

DETECTION OF HEAT RELATED QTL IN RICE AT FLOWERING STAGE USING SELECTED INTROGRESSED LINES

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ABSTRACT

To identify quantitative trait loci (QTL) underling heat tolerance in rice, four sets of BC₂F₅, Introgressed lines (ILs) were derived using four *indica* donors, (Jiangxisimiao, IR65600-27-1-2-2, Hanhui10 and Bala) with Minghui86 (MH86) restorer as the recurrent parent (RP). The heat stress index, HSI = (filled grain rate at normal condition – filled grain rate at heat stress condition)/ filled grain rate at normal condition, was employed to evaluate the heat tolerance of rice with other yield related traits exposing to heat stress during whole flowering period at two season in Hunan in the summer 2011 and 2012. There was no significant yield improvement of four populations under normal conditions in 2011 and 2012 except population MH86/Bala. Ranking was done according to the average HSI and grain yield (GY) for two years under stress condition. The best population was MH86/IR65600-27-1-2-2 (K) which shows the lowest HSI (0.43) and the highest GY (10 g/plant). The second one was the population MH86/Hanhui10 (L) (9.65 g/plant, HSI 0.44), Population MH86/Bala (M) (9 g/plant, HSI 0.57) and population MH86/Jianxisimiao (J) (6.95 g/plant, HSI 0.62) were third and fourth, respectively according to the ranking results. A total of 13 QTLs were detected for HSI, including three for population J, six for K and two for L and two for population M. QTL associated with SSR marker RM180 was detected from 3 populations except population L. RM473, RM474, RM202 and RM237 were found at least from two populations suggesting that these are important in selection of heat tolerance QTLs in *indica* background.

Keywords: Heat tolerance, Introgressed lines (ILs), Quantitative Trait Loci (QTL), SSR markers

INTRODUCTION

High temperature is often a problem for stable rice production in many tropical and subtropical countries, such as Pakistan, India, Bangladesh, China, Thailand, Sudan and many African countries (Osada *et al.*, 1973; Matsushima *et al.*, 1982; Tian *et al.*, 2009). Spikelets at anthesis that are exposed to temperatures $>35^{\circ}\text{C}$ for about 5 days during the flowering period are sterile and set no seed (Satake and Yoshida, 1978). Global warming caused by greenhouse gases has a huge effect on sustaining agricultural development. Since the early 20th century, the earth's mean surface temperature has increased by 0.8°C , with about 0.6°C of this hike occurring since 1980. Global mean surface temperatures for 2081–2100, relative to 1986–2005, is likely to increase by 0.3°C to 1.7°C for the lowest and by 2.6°C to 4.8°C for the highest greenhouse gas emission scenarios (Ye *et al.*, 2015). Developing new rice varieties with heat tolerance is an essential way to sustain rice production in future climate change and global warming.

QTL mapping studies for heat tolerance have been conducted on various rice populations at booting (Zhao *et al.*, 2006) and flowering stages (Cao *et al.*, 2003; Chen *et al.*, 2008; Zhang *et al.*, 2008; 2009, Jagadish *et al.*, 2010; Xiao *et al.*, 2011; Ye *et al.*, 2012; 2015).

Objective of this study was identification of QTLs for rice heat tolerant at the flowering stage using $\text{BC}_2\text{F}_{2.5}$ and $\text{BC}_2\text{F}_{2.6}$ populations of four sets of ILs over two years 2011-2012) in Hunan under plastic shed condition and open field condition.

MATERIALS AND METHODS

Development of planting materials

An *indica* restorer MH86, which is the male parent of many elite *indica* hybrid cultivars commercially grown in South China, was used as the recurrent parent (RP). Four *indica* donor parents (Jiangxisimiao, IR65600-27-1-2-2, Hanhui10 and Bala) were used to develop back crossed Introgressed Lines (ILs).

In 2004 summer in Hainan, the initial crosses were made among the RPs and four donors to produce F_1 s, which were back crossed (2004-winter) with RP to produce the BC_1F_1 s. Twenty five randomly chosen plants from each BC_1F_1 population, were backcrossed (2005-summer) with RP to produce bulk BC_2F_1 populations. The bulk BC_2F_1 lines were planted in the 2005-winter season and allowed to self-produce BC_2F_2 seeds

which were bulk-harvested as a random BC_2F_2 seeds and stored them with cold storage facility in Institute of Crop Sciences, CAAS, Beijing. BC_2F_2 populations were screened for high temperature stress, using 400 plants for each cross, in Hainan 2008, summer and selected tolerant individuals which have shown more than 60% spikelet fertility while 29% for RP. Then seed increasing was done growing two rows, each having 12 plants in $BC_2F_{2.3}$ generation in Hainan, 2008, winter season. Progeny test was conducted in Hainan 2009-summer and verified the HT performance of lines. At the same time, genotype evaluation was done with SSR markers in Institute of Crop Sciences, CAAS, and using 20-30 g of $BC_2F_{2.4}$ seed of each line.

$BC_2F_{2.5}$ and $BC_2F_{2.6}$ introgression lines were used for collecting phenotypic data growing them during two summer seasons of the year 2011 and 2012 respectively in Hunan at Agricultural Research Station at Liu yang, China (28° 09' N, 113° 37' E). Seeds were sown (2011 May 10) in the nursery prepared in the field. 28 days old seedlings were transplanted in plastic sheds, with two replications, at the same time open field with 3 replications having 10-12 plants in a row with 20×17 cm space with Randomized Complete Block Design (RCBD). The RP, DP and heat tolerant check (CK), N22 were planted repeatedly after each set of introgressed lines. The field was managed according to standard practice in the area. Plants were grown under flooded condition for the whole growth period. Ventilation mechanisms in the plastic shed were kept open to make minimize the heat stress during the vegetative growth period and ripening period. Heat stress was created closing the side walls and top vent during the flowering period. The maximum temperature inside the shed was maintained within 37-40 °C and no control for night temperature (23-28 °C) during flowering period. Daily maximum and minimum air temperature and relative humidity at the canopy level were recorded with a digital electronic thermometer (Oregon, Scientific, IN-OUT Thermo-Hygrometer and Clock, Model: THG312). Heading date (HD, days) was recorded when 50% of the plants in each line at heading. Plant height (PH, cm) and panicle number (PN) were measured three middle plants in each line at maturity and harvested including RP, DP, and CK. Filled grain number per panicle (FGN), spikelet number per panicle (SNP), filled grain rate (FGR, %) calculated as $(FGN/SNP)*100$, thousand grain weight (TGW, g), yield (GY, g/plant) were evaluated under normal and heat stress conditions. Heat tolerant is evaluated using heat stress index, $HSI = (FGR \text{ under normal condition} - FGR \text{ under heat stress condition})/FGR \text{ under normal condition}$.

The experiment was continued with BC₂F_{2:6} populations for the year 2012 in the same field. All the ILs were grouped into 5, (104-100d, 99-96d, 95-92d, 91-88d and 87-82d) based on heading date observed in 2011 and sown 5 different days, transplanted with two times to ensure that all lines to be headed at the same time and exposed to the same heat stress condition at the flowering stage. All the other management practices and data collection were same as the previous year.

Analysis of genotype with SSR markers

DNA was extracted from bulked seedlings from BC₂F_{2:4} populations using the CTAB method with slight modification. SSR markers of RM series from 1 to 600 and some markers above RM 1000 (<http://www.gramene.org>) were used for the parents polymorphism and afterword for the populations. Polymorphic markers were found as 59, 62, 63 and 71 for the population MH86/Jianxisimiao, MH86/IR65600-27-1-2-2, MH86/Hanhui10 and MH86/Bala respectively with distribution among 12 chromosomes.

Data analysis

Mapchart 2.0 software was used to draw genetic linkage map with polymorphism markers reference to Cornell University (<http://www.gramene.org>) marker distance. One-way ANOVA performed with SAS 8.1 software. QTLs were identified for heat stress index and yield related traits under high temperature stress condition and the normal condition for two years with the significant level of $p < 0.05$. When a QTL was detected by two or more linked markers, the one with the highest F-value was presented.

RESULTS AND DISCUSSION

Selection efficiency for HT and genetic diversity in the selected ILs

Spikelet fertility (SF) was $28.7 \pm 22.8\%$ for the recurrent parents Minghui86 under high temperature screening in Hainan 2008. Individuals selected from Minghui86 backgrounds have shown SF from $63.4 \pm 10.4\%$ (for population Minghui86/IR65600-27-1-2-2) to $77.0 \pm 11.9\%$ (for population Minghui86/Bala). The average Selection Intensity (SI) was 3% ranging from 2.5% for population Minghui86/IR65600-27-1-2-2 to 3.3% for the population Minghui86/Bala (Table 1).

Table 1. Screening results of 4 Minghui86 (RP) BC2F2 backcross populations for heat tolerance at the flowering stage in Hainan, 2008

Shuhui527/ Donor Parents	Subspecies	Origin	Code	Population Size	No. of selected plants	SI ¹ (%)	SF (%)	
							Mean± SD	Range
Minghui86/Donor parents								
JiangxiSimiao	<i>Indica</i>	China	J	400	12	3.0	67.9±9.0	50.0-81.3
IR65600-27-1-2-2	<i>Indica</i>	Philippines	K	400	10	2.5	63.4±10.4	50.0-81.4
Hanhui10	<i>Indica</i>	China	L	400	12	3.0	75.0±10.5	50.0-90.9
Bala	<i>Indica</i>	India	M	400	13	3.3	77.0±11.9	54.5-90.7
Mean				400	12	3.0	70.8±6.3	
Minghui86							28.7±22.8	5.0-66.7

¹SI= selection intensity, SF= spikelet fertility.

Performances of the 4 populations under heat stress and normal conditions

Four populations of Minghui86 background were evaluated in 2011 and 2012 in Hunan under heat stress and normal conditions (Table 2). Compared to the normal condition in 2012, MH86 suffered with heat stress and reduced FGR by 69% (FGR under normal –FGR under stress; 2012) while 2011 less reduction 36.4%, reduced GY 36.4 g in 2012 while 11 g in 2011, reduced FGN by 137.3 per panicle in 2012 while 21.3 per panicle in 2011, reduced SNP by 62.8 per panicle while 2011 increased by 91.7 per panicle, reduced TGW by 7.5 g while 0.94 g in 2011, increased PH 0.1 cm in 2012 while 4.6 cm in 2011, increased PN by 0.6 in 2012 while decreased 3.7 in 2011, HD is unchanged in 2012 while 2011 reduced by 3.1 days . On average the selected ILs suffered much less damages compare to MH86.

Table 2. Mean performances of 47 ILs of Minghui86 background with 4 populations for 8 traits evaluated under normal and stress condition in Hunan 2011 and 2012

Trait N ¹	Minghui86 background-2011								Minghui86 background-2012							
	J 12	K 10	L 12	M 13	Mean	RP MH86	CK N22		J 12	K 10	L 12	M 13	Mean	RP MH86	CK N22	
Normal																
PH (cm)	122.6±6.6	124.2±6.5	124.8±5.4	126.4±3.9	124.5	124.2	139.2		128.8±6.0	131.2±5.4	133.4±6.2	131.5±4.4	131.2	128.0	154.8	
PN	7.2±1.7	8.2±1.4	7.6±1.3	7.4±1.4	7.6	8.7	9.1		10.1±2.1	10.1±1.0	10.0±0.6	9.9±2.2	10.0	9.1	10.8	
FGN	89.3±9.2	80.5±13.8	72.6±12.7	83.8±17.1	81.6	75.3	68.5		138.4±28.1	151.1±20.5	127.9±19.1	155.6±26.0	143.2	146.0	142.8	
SNP	132.9±22.9	139.4±22.9	113.5±31.5	116.8±28.5	125.6	120.3	82.8		180.9±38.8	194.2±26.7	156.7±32.3	192.9±29.3	181.2	190.8	154.6	
FGR	68.5±9.4	58.7±10.4	66.1±9.6	73.3±8.1	66.6	63.5	82.5		77.3±9.3	78.7±5.7	82.7±8.6	81.1±8.6	79.9	76.4	92.2	
TGW (g)	27.2±1.7	26.8±2.3	30.0±2.5	25.9±3.3	27.5	28.14	20.9		28.6±2.6	27.3±1.9	30.2±1.5	27.8±2.1	28.5	28.7	20.6	
GY(g/plt)	17.2±3.6	17.1±2.3	15.8±2.6	15.9±2.5	16.5	18.5	13.1		38.3±3.5	40.9±4.3	38.4±6.5	41.5±6.2	39.8	38.1	31.5	
HD (d)	92.8±3.0	97.2±3.2	97.1±2.2	96.0±1.3	95.8	98.2	86.6		81.7±6.1	86.5±4.2	91.4±6.7	87.0±6.7	86.6	90.9	70.6	
Stress																
PH (cm)	132.7±5.8	129.8±4.9	136.3±5.9	128.7±5.6	131.9	128.8	157.6		120.6±6.6	125.5±7.7	124.9±8.2	123.3±7.2	123.6	128.1	133.0	
PN	5.8±1.5	5.1±1.1	4.9±1.2	6.2±1.6	5.5	5.0	5.7		11.1±3.9	10.7±1.5	10.6±1.3	11.2±3.7	10.9	9.7	10.4	
FGN	57.5±22.9	87.6±28.9	87.1±27.0	76.0±12.9	77.1	54.0	117.8		21.6±14.2	30.2±13.0	23.0±9.8	21.9±9.6	24.2	8.7	36.5	
SNP	166.6±37.8	177.8±30.0	154.2±25.5	164.7±36.3	165.8	212.0	144.8		123.7±19.1	143.3±16.4	120.0±19.7	126.0±25.2	128.2	128.0	104.9	
FGR	36.3±14.5	48.4±10.5	59.1±21.5	47.2±8.1	47.7	27.1	77.4		17.7±11.1	21.0±7.9	20.5±11.0	18.5±8.9	19.4	7.4	33.8	
TGW (g)	26.9±1.8	26.1±1.9	28.4±1.6	25.6±1.8	26.7	27.2	18.6		24.2±2.2	24.0±1.3	25.4±2.1	23.8±2.0	24.4	21.2	17.4	
GY(g/plt)	8.4±2.5	12.5±4.0	13.2±3.8	12.2±2.6	11.6	7.5	13.5		5.5±3.5	7.5±2.9	6.1±2.5	5.8±2.9	6.2	1.7	6.25	
HSI	0.45±0.29	0.13±0.32	0.12±0.29	0.35±0.09	0.26	0.56	0.06		0.78±0.13	0.73±0.11	0.75±0.11	0.79±0.10	0.76	0.9	0.63	
HD (d)	91.3±2.7	95.1±1.9	95.2±3.0	93.5±1.8	93.8	95.1	87.6		82.5±4.3	87.1±3.8	88.4±6.9	85.2±6.6	85.4	90.1	75.3	

¹N Number of selected lines, PH= plant height, PN=panicle number per plant, FGN=filled grain number per panicle, SNP= spikelet number per panicle, FGR= filled grain rate per panicle, TGW= 1000-grain weight, GY= grain yield per plant, HSI= heat stress index, HD= heading date, RP= Recurrent Parent, CK= Check variety. Bolded numbers are significantly higher or lower than Shuhui527 (RP) based on t tests.

Temperature and relative humidity combine effect for spikelet fertility

The average daily maximum (inside, $38.54\text{ }^{\circ}\text{C} \pm 4.5$, outside $33.6\text{ }^{\circ}\text{C} \pm 3.5$) temperature and humidity (inside, $68\% \pm 7.1$ outside, $64\% \pm 7.5$) were observed during the flowering period in year 2011. In the year 2012 stress was more severe and average maximum temperature (inside $40.3\text{ }^{\circ}\text{C} \pm 3.5$, outside $33.6\text{ }^{\circ}\text{C} \pm 1.8$) and RH (inside $70\% \pm 5.7$, outside $67.7\% \pm 7.8$) recorded. The higher maximum temperature $40.3\text{ }^{\circ}\text{C}$ with 70% maximum humidity reduced the spikelet fertility significantly in 2012 compared to 2011 and thereby low yield per plant observed. But at the same time, outside temperature and humidity would be desired to increase the fertility so, grain yield per plant higher at outside in 2012 compared to the 2011 (Table 2). However, there was genotype variability for withstanding high temperature at flowering period, suggesting that introgression of favorable allele will increase the heat tolerant ability in rice plant during flowering period.

Mapping QTL for heading date

A total of 22 QTLs were found for Heading date (HD) including 3 (2 in normal, 1 in both conditions) for MH86/Jianxisimiao (J), 8 (2 in normal, 6 in both conditions) for MH86/IR65600-27-1-2-2 (K), 4 (1 in normal, 2 in stress, 1 in both) for MH86/Hanhui10 (L), 7 (1 in normal and 6 in stress) for MH86/Bala (M) populations, respectively.

Three QTLs were found on chromosome 1, 6 and 10 in the population MH86/Jiangxisimiao. *QHd6* has negative value for the additive effects which shows it comes from donor alleles (Table 3). In second population, MH86/IR65600-27-1-2-2 all the additive effects show negative value except *QHd3* and *QHd6* which shows negative dominance effect (Table 4). It indicates that all the alleles belong to donor reduce the flowering time their phenotypic variation explain (PVE) values are much higher and ranging from 47%- 69%. Four QTLs, one from donor allele, two from recurrent parent alleles while one shows positive dominant effect, were found in the population MH86/Hanhui10 (Table 5). In the population MH86/Bala (Table 6), 3 alleles from donor and four alleles from recurrent parents were found showing that comparatively variety Bala has short heading period. Seven QTLs were found linkage in the Chi-square test including RM488, RM474 in population J, RM 442 in population K, RM423 and RM474 in population L and RM231 and RM19 in population M (bolded markers in Tables 5.1-.5.4). RM474 repeatedly appeared in population J showing -7.5 dominant effect and population L showing 5.16, 5.37 additive and dominant, respectively.

Mapping QTLs for plant height

A total of 18 QTLs were recorded for plant height including 3 (1 in normal, 1 in stress, 1 in both) for the population J, 2 (1 in stress, 1 in both) for population K, 6 (2 in normal and 3 in stress, 1 in both) for population L and 7 (2 in normal, 4 in stress, 1 in both) for the population M, respectively.

In the population J (Table 3), all three favorable alleles for plant height come from Jiangxisimiao donor segments ranging PVE values from 49% to 58%. *QPh3* and *QPh6* were found in population K (Table 4) belongs to IR65600-27-1-2-2 donor and MH86 respectively. In the population L (Table 5), *QPh3*, *QPh4* and *Qph11* belong to MH86 while *Qph7* and *Qph10* alleles coming from Hanhui10 donor segments ranging PVE from 42% to 67%. *Qph1* shows the positive dominant effect. In population M (Table 6), 4 favorable alleles for plant height belong to Bala donor segment while two for MH86 ranging PVE from 35% to 64%. *QPh6* shows negative dominance effect.

Interestingly, favorable alleles for plant height found one (population K and L) or two (in population J and M) from the chromosome 3 suggesting that important alleles recite in chromosome 3.

Mapping QTLs for panicle number

A total of 32 QTLs were declared for panicle number including 9 (2 in normal, 5 in stress, 2 in both) for population J, 11 (1 in normal, 3 in stress, 7 in both) for population K, 4 (3 in normal and 1 in stress) for population L, 8 (1 in normal, 5 in stress, 2 in both) for population M, respectively. There were 8 QTLs which were confirmed by the chi square test including, RM474 and RM202 in population J, RM237 and RM55 in population K, RM231, RM334, RM70 and RM407 in population M and no markers found in population L.

Eight favorable alleles for high number of panicle come from Jiangxisimiao donor segments while one belongs to MH86 in population J (Table 3) ranging PVE from 46% to 68%. In the population K (Table 4), 5 favorable alleles come from the MH86 while 4 favorable alleles belong to IR65600-27-1-2-2 donor segments PVE ranging from 41% to 64%. There were 2 positive dominant effects with *QPn2* and *QPn6*. Three favorable alleles from MH86 and one allele from Hanhui10 donor segment were found in population L, with PVE ranging from 35% to 58%. 6 favorable QTLs from Bala

donors and one from MH86 with one positive dominance effect allele were found in the population M.

There were repeated QTLs between populations in different year under different conditions. *QPn2* was found 2011 under normal condition in population M (Table 6) and same was found in population J (Table 3) in 2012 under stress condition. *QPn12* was found in 2011 under stress condition in population K and again observed under normal condition in population L in 2012. *QPn1a* was recorded in 2011 under normal condition in population K and the same time observed *QPn1* in M population under normal condition in 2011. The associated markers are RM145, RM519 and RM490 respectively.

Mapping QTLs for filled grain number per panicle

A total of 23 favorable QTLs were recorded for filled grain number including 5 (2 in normal, 2 in stress, 1 in both) for population J, 7 (3 in normal, 3 in stress, 1 in both) for population K, 3 (2 in normal and 1 in stress) for population L, 8 (5 in normal, 2 in stress, 1 in both) for population M respectively. Chi-square test confirmed linkage markers as, RM202 for population J, RM237, RM55, RM565, RM481 and RM 286 for population K, all the 3 markers, RM340, RM481 and RM278 in population L, RM178, RM70 and RM304 for the population M.

In the population J, 3 favorable alleles come from MH86 while 2 alleles belong to Jiangxisimiao donor parent PVE ranging from 34% to 64%. Five favorable alleles come from IR65600-27-1-2-2 donor while two come from recurrent parent PVE ranging from 46% to 68% in the population K. in population L, one allele comes from Hanhui10 donor while two favorable alleles come from MH86 of which *QFgn7* shows -31.92 negative dominance effects. Four favorable QTLs were found from MH86, 3 from Bala donor while one allele shows negative dominance effect ranging PVE from 36% to 64%.

QFgn1 associated with RM490 was found in population M under normal condition in 2011 and the same QTL observed as *QFgn1a* in population K under stress condition in 2012. *QFgn7* linked with RM481 was found from both K and L population under normal condition in 2012. *QFgn11* associated with RM286 was observed in both M and K populations in 2011 normal and 2012 normal conditions respectively suggesting that those are important favorable loci for filled grain number per panicle.

Mapping QTLs for spikelet number per panicle

A total of 28 favorable loci for spikelet per panicle were detected including 8 (6 in normal and 2 in both) for population J, 4 (3 in stress and 1 in both) for population K, 3 (1 in normal, 1 in stress, 1 in both) for population L and 13 (3 in normal, 4 in stress, 6 in both) for population M respectively. Chi-square test confirmed some QTLs associated with markers as, RM237, RM109, RM180, RM474 and RM202 for population J, RM565, RM418 in population K, all the markers RM340, RM478 and RM310 in population L, RM473, RM178, RM180, RM304, RM021 and RM19 for population M.

Interestingly, all the favorable loci for spikelet number per panicle come from MH86 fragment in population J with PVE ranging from 40% to 66%. In the population K, 2 alleles come from IR65600-27-1-2-2 donor and 2 from MH86 with PVE ranging from 45% to 68%. All desirable alleles come from MH86 for the population L with PVE ranging from 49% to 60%. Nine favorable loci come from Bala donor while 4 loci from the MH86 with PVE ranging from 36% to 66% for the population M.

QSn7a associated with RM180 was found under normal condition in 2011 from population M and same QTL was observed as *QSn7* under normal condition from population J in 2012.

Mapping QTLs for filled grain rate

A total of 24 QTLs were found for filled grain rate including 7 (3 in normal, 1 in stress, 3 in both) for population J, 4 (3 in stress and 1 in both) for population K, 4 (3 in normal and 1 in both) for population L and 9 (8 in normal and 1 in stress) for population M, respectively. Chi-square test confirm the association some of those markers with QTLs as, RM237, RM180, RM474 and RM202 for population J, RM565, RM180 and RM210 for population K, RM340 and RM457 for population L, RM178, RM336, RM202 and RM19 for the population M.

In the population J, all the favorable loci for filled grain rate come from Jiangxisimiao donor segments with PVE ranging from 48% to 65%. 3 desirable loci come from IR65600-27-1-2-2 donor while one locus found in MH86 in the population K with PVE ranging from 49% to 62%. For the population L, 3 alleles from Hanhui10 donor and one from MH86 having PVE ranging from 33% to 39%. More favorable alleles, 6 come

from MH86 while 3 alleles come from Bala donor segment in population M with PVE ranging from 37% to 68%. *QFgr7* linked with RM180 was found from both populations J and K under stress condition in 2011. *QFgr11* associated with RM202 was found from both J and M populations under normal condition in 2011.

Mapping QTLs for thousand grain weight

A total of 30 QTLs were mapped for thousand grain weight including 4 (all in stress) for population J, 5 (3 in normal and 2 in stress) for population K, 12 (5 in normal, 5 in stress, 2 in both) for population L, 9 (2 in normal, 3 in stress and 4 in both) for population M, respectively. 12 out of 30 QTLs was confirmed by Chi-square test as follows, RM474 in population J, RM18 and RM216 for population K, RM575, RM473, RM163, RM136, RM515 and RM278 for the population L, RM231, RM178 and RM342 for the population M.

In population J, 2 favorable alleles come from MH86 one for Jiagxisimiao donor while one shows positive dominance effect with PVE ranging from 43% to 53%. For the population K, 2 loci from IR65600-27-1-2-2 donor and 2 loci from mH86 while one locus shows positive dominance effect with PVE ranging from 44% to 60%. In population L, all the favorable alleles come from Hanhui10 donor with PVE ranging from 34% to 68%. For the population M, 5 loci come from MH86 and 4 loci come from donor Bala with PVE ranging from 34% to 62%. *QTgw4b* associated with RM119 was found both J and L populations under stress condition in 2012.

Mapping QTLs for grain yield per plant

A total of 24 QTLs were detected for grain yield per plant including 7 (4 in normal, 1 in stress and 2 in both) for population J, 5 (1 in normal, 3 in stress and 1 in both) for population K, 5 (4 in normal and 1 in stress) for population L, 7 (3 in normal and 4 in stress) for population M, respectively. Chi-square test found linkage markers which support to linkage markers with QTLs as, RM237, RM145, RM180 and RM474 for population J, RM180, RM210 for population K, RM442, RM401 and RM278 for population L, RM283, RM334, RM180 and RM407 for the population M.

In population J, 4 favorable alleles come from donor Jiangxisimiao, 2 from MH86 and two dominance having one positive and one negative value. In population K, 3 loci

come from donor IR65600-27-1-2-2 loci, one from MH86 and one positive dominance effect with PVE ranging from 46% to 64%. 4 favorable alleles are from Hanhui10 while 2 from MH86 for the population L, with PVE ranging from 36% to 62%. In population M, 5 favorable alleles come from MH86 and one from Bala with one allele positive dominance effect. *QGy7* associated with RM180 was found from both populations J and K under stress condition in 2011, at the same time *QGy7* was found from population M under normal condition in 2011 indicating that important locus for grain yield per plant.

Mapping QTLs for heat tolerant index

A total of 13 QTLs were found for heat stress index including 3 for population J, 6 for population K, 2 for population L and 2 for population M, respectively. Chi-square test found linkage markers as, RM237 and RM180 for population J, RM565, RM180 for population K, RM515 for population L and RM564 for the population M.

In population J, all favorable alleles for HSI come from Jiangxisimiao donor with PVE ranging from 36% to 48%. For the population K, 4 favorable alleles come from MH86 and 2 alleles from IR65600-27-1-2-2 donor with PVE ranging from 41% to 57%. In population L, *QHsi7* from Hanhui10 donor and *QHsi8* from MH86 were found with PVE value 37% and 34%, respectively. For the population M, one allele from Bala donor and one from MH86 were detected with PVE ranging from 42% to 68%. Phenotypic variation explains (PVE) for each trait for the all four populations is comparatively high. The reason might be directional selection under strong selection pressure and selected lines may belong to the upper tail of the normal distribution population for the heat tolerant trait. Moreover, small population size also may lead to loss of detection of minor QTLs and thereby increase the PVE for the detected QTLs. *QHsi7* associated with RM180 was found from both J and K populations under stress condition in 2011 suggesting that important locus for heat tolerant trait in rice.

Table 3. QTLs detected by one-way ANOVA of Minghui86/Jiangxisimiao

Trait	QTL	Envt.	Marker	Chrom	Distance	F value	Prob	R ² (%)	ADD	DOM
HD	<i>QHd1</i>	2011N	RM488	1	101.4	5.80	0.0240	56.3		-7.95
		2011S	RM488	1	101.4	5.56	0.0268	0.55		-6.61
	<i>QHd6</i>	2011N	RM539	6	45.1	8.32	0.0204	51.0	-3.66	
	<i>QHd10</i>	2011N	RM474	10	0	4.82	0.0378	51.7		-7.50
PH	<i>QPh2</i>	2011S	RM109	2	0	8.17	0.0288	57.7	3.05	
	<i>QPh3a</i>	2011N	RM231	3	15.7	9.92	0.0103	49.8	5.98	
	<i>QPh3b</i>	2011S	RM442	3	224.2	9.47	0.0117	48.6	7.01	
		2011N	RM442	3	224.2	6.16	0.0024	0.62	9.01	
PN	<i>QPn1a</i>	2012N	RM442	3	224.2	6.51	0.0288	0.39	6.36	
		2012N	RM442	3	224.2	6.51	0.0288	0.39	6.36	
	<i>QPn1a</i>	2011S	RM212	1	148.7	12.55	0.0053	55.6	1.20	
	<i>QPn1b</i>	2011S	RM14	1	194.1	8.47	0.0156	45.9	1.09	
	<i>QPn2</i>	2012S	RM145	2	49.8	34.03	0.0001	68.3	-2.35	5.16
		2012N	RM53	2	32.7	9.78	0.0122	0.52	1.78	
	<i>QPn4</i>	2012N	RM119	4	76.1	0.06	0.0012	66.7	1.78	
	<i>QPn5</i>	2012S	RM413	5	26.7	20.36	0.0011	67.1	5.38	
	<i>QPn6</i>	2011S	RM539	6	45.1	12.25	0.0081	60.5	1.73	
		2012S	RM510	6	20.8	5.98	0.0345	0.37	3.09	
	<i>QPn6</i>	2011N	RM539	6	45.1	7.78	0.0236	0.49	-1.99	
		2012N	RM474	10	0	5.02	0.0344	52.7	1.83	
	<i>QPn10b</i>	2012S	RM304	10	73.0	20.36	0.0011	67.1	5.58	
	<i>QPn11</i>	2011S	RM202	11	54.0	18.21	0.0016	64.6	1.14	
FGN	<i>QFgn1</i>	2012S	RM212	1	148.7	5.27	0.0446	34.5	9.24	
	<i>QFgn2a</i>	2011N	RM53	2	32.7	16.02	0.0031	64.0	-8.90	
	<i>QFgn2b</i>	2012S	RM29	2	68.9	7.95	0.0225	49.8	8.25	
	<i>QFgn4</i>	2011N	RM119	4	76.1	10.47	0.0089	51.1	-7.25	
	<i>QFgn11</i>	2011S	RM202	11	54.0	5.17	0.0464	34.1	-13.0	
		2012N	RM202	11	54.0	0.76	0.0083	0.52	-17.5	
SNP	<i>QSnpl1a</i>	2012N	RM237	1	115.2	6.73	0.0267	40.2	-21.4	
	<i>QSnpl1b</i>	2012N	RM212	1	148.7	9.51	0.0116	48.8	-25.6	
		2011N	RM212	1	148.7	5.37	0.0430	0.35	-15.0	
		2011S	RM212	1	148.7	7.23	0.0228	0.42	-27.0	
	<i>QSnpl2a</i>	2012N	RM109	2	0	11.47	0.0147	65.6	-20.9	
	<i>QSnpl2b</i>	2012S	RM53	2	32.7	10.16	0.0111	53.0	-17.2	
		2012N	RM53	2	32.7	6.56	0.0306	0.42	-26.7	
	<i>QSnpl4</i>	2012N	RM119	4	76.1	6.80	0.0262	40.5	-23.4	
	<i>QSnpl7</i>	2012N	RM180	7	30.1	6.73	0.0267	40.2	-21.4	

HEAT RELATED QTL IN RICE AT FLOWERING STAGE

Table 3. (Continued)

Trait	QTL	Env.	Marker	Chrom	Distance	F value	Prob	R ² (%)	ADD	DOM
FGR	<i>QSnpl0</i>	2012N	RM474	10	0	4.64	0.0412	50.8	-29.6	
	<i>QSnpl1</i>	2012N	RM202	11	54.0	8.64	0.0148	46.3	-22.0	
		2011N	RM202	11	54.0	6.32	0.0307	0.39	-13.9	
	<i>QFgr1a</i>	2011S	RM237	1	115.2	9.34	0.0121	48.3	10.2	
		2012N	RM237	1	115.2	8.36	0.0161	0.46	5.77	
	<i>QFgr1b</i>	2011N	RM212	1	148.7	9.57	0.0114	48.9	7.29	
		2012S	RM212	1	148.7	5.28	0.0445	0.35	7.21	
	<i>QFgr2a</i>	2012N	RM53	2	32.7	9.49	0.0131	51.3	7.77	
	<i>QFgr2b</i>	2012S	RM29	2	68.9	11.35	0.0098	58.6	6.76	
	<i>QFgr7</i>	2011S	RM180	7	30.1	9.34	0.0121	48.3	10.2	
		2012N	RM180	7	30.1	8.36	0.0161	0.46	5.77	
	<i>QFgr10</i>	2012N	RM474	10	0	8.24	0.0093	64.7	8.32	
TGW	<i>QFgr11</i>	2011N	RM202	11	54.0	6.00	0.0025	61.5	7.18	
	<i>QTgw4a</i>	2011S	RM518	4	25.5	10.47	0.0089	51.2	-1.39	
	<i>QTgw4b</i>	2012S	RM119	4	76.1	7.44	0.0213	42.6	-1.57	
	<i>QTgw6</i>	2012S	RM539	6	45.1	8.93	0.0174	52.8	2.41	
	<i>QTgw10</i>	2012S	RM474	10	0	4.84	0.0374	51.8		5.51
GY	<i>QGyl</i>	2011S	RM237	1	115.2	9.13	0.0128	47.7	1.78	
		2011S	RM488	1	101.4	4.75	0.0391	0.51	1.99	
	<i>QGy2</i>	2012N	RM145	2	49.8	11.96	0.0029	62.7		18.4
		2012N	RM29	2	68.9	8.56	0.0191	0.52	5.00	
		2012S	RM29	2	68.9	7.48	0.0256	0.48	2.59	
	<i>QGy5</i>	2012N	RM413	5	26.7	26.43	0.0004	62.6	9.28	
	<i>QGy6</i>	2011N	RM539	6	45.1	8.16	0.0213	50.5	-4.46	
	<i>QGy7</i>	2011S	RM180	7	30.1	9.13	0.0128	47.7	1.78	
		2011N	RM70	7	64.6	6.77	0.0161	0.60		-7.29
	<i>QGy10a</i>	2011N	RM474	10	0	6.65	0.0169	59.6		-8.02
	<i>QGy10b</i>	2012N	RM304	10	73.0	26.43	0.0004	62.6	9.28	
HSI	<i>QHsi1</i>	2011S	RM237	1	115.2	5.54	0.0404	35.6	-0.17	
	<i>QHsi2</i>	2012S	RM29	2	68.9	7.43	0.0260	48.1	-0.07	
	<i>QHsi7</i>	2011S	RM180	7	30.1	5.54	0.0404	35.6	-0.17	

HD= heading date; PH= plant height; PN= panicle number; FGN= filled grain number per panicle; SNP= spikelet number per panicle; FGR= filled grain rate TGW= thousand grain weight; GY= grain yield; HSI= heat stress index, S= heat stress condition; N= normal condition; R²= phenotypic variation explained; ADD= additive effect; DOM= dominant effect. The markers those bolded are detected as linkage by Chi-square test.

Table 4. QTLs detected by one-way ANOVA of Minghui86/IR65600-27-1-2-2

Trait	QTL	Envt.	Marker	Chrom	Distance	F value	Prob	R2(%)	ADD	DOM
HD	<i>QHd1</i>	2012N	RM490	1	51.0	6.28	0.0406	47.3	-3.26	
	<i>QHd2</i>	2011N	RM106	2	123.2	27.72	0.0005	68.8	-1.55	-7.86
		2011S	RM106	2	123.2	5.47	0.0371	0.61		-4.06
		2012N	RM106	2	123.2	14.40	0.0051	0.63		-12.2
	<i>QHd3</i>	2012N	RM442	3	224.2	7.21	0.0254	60.6		-10.6
	<i>QHd4</i>	2011N	RM518	4	25.5	30.98	0.0005	69.5	-4.53	
		2011S	RM518	4	25.5	10.80	0.0111	0.57	-2.25	
		2012N	RM518	4	25.5	16.14	0.0051	0.70	-5.25	
	<i>QHd6</i>	2011N	RM340	6	133.5	13.55	0.0039	59.5		-9.07
		2011S	RM340	6	133.5	5.01	0.0446	0.59		-4.17
		2012N	RM340	6	133.5	7.04	0.0267	0.60		-10.4
	<i>QHd8</i>	2011N	RM447	8	124.6	16.67	0.0022	62.6	-4.43	
		2011S	RM447	8	124.6	6.62	0.0243	0.65	-2.15	
		2012N	RM447	8	124.6	6.92	0.0277	0.60	-5.25	
	<i>QHd10</i>	2011N	RM184	10	58.3	30.98	0.0005	69.5	-4.5	
		2011S	RM184	10	58.3	10.80	0.0111	0.57	-2.25	
		2012N	RM184	10	58.3	16.14	0.0051	0.70	-5.25	
	<i>QHd12</i>	2011N	RM519	12	62.6	30.98	0.0005	69.5	-4.50	
		2011S	RM519	12	62.6	10.80	0.0111	0.57	-2.25	
		2012N	RM519	12	62.6	16.14	0.0051	0.70	-5.25	
		2012N	RM463	12	75.5	16.14	0.0051	0.70	-5.25	
PH	<i>QPh3</i>	2011S	RM55	3	168.2	17.11	0.0033	58.1	4.19	
	<i>QPh6</i>	2012S	RM340	6	133.5	30.29	0.0007	61.0	-7.24	
		2012N	RM340	6	133.5	13.14	0.0064	0.61	-3.81	
PN	<i>QPn1a</i>	2011S	RM490	1	51.0	7.91	0.0227	49.7	-0.82	
		2011N	RM490	1	51.0	6.53	0.0339	0.45	0.95	
	<i>QPn1b</i>	2011N	RM237	1	115.2	5.90	0.0413	42.4	0.84	
	<i>QPn2</i>	2012N	RM106	2	123.2	7.89	0.0209	72.4		1.94
		2011S	RM106	2	123.2	6.04	0.0299	0.63		2.69
	<i>QPn3</i>	2012S	RM55	3	168.2	7.85	0.0265	52.9	-1.12	
	<i>QPn4</i>	2011S	RM518	4	25.5	13.18	0.0067	62.2	1.42	
		2012N	RM518	4	25.5	7.92	0.0260	0.53	1.25	
	<i>QPn5a</i>	2011S	RM122	5	0	5.50	0.0470	40.7	-0.75	
	<i>QPn5b</i>	2012S	RM31	5	118.8	6.94	0.0388	53.6	-1.25	
	<i>QPn6</i>	2011N	RM340	6	133.5	5.65	0.0346	61.7		2.47
		2011S	RM340	6	133.5	5.79	0.0328	0.62		2.84

HEAT RELATED QTL IN RICE AT FLOWERING STAGE

Table 4. (Continued)

Trait	QTL	Env.	Marker	Chrom	Distance	F value	Prob	R2(%)	ADD	DOM
FGN	<i>QPn8</i>	2011S	RM447	8	124.6	5.83	0.0323	0.62	-1.40	
		2012N	RM447	8	124.6	5.32	0.0469	63.9	1.18	
	<i>QPn10</i>	2011S	RM184	10	58.3	13.18	0.0067	0.62	-1.41	
		2012N	RM184	10	58.3	7.92	0.0260	53.1	1.25	
	<i>QPn12</i>	2011S	RM519	12	62.6	13.18	0.0067	62.2	-1.41	
		2012N	RM463	12	75.5	7.92	0.0260	0.53	1.25	
	<i>QFgn1a</i>	2012S	RM490	1	51.0	9.61	0.0173	57.9	11.2	
		2012N	RM490	1	51.0	9.39	0.0182	0.57	-14.7	
	<i>QFgn1b</i>	2012N	RM237	1	115.2	9.21	0.0190	56.8	-12.3	
	<i>QFgn3a</i>	2011S	RM555	3	168.2	6.26	0.0368	43.9	19.8	
	<i>QFgn3b</i>	2011S	RM565	3	215.5	14.08	0.0056	63.8	21.9	
	<i>QFgn7</i>	2012N	RM481	7	3.2	5.94	0.0450	45.9	11.6	
	<i>QFgn8</i>	2012S	RM38	8	28.0	6.09	0.0429	46.5	10.0	
	<i>QFgn11</i>	2012N	RM286	11	0	29.72	0.0055	68.1	-17.4	
SNP	<i>QSn3</i>	2011S	RM565	3	215.5	6.49	0.0343	44.8	-19.0	
	<i>QSn6a</i>	2011S	RM469	6	2.2	8.32	0.0203	51.0	-25.4	
	<i>QSn6b</i>	2011S	RM340	6	133.5	5.75	0.0333	62.2	21.1	
	<i>QSn7</i>	2011S	RM418	7	42.1	10.38	0.0113	67.6	24.3	
		2012N	RM418	7	42.1	42.66	0.0006	0.68	-23.2	
FGR	<i>QFgr1</i>	2012S	RM490	1	51.0	9.44	0.0180	57.4	6.78	
	<i>QFgr3</i>	2011S	RM565	3	215.5	7.61	0.0247	48.8	6.98	
	<i>QFgr7</i>	2011S	RM180	7	30.1	11.33	0.0099	58.6	-8.35	
		2012N	RM418	7	42.1	7.82	0.0313	0.57	6.47	
	<i>QFgr7</i>	2012S	RM210	8	90.3	6.44	0.0414	62.0	4.45	
TGW	<i>QTgw2</i>	2011N	RM341	2	82.7	6.36	0.0357	44.3	1.81	
	<i>QTgw6</i>	2011N	RM541	6	75.5	14.30	0.0034	60.3		6.56
	<i>QTgw7</i>	2012S	RM18	7	90.4	6.90	0.0340	49.7	1.02	
	<i>QTgw9</i>	2012S	RM257	9	66.1	8.58	0.0220	55.1	-1.08	
	<i>QTgw10</i>	2011N	RM216	10	17.6	6.36	0.0357	44.3	-8.10	
GY	<i>QGy1</i>	2012S	RM490	1	51.0	16.82	0.0046	60.6	2.72	
	<i>QGy6</i>	2011N	RM541	6	75.5	13.01	0.0044	58.8		6.58
		2012N	RM541	6	75.5	8.76	0.0166	0.74		18.31
	<i>QGy7</i>	2011S	RM180	7	30.1	6.77	0.0315	45.9	-2.78	
	<i>QGy8a</i>	2011S	RM38	8	28.0	7.08	0.0288	46.9	3.22	
		2012N	RM38	8	28.0	6.11	0.0427	0.47	-5.15	
	<i>QGy8b</i>	2012S	RM210	8	90.3	12.91	0.0106	63.8	1.46	

Table 4. (Continued)

Trait	QTL	Envt.	Marker	Chrom	Distance	F value	Prob	R2(%)	ADD	DOM
HSI	<i>QHsi3</i>	2011S	RM565	3	215.5	7.75	0.0238	49.2	0.21	
	<i>QHsi6</i>	2011S	RM439	6	139.9	5.61	0.0454	41.2	0.32	
	<i>QHsi7</i>	2011S	RM180	7	30.1	6.22	0.0373	43.8	-0.21	
	<i>QHsi8</i>	2012S	RM38	8	28.0	5.98	0.0445	46.1	-0.08	
	<i>QHsi9</i>	2011S	RM257	9	66.1	10.68	0.0114	57.2	0.28	
	<i>QHsi12</i>	2011S	RM20	12	3.2	5.61	0.0454	41.2	0.32	

HD= heading date; *PH*= plant height; *PN*= panicle number; *FGN*= filled grain number per panicle; *SNP*= spikelet number per panicle; *FGR*= filled grain rate *TGW*= thousand grain weight; *GY*= grain yield; *HSI*= heat stress index *ADD*= additive effect; *DOM*= dominant effect, The markers those bolded are detected as linkage by Chi-square test.

Table 5. QTLs detected by one-way ANOVA of Minghui86/Hanhui10 population

Trait	QTL	Envt.	Marker	Chrom	Distance	F value	Prob	R2(%)	ADD	DOM
HD	<i>QHd2</i>	2011N	RM423	2	28.7	4.60	0.0420	50.6		4.11
	<i>QHd4</i>	2011S	RM307	4	0	5.75	0.0476	45.1	2.53	
	<i>QHd9</i>	2011N	RM105	9	32.1	10.32	0.0093	0.51	-1.73	
		2011S	RM105	9	32.1	7.98	0.0180	0.44	-2.22	
		2012N	RM105	9	32.1	18.10	0.0017	64.4	-5.38	
		2012S	RM105	9	32.1	12.33	0.0056	0.55	-5.69	
PH	<i>QHd10</i>	2012S	RM474	10	0	6.71	0.0164	59.9	5.16	5.37
	<i>QPh1</i>	2011N	RM473	1	120.2	11.55	0.0033	62.0		11.8
		2012N	RM473	1	120.2	10.16	0.0049	0.59		11.1
	<i>QPh3</i>	2011S	RM514	3	216.4	7.30	0.0222	42.2	-3.68	
	<i>QPh4</i>	2012S	RM307	4	0	6.05	0.0435	46.4	-8.93	
	<i>QPh7</i>	2012N	RM481	7	3.2	5.93	0.0228	56.9	4.02	
	<i>QPh10</i>	2011S	RM474	10	0	9.18	0.0067	67.1	5.25	
		2011N	RM474	10	0	5.36	0.0293	0.54	4.36	
	<i>QPh11</i>	2011S	RM286	11	0	5.82	0.0365	36.8	-3.64	
PN	<i>QPn5</i>	2012S	RM592	5	31.4	5.45	0.0417	35.3	0.76	
	<i>QPn7</i>	2012N	RM501	7	33.3	8.15	0.0290	57.6	-1.45	
	<i>QPn8</i>	2012N	RM506	8	0	8.52	0.0153	46.0	-1.45	
	<i>QPn12</i>	2012N	RM519	12	62.6	8.52	0.0153	46.0	-1.45	
FGN	<i>QFgn6</i>	2011S	RM340	6	133.5	5.92	0.0352	37.2	18.2	
	<i>QFgn7</i>	2012N	RM481	7	3.2	9.04	0.0070	66.8	-13.9	-31.9
	<i>QFgn9</i>	2012N	RM278	9	77.5	5.52	0.0406	35.6	-12.2	

HEAT RELATED QTL IN RICE AT FLOWERING STAGE

Table 5. (Continued)

Trait	QTL	Envt.	Marker	Chrom	Distance	F value	Prob	R2(%)	ADD	DOM
SNP	<i>QSn_p6</i>	2011N	RM340	6	133.5	9.48	0.0117	48.7	-24.3	
	<i>QSn_p7</i>	2012N	RM481	7	3.2	5.98	0.0222	0.57	-17.5	
		2012S	RM478	7	93.8	14.78	0.0032	59.6	-14.7	
	<i>QSn_p8</i>	2011S	RM310	8	57.0	5.55	0.0268	55.2	-22.2	
FGR	<i>QFgr2</i>	2011N	RM263	2	127.5	6.31	0.0308	38.7	-7.63	
	<i>QFgr3</i>	2011N	RM340	6	133.5	6.12	0.0329	38.0	6.53	
	<i>QFgr7</i>	2012N	RM234	7	88.2	6.03	0.0339	0.38	5.06	
		2012S	RM234	7	88.2	6.13	0.0327	38.0	7.48	
	<i>QFgr11</i>	2011N	RM457	11	83.0	4.97	0.0499	33.2	5.36	
TGW	<i>QTgw1a</i>	2012S	RM575	1	51.0	9.79	0.0121	52.1	1.19	
	<i>QTgw1b</i>	2011N	RM306	1	98.1	10.24	0.0095	0.51	-2.27	
		2012N	RM473	1	120.2	16.06	0.0011	68.1	2.20	0.98
	<i>QTgw2</i>	2011S	RM71	2	49.8	11.30	0.0121	61.7	1.64	
	<i>QTgw3a</i>	2012N	RM7	3	64.0	7.37	0.0127	62.1	2.01	
	<i>QTgw3b</i>	2012N	RM282	3	100.6	7.07	0.0288	46.9	1.58	
	<i>QTgw4a</i>	2011N	RM307	4	0	10.51	0.0142	60.0	2.78	
	<i>QTgw4b</i>	2012S	RM119	4	76.1	5.32	0.0438	34.7	1.34	
	<i>QTgw5a</i>	2012N	RM163	5	78.7	30.11	0.0003	65.1	1.95	
	<i>QTgw5b</i>	2011N	RM31	5	118.8	7.34	0.0219	42.3	2.80	
		2011S	RM334	5	141.8	4.82	0.0378	0.52		-3.6
	<i>QTgw6</i>	2011S	RM136	6	51.2	4.70	0.0399	51.1	1.23	
	<i>QTgw8</i>	2011S	RM515	8	80.5	5.16	0.0464	34.1	0.91	
	<i>QTgw9</i>	2011N	RM278	9	77.5	5.40	0.0425	35.1	1.49	
		2011S	RM278	9	77.5	5.26	0.0448	0.34	0.96	
GY	<i>QGy2</i>	2011N	RM263	2	127.5	9.28	0.0123	48.1	-2.28	
	<i>QGy3</i>	2011N	RM442	3	224.2	5.55	0.0402	35.7	1.46	
	<i>QGy4</i>	2011N	RM401	4	8.5	11.36	0.0138	62.0	1.46	
	<i>QGy7</i>	2012S	RM234	7	88.2	5.72	0.0378	36.4	1.69	
	<i>QGy9</i>	2012N	RM278	9	77.5	10.73	0.0084	51.8	-3.83	
HSI	<i>QHsi7</i>	2012S	RM234	7	88.2	5.77	0.0372	36.6	-0.07	
	<i>QHsi8</i>	2011S	RM515	8	80.5	5.10	0.0474	33.8	0.16	

HD= heading date; PH= plant height; PN= panicle number; FGN= filled grain number per panicle; SNP= spikelet number per panicle; FGR= filled grain rate TGW= thousand grain weight; GY= grain yield; HSI= heat stress index S= heat stress condition; N= normal condition; R2= phenotypic variation explained; ADD= additive effect; DOM= dominant effect, The markers those bolded are detected as linkage by Chi-square test

Table 6. QTLs detected by one-way ANOVA of Minghui86/Bala population

Trait	QTL	Env.	Marker	Chrom	Distance	F value	Prob	R2 (%)	ADD	DOM
HD	<i>QHd3</i>	2011S	RM231	3	15.7	5.00	0.0493	33.3	-1.00	
	<i>QHd4a</i>	2011S	RM335	4	21.5	8.00	0.0179	44.4	1.33	
	<i>QHd4b</i>	2011S	RM317	4	118.3	10.17	0.0097	50.4	1.65	
	<i>QHd10a</i>	2011S	RM184	10	58.3	10.17	0.0097	50.4	1.65	
	<i>QHd10b</i>	2012S	RM147	10	99.8	6.73	0.0267	40.2	-4.03	
	<i>QHd11</i>	2011N	RM286	11	0	5.98	0.0402	42.8	-0.59	
	<i>QHd12</i>	2011S	RM19	12	20.9	14.15	0.0037	58.6	1.41	
PH	<i>QPh1</i>	2012N	RM490	1	51.0	10.73	0.0169	64.1	7.14	
		2012S	RM490	1	51.0	7.39	0.0347	0.55	6.87	
	<i>QPH2</i>	2012N	RM145	2	49.8	6.86	0.0256	40.7	3.99	
	<i>QPh3a</i>	2011S	RM545	3	35.3	7.10	0.0237	41.5	-6.28	
	<i>QPh3b</i>	2011S	RM7	3	64.0	7.10	0.0237	41.5	-6.28	
	<i>QPh6</i>	2011S	RM136	6	51.2	4.29	0.0492	48.8		-13.3
	<i>QPh9</i>	2011S	RM257	9	66.1	5.40	0.0425	35.1	3.19	
	<i>QPh10</i>	2012N	RM333	10	110.4	5.91	0.0354	37.1	6.80	
	<i>QPn1</i>	2011N	RM490	1	51.0	20.53	0.0040	67.4	1.81	
PN		2011S	RM490	1	51.0	14.88	0.0084	0.61	1.29	
		2012N	RM283	1	31.4	7.78	0.0191	0.44	1.37	
	<i>QPn2</i>	2011N	RM145	2	49.8	10.59	0.0087	51.4	0.94	
	<i>QPn3</i>	2012S	RM231	3	15.7	7.21	0.0229	41.9	2.26	
	<i>QPn5</i>	2011S	RM334	5	141.8	10.45	0.0090	51.1	1.29	
		2012S	RM178	5	118.8	5.50	0.0437	0.38	2.05	
	<i>QPn7</i>	2011S	RM70	7	64.6	5.59	0.0265	55.4		4.10
	<i>QPn8</i>	2012S	RM407	8	5.7	5.37	0.0430	34.9	-1.54	
	<i>QPn9</i>	2011N	RM108	9	73.3	36.22	0.0018	67.9	1.74	
		2011S	RM108	9	73.3	23.87	0.0045	0.63	1.74	
		2012S	RM333	10	110.4	9.80	0.0107	0.49	4.44	
	<i>QPn10</i>	2012S	RM333	10	110.4	9.80	0.0107	49.5	4.44	
	<i>QFgn1</i>	2011N	RM490	1	51.0	31.48	0.0014	64.0	-12.1	
	<i>QFgn2</i>	2011N	RM233	2	16.3	6.79	0.0262	40.5	-10.1	
FGN	<i>QFgn5a</i>	2011S	RM163	5	78.7	5.51	0.0408	35.5	8.50	
	<i>QFgn5b</i>	2011N	RM178	5	118.8	5.85	0.0387	39.4	-10.1	
	<i>QFgn7</i>	2011S	RM70	7	64.6	4.26	0.0499	48.6		-22.6
	<i>QFgn9</i>	2011N	RM108	9	73.3	50.59	0.0009	61.0	-13.4	

HEAT RELATED QTL IN RICE AT FLOWERING STAGE

Table 6. (Continued)

Trait	QTL	Envt.	Marker	Chrom	Distance	F value	Prob	R2 (%)	ADD	DOM
SNP	<i>QFgn10</i>	2011S	RM107	9	82.4	5.43	0.0421	0.35	-9.82	
		2012N	RM107	9	82.4	8.64	0.0148	0.46	-22.3	
		2011N	RM304	10	73.0	7.36	0.0218	42.4	10.3	
		2011N	RM286	11	0	5.59	0.0457	41.1	14.2	
		2012S	RM473	1	120.2	8.64	0.0353	61.2	19.0	
	<i>QSn2</i>	2011N	RM233	2	16.3	10.20	0.0096	0.50	-19.6	
		2012S	RM233	2	16.3	11.88	0.0063	54.3	-18.8	
		2011N	RM335	4	21.5	10.85	0.0081	52.0	21.7	
		2011S	RM335	4	21.5	7.92	0.0183	0.44	26.7	
		2012N	RM335	4	21.5	7.83	0.0189	0.44	25.1	
	<i>QSn4b</i>	2012N	RM317	4	118.3	6.10	0.0331	37.9	27.1	
		2012S	RM317	4	118.3	5.21	0.0456	0.34	18.9	
		2011N	RM178	5	118.8	17.60	0.0023	66.2	-18.9	
		2012S	RM178	5	118.8	13.39	0.0052	0.60	-19.5	
		2012S	RM510	6	20.8	5.7	0.0381	36.3	26.3	
SNP	<i>QSn6b</i>	2012S	RM439	6	139.9	5.7	0.0381	36.3	26.3	
		2011N	RM180	7	30.1	4.78	0.0385	51.5	-15.7	
		2012S	RM47	7	90.4	5.85	0.0387	39.4	16.8	
		2011N	RM107	9	82.4	9.67	0.0111	0.49	-24.4	
		2012N	RM107	9	82.4	10.18	0.0097	50.4	-31.2	
	<i>QSn10</i>	2011N	RM304	10	73.0	12.48	0.0054	55.5	19.7	
		2012N	RM184	10	58.3	6.1	0.0331	0.38	27.1	
		2012S	RM184	10	58.3	5.21	0.0456	0.34	18.9	
		2011N	RM21	11	85.7	7.63	0.0200	43.3	18.2	
		2012N	RM21	11	85.7	5.99	0.0344	0.37	21.3	
	<i>QSn12</i>	2011N	RM19	12	20.9	6.91	0.0252	0.41	17.6	
		2011S	RM19	12	20.9	8.89	0.0138	0.47	25.3	
		2012N	RM19	12	20.9	12.34	0.0056	55.2	25.8	
		2012S	RM247	12	32.3	7.13	0.0235	0.42	16.5	
		2012N	RM324	2	66.0	9.32	0.0185	57.1	-3.11	
FGR	<i>QFgr3</i>	2011S	RM545	3	35.3	5.19	0.0460	34.2	8.24	
		2011N	RM335	4	21.5	7.74	0.0194	43.6	-5.63	
		2012N	RM335	4	21.5	7.67	0.0198	0.43	-5.32	
	<i>QFgr5</i>	2011N	RM178	5	118.8	5.34	0.0462	37.2	3.73	
		2012N	RM510	6	20.8	6.53	0.0286	39.5	-7.95	

Table 6. (Continued)

Trait	QTL	Envt.	Marker	Chrom	Distance	F value	Prob	R2 (%)	ADD	DOM
TGW	<i>QFgr6b</i>	2012N	RM439	6	139.9	6.53	0.0286	39.5	-7.95	
	<i>QFgr7</i>	2011N	RM336	7	61.0	17.04	0.0021	63.0	5.94	
	<i>QFgr11</i>	2011N	RM202	11	54.0	9.37	0.0063	67.6	-6.57	
	<i>QFgr12</i>	2011N	RM247	12	32.3	6.4	0.0298	0.39	-4.89	
		2012N	RM19	12	20.9	8.49	0.0155	45.9	-5.03	
	<i>QTgw1</i>	2012S	RM5	1	94.9	5.25	0.0449	34.4	-1.32	
	<i>QTgw2</i>	2011N	RM324	2	66.0	11.2	0.0123	61.5	-4.57	
	<i>QTgw3a</i>	2011N	RM231	3	15.7	7.31	0.0222	42.2	2.07	
	<i>QTgw3b</i>	2012S	RM168	3	171.2	6.13	0.0328	38.0	-1.38	
	<i>QTgw5</i>	2011N	RM178	5	118.8	5.68	0.0411	0.39	2.08	
		2011S	RM163	5	78.7	5.58	0.0398	0.36	-1.15	
		2012N	RM178	5	118.8	6.25	0.0338	41.0	1.57	
	<i>QTgw7</i>	2011N	RM47	7	90.4	9.43	0.0133	51.2	-1.75	
		2012S	RM47	7	90.4	5.49	0.0438	0.38	-1.4	
	<i>QTgw8</i>	2012N	RM342	8	78.4	5.34	0.0434	0.35	1.42	
		2012S	RM342	8	78.4	25.33	0.0005	61.7	1.67	
	<i>QTgw9</i>	2012N	RM107	9	82.4	5.24	0.0451	0.34	1.87	
		2012S	RM107	9	82.4	6.31	0.0308	38.7	1.62	
	<i>QTgw11</i>	2011S	RM286	11	0	5.79	0.0427	42.0	-1.92	
GY	<i>QGy1</i>	2012N	RM283	1	31.4	7.79	0.0191	43.8	3.54	
	<i>QGy2</i>	2011N	RM324	2	66	7.57	0.0284	52.0	-2.41	
	<i>QGy4</i>	2012S	RM317	4	118.3	5.43	0.042	35.2	-2.23	
	<i>QGy5</i>	2011S	RM334	5	141.8	7.84	0.0188	44.0	-1.65	
	<i>QGy7</i>	2011N	RM180	7	30.1	4.45	0.0452	49.7		5.00
	<i>QGy8</i>	2012S	RM407	8	5.7	5.34	0.0434	34.8	-1.67	
	<i>QGy10</i>	2011S	RM147	10	99.8	5.13	0.0469	0.34	-1.47	
		2012S	RM184	10	58.3	5.43	0.042	35.2	-2.23	
HIS	<i>QHsi3</i>	2011S	RM545	3	35.3	7.27	0.0225	42.1	-0.1	
	<i>QHsi4</i>	2012S	RM564	4	73.1	8.44	0.0439	67.8	0.07	

HD= heading date; PH= plant height; PN= panicle number; FGN= filled grain number per panicle; SNP= spikelet number per panicle; FGR= filled grain rate TGW= thousand grain weight; GY= grain yield per plant; HSI= heat stress index; S= heat stress condition; N=normal condition; R2= phenotypic variation explained, ADD= additive effect; DOM= dominant effect The markers those bolded are detected as linkage by Chi-square test.

CONCLUSION

The best population for tested traits was K; Minghui86/IR65600-27-1-2-22 which shows the lowest HSI (0.43) and the highest GY (10 g/plant). The second one was the population L; Minghui86/Hanhui10 (9.65 g/plant, HSI 0.44). Population M; Minghui86/Bala (9 g/plant, HSI 0.57) and population J; Minghui86/Jianxisimal (6.95 g/plant, HSI 0.62) were third and fourth according to the ranking, respectively.

A total of 13 QTLs were detected for HSI, including three for population J, six for K and two for L and two for population M. IRM473, RM474, RM202 and RM237 were detected at least from two populations suggesting that these are important and stable QTLs in MH86 background. Moreover, *QHsi7* associated with RM180 was found from both J and K populations under stress condition in 2011 suggesting that important locus for heat tolerant trait in rice.

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