FIELD EVALUATION OF CONDE PROGENIES WITH EARLY HEADING DATE AND RESISTANCE TO BACTERIAL LEAF BLIGHT

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Abstract

Heading date is one of key traits in rice adaptation to different environments. Rice with early maturity is very useful for increasing rice production extensively especially in Indonesia. The improvement of rice variety Conde for heading date and resistance to bacterial leaf blight (BLB) was developed through Marker Assisted Backcrossing approach (MAB). Xa7 derived from Conde as recipient parents for resistance to BLB and Hd2 gene derived from Nipponbare as a donor parent for heading date. The aim of this research was to evaluate the performance of heading date and agronomic traits of 85 BC2F4 lines in two field stations, Sukamandi (West Java) and Maros (South Sulawesi). Molecular analysis of Xa7 on chromosome 6 and Hd2 gene on chromosome 7 and agronomic performance was evaluated. Foreground analysis resulted 41% for Xa7 and 66.7% for Hd2 gene in homozygous condition. The majority of lines have similar heading date and yield with Conde and more resistance to bacterial leaf blight (BLB) than Conde. Six lines flowered earlier 5 days than Conde in Sukamandi and three lines flowered earlier 3 days in Maros. Twelve lines with flowered earlier than Conde, resistance to BLB and similar yield with Conde were selected for background analysis resulted 93% genome recovery. These lines would be further evaluated in preliminary yield trail for their stability.

Keywords: Hd2, Maros, Sukamandi, Tropical region, Xa7

Introduction

Flowering time is closely related to the grain yield for crop attribute to maintain an appropriate balance between full use of resources and avoidance of environmental stresses such as high temperature, low temperature, and drought. Abiotic stresses can pose a serious threat to spikelet fertility and consequently induce yield loss (Zhang et al., 2019).

Furthermore, early maturity allows farmers to increase their cropping intensity from two to three cropping of rice per year in tropical regions. Breeding for high yielding rice varieties with early maturity is considered important to increase cropping indexes in the fully irrigated farm lands (Fatimah et al., 2014; Pramudyyawardani et al., 2015).

Until now, a number of genes/QTLs involved in the photoperiodic flowering pathway/heading date have been identified and mapped in rice (Hori et al., 2016). Eighteen QTLs (Hdl-Hd18) were detected with the different populations (Liu et al., 2018). They derived from crosses between Nipponbare and Kasalath and between Koshihikari and Hayamasari, and most of the QTLs have been cloned (Matsubara, 2008, Lin, 2000, Yano, 2001, Shibaya 2016).

Hd2 derived from a cross between Nipponbare and Kasalath (Yano et al., 1997; Yamamoto et al., 1998) and confirmed as OsPRR37 gene (pseudo-response regulator gene) (Koo et al., 2013). Hd2 is allelic with Ghd7.1 (Yan et al., 2013) and through map based cloning approach it was confirmed that Ghd7.1 is the OsPRR37 gene, or Gao et al., (2014) reported Days to heading 7 (DTH7) and Zhang et al., (2016) detected qHD7.2, both of them encodes a pseudo-response regulator protein (OsPRR37).

Hd2/Ghd7.1/DTH7/OsPRR37/qHD7.2, or later named Hd2, was located in
LOC_Os07g49460 putative gene of 96.3-kb region in chromosome 7 (MSU Rice Genome Annotation Project). It involved in regulating rice heading date that suppresses flowering under short day and long day conditions (Koo et al. 2013; Yan et al. 2013) and played important roles in the expansion of rice cultivation to temperate areas and rice adaptation from low to high latitudes (Koo et al., 2013).

Farmers prefer grows short duration rice cultivar than long duration of rice cultivars because its easier and more efficient in crop management and field practice. They will save more energy, including water, fertilizer and labor, when they grow in short duration (Ahadiyat et al., 2012).

BLB caused by Xanthomonas oryzae pv. oryzae (Xoo) is a disastrous disease in rice worldwide. Yield losses caused by Xoo can be as high as 50% in some areas of Asia (Adhikari et al., 1995). In Indonesia, Suparyono and Sudir (1992) reported that damage threshold due to BLB was ca. 20% at about two weeks before harvest. Above the threshold, each 10% increase in the BLB severity the yield losses increased by 5 to 7%. The evaluation of disease resistance in early breeding generations of rice is important to develop varieties with better resistance and the selection of appropriate donor parents which show broad spectrum of resistance is important for the breeding program.

Conde, Indonesian rice varieties, was nationally released on 2002 as new lowland rice varieties. It derived from IR64, an existing popular variety, this variety is well accepted by farmers and consumers (Toenniessen, 2003; Jena & Mackill, 2008). The improvement of Conde rice variety that containing Xa7 gene was transferred with Hd2 gene from Nipponbare for earliness heading date and productivity has already developed through Marker Assisted Backcrossing approach (MABc) (Fatimah et al., 2014; Fatimah et al., 2018). MABc is using markers to select for target loci (donor), minimize the length of the donor segment containing a target locus, and/or accelerate the recovery of the recurrent parent genome during backcrossing (Hospital, 2001).

The aim of this research was to evaluate the performance of heading date and agronomic traits of BC2F4 lines with Xa7 and Hd2 gene in two field stations, Sukamandi, West Java Province in Western Indonesia and Maros, South Sulawesi Province in Eastern Indonesia.

Materials and Methods

Plant materials

This study was carried out using 85 BC2F4 lines of backcross population and their parents Conde (resistance to bacterial leaf blight, Xa7+Xa4 gene, recipient) and Nipponbare (Hd2 gene, donor). Two Indonesian elite rice varieties Inpari 13 and Ciherrang also included as check variety for productivity and IRBB7 containing Xa7 gene as resistant check.

Molecular Analysis

The foreground selection :PCR amplification was generated using Bioread Thermal Cycler PCR machine using SSR primer RM1362 (F:TGATCTAAACAGGCCCTTAG and R:CATCATCAAGACCACACACAT C) and RM7601 (F: GCCTCGCTGCTGCTTATTATC and R: CAGCCTCTCCTTGTGTTGTG TG) associated with the QTLs for Hd2 locus located on chromosome 7 at the genetic distance of 116.1 cM and 116.6 cM (Fujino and Sekiguchi, 2005; Fujino and Sekiguchi, 2008). SSR Primer RM20582 (F: AGAGCGTCGTCCTTCACCATCC and R: GGCCAATACGACGATACATTACG) linked to Xa7 locus located on chromosome 6 at the genetic distance of 118.5 cM (Chen et al., 2008). For the background selection: two hundred and forty three polymorphic SSR primers distributed on 12 chromosomes (Fatimah et al., 2014) were used for background selection. Amplified products was separated by electrophoresis in 8% polyacrylamide gel (Dual Triple-Wide Mini-Vertical System, C.B.S. Scientific, CA, USA) and observed by ethidium bromide and photographed under ultraviolet light using the gel documentation system (BioRad).

BLB Evaluation

These varieties were first sown in plastic boxes. The seedling was transplanted into pot containing natural paddy soil. Rice plants were grown under greenhouse condition. The cultivation and management of the rice proceeded as usual. The parents and check (Conde, Nipponbare and IRBB7) were inoculated with 39 Indonesian Xoo isolates at seedling stage (40 days old). Three isolates
(Xoo1110, Xoo1122 and Xoo1130) that showed different patterns of resistance between Nipponbare (susceptible) and Conde or IRBB7 (resistant) continued for disease evaluation in the BC2F4 population.

The fully expanded leaves were clip-inoculated (Kauffman et al., 1973) with scissors, which were dipped, prior to inoculation, into a bacterial cell suspension containing approximately $10^9$ cfu ml$^{-1}$. The suspension was prepared from 48-h old actively growing cultures of each isolate grown on NB medium. The length of the lesion was measured at 14 days after inoculation. The resistance reaction was classified into susceptible and resistant based on the BLB intensity of Conde as the cut off. The resistant lines gave similar BLB intensity with Conde and susceptible lines gave higher BLB intensity than Conde.

**Field Experiments**

Heading date and agronomic performance were evaluated in two locations, at Indonesian Center for Rice Research, Sukamandi, West Java Province and Indonesian Cereals Research Institute, Maros, South Sulawesi Province. All experiments were conducted during the months of March to July. The experiments were laid out following a Randomized Complete Block Design (RCBD) which the 85 BC2F4 lines as treatment with three replications. The seeds of improved lines and checks were sown in a seed bed nursery. Two weeks-old seedlings were then manually transplanted into the rice field with one seedling planted per hill. The plot size was 1.5 m x 2 m. Each plot had a planting density of 25 cm between plants (within a row), and 25 cm between rows. In all experiments, fields were fertilized by hand broadcasting with 115 kg/ha of urea, 38 kg/ha of P$_2$O$_5$ and 50 kg/ha of K$_2$O. Weed control was performed using chemical herbicide and hand weeding. From each breeding lines, five individual plants were selected for characterization of their agronomic performance.

**Data Collection**

Traits measurement of the agronomic performance were heading date (DH), plant height (PH), numbers of tiller (NT), and grain yield (GY). DH was recorded when 80% of the individual plants in each plot flowered. PH and NT were measured at maturity stage. PH was measured from the soil surface to the tip of the panicle. NT was counted manually. To measure GY in each plot, only the inner rows were used in square (1m x 1m) consisted of 16 clumps. Two border rows and the border plants of each row were discarded. GY of each plot was adjusted to 14% moisture content. The GY per plot was extrapolated to tons per hectare.

**Data Analysis**

The marker data were scored as “A”, “B” and “H” analyzed as homozygous recipient allele, homozygous dominant allele and heterozygous allele respectively. The marker data was analyzed using the software Graphical Genotyper (GGT 3.2) (Berloo, 2008). All agronomic traits in each experiment were subjected to statistical analysis using the SPSS v.17 program. Analysis of variance (ANOVA) was calculated based on the randomized complete block design (RCBD). A combined analysis of variance was performed using the mean value of data in all traits of each experiment. Duncan significant difference (DMRT) was determined at a five percent probability level to make the comparison between the mean values of each breeding line and parents.

**Results**

**Molecular Analysis**

Foreground analysis of the 85 BC2F4 lines revealed 56 lines (66.7%) were homozygous to Nipponbare for the marker RM7601 and RM1362 linked to $Hd2$ and 35 lines (41%) were homozygous to Conde for the marker RM20582 for $Xa7$ detection (Figure 1). Based on molecular data of $Xa7$ and $Hd2$ gene, heading date and grain yield of 85 BC2F4 lines, it was selected 26 lines that homozygous to $Xa7$ and $Hd2$ gene, flowered earlier and gave similar yield with Conde variety.

The background analysis was conducted on 12 selected lines that flowered earlier, resistance to BLB and similar yield with Conde. It resulted the average of genome recovery of the selected BC2F4 progenies in 12 chromosomes with the value was 93% (Figure 2).
Figure 1. Foreground selection of BC$_2$F$_4$ individues (Conde/Nipponbare) using marker a) RM7601 and b) RM20582. From left to right, lane 1: 100 bp marker, lane 2: Conde, lane 3: Nipponbare, lane 4: BC$_2$F$_4$ individues on 8% polyacrilamid gel electrophoresis.

Figure 2. The background selection of the selected BC$_2$F$_4$ lines using 243 SSR primers distributed on 12 chromosomes.

BLB Evaluation

Conde, Nipponbare and IRBB7 were inoculated with 39 Indonesian Xoo isolates at seedling stage (40 days old). Conde was resistant to 39 isolates whereas IRBB7 was resistant to 24 isolates and Nipponbare was resistant to 23 isolates. Out of 39, 10 isolates showed the different patterns of resistance between Nipponbare (susceptible) and Conde/IRBB7 (resistance) (data not shown). This result indicated that resistance gene possessing by Nipponbare and Conde/IRBB7 were different genes and their resistant reaction were difference while Conde and IRBB7 giving the same reaction pattern against Indonesian Xoo isolates.

The resistance of Conde to bacterial blight within 14 days after inoculation (DAI) was evaluated with three selected Xoo strains, Xoo1110, Xoo1122, and Xoo1130 (Figure 3). Nipponbare was susceptible to the three Xoo strains. The BLB intensity of Conde were 4% (Xoo1110), 5.38% (Xoo1122) and 9.5% (Xoo1130). The number of resistant BC$_2$F$_4$ lines were 42% ($\chi^2=1.98$, p=0.16) with the BLB intensity of the BC$_2$F$_4$ lines were lower than Conde (<4%) (Figure 4).

Field Experiment

Maros is located in eastern part of Indonesia (40°45´-50° 07´ South Latitude and 109°205´-129° 12´ East longitude) while Sukamandi located in western part of Indonesia (60 11' - 60 49' South Latitude and 1070 31' - 1070 54' East longitude) that lead to some different climate parameter. Both field stations were located in the same altitude. Sukamandi in West Java Province was 16 m above sea level in Western Indonesia and Maros in South Sulawesi Province was 15 m above sea level in Eastern Indonesia (Figure 5).
Agronomic and yield performance

Analysis of variance (ANOVA) of four traits is presented in Table 2. In BC2F4 population showed significant effects (P<0.05) were detected for all traits among the breeding lines at both Sukamandi and Maros field station. The agronomic performance of parents, check varieties and BC2F4 lines from both field station is presented in Table 3.

Table 2. The ANOVA of four traits in Conde/Nipponbare BC2F4 population.

<table>
<thead>
<tr>
<th>Location</th>
<th>Trait</th>
<th>MS</th>
<th>F</th>
<th>P</th>
<th>CV (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Maros</td>
<td>Heading date</td>
<td>157.2*</td>
<td>4.38</td>
<td>0</td>
<td>1.9</td>
</tr>
<tr>
<td></td>
<td>Tiller number</td>
<td>33.46*</td>
<td>1.94</td>
<td>0.002</td>
<td>11.6</td>
</tr>
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<td></td>
<td>Plant Height</td>
<td>461.36*</td>
<td>11.31</td>
<td>0</td>
<td>10.0</td>
</tr>
<tr>
<td></td>
<td>Grain Yield</td>
<td>4.40*</td>
<td>1.66</td>
<td>0.005</td>
<td>31.2</td>
</tr>
<tr>
<td>Suka mandi</td>
<td>Heading date</td>
<td>23.94*</td>
<td>6.11</td>
<td>0</td>
<td>2.82</td>
</tr>
<tr>
<td></td>
<td>Tiller number</td>
<td>17.77*</td>
<td>2.95</td>
<td>0</td>
<td>10.80</td>
</tr>
<tr>
<td></td>
<td>Plant Height</td>
<td>653.82*</td>
<td>35.23</td>
<td>0</td>
<td>13.21</td>
</tr>
<tr>
<td></td>
<td>Grain Yield</td>
<td>2.77*</td>
<td>2.88</td>
<td>0</td>
<td>17.11</td>
</tr>
</tbody>
</table>

*Significantly different at 5% level of Duncan significant difference.

MS: Mean square, F: FStat, P: Pvalue, CV: Coefficient of variation.
Figure 6. Distribution of agronomic trait on BC2F4 population and parents for A) heading date, B) tiller number, C) plant height and D) grain yield in Sukamandi and Maros field station.

The majority of the BC2F4 lines in Sukamandi and Maros have similar heading date with Conde (not with Nipponbare) however it was found three different type of heading date. In Sukamandi: early-fixed ranged 73-74 DAS (11,8%), middle-fixed ranged 75-79 DAS (77,6%) and late-fixed ranged 80-83 DAS (10,6%) while in Maros: early-fixed 73 DAS (3,5%), middle-fixed ranged 74-79 DAS (87%) and late-fixed 81 DAS (9,4%) (Figure 5). In Sukamandi, the BC2F4 lines flowered earlier 5 days than Conde were line number #31, #43, #44, #45, #48, and #49 and in Maros, the BC2F4 lines flowered earlier 3 days than Conde were #09, #72, #74 (Figure 6).

Genotype variances were found for number of tiller among the BC2F4 lines and Conde. The mean value of BC2F4 lines was 17-30 in Sukamandi and 16-34 in Maros while Conde was 20. The majority of BC2F4 lines have similar number of tiller with Conde was 81% in Sukamandi and 43,5% in Maros (Figure 6). Line number #28, #30, #31, #33, #78, #83, #84, and #85 (Sukamandi) and #04, #15, and #26 (Maros) gave higher number of tiller than Conde.

Genotype variances were found for plant height among the BC2F4 lines and Conde. The mean value of plant height of BC2F4 lines ranged from 100 to 133 cm in Sukamandi and 82 to 124 cm in Maros while Conde was 91 cm in Maros and 100 cm in Sukamandi (Figure 6). The majority of BC2F4 lines have similar plant height with Conde was 72% in Sukamandi and 53% in Maros (Figure 6).

There is no significant difference of grain yield observed in Sukamandi among the BC2F4 lines and Conde. The mean value of grain yield of the breeding line ranged from 2.5 to 7.0 ton/ha while Conde was 6,5 ton/ha (Figure 6). The majority of BC2F4 lines have similar yield with Conde (74,2%). Line number #03, #9, and #78 were giving higher yield than Conde and resistant to BLB however the heading date of these lines was similar with Conde (77 DAS).

Significance differences of grain yield observed in Maros among BC2F4 lines and Conde. The mean value of grain yield of the breeding line ranged from 1.1 to 7.7 ton/ha while Conde was 2.8 ton/ha (Figure 6). The majority of the breeding lines have similar yield with Conde (83,5%). Line number #01, #05, and #06 were flowered earlier than Conde, resistance to BLB and higher yield than Conde.

**Correlation analysis**

Based on their correlation using Pearson correlation analysis showed that there is a low correlation on BC2F4 lines between heading date and tiller number however both of them are statistically significant. Low correlation also revealed between heading date and plant height however it was not significant. The low correlation also showed between heading date and yield however both of them are statistically significant. The low correlation also showed between heading date and resistance to bacterial leaf blight however it was not significant (Table 4).

**Breeding Selection**

The BC2F4 lines were selected based on the molecular analysis in foreground selection that
homozygous to Conde for Xa7 and homozygous to Nipponbare for Hd2 gene, and background selection with genome recovery higher than 84%, early heading date, resistance to bacterial leaf blight, and similar or higher yield than Conde, then it was selected 16 BC2F4 lines for further evaluation in preliminary yield trail for their stability (Table 5).

### Tabel 4. Coefficient of Pearson Correlation.

<table>
<thead>
<tr>
<th>Maros Parameter</th>
<th>Correlation</th>
<th>Heading date</th>
<th>Plant Height</th>
<th>No.of tiller</th>
</tr>
</thead>
<tbody>
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<td>0.141</td>
<td>0.256</td>
</tr>
<tr>
<td>Correlation</td>
<td></td>
<td>-0.192</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sig. (1-tailed)</td>
<td></td>
<td>0.256</td>
<td>0.192</td>
<td>1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Sukamandi Parameter</th>
<th>Correlation</th>
<th>Heading date</th>
<th>Plant Height</th>
<th>No.of tiller</th>
</tr>
</thead>
<tbody>
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<td>Pearson</td>
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<td>-0.014</td>
<td>0.325</td>
<td></td>
</tr>
<tr>
<td>Correlation</td>
<td></td>
<td>-0.28</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sig. (1-tailed)</td>
<td></td>
<td>0.325</td>
<td>-0.28</td>
<td>1</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Greenhouse Parameter</th>
<th>Correlation</th>
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<th>BLB Intensity</th>
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<td>-0.019</td>
<td>-0.119</td>
</tr>
<tr>
<td>Correlation</td>
<td></td>
<td>-0.119</td>
<td>1</td>
</tr>
<tr>
<td>Sig. (1-tailed)</td>
<td></td>
<td>0.001</td>
<td>0</td>
</tr>
</tbody>
</table>

### Tabel 5. Agronomy performance of the selected BC2F4 of Conde in Sukamandi (S) and Maros (M) field station.

<table>
<thead>
<tr>
<th>No.</th>
<th>Lines</th>
<th>Hd</th>
<th>NT</th>
<th>PH</th>
<th>Yield</th>
<th>BLB</th>
<th>GR</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>#01</td>
<td>74*</td>
<td>E</td>
<td>22</td>
<td>95</td>
<td>5.64</td>
<td>5.10</td>
</tr>
<tr>
<td>2</td>
<td>#02</td>
<td>74*</td>
<td>E</td>
<td>23</td>
<td>93</td>
<td>5.43</td>
<td>3.85</td>
</tr>
<tr>
<td>3</td>
<td>#03</td>
<td>76</td>
<td>M</td>
<td>23</td>
<td>97</td>
<td>5.42</td>
<td>4.48</td>
</tr>
<tr>
<td>4</td>
<td>#05</td>
<td>75</td>
<td>E</td>
<td>23</td>
<td>96</td>
<td>6.13*</td>
<td>3.78</td>
</tr>
<tr>
<td>5</td>
<td>#07</td>
<td>75</td>
<td>E</td>
<td>22</td>
<td>97</td>
<td>4.23</td>
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<tr>
<td>6</td>
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<td>78</td>
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<td>87</td>
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<td>3.81</td>
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<td>3.63</td>
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<td>24*</td>
<td>83</td>
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<td>4.28</td>
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<td>5.02</td>
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<td>E</td>
<td>24*</td>
<td>86</td>
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<td>5.32</td>
</tr>
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<td>12</td>
<td>#35</td>
<td>81</td>
<td>L</td>
<td>22</td>
<td>113*</td>
<td>3.72</td>
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<td>E</td>
<td>23</td>
<td>122*</td>
<td>5.35</td>
<td>5.03</td>
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<tr>
<td>15</td>
<td>#76</td>
<td>78</td>
<td>M</td>
<td>19</td>
<td>108</td>
<td>4.65*</td>
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<td>78</td>
<td>L</td>
<td>22</td>
<td>92</td>
<td>4.58</td>
<td>4.66</td>
</tr>
</tbody>
</table>

**Table 6.**

Nipponbare 61 E 17 68 1.08 16.84 S
Conde 77 M 20 95.5 4.68 15.39 S
Impari 13 73 E 30 111 5.16 - S
Ciherang 76 M 36 97 5.62 - S

*Significantly different at 5% level of Duncan significant difference.

Hd: Heading date (DAS), E: Early, M: Middle, L: Late, NT: Number of tillers, PH: Plant Height (cm), Yield: ton/ha, BLB: BLB Intensity (%), R: Resistant, S: Susceptible, GR: Genome Recovery (%).

### Discussion

Rice heading date is one of the most important agronomic traits for season adaptation and grain yield, which is affected by both genetic and environmental factors (Ebana et al. 2011). Rice is a facultative short-day (SD) plant whose flowering is accelerated under SD conditions (<10-h light/day) and is delayed under longday (LD) conditions (>14-h light/day) (Izawa, 2007; Tsuji et al., 2008). In tropical regions, the daylength is less than 13.5 h, and the daily temperature is high, which ensures that rice can grow all year (Liu et al., 2018).

Nipponbare is a *japonica* rice variety with photoperiod-sensitive identified *Hd2* and *Hd4* gene (Yano et al., 1997) used as donor in this study while Conde is an *indica* rice variety and an elite cultivar used as recipient parent. Many heading-date quantitative trait locus (*Hd-QTLs*) (*Hd1-Hd3a, Hdb-Hd17*) were found in the crosses of *japonica* and *indica* cultivars with distinct heading dates and photoperiod sensitivity (Yano et al., 2001; Monna et al., 2002; Uga et al., 2007). Yano et al. (1997) indicated that five QTL (*Hd1-Hd5*) cause variation in rice heading date in crosses between Nipponbare and Kasalath. Koo et al. (2013) demonstrate that natural variation in *PRR37/Ghd7/Hd2* has contributed to *japonica* rice adaptation to growth in the northernmost regions of rice cultivation as well as double cropping of an *indica* variety in low-latitude regions (tropical region) by reducing days to heading and photoperiod sensitivity.

In this study, it was found three different phenotype of heading date of *Hd2* gene in BC2F4 lines. Six lines flowering earlier 5 days than Conde in Sukamandi and three lines flowering earlier 3 days in Maros. In line with Prasetyono et al. (2014) reported that the earliest flowering line in the improved Cihergang was 4 days earlier than Cihergang. Yamamoto et al. (1998) reported that large variation in days to heading of *Hd2* was observed in the population of crossing between Nipponbare and Kasalath. Zhang et al. (2019) mentioned the genetic interactions among *Ghd7, Ghd8, OsPRR37/Hd2* and *Hd1* contribute to large variation in heading date in rice.

Grain yield is positively correlated with heading date, especially in low latitude areas (tropical region) where the temperature is
warm year-round (Gao et al. 2014; Li et al. 2018). In this study, in Maros, the average minimum air temperature was 24°C and average maximum air temperature was 30.8°C while in Sukamandi, the average minimum air temperature was 23.2°C and average maximum air temperature was 31.3°C. It was reported that Hd2 is not only photoperiod-related, but also a temperature-related QTL (Nakagawa et al., 2005). Under low temperature in long day conditions it delays heading (Song et al., 2012).

In this study also showed that the majority of BC2F4 lines had heading date and yield similar to Conde and well adapted to different part of Indonesia. This also maintained the yield potential and stability of the Conde across two experimental locations in Indonesia with little difference among both locations. Yan et al. (2013) mentioned that Hd2 contributes greatly to regulating rice photoperiodic flowering, plant architecture and grain productivity and provides an opportunity to breed high-yield varieties with improved adaptive flexibility for special farming regions.

The use of resistant cultivars is the most economical and effective way to control BLB disease and has played a key role in sustaining rice productivity that requires no additional cost to farmers and is environmentally safe. Fatimah et al. (2018) reported that Conde revealed the similar gene action with Xa7 gene for BLB that exhibits high resistance to most of the Indonesian races of (BLB). In this study, the majority of BC2F4 lines gave more resistance to BLB than Conde.

This study provides a marked improvement of heading date and BLB resistance in Conde progenies. The preliminary yield trial needs to be done before amplifying seed for large-scale testing and validation in farmers fields at target areas. The result of this study contributes to enhancing and sustaining future livelihoods and food security in Indonesia versus climate change.

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