

MECHANISMS OF PHOTOPERIOD IN REGULATION OF RICE FLOWERING

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Abstract— A study on the photoperiodic control of flower in rice is advancing and rice has become an of short day plant. Many genes used in flowering time determination in rice have been identified by many methods. The conclusion from these molecular studies is a remarkable conservation of genes which play an important role in the control of flowering time in rice. The rice photoperiod sensitivity gene Hd3a was originally detected as a heading date related quantitative trait locus found on chromosome 6 of rice. High resolution linkage mapping of Hd3a was carried using a huge segregating population derived from advanced backcross progeny between a japonica variety, Nipponbare, and an indica variety, Kasalath. Researchers revealed that there are three (3) pathways for the day length regulation of flowering in rice, short day activation pathway and long day suppression pathway lastly the long day activation pathway. Some genes were used in multiple pathways and others are specific to a particular pathway. Their regulation also depends on the developmental stages. Rice may be an ideal plant to study the night break effect on flowering. In the near future there is need for better understand the controlled of flowering in rice at the genetic level.

Index Terms— Heading date, Short day plant, Long day plant

I. INTRODUCTION

Rice is the mainly world most important cereal crop which serve as a primary source of food for almost half of the world population[1]. Rice is a tropical legumes plant and mainly source of food which third of the world population depend on it[2]. About three billion people of the world use it as a major or basic food which provide 50-80% of the calories needed[3]. It grown in almost 148 million hectares annually or on 11% of the world planted land [2]. It's a member of graminaceae of grass family consist of two (2) cultivars mainly: *Oryza stiva* which originate from Asia and is found all over the world the last one *Oryza glaberrima* mostly found in only one region of the world west africa and is grown in small proportion. *Oryza* as the rice belong to has come in existence about 130million years ago which is evenly distributed all over the world apart from the the Antarctica[2]. Rice is the mainly cereal plant that is ate only by human, Wheat cover a significant proportion of land but majority of it is utilized as animal feed [2]. Rice is very important source of our food. Rice is grown in about one hundred and fifty four million hectares annually or in 11% of the worlds cultivated areas, in 200 world rice production was approximated to be 600 million tones[1]. Its production

increased at the rate of 2.3-2.5% during 1970s and 1980s however during the1990s the growth rate decline yearly by 1.5% up to present decade[4]. The number of rice consumption is increasing at the rate of 1.5% annually where as its production at present increase only at the rate of 1.0% annually[4]. According to the UN estimation, the world population will increase from 6.7 billion at present to about 8 billion by 2025, therefore its production must increase from 440 million tones at present to 475 million tones by 2020[4]. FAO estimates that by 2050 the world rice requirement will be 524 million tones which required annual increase of 2 million tones from the present level of production[4]. To meet with challenge of producing more rice from the existing land resources, therefore rice varieties with a high yield potential are required, to achieve this there is need to know how photoperiod regulate flowering in rice which is the key success to a high potential yields. In this review we summarize the various molecular and genetic approach that are currently adopted through photoperiod to increase the potential yield of rice. Flowering date act as the most considerable aspect of agricultural trait of rice, rice farmers entire the world have been advancing rice collections whose flowering time are most applicable for the place where they are planted. The formation of a flower is important for successful sexual reproduction, therefore the actual timing of it has adaptive value[5]. Especially in non-self-fertile species where flowering has to be synchronize among them, even in self fertile species, the induction of flowering is regulated by environmental and endogenous factors such as day length, temperature and hormonal constituents[5]. Regulation of flowering time has been investigated about 100 years ago. This early studies revealed that plant flowering is controlled by factors that included day length i.e photoperiod[5]. Photoperiod is one of the most important characteristic of plants because it helps to provide the plants with the suitable signals that are necessary for flowering. Plants in general consists of three sensing photoperiods classes; short and long day which play a vital role in promoting flowering by sensing the short and long day photoperiods respectively and lastly, the neutral day flowering plants which photoperiods have no effects on it [6]. Most all cultivars of rice are short day plants, and mature in a shorter time under a short photoperiod (about 10 hours) compared to long photoperiod (14 hours). However, the photoperiod sensitivity varies greatly among cultivars[5]. Advancement in the establishment of rice genomic sequence and the possible production of transgenic rice makes it an

interesting model organism for molecular studies in monocots [7].

II. PATHWAYS REGULATING THE PHOTOPERIODIC DURING RICE FLOWERING

In rice, flower is determined by short day and withheld by long day condition, thus, short day inhibiting pathway while long day withholding pathway are present in rice while there are so many rice that flowering is determined during long day although it takes longer time than short day and therefore there is a third pathway in rice which is long day inhibiting pathway[6]. Pathways for long day suppression and long day inhibition can be differentiated by advancing stage of the plant. Long day withholding sustains from undeveloped stage to the developmental stage[10]. Then the long day inhibition pathway becomes activated at later stage and it is independent of the long day suppression pathway, therefore in long day, both the activating pathway and the suppression pathway function simultaneously in the late developmental stage[17]. As it will describe, the OsGI-Hd1-Hd3a pathway are the main pathway for the regulation of flower in rice and it forms both short day inhibiting pathway and long day suppression pathway depending on the regulation of Hd3a by Hd1[10]. Behaviour of these pathways is also developmentally controlled. The short day inhibition pathway becomes activated at undeveloped stage while the long day suppression pathway functions entire the growth stage[8]. The molecular situation of the last pathway i.e. the long day inhibiting pathway, has not been known. It is going to be important to know constituents of this pathway[9].

3. Major Pathways Responsible for the Flowering Control in Rice

Three(3) genes which serve as a major genetic pathway in the photoperiodic control of flower in rice have been identified as: OsGI, an ortholog of Arabidopsis GI, Hd1, an ortholog of Arabidopsis CO, and Hd3a, an ortholog of Arabidopsis FT are shown to form the major pathway for the photoperiodic control of flower in rice[10]. OsGI was isolated as a gene whose mRNA was withheld in the *se5* mutant which is insensitive to the photoperiod by many array method [11]. OsGI has high similarity with GI and contains a nuclear localization signal. Hd1 was identified by map-based cloning after the isolation by quantitative trait locus (QTL) analysis which is closely associated to Arabidopsis CO, which play the major role in the photoperiodic regulation of flower. Two motifs, zinc finger motif and CCT motif, are highly conserved in Hd1 and CO[10]. Hd3a was similarly isolated by map-based cloning after the identification by QTL analysis[11]. Hd3a and FT are highly conserved and both function as activators of flowering under inductive conditions[11]. Heading date are found on the short arm of chromosome 6 which involved in the photoperiodic response and promoting flowering in short-day conditions are identified through a map-based strategy which show a high level of similarity with FT gene that promote flowering during long-day condition[10]. Transgenic analysis also show that the introduction of Hd3a gene result in early flowering in SDPs and LDPs conditions, moreover Hd3a mRNA is up-regulated in the short-day conditions that induce flowering in rice this that Hd3a plays an important role in the production of flowering in rice[10]. Overexpression of Hd3a and FT lead to early heading in rice and early flowering in Arabidopsis, the fact revealed that Hd3a promotes the floral transition as in FT sequence and

function similarity show that Hd3a is an ortholog of FT[11]. It also revealed that several copies of FT like genes found in the rice genome: such as RFT1 locate closed to Hd3a which its presumed amino acid sequence with 91% similarity with Hd3a[11]. Advancement in the establishment of rice genomic sequence and the possible production of transgenic rice makes it an interesting model organism for molecular studies in monocots [7]. Heading date 3 gene (Hd3a), which is found on the chromosome six (6) play an important role in short day flowering plant by promoting photoperiodic response [10]. Hd3a together with hd1 are positive regulator under short day condition and the transgenic analysis rice plants shows that over expressing or suppressing of OsGI gene activates hd1 in short day as well as in long day rice but however, OsGI, together with Hd1 suppresses the expression of Hd3a gene in long day condition thereby serving as negative regulators for the flowering [10]. These shows that OsGI-Hd1-Hd3a is the major genetic pathway for the regulation of photoperiod in flowering rice plants and these is also conserved in Arabidopsis which is a long day plant[12]. Hd1 is only activated in the dark period which give room for the expression of Hd3a gene [13]. The dual function of Hd1 for the regulation of Hd3a gene is dependent on the photoperiod.

III. NIGHT BREAK EFFECT IN RICE

A short exposure to light in the middle of the night promotes flowering in short day plants. The phenomenon is called night break and has been used previously and presently by researchers as a tool to study the photoperiodic regulation of flowering for many years. However, at the molecular level not much is known about this phenomenon. In *Oryza sativa* 10 min of light exposure in the middle of a 14-h night caused a delay in flowering[14]. A single NB strongly suppressed the mRNA of Hd3a, a homolog of Arabidopsis thaliana FLOWERING LOCUS T (FT), whereas the mRNAs of OsGI and Hd1 were not affected. The NB effect on Hd3a mRNA was maximal in the middle of the 14-h night[15]. The phyB mutation abolished the NB effect on flowering and Hd3a mRNA, indicating that the NB effect was mediated by phytochrome B. Because expression of the other FT-like genes was very low and not appreciably affected by NB, our results strongly suggest that the suppression of Hd3a mRNA is the principal cause of the NB effect on flowering in rice[15].

IV. GENETIC TIME OF RICE FLOWERING

The genetics of flowering is quantitative in nature. To know the determinants of heading date in rice, several groups have used quantitative trait loci (QTL) analyses [10]. Exploiting phenotypic differences and DNA polymorphisms within cultivated rice varieties and wild relatives of rice, researchers revealed that the loci are responsible for regulating heading date; determine their relative contribution to phenotypic variance, which establish genetic relationships between loci[16]. Adopting different segregating populations obtained by crossing a Nipponbare and Kasalath M. Yano's group identified most of the QTLs controlling heading date in rice, and pioneered the genetics of photoperiodic flowering [17]. Hd1 to Hd5 are the dominant loci regulating photoperiodic flowering responses which act as single Mendelian factors in a

segregating F2 population[18]. The Nipponbare alleles of Hd1 and Hd2 were shown to be short day flowering promoters with the largest effects on phenotype, acting independently of one another [17]. Hd3a genetically interacts with Hd1 and Hd2 to inhibit flowering under short day conditions[19]. The Kasalath alleles of Hd4 and Hd5 delayed flowering under long day conditions [16]. The genetic effect of Hd4 identified to be additive to that of Hd1 and Hd2, whereas an epistatic relationship was detected among Hd5 and Hd1[20]. With the exception of heading date 2 (Hd2) these QTLs have been fine mapped and the underlying genes cloned[21]. Backcross progenies derived from the same original cross allowed initial identification and cloning of other QTLs, often with minor effects, for many of these, the underlying genes still need to be identified[22]. Researchers revealed that by analyzing rice populations mutagenized through transgenes, transposons or γ -radiation, researchers identify the several genes implicated in flowering time control or day length perception, and position them into regulatory networks [17]. Phenotypic and functional analyses have suggested that photoperiodic flowering in rice is control by a genetic cascade that have similarities with that described for Arabidopsis, both in the components involved and in their mode of action. It also became clear that a parallel pathway unique to rice can control flowering own its own and both pathways eventually converge on the control of a group of genes encoding florigenic proteins [16].

V. CONCLUSION

Researches on the photoperiodic control of flowering in rice have advanced and rice has become a model of short-day plant. Many genes are involved in flowering time determination in rice have been identified by various methods. One striking conclusion from these molecular studies is a remarkable conservation of genes which play important roles in the regulation of flowering time in rice. Scientist revealed that there are three pathways for the day length control of flowering in rice: Short day activation pathway, long day suppression pathway and the long day activation pathway. Some genes are used in multiple pathways and others are pathway specific. They are also differentially regulated depending on developmental stages. Rice may be an ideal plant to study the night break effect on flowering. In the near future we hope better understand the regulation of flowering rice at the molecular level.

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