-Bahru, Johor, Malaysia

³Department of Biological Sciences, Faculty of Science, Gombe State University, PMB0127 Gombe, Nigeria

* **Corresponding Author:** Zaidah Rahmat, Department of Biotechnology and Medical Engineering, Faculty of Biosciences and Medical Engineering, Universiti Teknologi Malaysia, 81310, Johor-Bahru, Johor, Malaysia, E-mail: zaidahrahmat@utm.my

Citation: Sulaiman Mohammed, Azman Abd Samad and Zaidah Rahmat (2016) Long-Day Flowering Regulation Network in Rice by *RFT1* Gene: A Review. Cell Mol Biol 2: 010.

Copyright: © 2016 Sulaiman Mohammed, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted Access, usage, distribution, and reproduction in any medium, provided the original author and source are credited.

Abstract

Reproductive stage is the third phase in flowering plant life cycle. It is the most significant where vegetative organs transit from vegetative to reproductive stage. This comprises of flowering and fruiting events. Rice '*Oryzasativa* L.' is a modern short day (SD) plant, but equally flower during non-inductive long day (LD) condition due the possession of second florigen named *Rice Flowering locus T1 (RFT1)*. Classical experiments imply that flowering time (heading-date) in rice is governed by both endogenous hormonal signals (florigens) and environmental cues (photoperiod), which provides necessary signals to the species for flowering regulation through a complex genetic network. Recent molecular analysis revealed that several proteins are also involved in response to LD photoperiodic flowering regulation in rice, and then *RFT1* gene is the precise florigen which is positively activated by early heading date 1 (Ehd1) regulator. Interestingly, numerous genetic pathways mostly converge to regulate the expression of this florigen and the regulation integrates the presence of complex layers of gene networks to promoting such event. Rice species serves as a powerful model monocot plant for flower development analysis at molecular level. In the present review, rice flowering development and molecular genetic networks of LD flowering are highlighted; focusing on recent advances made in understanding the *RFT1* gene photoperiodic-dependant regulation.

Keywords: Rice; Reproductive phase; Florigen; Photoperiod; Long-day.

Introduction

Rice; *Oryzasativa* L. (*O. sativa*) belongs to the family *Poaceae* and regarded as the most essential cereal crop with close relation to other cereals. It is a suitable source of food and model species for studies of gene expression, genome organization as well as transgenes behaviour [1-3]. The plant is apposite for flower development analysis due to its relatively small genome size (approximately 430 Mb), diploid origin ($2n = 24$) and high commercial value. *Oryzasativais* a facultative short-day (SD) plant [4, 5] and equally produces flower during non-inductive long-day (LD) condition [6,7]. The flowering process in rice comprises of four (4) major series of developmental stages[8, 9]. First, the plant develops from embryonic to post-embryonic stage called germination phase, followed by vegetative phase; which characterized as a transition from a juvenile to an adult state. The third phase is the flowering occurrence and considered the most significant phase in which vegetative organ(s) of the plant transits from vegetative to reproductive stage (called reproductive phase) and senescence is the last phase [8].

Growth and development activities leading to flowering transition comprises both the second (vegetative) and the third (reproductive) phase respectively. Vegetative structure(s) evolve from shoot apical meristem (SAM) and later transit to the reproductive stage that produces flower and fruits/seeds [10]. Thus, the flowering process in flowering plants is measured as a key agronomic determinant for acclimatization to specific cropping locality. Similarly, in rice cultivation is considered as growing season's determinant [11]. Fascinatingly, rice inflorescence architecture has greatly differed from other eudicots species, because it possesses a great agronomic value and attracted plant scientist attention in previous years. For this reason, meaningful achievement has been made in understanding the rice inflorescence architectural mechanistic control and its possible high grain production potentials [12].

Now, rice is cultivated across the globe due to its flowering time diversification characteristics. Flowering gene (florigen) is the molecule that triggers such floral induction processes [13]. Scientific proofs via molecular approach have indicated the existence of diverse evolutionary genes in rice, which uniquely acquired for flowering promotion [14]. This have demonstrated that the timing of rice flowering is basically determined by expressing two essential rice florigens which includes *Heading date 3a (Hd3a)* (under SD condition) and *Rice Flowering Locus T1 (RFT1)* (under LD condition) [10,15-18]. Additional evidences demonstrated that other *FT* genes/proteins as are found helpful towards floral production either as a promoter, regulator or repressor [6,18,19]. Similarly, 90% of the rice genome has been sequenced and found the most homolog of *Arabidopsis*

thaliana (*A. thaliana*) in terms of flowering time genes [5]. This has made it possible to analyse gene expression and function of the plant [20]. This is because the determination of the nature, characteristics and molecular function of such homologous genes would be a major approach to drawing a research frame work for flowering time control. Equally, such analysis will help toward understanding the system and reveal on the species origin/evolution. So far, review on rice flowering network focused on SD transition network, while few or no report on LD flowering mechanism network. Therefore, this review highlighted on the current information on the molecular mechanism of *RFT1* photoperiod-dependent flowering under LD condition and contribution of other genes/proteins toward regulating the process. The paper gave the different molecular networks that led to flowering in rice under LD condition and strongly point-out the specificity of *RFT1* gene as rice LD florigen.

Rice Flowering System

Plants species capable of producing conspicuous flower (the state of bloom or efflorescence) are called *Angiospermae* or popularly known as flowering plants. In the case of rice research, flowering state has several meanings which include flower structure development, inflorescence initiation, anthesis (opening of the flower) and heading (panicle extrusion).Tsuji H, et al. [18], described heading date as the suitable word to describe the flowering period in cereal crops and an important agronomic trait in determining the rice cropping season and cultivation area of a given cultivar/variety [15, 21]. This reproductive event is considered as the best ecological examples between plant and its existing ecosystem because of its unpredicted appearance in rice cultivars within a year round [11]. Also, rice possesses a unique inflorescence structure which greatly diverged from that of other model *eudicots* plants such as *Antirrhinum majus* and *A. thaliana*. This makes it a fascinating model plant to investigate the flowering event as communicated by Noorzuraini AS,et al. [22].

The crop panicle [23] and its inflorescence are composed of a grass specific structural unit called spikelet (inflorescence primary unit) [24]. The spikelet comprises of florets and glumes (bract-like organs) as shown in Figure 1A and B. While, the floret contains a pair of bract-like organs called lemma and palea, stamens, carpel and lodicules that are equivalent to eudicot's petals. Both the palea and the lemma are grass-specific organs, but their identities are still controversial as demonstrated by Yoshida H and Nagato Y [24]. Naturally, the initial step of floral induction in rice is the inflorescence meristem (IM) specification, sequentially followed by branch meristem (BM), spikelet meristem (SM) and floral meristem (FM) (Figure 1A) respectively. All the following stages of development occurred at the SAM of the crop [19].

These transitions are one of the major reproductive changes in the course of the species lifecycle and complex trait that involves several developmental patterns of floral incident [25, 26, 9]. This trend is intensively regulated by a range of environmental signals (photoperiod/day-length, spectrum composition/light quality, light intensity, and ambient temperature), then endogenous hormonal engage which provides suitable indication for heading season [27, 10, 9].

Specifically, the hormonal signals must integrate into a single decision-to flower or not to flower in the plant[28]. This led to broad variation in rice flowering time, hence, the crucial factor in determining the species seasonal and regional adaptation and possibly the main target for breeding programs [25].With upsurge interest on flowering time regulation mechanisms, researches on the responsible hormones and their transition network in rice SD flowering system have been observed [29, 30]. In the last decades, DNA markers and mapping population analysis have identified multiple quantitative trait loci (QTLs) for rice heading-date [18]. These have revealed on the involvement of several genes toward photoperiodic flowering regulation in rice [31, 32]. Besides, certain activators or repressors of the transition are also determined, viz. such regulators makes rice possible to flower equally under both conditions (LD and SD) as described below [7, 33]. Accordingly, the molecular techniques contributed substantially toward understanding the mechanisms and prevail vital as it's led to the successful increase in rice yield production [7, 18] and probably will induce early flowering [30].

Photoperiodic Flowering Control in Rice

The precise environmental signal that induces the floral transition in flowering plants is the daylight or photoperiod. This measurement totally depends on the plant's ability to detect light and existence of a time keeping mechanism which referred to as 'circadian clock'. The involvement of circadian clock system in the control of biological activities permit plants species adaptation to seasonal environmental vagary and maximizes their survival opportunities efficaciously. Specifically, the system comprises of input pathways (that provides temporal information to the plant clock) and central oscillator mechanism itself (responsible for driving rhythms with a period of 24h). Thus, a number of output pathways for regulating developmental and metabolic processes using the temporal information are also provided by the clock [33].

In temperate regions, daylight duration normally changes with seasons, while other environmental factors also changed from period to period following a predictable pattern. Due to such time variation, plant species evolved a mechanism to prepare for the upcoming seasonal alteration by integrating daylight information into developmental programs such as flowering. By such advanced methods, the organism(s) enhance survival and reproductive victory, as earlier described by Wightman Garner and Henry Allard (1920). They introduced the terms 'photoperiod'; a daily recurring prototype of light and dark periods and 'photoperiodism'; the ability or response to respond to photoperiod [6]. For that, numerous plant species monitor their seasonal photoperiodic changes just to initiate the flowering event. Apart from that, such photoperiod-dependent has a direct effect on other developmental processes such as crops and livestock production and it is also crucial to migrating animal species towards regulating their physiological responses such as migration and resizing sexual organ. Hence, understanding of these pathways would be essential for determining the organism-ecosystem interaction and as an agronomical application that may increase productivity [34].

The photoperiod-sensing plants fall into one of the three classes' viz., short day plants (SDP), day neutral plants and long day plants (LDP) [14, 35]. SD and LD plants are varying distinctly in their sensitivity to day length changes. Such signaling cascades of photoperiodic flowering have been studied in *A. thaliana*, a modern LDP [8, 14] and *O. sativa*, a modern SDP [7]. The rice photoperiod sensing is measured in the leaf, but the distal bud develops into a flower; hence, there must be transmittable signal(s) from the leaf to the shoot apex [36, 37]. As a good example of SDP, rice has acute daylight threshold for floral induction, while no such critical condition exists in various LDP [35]. SDP flower in condition with 10-10 hours light, whereas LDP inflorescence appearance begins between 11-13 hours of light [10]. Therefore, this floral transition is considered the most important factor for ensuring successful sexual reproduction in the species [31]. As reported by Song YH et al. [34] and Matsubara K, et al. [38], recent advances in molecular biology have demonstrated that external light signals perceived by photoreceptors activates the flowering gene promoter(s), which is mediated by the circadian clock. This favours the flowering process in response to day-length in monocot species and also interesting results were produced in terms of regulating plant development genetically [39]. Though little was reported on the LD flowering regulation pathway in rice [17].

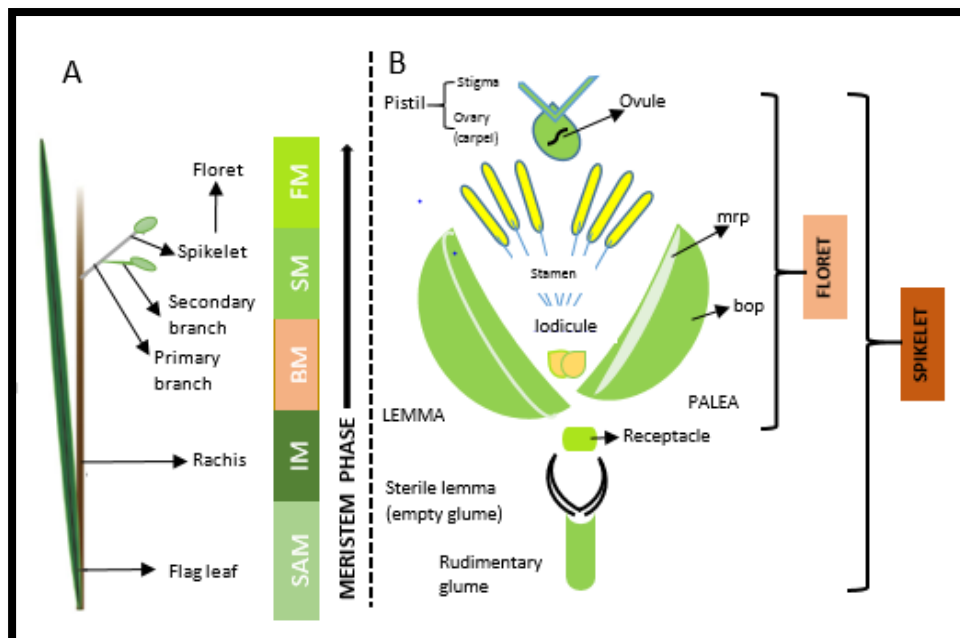


Figure 1: Schematic representation of rice flower showing: (A) inflorescence and (B) spikelet. SAM, IM, BM, SM, FM and other important floral parts as adapted from Yoshida and Nagato [24].

Rice Flowering Locus T1 (*RFT1*) Gene

Florigen has been hypothesized as a hormone-like molecule for promoting and/or triggering flowering processes in flowering plants. The gene is normally produced in the species leaf and act as a mobile signal in the SAM of buds as well as growing tips. Overexpression of these protein molecules with vascular-specific promoter or constitutive promoter results in an early-flowering phenotype, while its suppression by RNA-interference (RNAi) procrastinate flowering occurrence [10, 14]. This is known to be a graft-transmissible factor and even function between species.

Evidences exist to show that diverse evolutionary conserved genes are associated with the flowering process in *O. sativa*[14]. In fact, molecular understanding of such action has provided an answer to the *FT* gene networks i.e. how it is being regulated. This implies that flowering in rice is basically as a result of *Hd3a* and *RFT1* expression, which are the two highly conserved rice florigens [4, 10, 31, 40].*RFT1* is about 22 kDa size and 11.5 kb away from *Hd3a* all on chromosome 6. The florigen is typically producing in the leaf blades, interact with transcription factor *FD* (*flowering locus D*) by the competency of the SAM and switch-on flowering processes [18] as shown in Figure 2. The gene is a member of phosphatidyl-ethanol-amine-binding protein (PEBP) family. PEBPs is an anion, small globular-protein with pocket shape and vastly conserved across the living kingdom (unicellular-multicellular organisms) [17].

As reported by Osugi A et al. [41], after interacting with *FD* transcriptional factor, the gene acts as a mobile

signal via protein or mRNA [10,41]. Also, its interact with bZIP transcription factor *FD* that only expresses in the SAM and promote flowering under LD condition (e.g. *FT* in *Arabidopsis*) [10,17]. Consequently, a number of mobile flowering signals have been identified in rice and characterized for their roles toward encoding zinc-finger transcriptional activator and induces expression of floral integrator '*Flowering Locus T (FT)*' under LD condition [10, 14, 42].Nevertheless, expression of florigens faces a critical day-length threshold as described by Itoh H, et al. [43].

Molecular Mechanism of *RFT1* Gene Activation under Long-Day Condition

Early research on flowering promotion gene indicated that *Hd3a* was the actual rice florigen under SD condition, while RNAi strongly suppresses it and delays the flowering development under the same condition. Virtually, *Hd3a*-RNAi species indicates flower appearance during LD period. This natural variation signifies the existence of different key factor(s) responsible for promoting flowering during non-inductive LD condition. *RFT1* is the authentic rice florigen under LD condition as discovered by Komiya, et al. [10], Komiya, et al. [14], reviewed by Tsuji, et al. [44], Brambilla and Fornara[11] and Xiang, et al. [9]. The authors equally reported that regular *RFT1* expression occurs in leaf blade, which transferred using *RFT1*-GFP fusion from leaves to the shoot apex. Therefore, the different molecular networks that led to flowering or flower development in rice under LD condition and the specificity of *RFT1* gene as real rice LD florigen are discussed here.

The proteins associated with rice florigen have been identified through a molecular study as tabulated in Table 1. They act as promoters and regulators in activating or suppressing the flowering processes, which accelerates the event under LD condition. Among the mobile-protein signals recognized includes *Early heading date1 (Ehd1)* and *Heading date1 (Hd1)* which control the florigen activation [45]. Some signals were really determined and characterized for their roles toward encoding zinc-finger transcriptional activator and induces expression of the floral integrator *FT* under LD condition [10, 14, 42]. Itoh, et al. [43] reported that at the early age of rice it normally accumulates mRNA in the morning at below 13 hours daylight, but the expression of the messenger is almost one-tenth down-regulated when the daylight duration exceeded 13.5 hours. Therefore, these responses by the rice varieties have clearly indicated a conceivable link between critical day-length and florigen transcriptional regulation. Similarly, most SD plants experience a severe day-length threshold for floral initiation than LD species [6].

This reviewed by Itoh and Izawa[6], Xiang, et al. [9] and reconfirmed by Sun, et al. [5], they described that *Hd1* is an orthologue of *CONSTANT (CO)* and a member of *CONSTANS-like (COL)* family that promote floral induction under SD condition in rice as communicated by Lee and An [45]. It was first identified by QTL mapping due to crossing of two rice cultivars as reviewed by Lee and An [6] from Lin, et al. [46]. It acts as floral regulator upstream of the florigen during transcriptional regulation and remains responsible for diverse flowering time especially under SD condition. Equally, under LD condition rice flowering is regulated by *Ehd1* promoter; a B-type response regulator of *FT*-like genes (up-regulates the positive regulator *RFT1*), a constitutive activator and flowering inducer [45, 47]. Additionally, *Ehd1* positively regulate *Hd3a* under SD environment either in the absence of functional *Hd1* alleles and led to the floral transition [44]. *Hd1* and *Ehd1* (an activator and a promoter of heading) function redundantly by promoting floral transition preferentially under SD and antagonistically under LD condition. This indicated the double function of *Ehd1* under both conditions [47]. While, another signal named *OsCOL4 (Oryzasativa CONSTANT LIKE 4)* encodes the *Ehd1* repressor and activate the promoter at both condition [4]. Also, similar was reported by Tan, et al. [48], on *OsCOL10* a constant like gene that act downstream to repress the flowering process.

Ehd1 and *Hd1* presence marks the possibility of rice to flower under LD condition. Moreover, *Hd1* deficiency delays the flowering under SD condition and promote early flowering under LD condition [6, 9]. Kim, et al. [48], described *Hd1* as a key integrator of rice photoperiodic flowering pathway. Its expression is up-regulated by *OsGI(Oryzasativa Gigantea)* (an orthologue of *Gigantea* and main regulator of heading in *A. thaliana*)

which acts upstream of *Ghd 7/8 (Grain yield, heading date, and plant height 7/8,)* [21, 45, 50] as shown in Figure 3. Also, the same *Hd1* represses *Ehd1* under LD condition by interacting monocot-specific CCT-domain *Ghd1* as described by Nemoto, et al. [51]. In *Ghd7/8*-mediated flowering network; *Ehd3* (another florigen promoter) up-regulate *Ehd1* suppression through *Ghd7* which permit the activation of *Ehd1* under LD condition (Figure 2) [9]. On the other hand, *Ehd3* is responsible for regulating the *Ghd7*-independent pathway which up-regulates the *RFT1* promoter (*Ehd1*) under SD conditions.

Equally other molecular networks also exist such as *Ghd7*-independent pathways as proposed by Xue, et al. [33] and Jeong, et al. [52]; where CCT motif encode and regulate *FT* transcription by deactivating the *Ehd1* and/or regulated by *OsVIL1 (Oryzasativa VERNALIZATION INSENSITIVE3-LIKE 1)*. Certainly, this may indicate that under LD condition there are alternative activation pathways of flowering viz. *Ehd3-Ghd7-Ehd1-RFT1* (Figure 2A)[19]. This has also shown that *Ehd2/RID1/OsID1* is positive activators of *Ehd1* as earlier described by Komiyama, et al. [14]. Besides, these have shown the independent pathway from *OsMADS50 (Oryzasativa MADS-box 50)* pathway [14]. This simple network of *Ehd2/RID1/OsID1* (as a promoter and/or floral transition master switch) promotes LD *RFT1* flowering transition directly after *Ehd1* is been activated (Figure 2 and 3). Hence, *Ehd2/RID1/OsID1-Ehd1-RFT1* is another flowering activation pathway as shown in Figure 2A and 3 [9,44]. As a novel regular, *HDR1 (Heading Date Repressor1)* activation display early flowering phenotype in a different pathway by encoding a nuclear protein having a diurnal expression pattern [5].

Evenly, *OsMADS50* (the nearest homolog to Suppressor of Overexpression of *CONSTANS1 (SOC1)* in *A. thaliana*), acts as a floral promoter in response to LD by suppressing *OsLFL1 (Oryzasativa LEC2 and FUSCA3 like1)* (a B3 domain transcription factor and repressor of *Ehd1*) [53, 54]. This indicated that *OsMADS50* induces flowering specifically under LD as reviewed by Lee and An [26]. The *OsLFL1* acts as *Ehd1* suppressor, therefore, *OsMADS50* represses the expression of *OsLFL1* in response to day-length and activate the *Ehd1-RFT1*. Almost all *RFT1* activation networks at this stage are regularly observed in leaf blade, then to SAM [6, 33]. Consequently, this has demonstrated on either *Ehd3*, *OsMADS50* or *OsMADS51* is responsible for *Ehd1* activation (Figure 3). This corresponds with Shrestha, et al. [19] review. The *Ehd1* is generally considered as a real activator of *RFT1* and positively regulate the flowering transition under LD condition. Thus, going by the above-described regulation networks, it may indicate that *Ghd7/8* connect both *Ehd1* and *Hd1* dominated pathways through up or down regulation of flowering in rice cultivars [9, 50] as illustrated in Figure 2A and 2B.

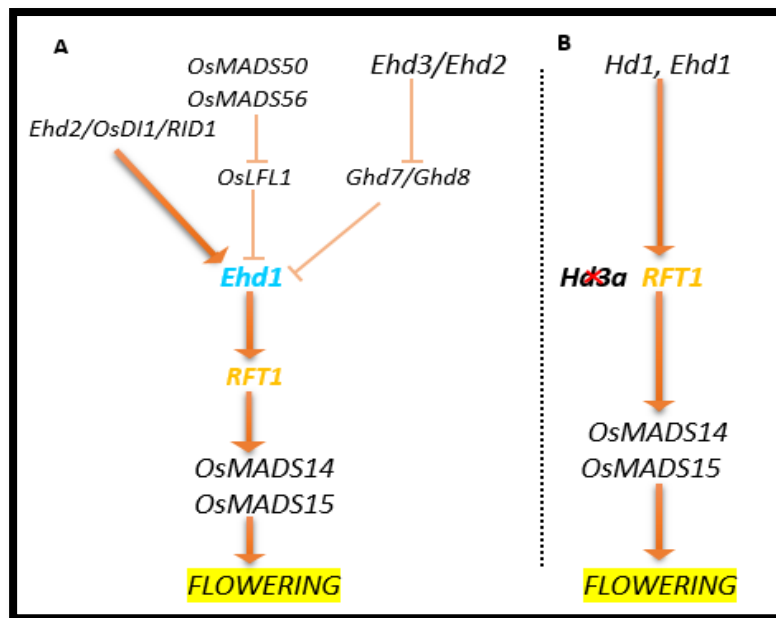


Figure 2: The different flowering networks (A and B) in rice through activation of *RFT1* gene under LD condition.

Komiya, et al. [14] communicated that activation of *RFT1* is usually when *Hd3a* is repressed, however, this led to the expression of *OsMADS14* and *OsMADS15* (the two rice orthologues of *A. thaliana* *API* (*APEZAKAI*)) that equally induce flowering [14]. It has also reported by Komiya, et al. [10] that the presence of double *RFT1-Hd3a* RNAi plants terminate flower initiation even at 300 days after sowing (DAS). After the actual regulation of *RFT1*, *OsMADS14* and *OsMADS15* the rice species instantly begins to show panicles. Hence, *OsMADS50-OsLFL1-Ehd1-*

RFT1-OsMADS14/OsMADS15 constitutes another *RFT1* LD flowering regulation network (Figure 2A) [6, 9, 33]. Additionally, *RFT1* suppression analysis specified that RNAi suppression act has shown a contrasting phenotype from *Hd3a-RNAi*. The suppression act shows no flowering effect under SD conditions but precisely weakened flowering under LD. Meanwhile, in a situation where *Hd3a* and *RFT1* activities are suppressed, flower production must cease. This implies that rice flowering process completely depend on florigen activities and photoperiod [44].

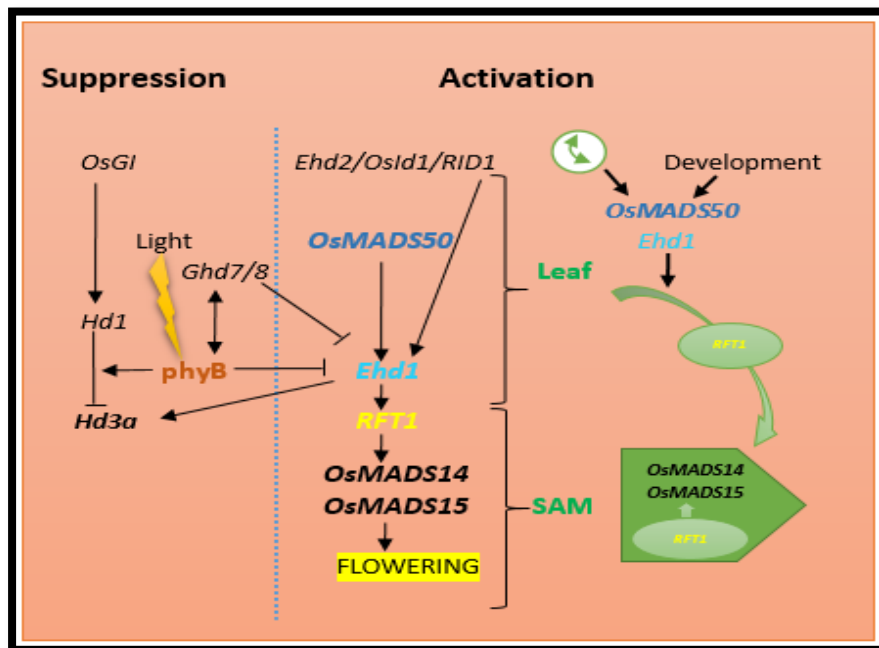


Figure 3: Molecular activation and suppression network of *Oryza sativa* L. photoperiodic flowering control under LD condition.

Long-Day Flowering Suppression in Rice

Flowering repression under LD condition have been reported [7, 11, 44]. As an SD plant, flowering repression under LD photoperiod occurred by repressing the *Hd3a* and seems to be ordinary due to the environmental changes and proteins function. Under such condition, *OsGI* receives light signals and effectively regulates the diurnal expression of *Hd1*[49]; as a result of this *Hd3a* expression is suppress by the *Hd1*. Thus, the *OsGI* action on *Hd1* may be affected by signaling from phytochrome (*Phy*) and *CK2a* activity. This is in agreement with the result of Yano, et al. [55], Ishikawa, et al. [56] and Matsubara, et al. [57] which showed that *Hd1*-mediated expression of *Hd3a* is regulated by *PhyB* (which codes for plant photoreceptor) and equate *CK2a* activity (Figure 3). Ideally, the *Hd1*-mediated regulation at LD period promotes the repressional effect of *Hd1* on *Hd3a* (Table 1) and delays the flowering process caused by the *Hd3a* florigen. This LD suppression pathway is suggested as *OsGI-Hd1-Hd3a* pathway [9, 47] as shown in Figure 3.

The diverse function of *Ehd1* and *Hd1* under SD (preferentially) and LD (antagonistically) condition, demonstrate the repression of *Hd3a* expression and activation of *RFT1* respectively. The *Ehd1* promotes the flowering process by activating the *RFT1*, whereas the *Hd1* repressed the *Hd3a* all under LD environment [58]. In addition, *OsCOL4* (member of *COL* family) and *OsBBX14-OX* (*Oryzasativa B-box14* (a zinc finger protein containing B-box domain)); are constitutively suppressed the flowering under such condition[58]. As reported by Wei, et al. [60], *OsCOL4* null mutants indicates early flower appearance under same LD, while *OsCOL4* activation-tagging mutants

(*OsCOL4-D*) indicate late panicle extrusion. The *oscol4* mutant enhances the *Ehd1* activation which indicates the upstream function of *OsCOL4* on *Ehd1*. But, *osphyB* (*Oryzasativaphytochrome B*) mutant decreases the *OsCOL4* transcript which confirms the *OsCOL4* downstream function on *osphyB*. These have indicated that multiple *Ehd1* regulators are involved in LD flowering regulation in rice as shown in Figure 2 and 3 respectively. Those regulators include; *OsCOL4*, *OsCOL10*, *Ghd7/8* [48, 52], *OsMADS56*, *DHT8*, *PhyBand Ehd2/RID1/OsIDI* [9]. Therefore, these results suggested the actual function of *PhyB* as a negative regulator of LD flowering in rice via suppressing the *Ehd1* by *OsCOL4*. Then, it further clarifies on the integration of multiple signals in *Ehd1* regulation toward LD flowering control.

Alternatively, in another unique pathway by *Gd7/8* signal(s); the *Ehd1* suppression by *OsMADS56* delays LD flowering certainly by encoding *OsMADS50* to form a complex. Ordinarily, *OsMADS56* acts as a repressor through *OsLFL1-Ehd1* to control flowering [35, 52]. Further to the above, alternative protein signal named *DHT8* [Table 1] plays a vital role towards providing a signal for photoperiodic flowering control under LD condition. It act as a novel repressor by down regulating the expression of *Ehd1*[60, 4] reported that for both rice florigens are not repressed in any condition either LD or SD. Considering all the diverse protein signals responsible for repressing the flowering process under LD photoperiod, this review suggested that different signal proteins are involved in down-regulation of *Ehd1*. Hence, they may re-unite to another suppression pathway under LD through the *Ehd1*-mediated expression of *Hd3a* and induce delay of inflorescence appearance.

Table 1: Rice flowering time genes and proteins involves in photoperiodic regulation of flowering under LD condition

Gene	Full-name of the gene	Function	Predicted product of the gene	Reference
<i>Ehd1</i>	Early heading date1	A specific promoter/regulator of rice flowering or signal integrator	B-type response regulator	[26, 47]
<i>Ehd2</i>	Early heading date2	Flowering promoter	Cys2/His2-type zinc finger transcription	[33, 61]
<i>Ehd3</i>	Early heading date3	Photoperiod pathway promoter	PHD finger gene	[57]
<i>RID/OsIDI</i>	Rice indeterminate1	Master switch of floral transition	Factor	[9]

<i>Ghd7</i>	Grain number, plant height and heading date7	Up-regulate <i>Hd3a</i> expression and delays flowering under LD by repressing the <i>Ehd1</i>	CCT domain protein	[14]
<i>Ghd8</i>	Grain number, plant height and heading date8	Delay flowering under LD by repressing the <i>Ehd1</i>	Encodes <i>OsHAP3</i> subunit of CCAAT-box binding protein; HAP complex	[21, 50]
<i>Hd1</i>	Heading date1	Represses/promotes <i>Hd3a</i> in response to photoperiod changes (SD or LD)	B-box, CCT-domain	[6, 9, 55]
<i>Hd3a</i>	Heading date 3a	Rice florigen under SD	Member of PEBP family; a putative kinase inhibitor	[10]
<i>HDR1</i>	(<i>Heading Date Repressor1</i>)	Flowering regulator under both LD and SD	Yet to identify	[5]
<i>OsMADS50</i>	Rice MADS-box protein gene50	Promoter of floral transition in response to LD by suppressing the <i>OsLFL1</i>	Homologous to <i>SOCI</i> in <i>Arabidopsis</i>	[5, 26, 44]
<i>OsLFL1</i>	<i>Oryzasativa LEC2</i> and <i>FUSCA3 like1</i>	Repressor of <i>Ehd1</i>	B3 domain transcriptional factor	[10,14]
<i>OsMADS51</i>	Rice MADS-box protein gene51	Involves in SD floral regulation	<i>MADS</i> box protein	[44]
<i>OsMADS56</i>	Rice MADS-box protein gene56	Inhibits flowering under LD probably by binding with <i>OsMADS50</i>	An orthologue of <i>SOCI/AGL20</i> far-red light/red light receptors	[35]
<i>OsMADS14</i>	Rice MADS-box protein gene14	Activates flowering	Orthologue of <i>API, MADS</i> box protein	[14, 49]
<i>OsMADS15</i>	Rice MADS-box protein gene15	Activates flowering	<i>MADS</i> box protein	[14, 49]
<i>OsGI</i>	<i>Oryzasativagigantea</i>	Flowering repressor	Orthologue of <i>GI</i> gene in <i>Arabidopsis</i>	[38, 55]
<i>OsFD1</i>	<i>Oryzasativa</i> flowering locus D1	Activates <i>OsMADS51</i> which leads to flowering activation under SD	<i>Hd3a-14-3-3</i> complex	[63, 64]
<i>14-3-3</i>	GF14c	Promotes/delays flowering under SD condition	Hd3a-OsFD1 complex; named Florigen	[28, 65, 44, 64]

			Activation Complex (FAC)	
<i>OsBBX-14</i>	<i>Oryzasativa B-box14</i>	Activator of <i>Hd1</i> at LD condition	Zinc finger protein containing B-box domain	[59]
<i>OsCOL4</i> / <i>OsCOL10</i>	<i>Oryzasativa CONSTANS-like4</i>	Flowering repressor	Member of <i>CONSTANS-like (COL)</i> family	[66, 52, 47]
<i>OsSOC1</i>	<i>Oryzasativa</i> Suppressor of Overexpression of <i>CONSTANS 1</i>	Promotes flowering with <i>OsMADS50</i> in LD environment	MADS-box transcriptional factor	[53, 67, 44]
<i>OsVIL1</i>	<i>Oryzasativa VERNALIZATION INSENSITIVE3-LIKE 1</i>	Inducer of <i>Ghd7</i> at LD condition	Homologous to many flowering promoters	[52]
<i>HAP</i>	HeamActivatory Protein	<i>FT</i> transcriptional regulator	Binds to CCAAT-box DNA sequence motif	[68, 69]
<i>DTH8</i>	Days to Heading on chromosome8	Repressor of <i>Ehd1</i> and <i>Hd3a</i> under LD condition	Putative HAP3 sub-unit of CCAAT-box-binding transcriptional factor	[60]
<i>DTH3b</i>	Days to Heading 3b	LD heading specific regulator; function upstream of <i>Hd3a</i> and <i>RFT11</i>	Orthologue of <i>FT</i> -like genes; <i>Ehd1</i>	[15]
<i>RFT1</i>	Rice Flowering Locus T1	Rice florigen under LD photoperiod	Orthologue of <i>FT</i> -like gene	[10]
<i>PHYB (OsPhyB)</i>	<i>Phytochrome B</i>	Hd1-mediated regulator	γ -ray radiation/T-DNA or Far-red light/red light receptor and constitutive repressor at both LD and SD	[56,16]
<i>FTL</i>	Ferritin light polypeptide	Promotes flowering by encoding light sub-unit of the ferritin protein.		[70-72]

Future Perspective

Numerous genetic molecules are eventually converging to regulate the expression of flowering gene(s). Determination of such genes molecular mechanism is of great value and would serve as a key regulator to decide the cereals photoperiod [50,61]. However, due to the complexity of genetic material of eukaryotes, numerous significant problems of molecular mechanism stay unexplained. These include the molecular mechanism underlying the critical night setting (long night flowering pathway) and diverse function of *Ehd1* under different conditions. The current flower development and *RFT1* flowering pathways summarized in this review really call for further substantiation of LD flowering mechanism including; the actual roles of some regulators that act only at temperate climatic regions and diverse biochemical roles of *Ghd7* and *Ghd8* proteins. Solving such problems will

provide an insight on how to genetically engineer the proteins and promote plant breeding system.

In addition, determining the role of such regulators may provide an answer to the key molecular question of bi-functionality of *Ehd1* (that regulate flowering under both daylight period) and its counterpart *Hd1* (the conserved photoperiodic key player for rice flowering regulation) as described by Izawa [62], as well as actual molecular act of *HDR1* as flowering regulator/repressor [5]. Therefore, as a fascinating model cereal crop, elucidating on the molecular nature of photoperiod sensitivity of *RFT1* and its various regulators will provide an insight into the heading molecular basis and the mechanisms behind the breeding approach at the temperate climatic region. These would also aid researchers to identify critical targets such as late flowering by some cultivars and led to the development of rice lines with increase productivity in the near future.

References

1. Bajaj, S. and Mohanty, A. (2005). Recent advances in rice biotechnology—towards genetically superior transgenic rice. *Plant Biotechnology Journal*. 3(3), 275-307.
2. Manimaran, P., Kumar, G. R., Reddy, M. R., Jain, S., RAO, T. B., Mangrauthia, S., Sundaram, R., Ravichandran, S. and Balachandran, S. (2013). Infection of early and young callus tissues of indica rice BPT 5204 enhances regeneration and transformation efficiency. *Rice Science*. 20(6), 415-426.
3. Saqib, M., Ehsanullah, N. A., Latif, M., Ijaz, M., Ehsan, F. and Ghaffar, A. (2015). Development and Appraisal of Mechanical Weed Management Strategies in Direct Seeded Aerobic Rice (*Oryza sativa* L.). *Pak. J. Agri. Sci.* 52(3), 587-593.
4. Gómez-Ariza, J., Galbiati, F., Goretti, D., Brambilla, V., Shrestha, R., Pappolla, A., Courtois, B. and Fornara, F. (2015). Loss of floral repressor function adapts rice to higher latitudes in Europe. *Journal of experimental botany*. erv004.
5. Sun, X., Zhang, Z., Wu, J., Cui, X., Feng, D., Wang, K., Xu, M., Zhou, L., Han, X. and Gu, X. (2016). The *Oryza sativa* Regulator HDR1 Associates with the Kinase OsK4 to Control Photoperiodic Flowering. *PLoS Genet*. 12(3), e1005927.
6. Itoh, H. and Izawa, T. (2013a). The coincidence of critical day length recognition for florigen gene expression and floral transition under long-day conditions in rice. *Molecular plant*. sst022.
7. Izawa, T. (2007). Adaptation of flowering-time by natural and artificial selection in *Arabidopsis* and rice. *Journal of experimental botany*. 58(12), 3091-3097.
8. Bäurle, I. and Dean, C. (2006). The timing of developmental transitions in plants. *Cell*. 125(4), 655-664.
9. Xiang, C., Qu, L.-j., Gao, Y.-m. and Shi, Y.-y. (2013). Flower development and photoperiodic control of flowering in rice. *Rice Science*. 20(2), 79-87.
10. Komiya, R., Ikegami, A., Tamaki, S., Yokoi, S. and Shimamoto, K. (2008). Hd3a and RFT1 are essential for flowering in rice. *Development*. 135(4), 767-774.
11. Brambilla, V. and Fornara, F. (2013). Molecular control of flowering in response to day length in rice. *Journal of integrative plant biology*. 55(5), 410-418.
12. Li, S., Qian, Q., Fu, Z., Zeng, D., Meng, X., Kyojuka, J., Maekawa, M., Zhu, X., Zhang, J. and Li, J. (2009). Short panicle1 encodes a putative PTR family transporter and determines rice panicle size. *The Plant Journal*. 58(4), 592-605.
13. Colasanti, J. and Sundaesan, V. (2000). 'Florigen' enters the molecular age: long-distance signals that cause plants to flower. *Trends in biochemical sciences*. 25(5), 236-240.

14. Komiya, R., Yokoi, S. and Shimamoto, K. (2009). A gene network for long-day flowering activates RFT1 encoding a mobile flowering signal in rice. *Development*. 136(20), 3443-3450.
15. Chen, L., Zhong, Z., Wu, W., Liu, L., Lu, G., Jin, M., Tan, J., Sheng, P., Wang, D. and Wang, J. (2015). Fine mapping of DTH3b, a minor heading date QTL potentially functioning upstream of Hd3a and RFT1 under long-day conditions in rice. *Molecular Breeding*. 35(11), 1-10.
16. Lee, Y. and An, G. (2015b). Complex Regulatory Networks of Flowering Time in Rice. *J Rice Res*. 3(141), 2.
17. Ogiso-Tanaka, E., Matsubara, K., Yamamoto, S.-i., Nonoue, Y., Wu, J., Fujisawa, H., Ishikubo, H., Tanaka, T., Ando, T. and Matsumoto, T. (2013). Natural variation of the Rice Flowering Locus T 1 contributes to flowering time divergence in rice. *PLoS One*. 8(10), e75959.
18. Tsuji, H., Tamaki, S., Komiya, R. and Shimamoto, K. (2008). Florigen and the photoperiodic control of flowering in rice. *Rice*. 1(1), 25-35.
19. Shrestha, R., Gómez-Ariza, J., Brambilla, V. and Fornara, F. (2014). Molecular control of seasonal flowering in rice, arabidopsis and temperate cereals. *Annals of botany*. mcu032.
20. Jain, M., Nijhawan, A., Tyagi, A. K. and Khurana, J. P. (2006). Validation of housekeeping genes as internal control for studying gene expression in rice by quantitative real-time PCR. *Biochemical and biophysical research communications*. 345(2), 646-651.
21. Hori, K., Nonoue, Y., Ono, N., Shibaya, T., Ebana, K., Matsubara, K., Ogiso-Tanaka, E., Tanabata, T., Sugimoto, K. and Taguchi-Shiobara, F. (2015). Genetic architecture of variation in heading date among Asian rice accessions. *BMC plant biology*. 15(1), 1.
22. Noorzuraini, A. S., Borromeo, T., Altoveros, N. and Kumar, A. (2012). Growth performance of selected Malaysian rice germplasm under drought stress environment. *J. Trop. Agric. and Fd. Sc.* 40(2), 169-179.
23. Asif, M., Chowdhury, F. and Saeed, M. (1997). Panicle structure, kernel quality and yield of fine rice as influenced by different NPK levels and per hill seedling density. *Pakistan J. Agril. Sci.* 34(1-4), 73-77.
24. Yoshida, H. and Nagato, Y. (2011). Flower development in rice. *Journal of experimental botany*. 62(14), 4719-4730.
25. Ebana, K., Shibaya, T., Wu, J., Matsubara, K., Kanamori, H., Yamane, H., Yamanouchi, U., Mizubayashi, T., Kono, I. and Shomura, A. (2011). Uncovering of major genetic factors generating naturally occurring variation in heading date among Asian rice cultivars. *Theoretical and applied genetics*. 122(6), 1199-1210.
26. Lee, Y. and An, G. (2015b). Complex Regulatory Networks of Flowering Time in Rice. *J Rice Res*. 3(141), 2.
27. Albani, M. C. and Coupland, G. (2010). Chapter Eleven-Comparative Analysis of Flowering in Annual and Perennial Plants. *Current topics in developmental biology*. 91, 323-348.
28. Putterill, J., Laurie, R. and Macknight, R. (2004). It's time to flower: the genetic control of flowering time. *Bioessays*. 26(4), 363-373.
29. Itoh, H. and Izawa, T. (2013b). The coincidence of critical day length recognition for florigen gene expression and floral transition under long-day conditions in rice. *Molecular plant*. 6(3), 635-649.
30. Purwestri, Y. A., Sari, R. D. K., Anggraeni, L. N. and Sasongko, A. B. (2015). *Agrobacterium Tumefaciens* Mediated Transformation of rolC:: Hd3a-GFP in Black Rice (*Oryza Sativa* L. cv. Cempo Ireng) to Promote Early Flowering. *Procedia Chemistry*. 14, 469-473.
31. Kojima, S., Takahashi, Y., Kobayashi, Y., Monna, L., Sasaki, T., Araki, T. and Yano, M. (2002). Hd3a, a rice ortholog of the Arabidopsis FT gene, promotes transition to flowering downstream of Hd1 under short-day conditions. *Plant and Cell Physiology*. 43(10), 1096-1105.
32. Shimamoto, K. and Yokoi, S. (2005). The photoperiodic control of flowering in rice, a short-day plant Light sensing in plants (pp. 339-346)Springer.
33. Xue, W., Xing, Y., Weng, X., Zhao, Y., Tang, W., Wang, L., Zhou, H., Yu, S., Xu, C. and Li, X. (2008). Natural variation in Ghd7 is an important regulator of heading date and yield potential in rice. *Nature genetics*. 40(6), 761-767.

34. Song, Y. H., Ito, S. and Imaizumi, T. (2010). Similarities in the circadian clock and photoperiodism in plants. *Current opinion in plant biology*. 13(5), 594-603.
35. RYU, C. H., Lee, S., CHO, L. H., Kim, S. L., LEE, Y. S., Choi, S. C., Jeong, H. J., Yi, J., Park, S. J. and HAN, C. D. (2009). OsMADS50 and OsMADS56 function antagonistically in regulating long day (LD)dependent flowering in rice. *Plant, cell & environment*. 32(10), 1412-1427.
36. Imaizumi, T. and Kay, S. A. (2006). Photoperiodic control of flowering: not only by coincidence. *Trends in plant science*. 11(11), 550-558.
37. Pennazio, S. (2003). "Florigen": an intriguing concept of plant biology. *Rivista di biologia*. 97(1), 33-51.
38. Matsubara, K., Ogiso-Tanaka, E., Hori, K., Ebana, K., Ando, T. and Yano, M. (2012). Natural variation in Hd17, a homolog of Arabidopsis ELF3 that is involved in rice photoperiodic flowering. *Plant and Cell Physiology*. 53(4), 709-716.
39. Itoh, J.-I., Nonomura, K.-I., Ikeda, K., Yamaki, S., Inukai, Y., Yamagishi, H., Kitano, H. and Nagato, Y. (2005). Rice plant development: from zygote to spikelet. *Plant and cell physiology*. 46(1), 23-47.
40. Tamaki, S., Matsuo, S., Wong, H. L., Yokoi, S. and Shimamoto, K. (2007). Hd3a protein is a mobile flowering signal in rice. *Science*. 316(5827), 1033-1036.
41. Osugi, A., Itoh, H., Ikeda-Kawakatsu, K., Takano, M. and Izawa, T. (2011). Molecular dissection of the roles of phytochrome in photoperiodic flowering in rice. *Plant physiology*. 157(3), 1128-1137.
42. Corbesier, L., Vincent, C., Jang, S., Fornara, F., Fan, Q., Searle, I., Giakountis, A., Farrona, S., Gissot, L. and Turnbull, C. (2007). FT protein movement contributes to long-distance signaling in floral induction of Arabidopsis. *Science*. 316(5827), 1030-1033.
43. Itoh, H., Nonoue, Y., Yano, M. and Izawa, T. (2010). A pair of floral regulators sets critical day length for Hd3a florigen expression in rice. *Nature genetics*. 42(7), 635-638.
44. Tsuji, H., Taoka, K.-i. and Shimamoto, K. (2011). Regulation of flowering in rice: two florigen genes, a complex gene network, and natural variation. *Current opinion in plant biology*. 14(1), 45-52.
45. Lee, Y.-S. and An, G. (2015a). Regulation of flowering time in rice. *Journal of Plant Biology*. 58(6), 353-360.
46. Lin, H., Yamamoto, T., Sasaki, T. and Yano, M. (2000). Characterization and detection of epistatic interactions of 3 QTLs, Hd1, Hd2, and Hd3, controlling heading date in rice using nearly isogenic lines. *Theoretical and Applied Genetics*. 101(7), 1021-1028.
47. Doi, K., Izawa, T., Fuse, T., Yamanouchi, U., Kubo, T., Shimatani, Z., Yano, M. and Yoshimura, A. (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 & Development*. 18(8), 926-936.
48. Tan, J., Jin, M., Wang, J., Wu, F., Sheng, P., Cheng, Z., Wang, J., Zheng, X., Chen, L. and Wang, M. (2016). OsCOL10, a CONSTANS-Like Gene, Functions as a Flowering Time Repressor Downstream of Ghd7 in Rice. *Plant and Cell Physiology*. pcw025.
49. Kim, S.-K., Yun, C.-H., Lee, J. H., Jang, Y. H., Park, H.-Y. and Kim, J.-K. (2008). OsCO3, a CONSTANS-LIKE gene, controls flowering by negatively regulating the expression of FT-like genes under SD conditions in rice. *Planta*. 228(2), 355-365.
50. Yan, W.-H., Wang, P., Chen, H.-X., Zhou, H.-J., Li, Q.-P., Wang, C.-R., Ding, Z.-H., Zhang, Y.-S., Yu, S.-B. and Xing, Y.-Z. (2011). A major QTL, Ghd8, plays pleiotropic roles in regulating grain productivity, plant height, and heading date in rice. *Molecular Plant*. 4(2), 319-330.
51. Nemoto, Y., Nonoue, Y., Yano, M. and Izawa, T. (2016). Hd1, a CONSTANS ortholog in rice, functions as an Ehd1 repressor through interaction with monocotspecific CCTdomain protein Ghd7. *The Plant Journal*. 86(3), 221-233.
52. Jeong, H. J., Yang, J., Cho, L.-H. and An, G. (2016). OsVIL1 controls flowering time in rice by suppressing OsLF under short days and by inducing Ghd7 under long days. *Plant cell reports*. 35(4), 905-920.

53. Lee, S., Kim, J., Han, J. J., Han, M. J. and An, G. (2004). Functional analyses of the flowering time gene OsMADS50, the putative Suppressor of Overexpression of CO 1/Agamous Like 20 (SOC1/AGL20) ortholog in rice. *The Plant Journal*. 38(5), 754-764.
54. Song, Y. H., Shim, J. S., Kinmonth-Schultz, H. A. and Imaizumi, T. (2015). Photoperiodic flowering: time measurement mechanisms in leaves. *Annual review of plant biology*. 66, 441.
55. Yano, M., Katayose, Y., Ashikari, M., Yamanouchi, U., Monna, L., Fuse, T., Baba, T., Yamamoto, K., Umehara, Y. and Nagamura, Y. (2000). Hd1, a major photoperiod sensitivity quantitative trait locus in rice, is closely related to the Arabidopsis flowering time gene CONSTANS. *The Plant Cell*. 12(12), 2473-2483.
56. Ishikawa, R., Aoki, M., Kurotani, K.-i., Yokoi, S., Shinomura, T., Takano, M. and Shimamoto, K. (2011). Phytochrome B regulates Heading date 1 (Hd1)-mediated expression of rice florigen Hd3a and critical day length in rice. *Molecular Genetics and Genomics*. 285(6), 461-470.
57. Matsubara, K., Yamanouchi, U., Nonoue, Y., Sugimoto, K., Wang, Z. X., Minobe, Y. and Yano, M. (2011). Ehd3, encoding a plant homeodomain finger-containing protein, is a critical promoter of rice flowering. *The Plant Journal*. 66(4), 603-612.
58. Izawa, T., Oikawa, T., Sugiyama, N., Tanisaka, T., Yano, M. and Shimamoto, K. (2002). Phytochrome mediates the external light signal to repress FT orthologs in photoperiodic flowering of rice. *Genes & development*. 16(15), 2006-2020.
59. Bai, B., Zhao, J., Li, Y., Zhang, F., Zhou, J., Chen, F. and Xie, X. (2016). OsBBX14 delays heading date by repressing florigen gene expression under long and short-day conditions in rice. *Plant Science*. 247, 25-34.
60. Wei, X., Xu, J., Guo, H., Jiang, L., Chen, S., Yu, C., Zhou, Z., Hu, P., Zhai, H. and Wan, J. (2010). DTH8 suppresses flowering in rice, influencing plant height and yield potential simultaneously. *Plant Physiology*. 153(4), 1747-1758.
61. Matsubara, K., Yamanouchi, U., Wang, Z.-X., Minobe, Y., Izawa, T. and Yano, M. (2008). Ehd2, a rice ortholog of the maize INDETERMINATE1 gene, promotes flowering by up-regulating Ehd1. *Plant Physiology*. 148(3), 1425-1435.
62. Izawa, T. (2012). Physiological significance of the plant circadian clock in natural field conditions. *Plant, cell & environment*. 35(10), 1729-1741.
63. Abe, M., Fujiwara, M., Kurotani, K.-i., Yokoi, S. and Shimamoto, K. (2008). Identification of dynamin as an interactor of rice GIGANTEA by tandem affinity purification (TAP). *Plant and cell physiology*. 49(3), 420-432.
64. Zhao, J., Chen, H., Ren, D., Tang, H., Qiu, R., Feng, J., Long, Y., Niu, B., Chen, D. and Zhong, T. (2015). Genetic interactions between diverged alleles of Early heading date 1 (Ehd1) and Heading date 3a (Hd3a)/RICE FLOWERING LOCUS T1 (RFT1) control differential heading and contribute to regional adaptation in rice (*Oryza sativa*). *New Phytologist*.
65. Taoka, K.-i., Ohki, I., Tsuji, H., Furuita, K., Hayashi, K., Yanase, T., Yamaguchi, M., Nakashima, C., Purwestri, Y. A. and Tamaki, S. (2011). 14-3-3 proteins act as intracellular receptors for rice Hd3a florigen. *Nature*. 476(7360), 332-335.
66. Lee, Y. S., Jeong, D. H., Lee, D. Y., Yi, J., Ryu, C. H., Kim, S. L., Jeong, H. J., Choi, S. C., Jin, P. and Yang, J. (2010). OsCOL4 is a constitutive flowering repressor upstream of Ehd1 and downstream of OsPHYB. *The Plant Journal*. 63(1), 18-30.
67. Tadege, M., Sheldon, C. C., Helliwell, C. A., Upadhyaya, N. M., Dennis, E. S. and Peacock, W. J. (2003). Reciprocal control of flowering time by OsSOC1 in transgenic Arabidopsis and by FLC in transgenic rice. *Plant Biotechnology Journal*. 1(5), 361-369.
68. Miyoshi, K., Ito, Y., Serizawa, A. and Kurata, N. (2003). OsHAP3 genes regulate chloroplast biogenesis in rice. *The plant journal*. 36(4), 532-540.
69. Thirumurugan, T., Ito, Y., Kubo, T., Serizawa, A. and Kurata, N. (2008). Identification, characterization and interaction of HAP family genes in rice. *Molecular Genetics and Genomics*. 279(3), 279-289.
70. Klintonäs, M., Pin, P. A., Benlloch, R., Ingvarsson, P. K. and Nilsson, O. (2012). Analysis of conifer FLOWERING LOCUS T/TERMINAL FLOWER1-like genes provides evidence for dramatic biochemical evolution in the angiosperm FT lineage. *New Phytologist*. 196(4), 1260-1273.

71. Park, Y. G., Muneer, S. and Jeong, B. R. (2015). Morphogenesis, Flowering, and Gene Expression of *Dendranthema grandiflorum* in Response to Shift in Light Quality of Night Interruption. *International journal of molecular sciences*. 16(7), 16497-16513.
72. Rao, N. N., Prasad, K., Kumar, P. R. and Vijayraghavan, U. (2008). Distinct regulatory role for RFL, the rice LFY homolog, in determining flowering time and plant architecture. *Proceedings of the National Academy of Sciences*. 105(9), 3646-3651.

Please Submit your Manuscript to Cresco Online Publishing
<http://crescopublications.org/submitmanuscript.php>