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AGRONOMIC PERFORMANCE AND YIELD OF DOUBLED HAPLOID RICE LINES IN ADVANCED YIELD TRIAL

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SUMMARY

Anther culture can be used to accelerate plant breeding program in producing superior variety of rice. The aims of this research were to determine agronomic performance and yield of doubled haploid (DH) lines of lowland rice and select the best genotypes for multilocation yield trials. The research was conducted in Indonesia at three locations, i.e. Subang (West Java), Cianjur (West Java) and Malang (East Java) using a randomized complete block design. It consisted of 35 genotypes and three check varieties (Ciherang, Inpari 13 and Inpara 5) as treatments. The treatments were repeated 3 times. The results showed that interaction of genotype and environment was significant on all traits. Genotypic variance and heritability estimates of all traits were in the high category and ranged between 1.57 – 458.51 and 0.58 - 0.96, except for tiller number and the productivity which were moderate. Fourteen DH lines were selected based on yield and selection index, which takes, into account a combination of traits, i.e. tiller number, filled grain per panicle, percentage of filled grain per panicle, 1000-grain weight, days to harvest and productivity, according to their relative weightage. The yield of the lines ranged between 4.82 - 6.60 ton/ha. Yield of Ciherang, Inpari 13 and Inpara 5 were 5.76, 4.85, and 4.82 ton/ha respectively. The selected DH lines will be used further in multilocation yield trial.

Key words: Doubled haploid lines, genetic variance, heritability, selection index, yield trial

Key findings: Fourteen doubled haploid rice lines with good agronomic performance and high yield were selected from advanced yield trials for further multilocation yield trials. They showed similar or higher productivity and weighted selection index value than three check varieties including Ciherang, a mega variety, which has the largest area of harvest in Indonesia.

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INTRODUCTION

Rice has an important role in producing food sources, especially in Asia. Based on harvested areas, Indonesia is in the third position among the ten highest rice producing countries in the world with average rice harvest area of 13.32 million hectares (8.23%) (Nuryati *et al*., 2015). However, rice fields keep dwindling due to land conversion as caused by increasing population. Global climate change also causes more biotic and abiotic stresses throughout the year. Thus, both of these become challenge in increasing rice production.

Conventional rice breeding has developed many new varieties with various advantages. However, conventional rice breeding takes significant amount of time, i.e. 6 to 8 generations, for conducting selection until the obtainment of pure lines (Fehr, 1987). Through application of anther culture, pure lines in the form of doubled haploid (DH) plants can be readily available in rice breeding at first generation of culture. Then, the desirable pure lines can be selected from those homogeneous and homozygous DH plants-derived microspore (Dewi and Purwoko, 2012).

The first stage of breeding is to make crosses to obtain high variability of lines. The variability is due to differences either in the genetic constitutions of the individual in the population or due to the differences in the environment in which they are grown. However for making any effective breeding programme, genetic improvement mainly depends on the amount of genetic variability presents in the lines (Fehr, 1987).

In Indonesia, Ciherang is one of the most widely grown rice varieties or "mega variety" (Toledo *et al*., 2015). Characteristics of Ciherang include short to moderate plant height (91-106 cm), moderate days to harvest (116-125 DTH), responsive to fertilization, upright plant form, relatively resistant to lodging, resistant to biotype 2 and moderately resistant to biotype 3 of brown plant hopper, ideal 1000-grains weight (27-28 g), high yield (> 6.0 ton per hectare), good eating quality (23% amylose content) and low glycemic index (54.9) (Suprihatno *et al*., 2011). Therefore, development of superior rice variety similar to Ciherang but with higher yield, more resistance to main pest and disease, more tolerance to certain abiotic stresses can be an alternative to increase rice productivity because such varieties can be easily accepted by farmers.

Selection as a part of breeding program will give optimum response when using the appropriate selection criteria. Selection can be done by using selection index when considering several traits simultaneously, because it is desirable to choose individuals with the best combination of these traits (Ibrahim *et al*., 2012; Fotokian and Agahi, 2014; Silva *et al.,* 2016). Construction of selection indices and their analysis would give the most appropriate economic weightage to the phenotypic values of each selected characters to be used simultaneously for selection (Ceron-Rojas 2008; Ferdous *et al*., 2010, Dutta *et al*., 2013).

Safitri *et al.,* (2016) obtained 125 DH rice lines from anther culture of 12 different F1s, derived from crossing of rice tolerant to salinity to high yielding rice. These lines have been evaluated in preliminary yield trials (PYT). The aims of this research were to conduct advanced yield trials (AYT) to determine agronomic performance and yield of 35 DH lowland rice lines and select genotypes, that are similar to or exceed the check varieties, including a mega variety “Ciherang”, suitable for multilocation yield trials.

MATERIALS AND METHODS

The research was conducted in three locations (Subang and Cianjur in West Java and Malang in East Java, Indonesia) during December 2015 - September 2016 using a randomized complete block design. It consisted of 35 genotypes and three check varieties (Ciherang, Inpari 13 and Inpara 5) as treatments. Codes in each line showed its parents, i.e. HS1 (Inpara 5/IR77674), HS2 (IR77674/Inpara 5), HS4 (IR77674 / Inpari 29), HS15 (IR78788 /Inpara 5), HS17 (Dendang/Inpari 30) and HS18 (IR64/Dendang). The treatments were repeated 3 times. The experimental unit was a 3 m x 3 m plot with plant spacing of 25 cm x 25 cm. Observations were done on plant height, tiller number, number of filled grain per panicle, percentage of filled grain per panicle, total number of spikelet per panicle, days to 50% flowering, days to harvest, panicle length, 1000-grain weight and productivity.

Data obtained were analyzed by normality test, if the tested character spread normally then continued with the analysis of the variety performed on the average of each genotype (Gomez and Gomez, 1984). If the F test was significant, Dunnett’s test was done and genetic parameters were predicted. The estimation of genetic parameters includes estimation of genotypic variance, environmental variance and phenotypic variance.

The value of the variances were obtained through:

$$\sigma^2_g = (\text{MS genotype} - \text{MS genotype x environment}) / rl$$

$$\sigma^2_{ge} = (\text{MS genotype x environment} - \text{MS error}) / r$$

$$\sigma^2 = \text{MS error}$$

$$\sigma^2_p = \sigma^2/rl + \sigma^2_{ge}/l + \sigma^2_g$$

r and l are the number of replications and environments, respectively.

Prediction of broad sense heritability (h^2_{bs}) based on entry means was calculated as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

σ^2_g is the genotypic variance
σ^2_p is the phenotypic variance
h^2 is the broad sense heritability

Grouping of broad sense heritability was done according to Stanfield (1983): high ($0.50 < h^2 < 1.00$), moderate ($0.20 < h^2 < 0.50$), and low ($h^2 < 0.20$). The experimental coefficient of variation (CV) and genotypic coefficient of variation (GCV) were calculated as follows:

$$CV = \frac{\sqrt{MSE}}{\bar{x}} x100\%$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} x100\%$$

MSE is the mean square error
σ^2_g is the genotypic variance
$\bar{x}$ is the grand mean

Selection index was used to select genotypes for multilocation yield trials. Several agronomic important traits representing yield and yield components were chosen simultaneously and economic weightage was given to the phenotypic values of each trait in such a way that expected gain in aggregate genotypic value would be maximized (Ramos *et al*., 2014; Gazal *et al*., 2017). The selected agronomic important traits (X) were weighted, i.e. productivity: +5, the tiller number: +1, the number of filled grain per panicle: +1, the percentage of filled grain per panicle: +1, total number of spikelet per panicle: +2, 1000-grain weight: +1 and days to harvest: -1. Determination of the selection index were conducted based on Falconer and Mackay (1996):

$$I = b_1X_1 + b_2X_2 + b_3X_3 + ... + b_nX_n.$$

I is the selection index
b_n is the weight of the variable to n
X_n is a standardized phenotype value for variables to n, where:

$$x_n = \frac{x - \bar{x}}{s}$$

x is the means of each genotype
$\bar{x}$ is the means of the variable
s is the standard deviation of the variable.

Then, the I values were ranked and used to select the best lines. The combined analysis of variance and the construction of weighted selection index were carried out using SAS 9.0 and STAR programs.

RESULTS AND DISCUSSION

Analysis variance and variance components

Analysis of variance showed that variation due to genotypes was significant for all studied traits, except for the tiller number (Table 1). Differences among locations were also significant for all traits, except for total number of spikelet per panicle. The interaction between genotype and location (G x E) were found significant for all traits. Similar findings showed significant variability due to G x E interaction for all traits which indicated the occurence of differential or a change in response of each genotype across the environments for these traits (Mutt *et al*., 2010, Ogunbayo *et al*., 2014, Sivakumar *et al*., 2017).

Character expression is determined by genetic and environmental factors. Therefore, variability can be observed through phenotypic variance (PV, σ^2_p) which is constructed from variance components caused by genotypic variance (GV, $\sigma^2_{g)}$ and environmental variance (σ^2_e). The highest genotypic variance (GV) and phenotypic variance (PV) were found in total number of spikelet per panicle trait with 458.5 and 516.4, respectively (Table 2). However, relationship between GV and PV showed that in all traits PV was

Table 1. Combined analysis of variance of doubled haploid lines of lowland rice.

Traits	F values of			Coefficient of variation (%)
	Genotype (G)	Environment (E)	G × E Interaction	
Plant height	8.45^{**}	130.22^{**}	19.13^{**}	1.82
Tiller number	1.30^{ns}	145.23^{**}	2.54^{**}	12.25
Number of filled grain/panicle	3.35^{**}	7.64^{**}	4.93^{**}	9.17
Percentage filled grain/panicle	2.72^{**}	104.08^{**}	6.15^{**}	4.93
Total number of spikelet per panicle	8.92^{**}	0.55^{ns}	4.74^{**}	6.44
1000-grain weight	17.15^{**}	86.48^{**}	2.94^{**}	2.57
Panicle length	25.91^{**}	18.86^{**}	4.63^{**}	2.41
Days to 50% flowering #	4.79^{**}	46.27^{**}	3.88^{**}	2.07
Days to harvest	2.37^{**}	3.80^{*}	7.34^{**}	1.09
Productivity	1.76^{*}	3.16^{ns}	2.69^{**}	14.45

#: location of Subang and Malang; ns, * and **: non-significant, and significant at $P < 0.05$ and $P < 0.01$, respectively.

Table 2. Mean basis variance analysis and heritability of agronomic traits of 38 rice genotypes.

Traits	σ^2p	σ^2g	σ^2	σ^2ge	GCV	$2\sigma\sigma^2g$	h^2
Plant height	66.99	59.07	3.73	22.53	7.22	15.90	0.88
Tiller number	2.02	0.48	5.49	2.81	3.62	1.04	0.24
Number of filled grain/panicle	241.10	169.09	131.42	172.23	10.40	69.69	0.70
Percentage filled grain/panicle	27.04	17.11	14.52	24.93	5.35	8.55	0.63
Total number of spikelet/panicle	516.40	458.51	109.89	137.04	13.16	122.01	0.89
1000-grain weight	2.74	2.58	0.49	0.32	5.90	0.63	0.94
Panicle length	5.64	5.42	0.42	0.51	8.64	1.28	0.96
Days to 50% flowering #	8.10	6.41	2.62	2.51	3.24	1.96	0.79
Days to harvest	2.71	1.57	1.40	2.96	1.16	0.92	0.58
Productivity	0.33	0.14	0.62	0.35	6.88	0.13	0.43

#: location of Subang and Malang, σ^2p: phenotypic variance; σ^2g: genotypic variance; σ^2: error variance; σ^2ge: variance of genotype and location interaction; GCV: genotypic coefficient of variation; $2\sigma\sigma^2g$: 2x standard deviation of genotypic variance; h^2: broad sense heritability.

slightly greater than GV, thus revealing little influence of environment for their expression.

Heritability influences the success of selection activity accross environment. Broad sense heritability ranged between 0.24 (tiller number) to 0.96 (panicle length) (Table 2). Based on the criteria of Stanfield (1983), the heritability estimates were high for all traits, except for number of tiller andproductivity (moderate), with coefficient of variation below 10% (Table 1). Previously, Vikram *et al.*, (2011) and Saikumar *et al.*, (2014) reported high to moderate heritability for different quantitative traits studied in rice. Traits having high heritability indicated that genetic factors contributed more to the traits than environmental factors. The success of selection is heavily relied on the occurence of variability controlled by genetic factor (Wicaksono, 2001).

Genotypic coefficient of variation (GCV) can be categorized as low (0-10%), moderate (10-20%) and high (> 20%) (Sivasubramanian and Madhavamenon, 1973). Table 2 showed that GCV ranged between 1.16% (day to harvest) to 13.16% (total number of spikelet per panicle). Broad or narrow genetic variability is determined by GV (σ^2_g) and standard deviation of GV ($\sigma\sigma^2$g). In this study, all traits except for tiller number had broad genetic variability, because σ^2g >2$\sigma\sigma^2$g. These findings were similar to that of Akinwale *et al.,* (2011) and Sadeghi (2011). Moreover, the trait that have broad genetic variability coupled with high heritability estimates will facilitate breeders in conducting selection activities (Zen, 2002).

Agronomic Traits

Agronomic trait performance including yield are presented in Table 3 and 4. The DH line of HS1-28-1-1 had the highest plant height (124.22 cm), while HS18-17-1-1 had the lowest plant height (86.39 cm) (Table 3). Plant height becomes the consideration of the farmer, because it is related to the lodging tendency and the ease of harvesting. Generally, tall genotypes (> 125 cm) tend to be very sensitive to lodging, while short one (< 80 cm) is relatively difficult for farmers to harvest (Dewi *et al*., 2009).

The tiller number ranged from 15.0 to 21.8 stems/hill (Table 3). According to IRRI (2002) the tiller number 10-19 stems/hill is grouped into medium category, tiller number 20 to 25 stems into high category, and tiller number more than 25 stems into very high category. Tiller number in the tested DH lines was medium to high. Most of the DH lines had medium tiller number similar to all check varieties.

The highest percentage of filled grain per panicle was achieved by Inpara 5 (87.1%), while the lowest percentage of filled grain per panicle was achieved by HS4-15-3-13 (68.6%) (Table 3). Generally DH lines had high percentage of filled grain per panicle and were similar to check varieties Ciherang and Inpari13. One of the traits contributing to ideal plant type, according to Ma *et al.,* (2006), was the high number of filled grains (180-240 grain/panicle) and percentage filled grain more than 85%. Percentage of filled grain per panicle leads to panicle fertility, so that high panicle fertility contributed to high potential yield (Dewi *et al*., 2009).

DH line having the highest total number of spikelet per panicle was HS4-17-1-1 and the line with the lowest total number of spikelet per panicle was HS2-5-1-2. Five DH lines had number of spikelet per panicle significantly higher than Ciherang (Table 3). Panicle length of DH lines ranged from 23.28 to 30.02 cm (Table 4). Eighteen DH lines had panicle length significantly longer than Ciherang (25.47 cm). Generally, number of spikelet per panicle and panicle length contributed to seed shape and size (Dewi *et al*., 2009). Seed index or 1000-grain weight of 8 DH lines were significantly heavier than Ciherang (27.07 g), namely HS1-5-1-1 (29.98 g), HS1-5-1-2 (29.77 g), HS4-8-1-2 (31.78 g), HS2-5-1-1 (30.57 g), HS2-5-1-2 (31.51 g), HS4-13-1-1 (29.01 g), HS4-15-1-9 (28.77 g) and HS4-15-3-39 (28.16 g).

Table 3. Mean performance of 38 genotypes for yield attributing traits.

Genotype	Plant height (cm)	Tiller Number (stems/hill)	Number of filled grain (FG)/ panicle	Percentage FG/panicle	Total number spikelet/panicle	Panicle length (cm)
HS1-5-1-1	103.39	19.7	119.7	86.7*	137.9*	26.09
HS1-5-1-2	101.62*	20.9	105.8*	86.8*	122.6*	25.40
HS1-15-1-1	109.07*	19.7	96.0*	73.7	131.9*	23.76*
HS1-28-1-1	124.22*	18.3	112.9*	74.1	152.3	24.54
HS1-28-1-3	119.69*	18.6	104.1*	75.0	138.9*	23.28*
HS1-28-1-4	119.94*	20.9	104.9*	72.4*	143.9*	23.89*
HS2-5-1-1	95.27*	18.3	96.9*	86.2*	112.3*	24.21*
HS2-5-1-2	88.46*	20.4	92.9*	86.6*	107.6*	24.10*
HS2-9-1-1	106.64	17.7	160.4*	81.3	197.6*	28.81*
HS4-8-1-2	106.70	17.0	123.6	74.2	166.9	29.44*
HS4-13-1-1	109.12*	16.4	148.0	80.8	184.6*	29.00*
HS4-13-1-3	116.68*	17.3	136.7	75.4	181.8	29.44*
HS4-13-1-4	115.22*	19.2	138.8	75.0	186.7*	28.79*
HS4-15-1-9	106.36	17.1	115.9	79.3	146.8*	29.94*
HS4-15-2-5	110.29*	19.3	122.2	72.0*	169.4	30.02*
HS4-15-3-13	110.70*	20.3	119.9	68.6*	174.8	30.02*
HS4-15-3-16	110.66*	19.8	117.7	71.7*	164.7	29.33*
HS4-15-3-39	108.28*	19.6	117.6	69.7*	169.1	29.88*
HS4-17-1-1	103.59	15.0*	137.9	68.7*	200.3*	29.43*
HS15-11-1-2	95.90*	20.9	136.6	77.1	177.2	25.10
HS15-13-1-1	122.79*	17.9	147.8	84.0	176.3	27.24*
HS17-1-1-1	115.58*	19.3	125.9	81.2	155.3	28.91*
HS17-3-1-1	105.60	21.3	131.7	78.1	168.2	29.47*
HS17-3-1-3	107.59	19.1	136.4	78.7	173.6	29.48*
HS17-3-1-4	106.13	20.9	137.6	76.0	180.7	29.63*
HS17-3-1-6	104.87	19.7	129.4	78.7	164.2	29.98*
HS17-3-1-7	105.16	19.4	135.2	80.1	168.3	29.06*
HS17-21-1-1	102.88	19.8	130.1	79.1	164.4	25.33
HS17-21-1-2	101.88*	20.1	129.6	79.2	162.9	25.12
HS17-21-1-5	100.17*	20.0	119.1	77.7	154.3	24.88
HS17-21-1-6	99.08*	21.8	124.7	76.4	162.9	24.71
HS17-21-1-7	102.69	19.2	117.8	75.0	156.7	24.82
HS17-31-1-1	105.73	18.6	131.7	72.6*	182.0	25.63
HS17-31-1-6	104.99	18.3	136.8	70.7*	194.3*	24.93
HS18-17-1-1	86.39*	19.2	118.6	71.6*	164.8	23.54*
Ciherang	105.16	18.7	132.1	78.8	166.8	25.47
Inpara 5	99.48*	18.3	110.4*	87.1*	127.1*	25.22
Inpari 13	105.28	18.4	150.2*	77.0	195.0*	27.08*
Average	106.40	19.1	125.1	77.3	162.8	27.26
LSD 0.05	2.81	3.41	16.70	5.55	15.28	0.95

*: significantly different to Ciherang at $P < 5\%$

Table 4. Mean performance of 38 genotypes for yield attributing traits and weighted index values.

Genotype	1000-grain weight (g)	Days to 50% flowering (DAS)	Days to harvest (DAS)	Productivity (ton/ha)	Weighted Index
HS1-5-1-1	29.98*	79.0	106.6*	6.60	10.15
HS1-5-1-2	29.77*	79.0	108.2*	6.30	4.23
HS1-15-1-1	25.37*	80.0	108.8*	5.04	-13.06
HS1-28-1-1	25.53*	79.8	108.7*	5.26	-7.56
HS1-28-1-3	25.74*	79.7	108.8*	4.37*	-15.63
HS1-28-1-4	25.36*	81.5	108.6*	4.33*	-14.89
HS2-5-1-1	30.57*	73.2*	104.8*	5.14	-3.96
HS2-5-1-2	30.51*	73.2*	104.7*	4.87	-5.69
HS2-9-1-1	26.60	80.0	107.6*	5.62	8.13
HS4-8-1-2	31.78*	76.3*	106.2*	5.90	9.38
HS4-13-1-1	29.01*	72.5*	105.8*	4.82	3.69
HS4-13-1-3	27.60	76.7*	107.6*	5.81	5.58
HS4-13-1-4	27.24	78.5	107.0*	6.03	8.54
HS4-15-1-9	28.77*	71.5*	105.7*	5.79	2.01
HS4-15-2-5	26.77	77.7*	108.3*	5.57	-0.23
HS4-15-3-13	27.73	79.2	109.2	5.67	1.82
HS4-15-3-16	27.19	79.2	108.1*	5.50	-0.84
HS4-15-3-39	28.16*	80.0	108.4*	5.70	1.93
HS4-17-1-1	26.07	76.2*	106.8*	5.59	2.85
HS15-11-1-2	23.71*	81.7	109.8	4.75	-7.09
HS15-13-1-1	27.12	78.5	108.1*	4.99	0.88
HS17-1-1-1	27.22	78.2*	108.1*	4.77	-5.01
HS17-3-1-1	27.06	75.3*	107.7*	6.21	7.33
HS17-3-1-3	27.04	74.8*	106.3*	5.47	3.33
HS17-3-1-4	26.90	76.3*	107.3*	5.16	1.99
HS17-3-1-6	26.80	75.3*	106.7*	5.35	0.35
HS17-3-1-7	26.32	77.7*	107.8*	6.41	7.30
HS17-21-1-1	26.82	80.5	110.8	5.75	1.07
HS17-21-1-2	27.50	81.0	109.9	6.29	5.32
HS17-21-1-5	27.02	82.0	110.1	6.29	2.84
HS17-21-1-6	26.43	81.5	109.9	5.62	-0.05
HS17-21-1-7	27.37	81.8	111.3	5.83	-1.00
HS17-31-1-1	27.29	78.8	108.2*	5.65	3.42
HS17-31-1-6	26.49	80.5	110.3	5.27	0.35
HS18-17-1-1	24.40*	80.2	109.2	4.82	-10.22
Ciherang	27.07	81.2	110.7	5.76	1.41
Inpara 5	27.13	77.8*	108.8*	4.74	-10.39
Inpari 13	26.29	73.8*	106.2*	4.85	1.71
Average	26.95	78.2	108.1	5.47	
LSD 0.05	1.01	2.90	1.72	1.15	

*: significantly different to Ciherang at $P < 5\%$; DAS: days after sowing

Inpari 13, Inpara 5 and 26 DH lines showed significantly shorter day to maturity compared to Ciherang (Table 4). According to classification of days to harvest (DTH) from days after sowing (DAS) made by Indonesian Center for Rice Research (ICRR) the tested DH lines fell into the early maturing classes (104 < DTH < 124 DAS) (Suprihatno *et al*., 2011). Therefore, all tested DH lines were categorized as early maturing. The tested DH lines had less days to 50% flowering or similar to Ciherang.

The average of productivity of DH lines obtained from the three locations ranged from 4.33 ton/ha (HS1-28-1-4) to 6.60 ton/ha (HS1-5-1-1). The three check varieties, i.e. Ciherang, Inpara 5, and Inpari 13 showed productivity of 5.76, 4.74, and 4.85 ton/ha, respectively. All DH lines exhibited similar yield with Ciherang, except for HS1-28-1-3 and HS1-28-1-4 (Table 4).

Selection based on weighted index

A better understanding of the relationship between grain yield and yield component traits becomes necessary in making an efficient selection for the development of new varieties with improved economically important traits (Kumar *et al.,* 2014). Therefore, as stated by Gazal *et al*., (2017), selection will give optimum response when using the appropriate selection criteria, especially for several traits of agronomic importance.

In this research several traits of agronomic importance such as productivity, number of tillers, number of filled grains per panicle, the percentage of filled grains per panicle, total number of spikelets per panicle, 1000-grain weight and days to harvest were chosen and weighted. As stated by Roy (2002) and Moeljopawiro (2002), the weighting should be based on the level of economic interests of each character in order to reduce subjectivity by breeders. In addition, positive and negative signs indicated the direction of selection, i.e. increased yield and decreased days to harvest. The selected traits were similar to those chosen by Shiv *et al*. (2008) and Bergale *et al.,* (2002) for wheat. Bergale *et al*., (*2002*) reported that grains per spike and tillers per plant had high positive direct effects on grain yield. Direct effect of number of spikelets per spike was negative and moderate. The direct effect of plant height was negligible and its correlation with grain yield per plant was negative and highly significant. Bergale *et al.,* (2002*)* also suggested that the number of spikes per plant, grains per spike and harvest index must be given preference in selection along with optimum plant height and days to flowering to select the superior wheat genotypes. Moreover, Shiv *et al.,* (2008) suggested that number of tiller per plant, number of spikelets per ear, number of grains per ear, grain weight per ear, 100-grain weight and biological yield could form effective selection indices for selection of high yielding genotypes of wheat.

Table 4 shows that the weighted index values ranged from -15.63 (HS1-28-1-3) to 10.15 (HS1-5-1-1). Based on the weighted index value, good agronomic performance including phenotypic acceptability and yield (> 4.8 t/ha), 14 lines were selected, i.e. HS1-5-1-1, HS2-9-1-1, HS4-8-1-2, HS4-13-1-1, HS4-13-1-3, HS4-13-1-4, HS4-17-1-1, HS15-13-1-1, HS17-3-1-1, HS17-3-1-3, HS17-3-1-4, HS17-3-1-7, HS17-21-1-2 and HS17-31-1-1.

CONCLUSION

Genotype and environment (G x E) interaction was significant for all traits. Broad sense heritability estimates of all observed traits was high and ranged between 0.58 – 0.96, except for tiller number and productivity which were moderate. Fourteen lines were selected (HS1-5-1-1, HS2-9-1-1, HS4-8-1-2, HS4-13-1-1, HS4-13-1-3, HS4-13-1-4, HS4-17-1-1, HS15-13-1-1, HS17-3-1-1, HS17-3-1-3, HS17-3-1-4, HS17-3-1-7, HS17-21-1-2 and HS17-31-1-1) based on weighted index value, good agronomic performance and productivity (4.82 – 6.60 ton/ha). The selected doubled haploid lines will be evaluated further in multilocation yield trials.

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