FROM A CROSS BETWEEN ASOMINORI *JAPONICA* AND IR24 *INDICA*AT THREE DIFFERENT LOCATIONS

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ABSTRACT

Field experiments were conducted to evaluate the adaptability of four promising rice lines, *viz.* IAS5, IAS37, IAS63, and DCG66, in both the Spring and Summer seasons of 2017 in Son La, Hanoi and Nghe An. The results showed that the growth durations of the lines varied depending on the growing areas. In each region, the growth durations of the IAS lines were shorter than that of IR24 variety, but only DCG66 had a short growth duration. The plant heights of the lines were equivalent to that of IR24, except for DCG66 which had significantly taller plants. The flag leaf lengths of the lines in the Summer were longer than in the Spring, but the flag leaf widths did not differ between seasons. Grain yields of the lines in the Spring season were higher than in the Summer season. The average grain yields of the IAS lines were not significantly different compared to those of IR24 across locations, but the grain yield of DCG66 was 13.6-33.5% and 15.9-34.7% higher than that of IR24 across three locations in Spring and Summer season, respectively. There were significant differences in the grain size of the studied lines, and among those only IAS63 was classified as having a long grain size. The amylose contents of the lines were around 24.2-30.5%, and thus the lines were classified as belonging to the hard rice group. Overall, the results showed that all the lines were able to adapt across the three locations, and DCG66 could be a new source of genes for breeding programs involving rice varieties with a short growth duration and large panicles.

Keywords: Chromosome segment substitution line, crop growth rate, spikelet number, grain yield.

1. INTRODUCTION

Rice (Oryza sativa L.) is the staple food crop in Vietnam and its productivity is critical for national food security (Mien, 2015). However, rice production in Vietnam is facing challenges due to climate change, limited cultivation area, and limited adaptable varieties (Bo, 2016). Improvement in rice yield in tropical environments depends mainly on the plants' ability to increase their panicle size as well as biomass production (Ibrahim et al., 2013). However, total aboveground biomass can be significantly affected by planting location. The final yield of a given cultivar depends on the magnitude of the interactions among the genotype, environmental conditions, and management practices (Messina et al., 2009). Under the same management practices, the genotype and environment interaction is the sole determinant of overall varietal performance (Dingkuhn et al., 2006). To develop new rice cropping systems in different environments, it is important to select cultivars that are adapted to the prevailing climatic conditions of the target growing environment.

Chromosome segment substitution lines (CSSLs) are produced when a particular chromosome segment in the genetic background of the recurrent line is substituted by the corresponding chromosome segment from the donor line (Hao *et al.*, 2009). The advantage of

these substitution lines is the complete integration of the substituted segment with the stability of a certain characteristic. Thus, these substitution lines can be used not only for the primary identification of quantitative trait loci (QTLs) for target genes, but also evaluation of as well as gene-environment gene-gene interactions for many types of traits (Doi et al., 2004; Yu et al., 2007; Wei et al., 2010) and are a good material source for breeding programs. Kubo et al. (2002) developed a set of 70 Asominori CSSLs with an IR24 genetic background. Using the Asominori CSSLs, several QTLs were found such as the QTLs for the heading date on chromosome 3, grain length on chromosome 3, plant height on chromosome 1 (Kubo et al., 2002), and aluminum resistance on chromosomes 1 and 9 (Xue et al., 2006). The Asominori CSSLs were consider good materials for breeding programs in Vietnam because of their cool temperature tolerance at the seedling stage (Loc et al., 2014) and drought tolerance at the tillering stage (Cuong et al., 2015). Based on the good traits of these CSSLs, we previously screened 24 Asominori CSSLs over two seasons under field conditions in Hanoi and found four promising rice lines (denoted IAS5, IAS37, IAS63, and DCG66) with good phenotypic traits including having a short growth duration, 5 to 8 active tillers per plant, around 200 spikelets per panicle, and a grain-filling rate of 90% (Hanh et al., 2017). In Vietnam, rice is grown in different ecological regions which differ in soil and climate characteristics. Therefore, this study aimed to evaluate the growth and ecological response of the four above promising rice lines in the various climate conditions of Son La, Hanoi, and Nghe An in Northern Vietnam.

2. MATERIALS AND METHODS

2.1. Time and place of study

Field experiments were conducted during the 2017 Spring and Summer seasons in Son La city (representing the North mountain region) (21015'-21031'N. 103045'-104000' E) from mid-February to mid-November, Hanoi city (representing the Red River Delta region) $(20^{\circ}53'-21^{\circ}23'N.$ $105^{\circ}44'-106^{\circ}02'E)$ from February to October, and in Nghe An province (representing the North Central region) $(8^{\circ}33'-19^{\circ}25'N.$ $102^{\circ}53'-105^{\circ}46'E)$ from the end of January to the end of September. The soil at the Son La site consisted of 0.29% total N, 0.035% P_2O_5 , 0.091% K_2O , and 2.71% OM. The soil at the Hanoi site consisted of 0.31% total N, 0.054% P_2O_5 , 0.083% K_2O , and 2.2% OM. The soil at the Nghe An site consisted of 0.25% total N, 0.038% P_2O_5 , 0.093% K_2O , and 1.61% OM.

2.2. Source of materials and experimental designs

Four promising rice lines, viz. IAS5, IAS37, IAS63, and DCG66, were selected for this experiment. Three of the lines were Asominori CSSLs in an IR24 genetic background (denoted as IAS lines) (Kubo et al., 2002) and the fourth line, DCG66, also named IAS66-1, was selected from a segregating population of IAS66 (Quang et al., 2014). These lines were selected from a field screening experiment grown over two seasons in Hanoi in 2016 (Hanh et al., 2017). In the Spring 2017 and Summer 2017 seasons, IAS5, IAS37, IAS63, DCG66, and IR24 were grown at the three test locations. These rice lines were arranged in a randomized complete block design (RCBD) with three replications in each location.

2.3. Cultural management practices

Each plot area was 20 m² and the planting density was 33 plants per m² at three seedlings per hill in all locations and in both seasons. Four to five leaf seedlings from wet-bed nurseries were transplanted into the plots. Chemical fertilizers were applied as follows: 90 kg N + 90 kg P_2O_5 + 68 kg K_2O per hectare. The sources of the fertilizers were urea (46% N), single superphosphate (12% P_2O_5), and potassium chloride (60% K_2O). The rate of fertilizer application was 20% (N & K_2O) at tillering, and 30% (N + K_2O) at panicle

initiation. Water, weeds, insects, and diseases were controlled as necessary to avoid yield loss. Pesticides were applied when the damage rate reached the control threshold.

2.4. Data collection

Growth duration was determined as the time from sowing to maturity (ripening of 90-95% of spikelets per panicle). Plant materials were harvested at tillering, heading, and maturity. Dry weight was determined after oven-drying materials at 80°C to a constant weight. At the maturity stage, 10 hills per genotype were sampled to determine the plant height and yield components. The height of each plant was measured from the ground to the top of the panicle. The number of panicles per hill, number of spikelets per panicle, grain filling percentage, and grain yield were calculated. Biomass yield was the total dry matter of straw and filled and unfilled spikelets after oven-drying to a constant weight at the harvesting stage. Grain yield was determined from a 5 m² area in each replication and adjusted to a standard moisture content of 14%. Twenty grains and husked grains were measured to determine grain length and width. Amylose content was determined by TCVN 5716-1:2008 (ISO 6647 - 1: 2007). Pests and diseases were monitored following the rice standard evaluation system (IRRI, 1996).

2.5. Statistical analyses

ANOVA analysis was performed to determine genotype and location effects, and their interaction using Statistix 10.0 software. The significance of mean values was analyzed using Tukey's test (0.05).

3. RESULTS AND DISCUSSION

3.1. Climatic conditions during the experiment

The mean temperatures in the Spring season were similar across locations. The average Spring and Summer temperatures throughout each growing season were 23.0°C and 24.3°C in Son La, 24.0°C and 28.6°C in Hanoi,

and 21.5°C and 29.2°C in Nghe An, respectively. The sunshine duration in Son La tended to be higher in the early growth stages and lower in the late-growth stages compared to the Hanoi and Nghe An locations in the Spring season. The sunshine duration in Nghe An was higher during the mid and late-growth stages in the Summer season than in Son La and Hanoi. These factors affected the growth duration of the genotypes as low temperatures lengthened the growth duration of the genotypes in Son La compared to Hanoi and Nghe An (Figures 1 and 2).

Precipitation rates in Son La in the Spring season were higher than in Nghe An for all growth stages, whereas the precipitation in Hanoi was high at the maturity stage, which led to lower grain filling rates of the genotypes (Table 3). In the Summer season, the number of rainfalls increased in Hanoi and Nghe An leading to floods at the harvesting stage, while rainfall in Son La was low.

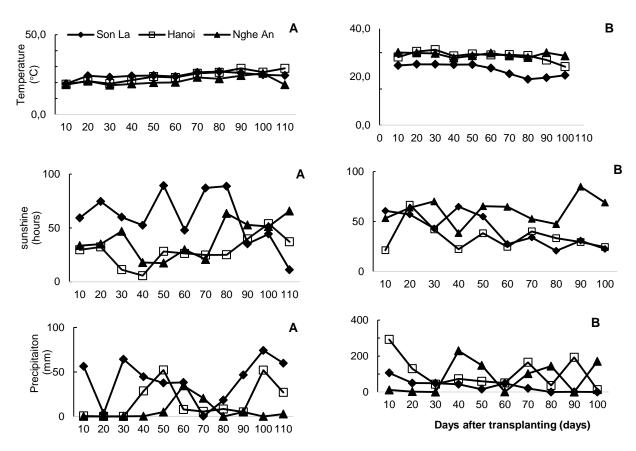
3.2. Growth duration, plant height, and flag leaf characteristics of the study lines

The growth duration of the lines varied by season and location, of which the growth duration of the lines in the Summer season was shorter than in the Spring season. In Son La, the growth duration of the lines was lengthened because of a later transplanting time and lower temperatures compared to the other locations in both seasons. In Nghe An, the growth durations of the lines were shortened in the Summer season due to a higher number of sunshine hours. According to QCVN 01-55-2011, only DCG66 had a short growth duration, 125 days and 115 days in Son La, 126 days and 105 days in Hanoi, and 125 days and 102 days in Nghe An in the Spring and Summer seasons, respectively (Figure 2). The IAS lines had shortened growth durations compared to IR24 because the substitution segments from the Asominori variety advanced the heading date of the IAS lines (Kubo et al., 2002).

The plant height data reflected the results of plant growth under different environmental conditions. In the Summer season, the plant Bio-agronomic characteristics of promising rice lines derived from a cross between *Asominori japonica* and IR24 *Indica* at three different locations

heights of the lines were taller than in the Spring. In each location, the plant heights of the lines in Son La in Spring were taller than in Hanoi and Nghe An, but in the Summer season, the plants were taller in Hanoi than in Son La and Nghe An. Most of the IAS lines were classified as semi-

dwarfs around 90 cm, equivalent to recurrent parent IR24, except the plant height of DCG66 which was classified as medium height (Figures 3a1 and 3b1). Increasing plant height has been found to be based on closed correlations with panicle size (Yoshida, 1981).



Note: each data point represents the mean of 10 days; A: Spring season, B: Summer season

Figure 1. Average temperatures, sunshine hours, and precipitation amounts from transplanting to maturity in Son La, Hanoi, and Nghe An

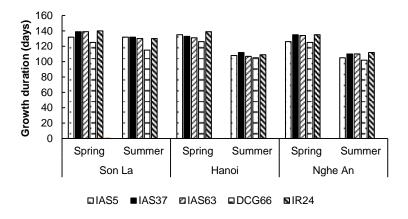
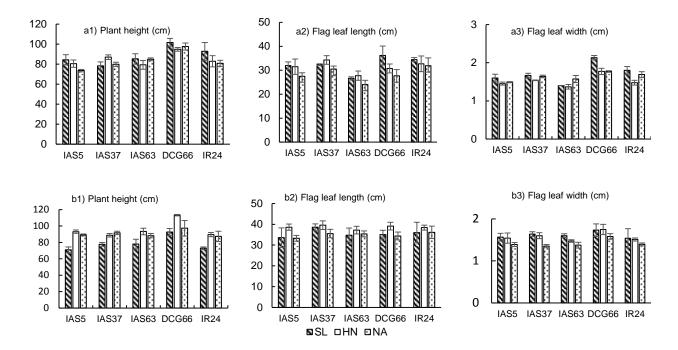


Figure 2. The growth duration of the promising rice lines at the three test locations



Note: SL: Son La; HN: Hanoi; NA: Nghe An

Figure 3. Plant heights, flag leaf lengths, and flag leaf widths of the lines at the three locations during the a) Spring season and b) Summer season

The chromosome segment substitution lines had darker green leaves than the check variety (data not shown), and the lengths of the flag leaves of the lines in the Spring season were shorter than those in the Summer season (Figure 2a1). In the Summer season, the lengths of the flag leaf in Hanoi had the highest values, but no significant differences between lines were observed. Differences in flag leaf widths were observed across locations and lines, of which DCG66 had the highest values of 2.1 cm in Son La, and 1.77cm in Hanoi and Nghe An (Figures 3a3 and 3b3).

3.3. Biomass yield, crop growth rate, and harvest index of the rice lines

Yoshida (1981) and Ibrahim et al. (2013) showed that higher grain yield in rice contributed to greater biomass production. Dry matter accumulation of the study lines in the Spring was higher than in the Summer season because of a longer growth duration. There were no significant differences between the average biomass yields of the IAS lines compared to IR24. The biomass yields of DCG66 had the highest values in both

seasons across all three locations and the values were significantly different to the yield of the recurrent parent IR24 (Table 1).

growth rate (CGR) crop transplanting to maturity was different between lines, seasons, and locations. The CGRs in the Spring season in Nghe An and Hanoi were larger than in Son La, but the Summer season values in Hanoi were the highest. The CGRs of the IAS lines were not significantly different compared to IR24, but the CGR of DCG66 was significantly different to IR24 in Nghe An. In the Summer season, the CGR of DCG66 had the highest value, and was significantly different to the CGR of IR24 across all three locations. The CGR during the late reproductive period and the grain yield in rice has been shown to have a significant positive relationship (Horie et al., 2003; Takai et al., 2006).

3.4. Pest and disease reactions of the study genotypes

The level of pest and disease damage depended on the season and the location. All

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lines were damaged by *Hydrellia philipina* at tillering across the three sites, but the damage score rate was only a score of 3 and did not affect the three upper rice leaves. In Son La, all the lines except DCG66 were infected by *Pirycularia oryzae* (Table 2). However, DCG66 was infected by *Ustilaginoidea virens* at the maturity stage in the Spring season, possibly

due to the high humidity in Son La. In Hanoi, the damage levels from pests and diseases were only slight. In Nghe An, because of high temperatures and varying weather, the lines were infected by rice black-streaked dwarf virus, but the damage score rate was low. Moreover, the Asominori CSSLs also have resistance to blast (Endo *et al.*, 2012).

Table 1. Physiological parameters of lines at three locations

Construe		Son La			Hanoi		Nghe An				
Genotype	BY	CGR	HI	BY	CGR	HI	BY	CGR	HI		
Spring 2017											
IAS5	875 ^b	8.2 ^b	0.54 ^a	1003 ^b	12.5 ^b	0.53 ^a	932 ^c	11.9 ^b	0.49 ^a		
IAS37	946 ^{ab}	8.5 ^b	0.45 ^b	986 ^b	12.4 ^b	0.54 ^a	950°	13.9 ^b	0.5 ^a		
IAS63	898 ^b	6.9 ^b	0.53 ^a	1016 ^b	13.6 ^{ab}	0.55 ^a	949 ^c	11.5 ^b	0.53 ^a		
DCG66	1237 ^a	13.6 ^a 0.57 ^a		1207 ^a	1207 ^a 18.1 ^a		1230 ^a	17.5°	0.54 ^a		
IR24	1130 ^{ab}	10.1 ^{ab}	0.53 ^a	1011 ^b	13.5 ^{ab}	0.54 ^a	1011 ^b	13.7 ^b	0.53 ^a		
Summer 2017											
IAS5	896 ^b	9.2 ^b	0.54 ^a	845 ^b	12.3 ^b	0.54 ^{ab}	853 ^b	12.0 ^b	0.5 ^a		
IAS37	956 ^b	9.5 ^b	0.54 ^a	804 ^b	10.3 ^b	0.53 ^{ab}	909 ^b	13.8 ^b	0.47 ^a		
IAS63	915 ^b	9.7 ^b	0.53 ^a	869 ^b	12.1 ^b	0.52 ^b	888 ^b	11.7 ^b	0.49 ^a		
DCG66	1190 ^a	14.9 ^a	0.55 ^a	1132 ^a	18.5 ^a	0.56 ^a	1134 ^a	17.6 ^a	0.52 ^a		
IR24	954 ^b	10.0 ^b	0.54 ^a	819 ^b	12.2 ^b	0.54 ^{ab}	920 ^{ab}	13.2 ^b	0.49 ^a		

Note: BY: biomass yield (g m $^{-2}$); CGR: crop growth rate (g m $^{-2}$ soil day $^{-1}$); HI: Harvest index Within a column for each season, values followed by the same letter are not significantly different according to Tukey's test at P = 0.05

Table 2. Pest and disease reactions of the study lines at the three test locations

Genotype		Son La	а		Hanoi	Nghe An		
Spring season	S. inceertulas P. oryzae U.virens R. solar		R. solani	S. inceertulas	S. inceertulas	C. medilalis	RBSDV	
IAS5	0	H.5	0	0	0	H.5	0	0
IAS37	0	H.5	0	0	0	H. 5	0	0
IAS63	0	H.5	0	0	0	H.5	0	0
DCG66	0	0	M.3	0	0	H.5	0	0
IR24	0	H.5	0	0	0	H.5	0	0
Summer season								
IAS5	H.5	S.5	0	0	2WAH.5	0	H.3	BT.5
IAS37	H. 5	S.5	0	0	2WAH.5	0	H.3	BT.5
IAS63	H.5	S.5	0	0	2WAH.5	0	H.3	BT.5
DCG66	H.5	0	M.3	C.3	2WAH.5	0	H.3	BT.3
IR24	H.5	S.5	0	0	2WAH.5	0	H.3	BT.5

Note: Hydrellia philipina Ferino, Scirpophaga Incertulas (Walker), Pirycularia oryzae Cav, Ustilaginoidea virens (Cooke), Rhizoctonia solani Kuhn, Cnaphalocrosis medilalis (Guenee), Rice black-streaked dwarf virus (RBSDV). Damage phase: S: seedling; T: tillering; BT: booting stage; 2WAH: two weeks after heading; H: heading; M: maturity. Damage score rate: from 1 to 9 (0: no scraping; 1: less than 1%; 3: 1-10%; 5: 11-25%; 7: 26-50%; 9: 51-100%).

Genotype	Number of panicles per m ²				Number of spikelets per panicle			Grain filling rate (%)			grain w	eight	Grain yield (quintal ha ⁻¹)			
	SL	HN	NA	SL	HN	NA	SL	HN	NA	SL	HN	NA	SL	HN	NA	
IAS5	321 ^a	234ª	312 ^a	147 ^b	126 ^{bc}	135 ^{bc}	87.1ª	90.5 ^{ab}	81.8 ^b	21.4 ^{ab}	24.7 ^d	24.8 ^b	48.0 ^b	59.9 ^b	48.7°	
IAS37	307 ^a	188ª	276 ^a	138 ^b	127 ^b	140 ^b	74.5 ^a	91.3 ^{ab}	86.8 ^b	23.5°	25.7°	28.5 ^a	40.9 ^b	56.7 ^b	58.0 ^b	
IAS63	245 ^a	218 ^a	293ª	122 ^b	109 ^c	98°	86.3ª	89.8 ^b	90.5 ^{ab}	22.3ª	27.2 ^b	28.4ª	42.0 ^b	61.9 ^b	57.3 ^b	
DCG66	283 ^a	172 ^a	205 ^a	238 ^a	178 ^a	197 ^a	81.2ª	94.0 ^a	96.1 ^a	19.2 ^b	22.5 ^e	22.3°	68.5 ^a	70.9 ^a	71.2 ^a	
IR24	316 ^a	213 ^a	315 ^a	172 ^b	121 ^{bc}	149 ^b	74.5 ^a	88.2 ^b	87.6 ^b	20.9 ^{ab}	27.5 ^a	25.6 ^b	51.3 ^b	62.2 ^b	62.7 ^b	
Location	0.0031** 0.004**			0.0047**				0.000**		0.171ns						
Line	0.0045** 0.000**			0.008**				0.000**		0.000**						
Location x	(0.3002n	s		0.051ns	6		0.0313*			0.000**		0.0049*			

Table 3. Grain yield and yield components of the study lines at the three test locations in the Spring season of 2007

Note: SL: Son La; HN: Hanoi; NA: Nghe An. Within a column, values followed by the same letter are not significantly different according to Tukey's test at P = 0.05. *, ** P value significance at 0.05 and 0.01 probability levels; ns: non-significant at P = 0.05 level

3.5. Yield and yield-related traits

Line

There were significant differences in the number of panicles per square meter between locations and lines, but the location x line interaction was not a significant factor (Table 3). In each location, the numbers of panicles per m² were not significantly different among lines, but the lowest value belonged to DCG66. However, there were significant differences (P < 0.01) between the three regions and lines in the number of spikelets per panicle, as the values were higher in Son La than in Hanoi and Nghe An. The numbers of spikelets per panicle of the IAS lines were not significantly different to IR24, except that of DCG66 which had the highest values with 238, 178, and 197 spikelets per panicle in Son La, Hanoi, and Nghe An, respectively, and were significantly different to the recurrent parent IR24 in each location. The grain filling percentage was variable across locations and was affected by weather (Table 3). The rate of grain filling of the five lines in Son La was lower than in Hanoi and Nghe An due to high rainfall at the heading stage. This rainfall amount led to lower 1000-grain weights of all the lines in Son La compared to Nghe An and Hanoi. The 1000-grain weights of DCG66 were the lowest with values of 19.2, 22.5, and 22.3 g in Son La, Hanoi, and Nghe An, respectively. The reason for these results could be a trade-off relationship between two components: spikelets per panicle and 1000-grain weight (Huang *et al.*, 2011).

There were no significant differences in grain yield between locations, but a significant difference between lines and the location x lines interaction was observed. Grain yield of all the lines in Hanoi and Nghe An were higher than in Son La, and the reasons for these results were low temperatures at the vegetative stage, and optimum high temperatures and sunshine at the heading and maturing stages which contributed to high grain-filling (Tables 1 and 3). DCG66 had the highest grain yield values with 68.5, 70.9, and 71.2 quintal ha⁻¹ in Son La, Hanoi and Nghe An, respectively (Table 3). The higher grain yield of DCG66 was mainly attributed to more grains per panicle, stronger CGR, and higher HI (Tables 1 and 3) (Yoshida, 1981). These results were in agreement with Ibrahim et al. (2013) who reported that rice yields in tropical environments depended mainly on the plants' ability to increase their panicle size as well as CGR during the growth phase.

There were no significant differences (P<0.01) in grain yield, the number of spikelets, and grain filling rate but significant differences were observed in the number of panicles per m² and 1000-grain weight between locations in the Summer season (Table 4). Yield component performance varied over locations. In each location, there were no significant differences in the number of panicles per square meter. The number of spikelets per panicle averages of the IAS lines were equal to IR24, but the values of DCG66 were much higher than those of all other genotypes. Only the grain yield of DCG66 was significantly different to IR24 with 62.6, 64.5, and 60.2 quintal ha-1 at Son La, Hanoi, and Nghe An, respectively. These results are consistent with the previously reported grain yield of DCG66 in Thai Nguyen and Lao Cai, which were 70.3 quintal ha-1 and 64.9 quintal ha⁻¹, respectively, in the Summer season (Hanh et al., 2014).

3.6. Grain characteristics and amylose content

Grain size was one of the few traits affected by locational conditions. According to the IRRI standard 2002, only kernel length of IAS63 was long, ranged from 6.62 to 7.29 mm through both seasons and three locations, and was followed by IAS37. The rice kernel length per width ratio of IAS63 was ranked as elongated, and may be due to the Asominori chromosome substitution. The grain size of the other genotypes belonged to the medium classification, except DCG66 which had a short size. The amylose contents of all the genotypes varied but were higher than 25%, and were thus classified as hard rices, of which the values of DCG66 were over 29% across all seasons and locations.

There was a significant relationship between the number of spikelets per panicle and grain yield in the three locations with r values of 0.67**, 0.63*, and 0.56* in the Spring season, and with r values of 0.74**, 0.69**, and 0.64* in the Summer season in Son

La, Hanoi, and Nghe An, respectively. Additionally, there was a positive relationship between the crop growth rate and grain yield with r values of 0.81**, 0.57**, and 0.56** in the Spring season in Son La, Hanoi, and Nghe An, respectively (Figure 4), but the correlations in the Summer season in Son La and Nghe An were non-significant with r values of 0.5ns and 0.44ns, respectively. These results were assumed to contribute to the number of spikelets per panicle and to the CGR and grain yield of the promising rice lines.

4. CONCLUSIONS

The results revealed that the study lines responded differently to each location in terms of growth duration, plant height, filled-grain rate, and grain yield. Among the locations, Hanoi was considered the most favourable place for all the genotypes because of stable grain yield. Among the promising lines, DCG66 was the most adaptable across the three locations. The grain yield of DCG66 was greater than the other IAS lines at all the study locations and ranged from 68.5-71.2 quintal ha⁻¹ and 60.2-64.5 quintal ha⁻¹ in the Spring and Summer seasons, respectively, in the three locations. From the viewpoint of plant type, the short growth duration, larger flag leaf width and length, and taller plant height were responsible for the greater grain yield of DCG66. With a short growth duration, DCG66 can avoid floods in the early Summer in Nghe An and can be transplanted later to wait for the rainy season in the rainfed lowland area in Son La. In addition, DCG66 was tolerant to Pirycularia oryzae disease at the seedling stage. Therefore, the DCG66 line can be an alternative variety to improve genetic diversity in these three locations.

Acknowledgements

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Table 4. Grain yield and yield components of the study lines at the three test locations in the Summer 2017 season

Genotype -	Panicles per m ²			Spik	Spikelets per panicle			Grain filling (%)			0-grain weig	ht(g)	Grain yield (quintal ha ⁻¹)			
	SL	HN	NA	SL	HN	NA	SL	HN	NA	SL	HN	NA	SL	HN	NA	
IAS5	243 ^a	254 ^a	195ª	115 ^b	124 ^b	128 ^b	81.6ª	78.0 ^b	88.4ª	21.2°	23.0 ^b	21.2 ^b	44.7°	51.0 ^b	46.7 ^b	
IAS37	256 ^a	222 ^a	189 ^a	142 ^b	133 ^b	130 ^b	85.5 ^a	85.5 ^{ab}	86.1 ^a	24.6 ^a	24.5 ^a	23.2 ^a	47.4 ^{bc}	47.9 ^b	42.1 ^b	
IAS63	258ª	252 ^a	193ª	137 ^b	143 ^b	118 ^b	85.6ª	76.7 ^b	85.7 ^a	25.1ª	24.6ª	23.4ª	48.7 ^{bc}	45.3 ^b	47.2 ^b	
DCG66	235°	216 ^a	189 ^a	230 ^a	221 ^a	187 ^a	82.6ª	92.5 ^a	89.4ª	20.7 ^c	20.1°	18.1°	62.6 ^a	64.5 ^a	60.2 ^a	
IR24	283ª	219 ^a	202 ^a	161 ^b	160 ^b	132 ^b	80.5 ^a	81.9 ^b	86.2 ^a	22.9 ^b	23.3 ^b	20.7^{b}	54.0 ^b	47.9 ^b	50.1 ^b	
Location	0.0013** 0.2070ns				0.2505ns				0.0006**		0.116ns					
Line		0.1080ns 0.000**			0.0084**				0.000**		0.000**					
Location x Line		0.093ns		0.4663ns			0.0068**				0.000**		0.0410*			

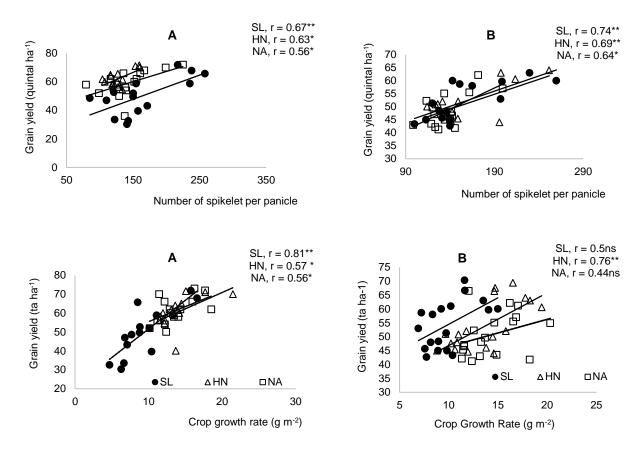
SL: Son La, HN: Hanoi; NA: Nghe An; Within a column, values followed by the same letter are not significantly different according to Tukey's test at P = 0.05 *, ** P value significance at 0.05 and 0.01 probability levels and ns means non-significant at P = 0.05 level.

Table 5. Grain and kernel rice sizes and amylose content of the study lines in the Spring and Summer 2017 seasons at the three test locations

Genotype	Grain length (mm)		Grain width (mm)		Kernel length (mm)			Kernel width (mm)			Length/	width ker	nel ratio	Amylose content (%)				
Spring season 2017	SL	HN	NA	SL	HN	NA	SL	HN	NA	SL	HN	NA	SL	HN	NA	SL	HN	NA
IAS5	9.19 ^{bc}	8.3 ^c	8.82 ^d	2.62 ^b	2.12^{d}	2.56 ^c	6.51 ^b	6.12 ^c	6.48 ^d	2.33 ^{ab}	2.01 ^a	2.27 ^c	2.79 ^a	3.04 ^c	2.88 ^b	24.2	26.8	27.6
IAS37	9.33 ^{ab}	9.0 ^b	9.67 ^b	2.7 ^a	2.36 ^{ab}	2.85 ^a	6.79 ^a	6.47 ^b	7.02 ^b	2.37 ^{ab}	2.05 ^a	2.37 ^{ab}	2.86 ^a	3.16 ^b	2.97 ^a	24.6	24.5	26.7
IAS63	9.05°	9.08 ^a	9.79 ^a	2.67 ^{ab}	2.38 ^a	2.78 ^{ab}	6.84 ^a	6.62 ^a	7.29 ^a	2.36 ^{ab}	2.04 ^a	2.38 ^a	2.90^a	3.36 ^a	3.06 ^a	24.0	26.4	26.8
DCG66	7.81 ^d	7.4 ^d	7.91 ^e	2.46 ^c	2.27 ^{bc}	2.72 ^b	5.7 ^c	5.27 ^d	6.05 ^e	2.26 ^b	2.09 ^a	2.28 ^{bc}	2.52 ^b	2.52 ^e	2.66°	28.8	29.8	30.0
IR24	9.38 ^a	8.32 ^c	9.12 ^c	2.75 ^a	2.18 ^{cd}	2.74 ^b	6.77 ^{ab}	6.04 ^c	6.79 ^c	2.39 ^a	2.09 ^a	2.4 ^a	2.84 ^a	2.88 ^d	2.83 ^b	24.3	26.3	25.4
Summer season 2017																		
IAS5	8.92 ^b	9.05 ^b	8.56 ^c	2.79 ^a	2.21 ^b	2.34 ^a	6.51°	6.45 ^b	6.3 ^b	2.37 ^b	2.01 ^b	2.11 ^a	2.75 ^b	3.21 ^a	2.99 ^b	26.8	28.5	28.3
IAS37	9.38 ^a	9.52 ^a	9.20 ^a	2.87 ^a	2.31 ^{ab}	2.33 ^a	6.85 ^{ab}	6.72 ^a	6.68 ^a	2.48 ^a	1.96 ^b	2.15 ^a	2.77 ^{ab}	3.43 ^a	3.1 ^{ab}	25.8	28.2	28.0
IAS63	9.49 ^a	9.45 ^a	8.98 ^b	2.75 ^a	2.27 ^{ab}	2.37 ^a	6.98 ^a	6.8 ^a	6.73 ^a	2.41 ^{ab}	2.04 ^{ab}	2.11 ^a	2.90 ^a	3.33 ^a	3.2 ^a	25.3	26.5	27.3
DCG66	8.26 ^c	8.04 ^c	7.99^{d}	2.85 ^a	2.38 ^a	2.38 ^a	5.98 ^d	5.67 ^c	5.62 ^c	2.5 ^a	2.16 ^a	2.1 ^a	2.39 ^c	2.63 ^b	2.67 ^c	29.2	29.7	30.5
IR24	9.12 ^b	9.13 ^b	8.69°	2.80 ^a	2.30 ^{ab}	2.35 ^a	6.65 ^{bc}	6.51 ^b	6.24 ^b	2.43 ^{ab}	2.03 ^{ab}	2.09 ^a	2.74 ^b	3.2 ^a	2.98 ^b	25.9	26.4	27.2

Note: SL: Son La; HN: Hanoi; NA: Nghe An. Within a column for each season, values followed by the same letter are not significantly different according to Tukey's test at P = 0.05. *, ** P value significance at 0.05 and 0.01 probability levels and ns means non-significant at P = 0.05 level

Bio-agronomic characteristics of promising rice lines derived from a cross between *Asominori japonica* and IR24 *Indica* at three different locations



Note: A: Spring season, B: Summer season; *, **, ns: significantly different at P<0.05, 0.01, and nonsignificant, respectively

Figure 4. The relationship between number of spikelets per panicle and crop growth rate with grain yield

REFERENCES

Bo N. V. (2016). Rice production development in the context of climate change and intergration in Vietnam. The 2nd National Workshop on Crop Science, Vietnam Academy of Agricultural Sciences. pp. 38-49 (in Vietnamsese).

Cuong P. V., Dien D. C, Tuan T. A and Hanh T.T. (2015). Evaluation on drought tolerance of rice lines with Indica genetic bacground carrying chromosome segment substitution from wild rice or japonica. Journal of Science and Development. Vol 13 (2). pp. 166-172.

Doi K., Izawa T., Fuse T., Yamanouchi U., Kubo T., Shimatani Z., Yano M. and Yoshimura A. (2004). *Ehd1*, a B-type response regulator in rice, confers short-day promotion of flowering and controls FT-like gene expression independently of *Hd1*. Genes Development. Vol 18. pp. 926-936.

Dingkuhn M., Luquet D, Kim H., Tambour L. and Clement-Vidal A. (2006). EcoMeristem, a model of morphogenesis and competition among sinks in rice. 2. Simulating genotype responses to phosphorus deficiency. Functional Plant Biology. Vol 33. pp. 325-337.

Dingkuhn M., Luquet D., Kim H., Tambour L. and Clement-Vidal A. (2006). EcoMeristem, a model of morphogenesis and competition among sinks in rice. 2. Simulating genotype responses to phosphorus deficiency. Functional Plant Biology. Vol 33. pp. 325-337.

Endo T., Yamaguchi M. and Kaji R. (2012). Close linkage of a blast resistance gene, Pias (t), with a bacterial leaf blight resistance gene, Xa1-as (t), in a rice cultivar 'Asominori'. Breeding Science. Vol 62. pp. 334-339.

Hao W., Zhu M. Z., Gao J. P., Sun S. Y. and Lin H. X. (2009). Identification of quantitative trait loci for rice quality in a population of chromosome