# Characterization of Introgression Lines for Yield-related Traits with Indica-type Rice Variety IR64 Genetic Background

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#### **Abstract**

A total of 334 introgression lines (INLs: BC<sub>3</sub>-derived lines) derived from crosses between Indica cultivar IR64 as a recurrent parent and 10 donor parents including new plant type lines (IR65600-87-2-2-3, IR65598-112-2, IR65564-2-2-3, IR66750-6-2-1, IR69093-41-2-3-2, IR69125-25-3-1-1, Hoshiaoba, IR66215-44-2-3, IR68522-10-2-2, and IR71195-AC1) have been developed by recurrent backcross breeding, to introduce unique traits into IR64 genetic background and to use for breeding materials. The agronomic traits of the 334 INLs were evaluated in International Rice Research Institute from 2005 to 2007 and the genotypes of the 334 INLs were detected using SSR markers. Particularly, 117 out of the 334 INLs which showed unique agronomic traits were selected as the "core set" for detailed evaluation. Variation in agronomic traits: days to heading (DTH), leaf length and width, culm and panicle length, number of panicles, total spikelet number per panicle (TSN), and 100-grain weight (GW), in the 117 INLs were characterized. As a result of comparison between the several INLs and IR64, significant differences were observed in DTH, TSN and GW in at least one season. The developed INLs with the IR64 genetic background are useful for both breeding and genetic dissection of agronomic traits across various environments.

Discipline: Plant breeding

Additional key words: days to heading, grain weight, new plant type, *Oryza sativa* L., total spikelet number

# Introduction

Since the 1960s, many International Rice Research Institute (IRRI)-bred varieties have been released and distributed worldwide and used by farmers as cultivated varieties and breeders as important parental varieties in breeding programs. IRRI has developed many highyielding Indica inbred cultivars such as IR8, IR36, IR 64, and IR72<sup>20</sup>. Especially, IR64, which was released in 1985, had been widely accepted as a high-quality rice variety in many countries<sup>7</sup>. To increase yield potential in inbred varieties under a tropical environment, new plant

# Background:

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type (NPT) rice have been developed using tropical Japonica varieties. The NPT lines have unique agronomic traits from tropical Japonica such as low tillering, large panicles, thick culm, and large and dark green flag leaves<sup>19</sup>.

Because of wide acceptability of IR64, several breeding materials with IR64 genetic background such as doubled haploid (DH) lines<sup>3</sup>, recombinant inbred lines (RILs), and thousands of mutant lines24 have been developed for genetic analysis and improvement of rice varieties. Additionally, recent progress in molecular biology has made it possible to conduct genetic analysis in complex agronomic traits which were governed by multiple quantitative trait loci (QTLs) and their interactions with other loci. For example, 135 DH lines derived via anther culture from a cross between IR64 and tropical Japonica cultivar Azucena were developed and the DH lines were used for QTL analysis of grain shape<sup>6</sup>, panicle number<sup>12</sup>, blast resistance<sup>22</sup>, and brown planthopper resistance<sup>6</sup>. These materials with IR64 genetic background are useful as not only the materials for detecting QTLs in genetic analysis but also breeding materials which are similar in elite traits to IR64.

Introgression lines (INLs) derived from crosses between IR64 and 10 donor varieties which were mostly NPT lines have been developed in the present study as breeding materials for enhancement of rice yield<sup>2</sup>. A total of 334 INLs were selected by agronomic traits related to yield such as days to heading, total spikelet number and grain size. Based on characterization of phenotype and genotype in the 334 INLs, associations

between agronomic traits and introgressed chromosomal segments were investigated. A total of 54 regions for eight traits were associated with agronomic traits: seven regions for days to heading (DTH), eight regions for culm length (CL), eight regions for leaf width (LW), four regions for leaf length (LL), six regions for panicle length (PL), three regions for panicle number (PN), seven regions for 100-grain weight (GW), and 11 regions for total spikelet number per panicle (TSN). These lines with IR64 genetic background are useful as research and breeding materials to enhance yield potential of IR64 using marker-assisted selection (MAS) in breeding programs.

In this study, 117 lines representing diversity of 334 INLs derived from crosses between IR64 and the 10 donors were characterized for agronomic traits: DTH, CL, PL, LW, LL, PN, TSN, and GW. Especially, several INLs which have unique agronomic traits such as DTH, TSN and GW, were compared with IR64.

#### Materials and methods

#### 1. Plant materials

A total of 334 INLs were developed by the back-cross breeding in the combinations between an Indicatype variety IR64 as a recurrent parent and 10 donor varieties: IR65600-87-2-2-3 (YP1), IR65598-112-2 (YP3), IR65564-2-2-3 (YP4), IR69093-41-2-3-2 (YP5), IR69125-25-3-1-1 (YP6), Hoshiaoba (YP7), IR66215-44-2-3 (YP8), IR68522-10-2-2 (YP9), IR71195-AC1 (YP10), and IR66750-6-2-1 (YP11) (Table 1). Among the

Table 1. List of 10 donor varieties which were used for development of introgression lines.

Entry No.	Donor variety	Number of INLs			
			Developed	Core set	
YP1	IR65600-87-2-2-3	Shen Nung 89-366, Ketan Lumbu	36	10	
YP3	IR65598-112-2	Shen Nung 89-366, Genjah Wangkal	23	12	
YP4	IR65564-2-2-3	NO 11, Bali Ontjer	45	19	
YP5	IR69093-41-2-3-2	Shen Nung 89-366, Ketan Lumbu, Gundil Kuning	56	19	
YP6	IR69125-25-3-1-1	Shen Nung 89-366, Ketan Lumbu, Gundil Kuning	29	7	
YP7	Hoshiaoba	Chugoku 113, Oochikara	21	11	
YP8	IR66215-44-2-3	Gaok, Chir 87-3-1, Moroberekan, Palawan	29	10	
YP9	IR68522-10-2-2	Moroberekan, Shen Nung 89-366, <u>Daringan</u>	16	7	
YP10	IR71195-AC1	Shen Nung 89-366, Pring, Akihikari, Cnax 1419-37-2-3-4, Mee Nteri	39	11	
YP11	IR66750-6-2-1	Shen Nung 89-366, Sri Kuning	40	11	

The underline indicates variety from Indonesia (tropical Japonica).

Donors were developed from the crossing among several varieties including Japonica-type.

10 donor varieties, nine which were designated with the IR number were the NPT varieties developed in IRRI using tropical Japonica-type varieties<sup>19</sup>. The other one donor parent, Hoshiaoba<sup>14</sup> (also known as Chugoku 146), was a high-yielding variety developed in Japan and derived from a cross between Indica and Japonica-types' varieties. These lines and a variety were used as donor parents to enhance yield potential.

The  $F_1$  plants which were derived from the crosses between IR64 and these donor varieties were recurrently backcrossed with IR64 for three times. Several BC<sub>3</sub>F<sub>1</sub> individuals were selected by agronomic traits related to yield such as heading date, tiller number, plant height, panicle size, and grain size. The selection of BC<sub>3</sub>F<sub>1</sub> individuals was conducted for selecting the individuals with unique agronomic traits related to yield. A single BC<sub>3</sub>F<sub>1</sub> plant from each donor parent was continuously selfpollinated and selected for maintaining variation of these traits in every generation by the BC<sub>3</sub>F<sub>7</sub> in 2005. The backcrossed inbred lines derived from crosses between IR64 and 10 donor parents were developed although the number of backcrossed inbred lines from each donor was small. The group of backcrossed inbred lines from each donor was called a "sib group". A total of 334 INLs were developed and consisted of 36 lines from YP1 (YTH 2-38), 23 lines from YP3 (YTH 55-78), 45 lines from YP4 (YTH 79-126), 56 lines from YP 5 (YTH 169-227), 29 lines from YP6 (YTH 229-258), 21 lines from YP7 (YTH 259-280), 29 lines from YP8 (YTH 282-311), 16 lines from YP9 (YTH 312-328), 39 lines from YP10 (YTH 329-369), and 40 lines from YP 11 (YTH 127-168) (Table 2).

# 2. Phenotypic evaluation for agronomic traits

The 334 INLs were grown at the field of IRRI, Los Baños, Laguna, Philippines, in the dry seasons (DS: January to May) and the wet seasons (WS: July to November) from 2005 to 2007. A total of 117 lines which represented variation of agronomic traits in the 334 INLs were also grown at the field of IRRI in the DS and the WS in 2008. Each line was represented by more than two rows of 12 individuals. A single plant at 21-days after sowing was transplanted at 20 cm between hills and at 30 cm between rows. A total of eight agronomic traits in the 117 INLs were evaluated from 2005 to 2008. The six traits: DTH, CL, PL, LW, LL, and PN, were evaluated in 2005WS, 2006DS, 2006WS, 2007DS, 2007WS, and 2008DS. Two yield components: TSN and GW were evaluated in 2007DS, 2007WS and 2008DS.

DTH was evaluated as the number of days from sowing seeds until 50% of the panicles flowered. A single value per plant of 10 individuals which were planted

in the middle of each line were measured for CL, PL, LW, LL, PN, TSN, and GW. CL was measured from the soil surface to the neck of the tallest tiller in a plant. PL was measured from panicle neck to the panicle tip of the tallest tiller. LW and LL were measured on the second leaf under the flag leaf of the tallest tiller. PN was counted as the number of productive panicles per plant. TSN was calculated as the sum of filled and unfilled spikelets per panicle. GW was measured as the weight of 100 filled grains for each plant. The averages of agronomic traits in the 117 INLs were calculated in 2005, 2006, 2007, and 2008. The averages of agronomic traits for DS were calculated using the data of DS in 2006, 2007 and 2008. Similarly, the averages of agronomic traits for WS were calculated based on the data of WS in 2005, 2006 and 2007. The averages of TSN and GW for DS in 2008 were used as the representative data of DS and those for WS in 2007 were used as the representative data of WS.

## 3. Genotyping using SSR markers

The whole genome DNA of the 334 BC<sub>3</sub>F<sub>8</sub> plants was individually extracted from fresh leaves using the CTAB method<sup>21</sup>. DNA of these INLs was analyzed using simple sequence repeat (SSR) markers<sup>15</sup> distributed across the 12 rice chromosomes. A total of 457 SSR markers of known chromosomal position were used to survey polymorphism between IR64 and 10 donor parents. More than 200 polymorphic markers for each sib group: 247 markers for YP1-INLs, 248 for YP3-INLs, 261 for YP4-INLs, 262 for YP5-INLs, 260 for YP6-INLs, 238 for YP7-INLs, 224 for YP8-INLs, 266 for YP 9-INLs, 280 for YP10-INLs, and 276 for YP11-INLs, were used for genotyping of the INLs.

To detect the introgressed segments of donor parents, genotypes of the 334 INLs were analyzed using the polymorphic SSR markers. Firstly, the genotypes of postulated BC<sub>3</sub>F<sub>1</sub> plants were analyzed using bulked DNA of sib INLs for each donor parent. The genotypes of 10 bulked DNA from each sib group were detected using about 200 polymorphic SSR markers. Secondly, the genotypes of the 334 INLs have been individually analyzed using the SSR markers which detected introgressed segment regions in the bulked DNA.

PCR amplification was conducted using a DNA engine dyad thermal cycler (Bio-Rad). The 15 μl PCR reaction mixture contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 1.5 mM MgCl<sub>2</sub>, 200 μM dNTP, 0.2 μM primer, 1 unit of Taq polymerase (SBS Genetech, China), and 5-10 μg/ml of genomic DNA as a template. The thermal cycler was programmed for a first denaturation step of 5 min at 95 °C, followed by 35 cycles,

Table 2. List of 334 introgression lines (INLs) bred from the crosses between IR64 as a recurrent variety and 10 different donor varieties.

Entry No. in 2005WS	IR designation number	Donor parent <sup>a)</sup>	Core set	Entry No. in 2005WS	IR designation number	Donor parent	Core set
	R84633-9-5-2-2-1-4-2-2-B	YP1		YTH 79	IR84642-8-1-2-2-3-2-2-B	YP4	
	R84633-9-5-2-4-4-3-2-2-B	YP1		YTH 80	IR84642-8-1-2-6-1-2-4-3-2-2-B	YP4	
	R84633-9-9-7-2-1-3-2-3-B	YP1		YTH 82	IR84642-8-1-2-7-2-3-2-2-B	YP4	
	R84633-9-9-7-6-1-4-2-2-B	YP1		YTH 83	IR84642-8-4-3-4-4-2-4-2-6-B	YP4	X
	R84633-9-9-8-3-3-3-2-2-B	YP1	X	YTH 84	IR84642-8-4-3-11-2-2-5-2-2-B	YP4	X
	R84633-9-9-8-8-3-3-2-2-B	YP1		YTH 85	IR84642-8-4-3-5-2-2-4-2-2-B	YP4	X
	R84633-9-12-3-4-1-2-2-2-B	YP1		YTH 86	IR84642-8-4-3-10-5-2-4-5-2-B	YP4	
	R84633-9-12-3-8-1-2-2-3-B	YP1		YTH 87	IR84642-8-6-4-6-3-4-2-2-B	YP4	
	R84633-9-14-4-5-3-3-2-2-B	YP1	X	YTH 88	IR84642-8-6-6-3-4-3-4-2-2-B	YP4	X
	R84633-9-14-4-10-3-3-2-2-B	YP1		YTH 89	IR84642-8-6-6-8-3-3-2-3-B	YP4	X
	R84633-9-14-6-4-1-3-2-2-B	YP1	X	YTH 90	IR84642-8-23-4-7-3-3-2-2-B	YP4	
	R84633-9-14-6-8-4-3-2-2-B	YP1	X	YTH 91	IR84642-8-23-4-8-2-2-4-2-2-B	YP4	
	R84633-9-16-5-7-3-2-4-2-2-B	YP1		YTH 92	IR84642-8-35-10-6-2-2-4-2-2-B	YP4	X
	R84633-9-16-5-11-2-2-4-3-2-2-B	YP1	X	YTH 93	IR84642-8-36-8-7-2-2-5-2-2-B	YP4	
	R84633-9-28-3-9-2-5-2-3-B	YP1	X	YTH 94	IR84642-8-36-8-8-2-2-4-2-2-3-B	YP4	
	R84633-9-28-10-8-2-3-5-2-2-B	YP1		YTH 95	IR84642-8-36-10-2-2-2-4-2-2-3-B	YP4	
	R84633-9-50-2-3-2-3-2-2-B	YP1		YTH 96	IR84642-8-36-10-6-3-2-5-2-2-B	YP4	
	R84633-9-50-2-6-2-4-2-2-B	YP1		YTH 97	IR84642-8-49-6-11-4-3-2-3-B	YP4	
	R84633-9-50-3-6-2-2-5-B	YP1	X	YTH 98	IR84642-8-61-8-9-2-3-2-4-B	YP4	
	R84633-9-50-3-10-1-2-2-9-B	YP1		YTH 99	IR84642-8-61-8-10-4-2-4-2-2-B	YP4	X
	R84633-9-58-6-3-3-2-4-2-2-B	YP1		YTH 100	IR84642-8-61-11-4-3-2-4-2-2-4-B	YP4	
	R84633-9-58-6-6-2-2-5-2-2-B	YP1	X	YTH 102	IR84642-8-61-11-8-3-2-4-2-2-B	YP4	
YTH 25 IR	R84633-9-58-6-8-1-2-4-2-2-3-B	YP1		YTH 103	IR84642-8-68-2-3-2-2-4-2-2-B	YP4	
	R84633-9-64-7-5-1-3-2-2-B	YP1		YTH 104	IR84642-8-68-2-6-2-2-4-2-2-B	YP4	
	R84633-9-77-3-10-3-3-2-2-B	YP1		YTH 105	IR84642-8-68-2-10-3-2-4-2-2-B	YP4	X
	R84633-9-77-10-5-2-2-4-2-3-2-B	YP1		YTH 106	IR84642-8-68-11-5-2-2-4-3-2-2-B	YP4	
	R84633-9-77-10-7-1-2-4-2-2-3-B	YP1		YTH 107	IR84642-8-68-11-9-2-4-2-4-B	YP4	X
	R84633-9-92-4-4-3-3-2-5-B	YP1		YTH 108	IR84642-8-97-3-3-3-2-4-2-2-B	YP4	X
	R84633-9-92-4-10-3-3-2-2-B	YP1		YTH 109	IR84642-8-97-3-9-2-2-4-2-2-B	YP4	
	R84633-9-92-5-3-3-2-4-2-2-B	YP1		YTH 110	IR84642-8-97-8-6-3-2-4-2-2-B	YP4	
	R84633-9-92-5-2-3-2-4-2-2-B	YP1	X	YTH 111	IR84642-8-106-3-5-3-4-4-2-2-B	YP4	
	R84633-9-92-10-4-2-3-2-2-B	YP1		YTH 112	IR84642-8-106-3-9-2-3-2-4-B	YP4	X
	R84633-9-94-2-2-3-2-2-B	YP1	X	YTH 113	IR84642-8-106-3-11-3-3-2-4-B	YP4	X
	R84633-9-94-2-11-2-3-2-2-B	YP1		YTH 114	IR84642-8-106-6-2-2-2-4-1-2-2-B	YP4	X
	R84633-9-107-10-5-3-3-2-2-B	YP1		YTH 115	IR84642-8-106-6-10-2-3-2-2-B	YP4	
	R84633-9-107-10-8-1-2-5-2-2-B	YP1		YTH 116	IR84642-8-106-6-11-2-3-2-2-B	YP4	
	R84635-10-10-10-3-3-2-4-2-2-B	YP3		YTH 117	IR84642-8-106-7-4-3-3-2-3-B	YP4	
	R84635-10-10-10-9-5-3-2-2-B	YP3		YTH 118	IR84642-8-106-7-6-2-2-4-3-2-2-B	YP4	X
	R84635-10-18-7-10-4-2-2-B	YP3	X	YTH 119	IR84642-8-106-7-11-3-3-2-2-B	YP4	X
	R84635-10-20-2-4-1-2-2-B	YP3	X	YTH 120	IR84642-8-115-2-3-3-4-2-2-B	YP4	
	R84635-10-20-2-7-1-2-2-B	YP3	X	YTH 122	IR84642-8-115-2-6-2-3-2-2-B	YP4	X
	R84635-10-44-7-1-3-4-2-2-B	YP3	X	YTH 123	IR84642-8-119-3-5-2-3-2-2-B	YP4	X
	R84635-10-44-7-4-5-4-3-2-2-B	YP3		YTH 124	IR84642-8-119-3-9-2-3-2-2-B	YP4	X
	R84635-10-59-4-2-2-3-4-2-2-8-B	YP3	X	YTH 125	I884642-8-119-10-8-3-2-4-2-2-B	YP4	X
	R84635-10-59-4-7-2-2-4-2-2-14-B	YP3		YTH 126	IR84642-8-119-10-10-3-2-4-2-2-B	YP4	
	R84635-10-59-4-8-3-3-2-4-B	YP3		YTH 127	IR84643-11-11-1-7-7-2-4-2-2-B	YP11	
	R84635-10-79-9-2-2-3-2-2-B	YP3		YTH 128	IR84643-11-1-7-10-4-2-4-2-2-B	YP11	
	R84635-10-79-9-6-2-3-2-2-B	YP3	X	YTH 129	IR84643-11-1-8-7-2-3-2-2-B	YP11	
	R84635-10-89-3-1-2-2-B	YP3	X	YTH 130	IR84643-11-1-8-8-2-2-4-2-2-B	YP11	
YTH 69 IR	R84635-10-89-3-61-2-4-2-2-9-B	YP3	X	YTH 131	IR84643-11-13-8-11-2-3-2-2-B	YP11	
	R84635-10-90-2-9-3-2-4-2-2-B	YP3		YTH 132	IR84643-11-15-6-2-3-2-4-3-2-2-B	YP11	
	R84635-10-90-2-11-2-2-4-2-2-B	YP3		YTH 133	IR84643-11-15-6-5-3-2-4-3-2-2-B	YP11	X
	R84635-10-91-3-1-3-4-2-2-3-B	YP3	X	YTH 134	IR84643-11-23-8-2-2-3-2-2-B	YP11	
	R84635-10-91-5-1-3-2-2-B	YP3	X	YTH 135	IR84643-11-23-8-8-2-2-4-2-2-4-B	YP11	X
	R84635-10-99-7-4-3-6-2-2-B	YP3	X	YTH 136	IR84643-11-47-6-2-2-4-2-2-3-B	YP11	
	R84635-10-99-7-11-3-3-2-5-B	YP3		YTH 137	IR84643-11-47-6-11-2-2-4-2-2-4-B	YP11	X
	R84635-10-111-3-10-1-2-2-B	YP3		YTH 138	IR84643-11-68-9-3-2-2-4-3-2-14-B	YP11	
YTH 77 IR	R84635-10-113-11-26-3-2-2-B	YP3	X	YTH 139	IR84643-11-68-9-6-2-3-2-2-B	YP11	
	R84635-10-113-11-98-2-4-2-3-B						

Table 2. Continued.

Entry No. in 2005WS	IR designation number	Donor parent	Core set	Entry No. in 2005WS	IR designation number	Donor parent	Core set
YTH 142	IR84643-11-68-11-8-3-2-4-2-2-3-B	YP11		YTH 205	IR84636-13-78-11-3-2-2-4-2-2-B	YP5	X
YTH 143	IR84643-11-69-3-6-2-2-4-2-2-B	YP11		YTH 206	IR84636-13-78-11-8-2-5-4-2-2-B	YP5	
YTH 144	IR84643-11-69-3-9-2-3-2-2-B	YP11		YTH 207	IR84636-13-80-4-4-2-2-4-2-2-B	YP5	
YTH 145	IR84643-11-74-3-2-3-3-2-2-B	YP11		YTH 208	IR84636-13-80-4-10-2-3-2-2-B	YP5	
YTH 146	IR84643-11-81-4-4-3-3-2-4-B	YP11	X	YTH 209	IR84636-13-80-5-3-2-3-4-2-2-B	YP5	
YTH 147	IR84643-11-81-4-6-3-2-4-2-2-B	YP11		YTH 210	IR84636-13-80-5-4-2-2-4-2-3-B	YP5	X
YTH 148	IR84643-11-82-8-2-3-3-2-3-B	YP11		YTH 211	IR84636-13-80-9-9-4-4-2-2-B	YP5	
YTH 149	IR84643-11-82-8-9-3-2-4-2-2-B	YP11		YTH 212	IR84636-13-82-2-2-1-2-4-2-2-B	YP5	
YTH 150	IR84643-11-105-5-5-2-3-2-6-8-B	YP11	X	YTH 213	IR84636-13-82-2-5-2-2-4-2-2-B	YP5	X
YTH 151	IR84643-11-105-5-8-3-3-2-2-B	YP11		YTH 214	IR84636-13-82-3-2-3-2-4-2-2-B	YP5	
YTH 152	IR84643-11-105-7-2-2-3-3-3-B	YP11		YTH 215	IR84636-13-82-3-7-3-2-4-2-2-B	YP5	
YTH 153	IR84643-11-105-7-9-2-3-2-2-B	YP11	X	YTH 216	IR84636-13-82-12-6-3-2-4-2-2-B	YP5	
YTH 154	IR84643-11-105-8-3-2-2-4-2-3-3-B	YP11		YTH 217	IR84636-13-82-12-8-3-2-4-2-2-3-B	YP5	
YTH 155	IR84643-11-105-8-7-2-2-4-3-2-3-B	YP11	X	YTH 218	IR84636-13-89-11-3-2-2-4-2-2-B	YP5	X
YTH 156	IR84643-11-105-11-6-1-2-4-2-2-3-B	YP11		YTH 219	IR84636-13-89-11-7-2-2-4-2-3-B	YP5	
YTH 157	IR84643-11-105-11-11-3-2-4-2-2-B	YP11	X	YTH 220	IR84636-13-90-2-2-2-4-2-2-4-B	YP5	
YTH 158	IR84643-11-106-3-3-2-1-2-3-B	YP11		YTH 222	IR84636-13-90-2-9-2-2-4-2-2-8-B	YP5	X
YTH 159	IR84643-11-106-3-10-2-2-2-B	YP11		YTH 223	IR84636-13-90-2-10-2-2-4-2-2-5-B	YP5	
YTH 160	IR84643-11-106-4-6-2-1-3-4-B	YP11	X	YTH 224	IR84636-13-91-3-6-1-2-4-2-2-4-B	YP5	
YTH 162	IR84643-11-106-4-8-2-8-4-2-2-B	YP11	X	YTH 225	IR84636-13-91-3-10-1-2-4-2-2-10-B	YP5	X
YTH 163	IR84643-11-114-5-7-2-6-2-2-B	YP11		YTH 226	IR84636-13-91-8-4-1-2-4-2-5-B	YP5	X
YTH 164	IR84643-11-114-5-9-2-3-4-2-2-B	YP11		YTH 227	IR84636-13-91-8-8-1-2-4-2-2-B	YP5	
YTH 165	IR84643-11-114-6-2-2-3-2-2-B	YP11	X	YTH 229	IR84637-4-7-8-2-2-3-4-3-2-2-B	YP6	
YTH 166	IR84643-11-114-6-3-2-4-4-3-2-2-B	YP11		YTH 230	IR84637-4-7-10-3-2-2-4-2-2-B	YP6	
YTH 167	IR84643-11-115-4-2-3-2-5-2-2-B	YP11		YTH 231	IR84637-4-7-10-8-3-3-4-4-2-2-B	YP6	
YTH 168	IR84643-11-115-4-5-3-2-4-2-2-B	YP11		YTH 232	IR84637-4-7-10-9-2-2-4-2-2-B	YP6	
YTH 169	IR84636-13-2-2-3-2-2-4-3-2-2-B	YP5		YTH 233	IR84637-4-29-5-2-3-1-2-2-B	YP6	
YTH 170	IR84636-13-2-2-9-2-2-4-2-2-B	YP5		YTH 234	IR84637-4-29-5-7-2-2-4-2-2-4-B	YP6	
YTH 171	IR84636-13-2-3-2-2-4-2-2-B	YP5		YTH 235	IR84637-4-63-8-3-1-2-5-2-2-B	YP6	
YTH 172	IR84636-13-2-3-5-2-3-3-6-B	YP5		YTH 236	IR84637-4-63-8-8-2-3-2-2-B	YP6	
YTH 173	IR84636-13-5-2-2-3-2-3-B	YP5		YTH 237	IR84637-4-63-8-11-2-2-4-2-2-B	YP6	
YTH 174	IR84636-13-5-2-9-2-2-4-2-2-B	YP5	X	YTH 238	IR84637-4-63-11-4-2-2-4-2-2-B	YP6	
YTH 175	IR84636-13-5-7-2-2-3-2-3-B	YP5		YTH 239	IR84637-4-63-11-10-2-3-2-2-B	YP6	
YTH 176	IR84636-13-5-7-7-2-3-2-2-B	YP5		YTH 240	IR84637-4-69-3-2-3-3-2-3-B	YP6	
YTH 177	IR84636-13-8-5-4-2-3-2-2-B	YP5		YTH 242	IR84637-4-69-3-5-1-3-4-2-2-B	YP6	
YTH 178	IR84636-13-8-5-8-2-2-4-2-2-3-B	YP5		YTH 243	IR84637-4-69-7-2-2-4-2-2-B	YP6	X
YTH 179	IR84636-13-8-6-5-2-2-4-2-2-8-B	YP5		YTH 244	IR84637-4-69-710-1-2-4-2-2-B	YP6	
YTH 180	IR84636-13-8-6-7-2-2-4-2-2-B	YP5	X	YTH 245	IR84b37-4-69-9-6-1-4-2-2-B	YP6	X
YTH 182	IR84636-13-12-2-2-2-4-2-2-B	YP5		YTH 246	IR84637-4-69-9-10-2-4-4-2-2-B	YP6	X
YTH 183	IR84636-13-12-2-6-3-3-2-2-B	YP5	X	YTH 247	IR84637-4-69-12-3-3-3-2-3-B	YP6	X
YTH 184	IR84636-13-12-3-5-2-2-4-2-3-3-B	YP5		YTH 248	IR84637-4-69-12-10-3-2-4-4-2-2-B	YP6	
YTH 185	IR84636-13-12-3-9-2-2-4-2-2-B	YP5		YTH 249	IR84637-4-72-9-4-1-2-4-2-2-B	YP6	
YTH 186	IR84636-13-53-5-7-2-2-4-2-2-B	YP5	X	YTH 250	IR84637-4-72-9-5-2-2-4-2-2-B	YP6	
YTH 187	IR84636-13-55-5-8-2-2-4-2-2-B	YP5	X	YTH 251	IR84637-4-72-9-10-1-2-4-2-2-B	YP6	
YTH 188	IR84636-13-55-8-5-2-3-2-7-B	YP5		YTH 252	IR84637-4-74-2-2-3-2-2-B	YP6	X
YTH 189	IR84636-13-55-8-11-2-2-4-2-3-B	YP5		YTH 253	IR84637-4-74-2-7-2-3-2-3-B	YP6	
YTH 190	IR84636-13-59-6-3-2-3-4-5-2-2-B	YP5		YTH 254	IR84637-4-89-2-9-2-3-2-2-B	YP6	X
YTH 191	IR84636-13-59-6-4-2-2-4-2-2-B	YP5	X	YTH 255	IR84637-4-106-7-11-2-2-2-B	YP6	X
YTH 192	IR84636-13-64-2-4-2-2-4-B	YP5		YTH 256	IR84637-4-113-6-6-2-Z-7-B	YP6	
YTH 193	IR84636-13-64-2-5-2-2-4-2-2-7-B	YP5		YTH 257	IR84637-4-113-6-10-2-3-2-14-B	YP6	
YTH 194	IR84636-13-71-7-3-2-3-B	YP5		YTH 258	IR84637-4-113-11-5-2-3-2-2-B	YP6	
YTH 195	IR84636-13-71-7-5-2-2-4-2-2-B	YP5		YTH 259	IR84638-11-6-3-2-1-1-2-2-B	YP7	X
YTH 196	IR84636-13-71-9-2-3-2-4-2-2-B	YP5	X	YTH 260	IR84638-11-6-3-7-1-2-5-4-2-2-B	YP7	X
YTH 197	IR84636-13-71-9-10-3-4-2-2-B	YP5	X	YTH 262	IR84638-11-11-9-2-1-2-4-2-2-B	YP7	X
YTH 198	IR84636-13-71-10-2-2-2-4-3-2-14-B	YP5	X	YTH 263	IR84638-11-11-9-7-1-2-4-2-2-B	YP7	21
YTH 199	IR84636-13-71-11-3-2-2-4-2-2-B	YP5	X	YTH 264	IR84638-11-11-9-9-1-2-5-2-2-B	YP7	X
YTH 200	IR84636-13-71-11-3-2-2-4-2-2-B	YP5	X	YTH 265	IR84638-11-17-10-4-1-2-4-2-2-B	YP7	21
YTH 200	IR84636-13-71-11-4-2-2-4-2-2-B	YP5	1	YTH 266	IR84638-11-17-10-9-1-2-4-2-2-B	YP7	X
YTH 203	IR84636-13-78-9-4-2-2-4-2-2-B	YP5	X	YTH 267	IR84638-11-60-6-3-1-2-4-2-2-B	YP7	11
YTH 204	IR84636-13-78-9-5-2-2-4-2-2-5-B	YP5	21	YTH 268	IR84638-11-60-6-10-1-2-4-2-2-B	YP7	
1 111 204	11XU+UJU-1J-70-7-J-4-4-4-4-5-D	113		1 111 200	110+030-11-00-0-10-1-2-4-2-2-B	11'/	

Table 2. Continued.

Donor Core

set

X

X

X

X

X

X

X

X X

X

X

Entry No.	IR designation number	Donor	Core	Entry No.	IR designation number	Donor
in 2005WS		parent	set	in 2005WS		parent
YTH 269	IR84638-11-66-8-3-1-2-4-2-2-B	YP7	X	YTH 329	IR84641-2-15-2-3-2-2-4-2-2-B	YP10
YTH 270	IR84638-11-66-8-4-1-2-4-2-2-B	YP7	X	YTH 330	IR84641-2-22-2-10-2-2-4-3-2-2-B	YP10
YTH 271	IR84638-11-66-8-7-1-2-4-4-2-2-B	YP7	X	YTH 331	IR84641-2-61-I1-7-2-2-4-2-2-B	YP10
YTH 272	IR84638-11-85-2-5-1-3-2-2-B	YP7	X	YTH 332	IR84641-2-71-5-11-2-3-2-2-B	YP10
YTH 273	IR84638-11-85-2-7-1-2-4-3-2-2-B	YP7		YTH 333	IR84641-2-76-2-9-1-2-4-2-2-B	YP10
YTH 274	IR84638-11-101-5-4-1-4-2-2-B	YP7		YTH 334	IR84641-2-76-4-2-2-4-4-2-2-B	YP10
YTH 275	IR84638-11-101-5-9-3-2-4-2-2-B	YP7		YTH 335	IR84641-2-76-4-4-2-3-2-2-B	YP10
YTH 276	IR84638-11-101-5-10-4-2-4-2-2-B	YP7	**	YTH 336	IR84641-6-5-2-2-3-2-2-B	YP10
YTH 277	IR84638-11-101-9-6-1-2-4-3-2-2-B	YP7	X	YTH 337	IR84641-6-5-2-3-2-2-4-2-2-B	YP10
YTH 278	IR84638-11-101-9-8-1-2-4-2-2-B	YP7	v	YTH 338	IR84641-6-5-2-6-1-2-4-2-2-B	YP10
YTH 279	IR84638-11-101-9-9-3-2-4-2-2-B	YP7	X	YTH 339	IR84641-6-12-6-2-3-3-2-2-B	YP10
YTH 280	IR84638-11-118-8-10-3-2-4-2-2-B	YP7 YP8		YTH 340	IR84641-6-12-6-6-2-3-2-2-B	YP10 YP10
YTH 282 YTH 283	IR84639-7-12-4-3-1-2-4-2-2-B IR84639-7-12-4-3-1-2-4-2-2-B	YP8		YTH 342 YTH 343	IR84641-6-12-8-2-2-4-2-2-B	YP10
		YP8	X		IR84641-6-12-8-10-1-2-4-2-2-B	YP10
YTH 284 YTH 285	IR84639-7-21-9-3-3-2-4-2-2-2-B	YP8	Λ	YTH 344 YTH 345	IR84641-6-17-5-7-2-2-4-2-2-B	YP10 YP10
YTH 286	IR84639-7-21-9-8-3-3-2-5-B IR84639-7-21-9-9-2-2-4-2-2-B	YP8		YTH 346	IR84641-6-23-11-3-1-2-4-2-2-B IR84641-6-23-11-10-2-2-4-2-2-B	YP10 YP10
YTH 287	IR84639-7-28-5-4-2-2-4-3-2-2-B	YP8	X	YTH 347	IR84641-6-30-5-11-2-3-2-3-B	YP10
YTH 288	IR84639-7-28-5-5-2-2-3-2-2-14-B	YP8	X	YTH 348	IR84641-6-39-3-3-2-2-4-2-2-3-B	YP10
YTH 289	IR84639-7-29-3-8-3-2-4-2-2-3-B	YP8	X	YTH 349	IR84641-6-39-3-9-1-3-2-2-B	YP10
YTH 290	IR84639-7-29-3-10-2-2-3-B	YP8	Λ	YTH 350	IR84641-6-46-10-2-2-3-2-2-B	YP10
YTH 291	IR84639-7-65-1-5-2-2-4-2-3-B	YP8		YTH 351	IR84641-6-63-2-3-1-3-2-3-B	YP10
YTH 292	IR84639-7-65-1-11-3-2-4-2-2-7-B	YP8	X	YTH 352	IR84641-6-63-2-9-4-3-2-2-B	YP10
YTH 293	IR84639-7-72-5-2-3-2-4-2-2-B	YP8	Λ	YTH 353	IR84641-6-63-2-11-3-3-2-2-B	YP10
YTH 294	IR84639-7-72-5-9-2-3-4-2-2-3-B	YP8		YTH 354	IR84641-6-66-3-2-1-2-2-B	YP10
YTH 295	IR84639-7-72-8-3-1-3-2-2-B	YP8		YTH 355	IR84641-6-66-3-11-1-3-2-2-B	YP10
YTH 296	IR84639-7-72-8-4-2-2-4-2-2-B	YP8		YTH 356	IR84641-6-84-8-2-3-3-2-2-B	YP10
YTH 297	IR84639-7-76-3-2-1-2-4-2-2-B	YP8	X	YTH 357	IR84641-6-84-8-3-3-3-2-2-B	YP10
YTH 298	IR84639-7-76-3-5-1-2-4-3-2-2-B	YP8	21	YTH 358	IR84641-6-85-8-11-5-3-2-3-B	YP10
YTH 299	IR84639-7-76-8-3-3-2-4-2-2-B	YP8		YTH 359	IR84641-6-87-2-7-1-3-2-2-B	YP10
YTH 300	IR84639-7-76-8-6-3-3-2-2-B	YP8		YTH 360	IR84641-6-87-2-10-1-2-4-2-2-B	YP10
YTH 302	IR84639-7-88-5-6-3-3-2-3-B	YP8	X	YTH 362	IR84641-6-96-3-3-2-2-2-B	YP10
YTH 303	IR84639-7-88-5-11-5-2-5-3-2-2-B	YP8	X	YTH 363	IR84641-6-111-5-4-2-2-2-B	YP10
YTH 304	IR84639-7-97-6-6-2-2-4-2-2-B	YP8	X	YTH 364	IR84641-6-111-5-9-1-3-2-2-B	YP10
YTH 305	IR84639-7-97-7-4-3-2-4-2-2-3-B	YP8		YTH 365	IR84641-6-111-5-10-3-3-2-2-B	YP10
YTH 306	IR84639-7-110-2-3-2-2-4-2-2-B	YP8	X	YTH 366	IR84641-6-116-2-8-3-3-2-2-B	YP10
YTH 307	IR84639-7-110-2-7-1-4-2-4-B	YP8		YTH 367	IR84641-6-116-2-10-1-3-2-2-B	YP10
YTH 308	IR84639-7-110-3-4-2-3-4-2-2-B	YP8		YTH 368	IR84641-6-119-9-2-2-4-4-B	YP10
YTH 309	IR84639-7-110-3-7-1-3-2-2-B	YP8		YTH 369	IR84641-6-119-9-7-2-3-2-2-B	YP10
YTH 310	IR84639-7-115-4-5-2-3-2-2-B	YP8				
YTH 311	IR84639-7-115-4-6-3-3-2-2-B	YP8				
YTH 312	IR84640-11-3-1-5-2-2-4-2-2-B	YP9				
YTH 313	IR84640-11-3-1-6-2-3-2-5-B	YP9				
YTH 314	IR84640-11-3-6-7-2-2-4-2-5-B	YP9				
YTH 315	IR84640-11-3-6-8-1-3-2-3-B	YP9				
YTH 316	IR84640-11-10-7-4-2-2-4-2-3-2-3-B	YP9				
YTH 317	IR84640-11-10-7-7-2-2-4-2-2-B	YP9				
YTH 318	IR84640-11-12-7-4-2-2-4-2-3-2-3-B	YP9	X			
YTH 319	IR84640-11-14-10-3-2-2-4-2-2-B	YP9	X			
YTH 320	IR84640-11-14-10-9-2-2-4-2-2-B	YP9				
YTH 322	IR84640-11-27-1-5-3-3-2-2-B	YP9				
YTH 323	IR84640-11-27-1-9-3-2-4-2-2-B	YP9	X			
YTH 324	IR84640-11-37-1-6-3-3-4-2-2-B	YP9	X			
YTH 325	IR84640-11-110-6-2-2-2-4-2-2-4-B	YP9	X			
YTH 326	IR84640-11-110-6-4-2-2-4-2-2-3-B	YP9	X			
YTH 327	IR84640-11-110-7-2-2-2-2-B	YP9				
YTH 328	IR84640-11-110-7-9-2-2-5-3-2-2-B	YP9	X			

a) see Table 1

each of 95 °C for 30 s, 55 °C for 30 s, and 72 °C for 30 s. The SSR products were resolved in 4.0% agarose gel by electrophoresis at 250 V for 1 h in  $0.5 \times TBE$  buffer. The gels were stained with ethidium bromide and photographed under ultraviolet light.

#### Results

# 1. Characterization of INLs in agronomic traits

The 334 INLs for agronomic traits from 10 donor varieties were developed by backcrossed breeding and used for association analysis between introgressed segments and agronomic traits (Table 2). The eight agronomic traits: DTH, CL, LW, LL, PL, PN, TSN, and GW in the 334 INLs were evaluated from 2005 to 2007. Based on the data obtained in WS and DS, a total of 117 INLs were selected as a 'core set' for further detailed characterization. The unique INLs that showed the top 30 and the least 30 values on six agronomic traits: DTH, CL, LW, LL, PL, and PN in 2005WS, 2006DS, 2006WS, and 2007DS were selected. Some unique INLs showed a similar phenotype and genotype to each other. In this case, a single line was selected among these INLs to avoid duplication. The core set consisted of 10 lines from YP1, 12 lines from YP3, 19 lines from YP4, 19 lines from YP5, seven lines from YP6, 11 lines from YP7, 10 lines from YP8, seven lines from YP9, 11 lines from YP10, and 11 lines from YP11 (Tables 1 and 2). The selected 117 INLs covered the variations of agronomic traits: DTH, CL, LW, LL, PL, PN, TSN, and GW, observed in the developed 334 INLs (Fig. 1).

On the selected 117 lines, eight agronomic traits: DTH, CL, PL, LW, LL, PN, TSN, and GW, were evaluated from 2005 to 2008 (Table 3). Some of the INLs among the same donor parents showed unique agronomic traits compared with IR64. For DTH, several INLs from YP1, YP7 and YP10 were shorter than IR64, while several lines from YP3, YP5, YP6, and YP8 were longer than IR64. For CL, several INLs from YP1, YP5, YP7, and YP10 were shorter than IR64, while several INLs from YP3, YP4, YP8, YP9, and YP11 were longer. For PL, several INLs from YP1, YP7 and YP10 were shorter than IR64, while several INLs from YP3 and YP 4 were longer. For LW, several INLs from YP1, YP5 and YP10 had a narrow leaf compared with IR64, while several INLs from YP3, YP4, YP8, YP9, and YP11 had a wider leaf. LL of several INLs from YP1, YP5 and YP 10 were shorter than that of IR64, while that of several INLs from YP3, YP4, YP8, YP9, and YP11 were longer. PN of several INLs from YP7 were higher than that of IR64, while that of several INLs from YP3 and YP4 were lower. TSN of several INLs from YP1, YP7 and

YP10 were lower than that of IR64, while that of several INLs from YP3, YP4, YP5, YP7, YP8, YP9, and YP 11 were higher. For GW, several INLs from YP1, YP5 and YP10 had heavier grain than IR64. The 117 INLs which showed variations in agronomic traits of DTH, CL, PL, LL, LW, PN, TSN, and GW, had different characteristics depending on donor varieties.

# 2. Determination of genotypes in the 334 INLs

The genotypes of the 334 INLs were analyzed using the polymorphic SSR markers (those of the selected 117 INLs are shown in Fig. 2). The common regions of introgressed segment for each donor parent were found on chromosomes 1, 2, 4, 5, and 6 among more than four sib groups. Twenty-nine lines out of them from YP 4, YP5 and YP11, had the introgressed segments at the region around 130 to 140 cM on the long arm of chromosome 1. Forty-two lines from YP1, YP5, YP6, YP8, YP9, and YP10 had the introgressed segments at from 0 to 10 cM on chromosome 2. Forty-five lines from YP1, YP4, YP5, YP8, YP9, and YP11 had the introgressed segments at from 110 to 120cM on chromosome 4. Thirty-five lines from YP1, YP3, YP5, YP9, YP10, and YP11 had the introgressed segments at from 40 to 60 cM on chromosome 5. Twenty-six lines from YP5, YP6, YP7, and YP10 had the introgressed segments at from 80 to 90 cM on chromosome 6.

# 3. Comparisons of DTH, TSN and GW between the INLs and IR64

Association analysis between genotype and agronomic traits in 334 INLs was conducted in a previous study and 54 associated regions for agronomic traits in nine sib groups were detected by analysis of variation<sup>2</sup>. Several associated regions for DTH, GW and TSN were located on chromosomes 1, 4, 5, 6, 8, and 12 (Fig. 3). Representative INLs showed significant difference in these traits with IR64 in 2007 WS and 2008 DS (Fig. 4). Most of these INLs had associated regions for DTH, GW and TSN, while several other lines didn't have associated regions for DTH, GW and TSN. DTH of two INLs in DS were shorter than that of IR64: by 10 days in YTH13 (derived from YP1) and by 11 days in YTH 259 (YP7) (Fig. 4A). DTH of two INLs in DS were longer than that of IR64: by 22 days longer in YTH59 (YP3) and by eight days longer in YTH246 (YP6). Three INLs for DTH had associated regions: YTH259 with YP7-DTH12 for short DTH, YTH13 with YP1-DTH8 for short DTH and YTH59 with YP3-DTH6 for long DTH. The name for an associated region, for example, YP7-DTH12, represented the donor parent YP7, followed by the trait DTH and chromosome number 12.

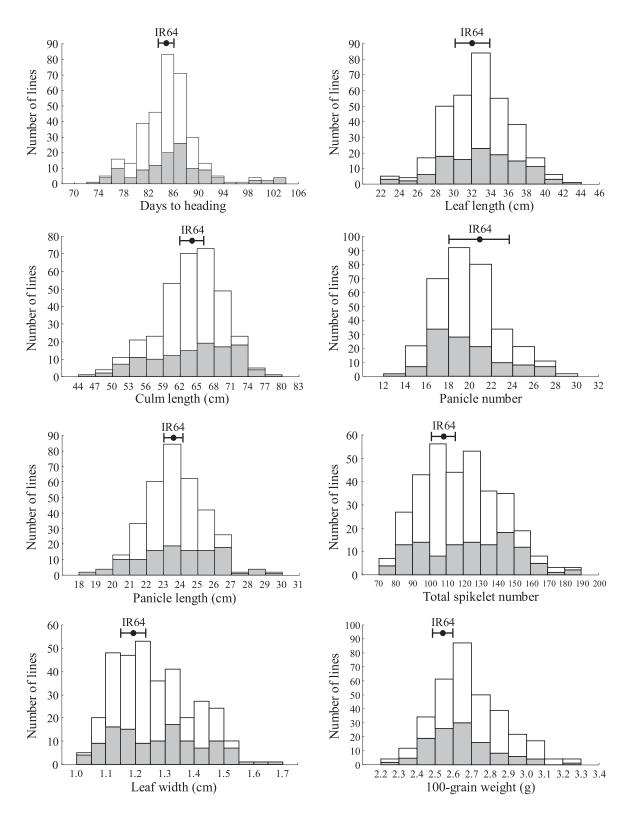


Fig. 1. Frequency distribution of eight agronomic traits: days to heading, culm length, panicle length, leaf width, leaf length, panicle number, total spikelet number per panicle, and 100-grain weight in 334 introgression lines at dry season

Gray area indicates 117 introgression lines, while white area indicates the remaining 217 lines in each trait. Error bar under IR64 showed standard deviation of IR64.

Table 3. Variation in agronomic traits of 117 introgression lines bred from the crosses between IR64 as a recurrent variety and 10 different donor varieties.

20053310						Ave	rage of									
2005WS Entry No.	Donor variety <sup>a)</sup>	DTH	(day)	CL(cm)	PI	L(cm)		(cm)		(cm)	P		TS	N	GV	V(g)
	variety	DS	WS	DS WS			DS	WS	DS	WS	DS	WS	DS	WS	DS	WS
IR64 YP1		86 104	90	63.5 64. 74.1 70.			1.2	1.2	34.4 40.2	33.0 39.9	21.0	18.2	108.8 154.6	104.7 142.2	2.6	2.4 3.7
YTH 6	YP1	78	93 88	54.0 68.			1.9	1.3	28.2	35.4	22.1	10.8 19.6	84.7	92.0	2.8	2.9
YTH 10	YP1	79	83	57.7 66.			1.1	1.2	32.5	37.3	22.6	19.4	84.7	83.4	2.7	2.5
YTH 12	YP1	76	80	57.9 66.			1.1	1.1	29.1	34.2	25.8	19.8	69.7	68.6	2.7	2.5
YTH 13	YP1	76	82	59.0 68.	7 20.3		1.1	1.1	29.2	34.3	24.5	19.0	69.8	75.8	2.7	2.6
YTH 15	YP1	84	91	69.2 76.	5 23.5	5 23.9	1.2	1.2	33.1	37.2	22.4	17.2	95.0	82.0	2.7	2.6
YTH 16	YPI	77	81	59.1 64.			1.1	1.2	30.0	36.1	21.2	19.3	87.6	89.2	2.6	2.5
YTH 20	YP1	77	82	51.9 64.			1.2	1.2	28.7	34.6	25.9	19.7	71.7	78.1	2.9	3.2
YTH 24	YP1	83	88	61.3 74.			1.1	1.2	29.8	33.6	23.4	19.0	83.8	82.2	2.8	2.9
YTH 33 YTH 35	YP1 YP1	81	89 83	60.3 72. 55.5 67.			1.0	1.2 1.3	32.5 31.7	39.0 36.5	20.9 20.0	17.3 16.8	91.5 86.2	88.6 98.7	3.0 3.0	3.0 2.9
YP3	111	77 104	96	61.4 62.			1.2	2.1	37.8	40.7	10.9	7.0	207.2	252.9	2.5	2.3
YTH 57	YP3	93	98	66.1 74.			1.3	1.4	35.4	41.0	17.8	15.2	146.0		2.5	2.5
YTH 58	YP3	106	125	66.3 78.			1.4	1.4	41.7	48.1	17.3	14.5	156.2		2.3	2.5
YTH 59	YP3	108	125	65.9 76.	9 29.3	3 29.7	1.4	1.4	43.5	47.8	152	14.4	158.4	122.8	2.3	2.4
YTH 60	YP3	105	116	69.8 82.	3 26.4		1.3	1.3	36.7	44.0	18.0	15.5	125.8	115.9	2.6	2.5
YTH 63	YP3	91	97	65.8 78.			1.4	1.4	36.0	43.9	17.7	14.7		142.1	2.6	2.6
YTH 67	YP3	89	94	67.7 76.			1.4	1.4	35.1	39.2	17.2	13.7	148.2		2.6	2.5
YTH 68	YP3	107	118	69.1 77.			1.4	1.4	40.2	49.0	16.6	13.7		136.3	2.4	2.5
YTH 69 YTH 72	YP3 YP3	103 105	114 120	72.9 81. 66.0 79.			1.3 1.4	1.4 1.4	38.1 38.4	47.6 48.4	16.8 18.5	13.7 16.6	153.5 150.8	130.5	2.6 2.4	2.4 2.5
YTH 73	YP3	103	120	66.8 79.			1.4	1.4	39.9	47.3	18.0	14.4		131.3	2.5	2.5
YTH 74	YP3	92	97	68.9 78.			1.3	1.3	36.7	40.2	19.2	16.7	143.5		2.6	2.6
YTH 77	YP3	100	115	69.9 82.			1.2	1.3	36.4	44.9	18.0	16.4		132.4	2.4	2.4
YP4		84	90	78.8 78.	7 23.8	3 25.2	1.5	1.6	39.7	40.7	10.3	8.6	180.5	210.9	2.6	2.7
YTH 83	YP4	90	92	74.4 77.			1.5	1.5	37.7	46.5	14.8	14.2	199.8	202.0	2.3	2.2
YTH 84	YP4	89	91	74.2 75.			1.5	1.5	40.4	44.9	17.3	14.4	176.5		2.4	2.2
YTH 85	YP4	89	90	69.7 77.			1.3	1.3	36.8	39.4	18.0	16.9		123.1	2.6	2.7
YTH 88 YTH 89	YP4 YP4	89 88	92 92	74.5 76. 73.8 77.			1.5 1.4	1.4 1.4	40.4 41.4	44.2 43.6	18.0 17.6	13.7 13.4	177.5 155.2	183.2	2.4 2.5	2.3 2.4
YTH 92	YP4	87	90	74.8 80.			1.4	1.4	37.4	41.2	19.0	16.5		122.9	2.6	2.6
YTH 99	YP4	86	89	73.1 80.			1.3	1.5	36.9	41.3	19.2	16.6	161.5		2.4	2.4
YTH 105	YP4	87	93	69.6 76.			1.5	1.5	37.2	43.3	17.0	14.5		152.9	2.4	2.5
YTH 107	YP4	89	92	73.9 75.	5 25.6	5 25.5	1.5	1.5	39.0	45.2	14.8	13.7	159.3	187.7	2.4	2.4
YTH 108	YP4	89	92	69.1 73.	25.8	3 26.2	1.3	1.4	36.4	42.6	17.8	17.7	147.4	133.4	2.6	2.5
YTH 112	YP4	88	91	75.3 83.			1.4	1.5	37.1	44.8	16.6	16.7		140.5	2.5	2.5
YTH 113	YP4	89	92	75.9 84.			1.4	1.5	38.4	44.5	17.7	15.6	164.8		2.5	2.6
YTH 114	YP4	87	92	74.0 82.			1.4	1.5	39.3	46.2	17.0	16.1	173.9	175.2	2.5	2.5
YTH 118 YTH 119	YP4 YP4	87 87	90 90	73.7 75. 71.5 74.			1.4 1.5	1.5 1.5	39.3 40.9	44.5 43.9	18.8 16.9	15.3 14.6	160.6 157.0	169.0	2.5 2.4	2.5 2.4
YTH 122	YP4	86	91	74.0 78.			1.5	1.6	39.9	47.7	16.7	14.1	175.2		2.4	2.4
YTH 123	YP4	88	92	73.4 77.			1.3	1.4	36.1	42.6	17.7	17.2	137.8		2.8	2.7
YTH 124	YP4	90	93	75.4 81.				1.4	37.2	43.7		15.7	148.9		2.4	2.6
YTH 125	YP4	86	91	74.0 81.	26.	7 28.4	1.3	1.4		44.2		15.9	136.6		2.6	2.6
YP5		93	91	70.9 69.			1.4	1.4	38.4		13.5	9.8	150.7		2.8	2.8
YTH 174	YP5	90	91	55.7 60.		22.6	1.1	1.2	23.9	28.7		19.9	96.7	95.2	2.6	2.5
YTH 180 YTH 183	YP5	93	93	59.4 59.			1.1	1.2	25.9	31.4	23.2		103.5		2.4	2.4
YTH 186	YP5 YP5	84 92	89 93	66.4 77. 78.3 86.			1.2 1.5	1.4 1.5	34.1	40.7 38.1	19.0	18.7	131.2 131.8		2.7 2.6	2.9 2.5
YTH 187	YP5	90	92	68.5 73.			1.4	1.4	32.1	36.9	17.9		130.8		3.0	2.5
YTH 191	YP5	87	91	75.3 85.			1.5	1.6	40.4			17.2	158.1		2.4	2.5
YTH 196	YP5	89	91	59.8 57.			1.4	1.4		34.1	21.3	22.7	120.9		2.7	2.7
YTH 197	YP5	86	90	47.8 48.	5 22.2	2 23.8	1.1	1.1	27.6	31.3	26.0	25.4	89.5	84.7	2.6	2.7
YTH 198	YP5	87	89	49.5 52.			1.1	1.2	24.9	29.1	25.9		97.7	82.4	2.7	2.7
YTH 199	YP5	89	93	67.7 76.			1.4	1.4		42.8	19.7		155.6		2.8	2.8
YTH 200	YP5	82	88	55.5 65.			1.0	1.1		34.6		18.2	122.2		2.8	2.7
YTH 203	YP5	83	88	57.2 63.			1.1	1.2	29.6	35.6		19.8	119.6		2.8	2.6
YTH 205 YTH 210	YP5 YP5	91 85	94 87	55.7 55. 53.3 58.			1.0 1.1	1.1 1.2	28.3 29.9	31.0 32.8	20.9 27.8	22.0 22.1	122.2 98.2	90.2	2.6 2.2	2.3 2.2
YTH 213	YP5	83	85	60.9 69.		25.2	1.1	1.6	32.9	38.4		15.4	107.6		2.6	2.6
YTH 218	YP5	89	90	58.1 63.			1.1	1.1	24.3	28.4	23.3	21.8	122.2		2.4	2.3
YTH 222	YP5	92	93	53.5 57.			1.3	1.4		39.8		17.7	149.9		2.4	2.4
YTH 225	YP5	85	88	58.9 62.		24.2	1.2	1.2		33.0		19.6	101.2		2.7	2.7
YTH 226	YP5	82	85	56.0 61.		23.6	1.1	1.3		32.6	21.0		86.4	88.8	2.6	2.7

Table 3. Continued.

		Average of agronomic traits in each INL															
2005WS	Donor	DTH(day)		CL(c	m)	PL(		rage of a			cm)		N	TS	SN	GW	/(g)
Entry No.	variety <sup>a)</sup>	DS	WS		WS	DS	WS	DS	WS	DS	WS	DS	WS	DS	WS	DS	WS
YP6		99	98	80.8	79.1	28.6	29.4	2.1	2.1	43.8	44.1	11.2	8.3	172.0	152.3	3.0	3.0
YTH 243	YP6	88	92		73.7	23.5	24.7	1.3	1.3	33.8	35.9	19.2	16.9	115.4	103.1	2.6	2.6
YTH 245	YP6	93	98		79.6	24.4	25.8	1.3	1.3	31.8	35.5	18.9	16.7		113.8	2.7	2.6
YTH 246	YP6	94	99		80.8	24.8	25.6	1.3	1.3	33.0	36.9	20.7	16.9	125.5	110.1	2.7	2.6
YTH 247 YTH 252	YP6 YP6	95 92	99 96		77.9 67.2	23.7 23.6	24.5 24.6	1.4 1.3	1.3 1.4	29.8 29.4	35.7 33.2	20.0 19.6	17.0 17.4	118.4 95.8	110.2 99.2	2.6 2.6	2.5 2.6
YTE 254	YP6	86	89		70.8	24.0	24.2	1.3	1.4	34.4	36.0	22.1	18.8	108.6	92.8	2.7	2.6
YTH 255	YP6	89	94		68.2	24.7	26.7	1.4	1.3	31.3	34.7	19.6	16.8	119.8	107.0	2.6	2.5
YP7		80	78		58.9	20.1	20.0	1.0	0.9	33.6	33.6	19.3	12.0	123.6	103.7	3.2	3.2
YTH 259	YP7	75	79	54.5	60.5	18.9	20.7	1.1	1.1	30.3	36.6	30.0	25.1	73.7	104.4	2.7	2.8
YTH 260	YP7	78	80		60.4	18.9	19.4	1.1	1.1	30.6	34.8	28.4	27.1	67.9	65.5	2.7	2.7
YTH 262	YP7	76	79		58.6	20.0	20.7	1.2	1.2	30.4	38.7	28.9	22.0	67.0	60.2	2.7	2.7
YTH 264	YP7	76 70	80		59.8	20.8	21.0	1.2	1.2	29.6	36.6	27.7	23.0	69.1	66.1	2.7	2.8
YTH 266 YTH 269	YP7 YP7	79 83	80 84		66.1 64.5	21.7 20.8	21.8 21.5	1.1 1.3	1.2 1.3	32.7 31.7	36.5 35.8	24.2 27.0	19.2 21.6	106.1 98.3	93.7 88.1	2.5 2.4	2.6 2.4
YTH 270	YP7	84	86		67.3	23.3	23.5	1.3	1.3	34.7	38.0	20.0	16.9	154.6	126.8	2.4	2.4
YTH 271	YP7	85	87		70.9	23.6	24.1	1.3	1.3	34.4	36.5	20.9	16.4	148.5	127.2	2.4	2.5
YTH 272	YP7	80	82		61.8	20.0	19.4	1.2	1.2	31.4	32.5	28.6	25.9	74.5	70.3	2.5	2.5
YTH 277	YP7	76	82	53.9	59.0	19.3	20.0	1.1	1.1	29.3	35.3	25.4	21.0	83.0	78.3	2.6	2.5
YTH 279	YP7	78	81	56.6	62.3	20.5	20.5	1.1	1.1	32.9	35.1	24.7	21.3	103.1	88.2	2.5	2.5
YP8		102	98		70.2	22.0	20.6	1.6	1.5	39.1	39.9	11.7	11.9	190.1	149.7	2.8	2.6
YTH 284	YP8	86	89		66.2	24.0	24.1	1.4	1.4	38.3	39.6	23.2	19.6	150.5	121.5	2.3	2.3
YTH 287	YP8	89	91		76.7	24.0	23.8	1.4	1.4	38.4	42.8	19.3	17.1	175.3	161.5	2.5	2.5
YTH 288 YTH 289	YP8 YP8	93 87	94 88		83.5 64.4	25.8 24.2	26.4 23.4	1.4 1.2	1.4 1.2	34.9	38.5 35.4	18.9 24.2	15.8 21.0	189.5	176.7 97.5	2.5 2.5	2.5 2.4
YTH 292	YP8	84	85		70.7	24.2	24.7	1.1	1.2	34.3 33.5	37.5	20.3	16.8	126.1 124.3	124.4	2.5	2.4
YTH 297	YP8	81	86		65.9	22.9	24.7	1.1	1.3	33.6	39.0	20.3	16.1		130.6	2.4	2.4
YTH 302	YP8	85	87		71.3	22.8	23.7	1.2	1.3	35.2	39.6	22.6	19.4	123.2	119.6	2.5	2.5
YTH 303	YP8	86	88	69.3	71.2	22.6	22.7	13	1.3	36.5	40.1	19.9	16.4	143.9	136.5	2.5	2.5
YTH 304	YP8	82	89	65.9	70.9	24.6	25.1	1.4	1.4	39.2	41.2	18.3	13.7	167.3	151.8	2.4	2.4
YTH 306	YP8	79	83		70.8	24.5	24.6	1.2	1.3	35.8	39.4	20.8	16.3		137.6	2.6	2.5
YP9	MDO	98	89		67.9	23.9	22.3	1.6	1.5	38.6	36.7	10.1	8.7	167.6		2.7	2.9
YTH 318 YTH 319	YP9 YP9	90 87	91 89		74.0 66.3	23.1 23.7	24.4 23.5	1.6 1.3	1.6 1.3	38.1 35.8	44.3 39.1	18.7 19.6	17.3 19.0	154.5 118.1	136.0 105.6	2.4 2.6	2.4 2.7
YTH 323	YP9	92	88		79.1	23.7	23.3	1.7	1.7	36.1	41.5	16.1	16.7	144.5	135.2	2.4	2.4
YTH 324	YP9	84	86		74.6	23.2	23.7	1.2	1.4	32.2	37.1	20.5	18.6	108.3	98.4	2.6	2.6
YTH 325	YP9	87	88		71.0	23.1	23.2	1.5	1.6	37.4	42.0	17.1	15.8	162.4	145.4	2.4	2.5
YTH 326	YP9	86	86	70.1	72.5	23.1	23.4	1.4	1.5	38.0	41.8	20.6	17.3	141.8	140.2	2.5	2.5
YTH 328	YP9	85	87	66.7	70.2	22.9	23.4	1.2	1.3	34.5	38.9	19.7	18.6	134.5	115.9	2.6	2.7
YP10		66	_		53.3	17.8	17.8	0.9	0.9	24.0	28.2	23.1	17.8	47.3	55.1	2.6	2.6
YTH 332	YP10	85	87		76.3	25.0	25.3	1.3	1.3	34.7	38.2	21.0	18.8	125.3	110.0	2.6	2.6
YTH 336 YTH 339	YP10 YP10	79 81	85 87		61.6 65.3	21.6 21.1	22.7 21.4	1.1 1.1	1.2 1.3	27.6 28.4	32.7 31.9	21.6 24.0	20.8 20.5	101.6 78.9	109.1 80.7	2.9 2.8	2.6 2.9
YTH 342	YP10	81	87		68.7	22.9	23.9	1.1	1.3	31.9	38.0	19.9	18.7	112.5	94.6	3.2	3.2
YTH 344	YP10	85	88		74.5	25.0	27.0	1.2	1.3	34.8	40.9	18.6	17.2		126.3	2.7	2.6
YTH 351	YP10	81	86		67.6	22.7	24.8	1.1	1.3	32.8	38.0	19.3	17.9	89.6	95.3	2.8	3.0
YTH 353	YP10	82	84	55.6	60.7	20.5	21.7	1.2	1.3	31.0	36.1		19.3	79.9	84.9	2.8	2.8
YTH 360	YP10	81	86		72.1	22.9	23.3	1.2	1.3	33.8	36.0	19.8	18.6	110.0	103.6	3.0	2.6
YTH 362	YP10	82	88		61.3	20.8	21.5	1.1	1.2	28.5		23.7		83.9	81.6	2.4	2.5
YTH 363	YP10	84	90		56.0	22.0	23.4	1.2	1.3	30.6	36.3	19.6	17.1	90.7	89.0	2.8	2.8
YTH 368 YP11	YP10	82 105	87 99		63.1 60.8	20.8	24.5	1.1	1.3	29.5 37.7	34.4 39.3	12.2	16.0 7.6	75.1	89.8	3.0	2.9
YTH 133	YP11	88	99 90		62.3	23.8	23.3	1.8	1.9	34.3	35.9	21.4	18.3	180.0 106.2	186.3 97.6	2.6 2.6	2.4
YTH 135	YP11	86	89		64.9	26.5	26.5	1.5	1.6	37.5	38.9	20.0	18.3	143.4		2.6	2.7
YTH 137	YP11	88	90		69.9	25.3	25.2	1.4	1.5	40.4	42.0	19.5	19.3	142.5		2.5	2.4
YTH 146	YP11	84	88		64.7	23.2	23.1	1.3	1.3	33.6		23.2	20.7	114.7		2.7	2.7
YTH 150	YP11	90	90		72.6	26.4	26.3	1.5	1.6	40.6		20.5	17.0	155.2		2.7	2.7
YTH 153	YP11	87	88		73.9	24.4	25.2	1.3	1.5	34.9	40.5	21.5	17.3	117.4	107.3	2.6	2.7
YTH 155	YP11	88	90		73.2	26.1	26.6	1.5	1.6		43.0	20.6	13.7	167.7		2.5	2.5
YTH 157	YP11	87	90		70.4	25.2	25.4	1.5	1.6	37.7	40.3		16.5	147.0		2.6	2.6
YTH 160	YP11	87	90		74.1	25.6	25.8	1.6	1.7	38.6	42.1		15.9	161.1		2.6	2.6
YTH 162 YTH 165	YP11 YP11	88 88	90 90		73.9 70.4	25.4	26.2 25.4	1.5 1.5	1.6 1.6		42.7 41.6		17.4 17.4	148.6 158.2		2.5 2.6	2.4 2.5
1111103	1111	00	90	07.7	70.4	20.0	43.4	1.3	1.0	50.4	41.0	20.2	1 / .4	130.2	140.4	۷.0	

DTH: days to heading, CL: culm length, PL: panicle length, LW: leaf width, LL: leaf length, PN: panicle number per plant, GW: 100-grain weight, TSN: total spikelet number per panicle.

The phenotypic averages of DS in 2006, 2007 and 2008 and of WS in 2005, 2006 and 2007 were shown.

a) See Table 1.

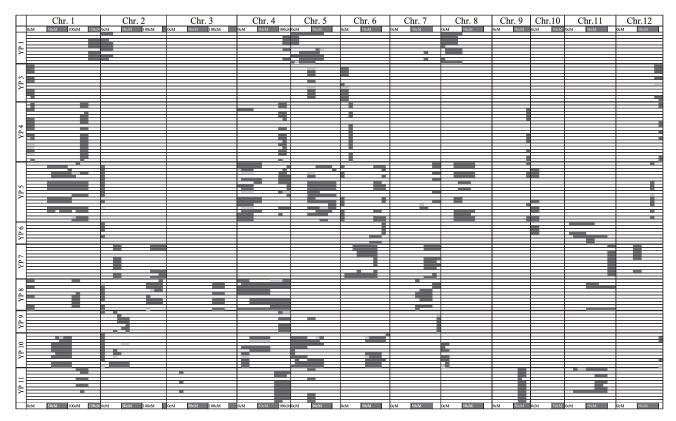


Fig. 2. Graphical genotypes of 117 introgression lines derived from crosses between IR64 and 10 donor parents

The black regions denote the homozygous for donor allele; the white regions denote the homozygous for IR

64 allele; the gray regions denote the heterozygous alleles.

GW of three INLs in DS was heavier than that of IR64: by 0.2 g in YTH199 (YP5), by 0.4 g in YTH33 (YP1), and by 0.5 g in YTH368 (YP10) (Fig. 4B). YTH33 had an associated region YP1-GW5 for heavy GW. TSN of three INLs were lower than that of IR64, while that of seven INLs was higher (Fig. 4C). TSN of three INLs in DS were lower than that of IR64: by 39 in YTH13 (YP 1), by 40 in YTH264 (YP7) and by 30 in YTH339 (YP 10). TSN of seven INLs in DS was higher than that of IR64: by 58 in YTH63 (YP3), by 91 in YTH83 (YP4), by 49 in YTH191 (YP5), by 46 in YTH270 (YP7), by 81 in YTH288 (YP8), by 54 in YTH325 (YP9), and by 52 in YTH160 (YP11). Three INLs which showed lower TSN compared with IR64 had the associated regions: YTH264 with YP7-TSN6, YTH13 with YP1-TSN1 and YP1-TSN5, and YTH339 with YP10-TSN6. On the other hand, five INLs which showed higher TSN compared with IR64 had the associated regions: YTH191 with YP5-TSN4, YTH160 with YP11-TSN4, YTH325 with YP9-TSN4, YTH288 with YP8-TSN4, and YTH83 with YP4-TSN4. The INLs which showed unique agronomic traits: short and long DTH, high and low TSN, and heavy GW, were found across multiple sib groups.

# Discussion

In our previous study, association analyses between agronomic traits and introgressed segments in the 334 INLs were conducted using SSR markers<sup>2</sup>. As a result, two regions for short DTH in YP1 and YP7 and five regions for long DTH in YP1, YP3, YP5, YP8, and YP10 were identified. The results estimated that several regions from the 334 INLs coincided with QTLs and genes which have been previously reported. For example, YTH13 which showed short DTH had an introgressed segment at the same region of the Hd5 locus on chromosome 813. YTH59 which showed long DTH had introgressed segments at the similar location of Hd3a and Hd3b on chromosome 68,17. Thus, these associated regions in these INLs which were responsible for DTH were thought to correspond with results of previous studies. A region for GW in YP1 contributed to increase GW in previous study and was located on the centromere region of chromosome 5. From this region of chromosome 5, qSW5 for grain size related to GW was isolated<sup>23</sup>. This fact suggested that YTH33 (derived from YP1) for heavy GW might have qSW5. Although an associated region for GW in analysis of variation was not

#### D. Fujita et al.

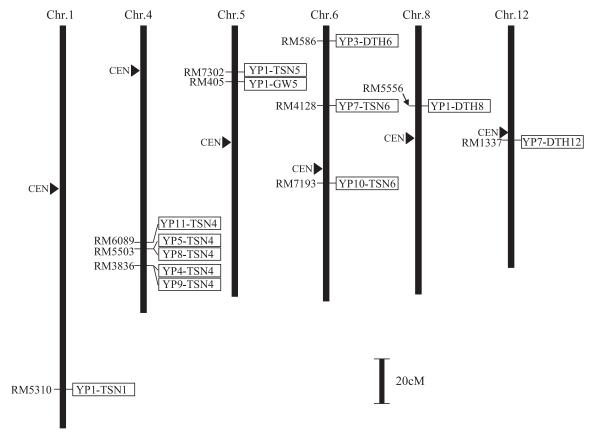


Fig. 3. Chromosomal locations of associated regions for agronomic traits in 334 introgression lines

The SSR markers associated with each agronomic trait in analysis of variation were quoted from Fujita et al. (2009)<sup>2</sup>. The rectangles indicate the regions of introgressed segments associated with agronomic traits. The name for an associated region in rectangles, for example, YP1-DTH8, represented the donor parent YP1, followed by the trait DTH, and chromosome number 8.

identified in YTH199 from YP5 and YTH368 from YP 10 which showed heavy GW, these lines had introgressed segments around qSW5 on chromosome 5. This result indicated that YTH199 and YTH368 may have qSW5. Additionally, a region contributing to increase TSN was detected in association analysis. The region for high TSN on the long arm of chromosome 4 was detected across five sib groups from YP4, YP5, YP8, YP 9, and YP11. In previous study, several QTLs for TSN have been detected on the same region of chromosome 4<sup>1, 4, 5, 9-11, 16, 18, 25, 26</sup>. YTH83 from YP4, YTH191 from YP 5, YTH288 from YP8, YTH325 from YP9, and YTH160 from YP11 had the common region on the long arm of chromosome 4. Although the associated regions for TSN in most of these INLs have been identified, the associated regions of YTH270 and YTH63 for high TSN have not been detected by analysis of variation. QTL analysis for agronomic traits using segregated populations derived from YTH246, YTH199, YTH368, YTH270, and YTH63, will reveal the location and effect of QTLs and will provide useful genetic information for MAS.

In this study, developed 334 INLs showed unique agronomic traits such as short and long DTH, heavy GW, and low and high TSN. Although the developed INLs are useful as breeding materials and for studying agronomic traits, each INL contained multiple introgressed segments. For instance, near isogenic lines (NILs) for agronomic traits can be easily developed based on these developed INLs. The NILs are more suitable materials for precise genetic studies, including the evaluation of gene effects, selection of enhanced molecular markers which are tightly linked with the target gene, gene expression, and gene isolation. If the target trait is decided, it is easy to develop NILs with IR64 genetic background by MAS using the developed INLs based on the information of associated regions. The NILs for agronomic traits can be used to reveal the gene-environment interaction. Understandably, the developed INLs in a uniform background of IR64 are useful not only as research materials but also as pre-breeding lines.

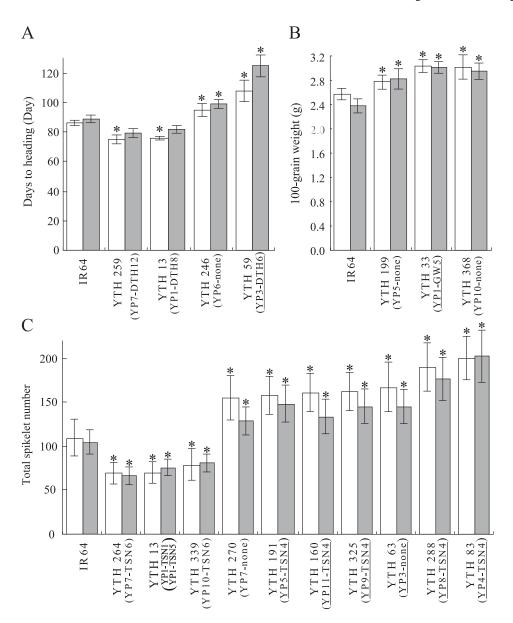


Fig. 4. Comparison for agronomic traits for wet season (WS) in 2007 and dry season (DS) in 2008: (A) days to heading, (B) 100-grain weight, (C) total spikelet number among typical line

The names in parenthesis indicate the regions associated with agronomic traits at 0.1% level and were designated as donor varieties followed by the traits and chromosome number. Bars indicate the average of each trait with standard deviation. Asterisks indicate a significant difference between IR64 and the INLs at 5% level by Dunnett's test.

: DS, | : WS.

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