Progress in Biological Sciences
Vol. 4, Number 2, Summer / Autumn 2014/153-166

Genetic worth and stability of selection indices in rice (*Oryza sativa* L.)

Received: December 20, 2013; Accepted: March 10, 2014

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ABSTRACT

Improvement of one trait on its own will affect the performance of other traits because of genotypic correlations between traits. Index selection is one of the tools used by plant breeders to overcome this problem. The purpose of this paper is to evaluate selection indices developed for improving grain yield in rice (*Oryza sativa* L.). Forty-nine rice genotypes were cultivated at Tonekabon Rice Research Station, Iran, in 2009 and 2010. Selection indices were developed based on phenotypic and genotypic correlations, path coefficients, broad-sense heritability of traits and stepwise multiple linear regression coefficients. Assessment of indices revealed that the stability decreased concurrently with increase in the genetic worth, and hence an inverse association existed between stability and genetic worth of indices. The results also suggested that selection for TP, GW, GP and GL and against PH using their multiple linear regression parameters as economic weights was an effective criterion for improving grain yield in rice genotypes. On the other hand, the most stable indices were those that were developed based on heritability of traits as well as genotypic path coefficients.

Keywords: broad-sense heritability, expected genetic advance, genotypic correlation coefficients, path analysis, rice, selection indices, Smith-Hazel index, stepwise multiple linear.

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Introduction

Selection for more productive genotypes has always been one of the basic goals in breeding programs. However, because of genotypic correlations, improving one trait will other traits. In rice, for example, the best families derived from selection for grain yield will have smaller panicles, smaller grain breadth and more days to maturity. Use of selection indices is one of the useful methods to overcome this problem.

Selection index theory was originally defined as a linear function of traits. The index is a linear weighted function of observations of an individual or its relatives that aims to rank the population for breeding values and thus expected progeny performance (1). To obtain an index, the economic values as well as the phenotypic and genotypic variance and covariances are necessary. The economic values may reflect the market situation, preferences, retrospective results, or simply arbitrarily fixed values. Ideally, the economic weight of a single trait should reflect the marginal benefit from a one-unit improvement (2). Samonte *et al.* (3), Rabiei *et al.* (4) and Sabouri *et al.* (5) have studied various economic weights and recommended path coefficients as the most appropriate economic values. Furthermore, the determination of traits contributing to or affecting the target trait is one of the most important steps. For this purpose, the inter-relationships between target trait and important characteristics should be accurately known. Various statistical techniques, such as correlation coefficient, path and regression analyses, were applied to this relationship.

Studies on rice have shown that grain yield is correlated with 1000-grain weight, number of tillers, plant height, number of panicles and productive tillers (3, 6-8).

Environmental factors strongly affect the parameters commonly used to develop selection indices. Therefore, Singh and Bellman studied the problems of generalization of selection indices (9). They reported that selection indices are specific. In other words, an index developed for a particular population does not have the same effect on other similar populations.

The aim of this research was to evaluate the efficiency and stability of different selection indices in order to propose a suitable criterion for improving grain yield in rice.

Materials and Methods

Plant materials and studied traits

Plant materials of this research comprised 49 genotypes, including 29 Iranian and 20 introduced lines of rice (Table 1). The field trial was arranged in a square lattice design with two replications. The experiment was conducted at the Tonekabon Rice Research Station, at 50°, 40' eastern and 36°, 54' northern in Iran during 2009 and 2010. The soil was a sandy loam with 1.67 to 2.2% organic matter, pH 7.5, and low to medium natural fertility. The mean temperature and the average annual rainfall were 15°C and 1100 mm, respectively.

Twenty single seedlings of each genotype were planted in two rows with a spacing of 25 cm. In each plot, 10 plants were randomly selected and evaluated to score their traits. The studied traits were plant height (PH), tillers for each plant (TP), panicle length (PL), flag leaf length (FL), flag leaf width (FW), length of the uppermost inter-node (LU), grain length (GL), grain breadth (GB), 100-grain weight (GW), grains for each panicle (GP), grain yield for each plant (GY), days to heading (DH) and days to maturity (DM), based on the standard evaluation system for rice published by IRRI.

Table 1. Plant materials studied in 2009 and 2010

Variety	**Origin**	**Land Race/Cross**	Growth duration (128.36±7.21 $_{\text{day}}$)	Grain length (9.26±1.17 $_{\text{mm}}$)	Grain yield per plant (6.72±2.32 $_{\text{gr}}$)
Ali Kazemi	Iran	Local Land Race	127	11.3	6.692
Amol1	Iran	IR8/Domsiah	137	8.5	10.022
Amol2	Iran	IR28 (Introduction)	135.8	9.98	7.902
Amol3	Iran	Sona (Introduction)	134.5	10.83	8.896
Anbarboo	Iran	Local Land Race	121.8	8.98	6.148
H124-36-1-1	Argentina	Dawn/IR594-34	123.8	8.9	5.468
Asgari Tarom	Iran	Local	136	9.8	12.272
Bejar	Iran	Domsiah/IR8/IR28	135.3	9.35	7.858
Binam	Iran	Local Land Race	135.3	9	3.908
Caloro	USA	CA, CI 1561-1	121.5	8.13	6.38
Century Patna231	USA	Texas Patna/Rexoro-Supreme Blue Rose	120.5	8.7	6.428
Champa Boudar	Iran	Local Land Race	127.8	9.65	5.196
Kanto51	Japan	Gin Bozu/To To	122	6.93	5.576
CY1819	USA	GID2953933	123.3	10.95	4.674
Dasht	Iran	IR29/Amol1	137.8	10.95	8.602
DC1	Malaysia	GID381148	121.5	8.83	3.544
DCL-Donghaechal	Korea	GID2274576	120.8	9.1	5.428
Deylamani	Iran	Local Land Race	121.5	8.8	10.032
Dular	India	Dumai/Larkoch	131.8	8.85	5.074
Domsiyah	Iran	Local Land Race	135.3	8.4	3.492
Fuji-Minori	Japan	Nourin17/Fujisaka5	122	7.4	5.474
Gharib	Iran	Local Land Race	123.5	8.4	5.19
Gharib Seyah Rayhani	Iran	Local Land Race	127	8.2	7.766
Gil1	Iran	Mosa Tarom /Ancitco	121.3	9.05	4.476
Gil3	Iran	IR498/Salari	119.3	10.1	4.606
Hassan Saraei Atashagah	Iran	Local Land Race	124.5	7.98	5.926
Hassan Saraei	Iran	Local Land Race	125.8	10	4.096
Hassan Saraei Pichide Ghalaf	Iran	Local Land Race	123.8	9.95	6.05
Hassani	Iran	Local Land Race	108	8.3	6.416
IR28	IRRI	IR833-6-2-1-1//IR 1561-149-1/IR 1737	129.8	9.95	10.088
IR36	IRRI	IR1561-228-1-2/IR 1737//CR 94-13	140.3	9	6.246
IR50	IRRI	IR2153-14-1-6-2/IR 28//IR 36	133.5	9.93	5.024

Table 1. Plant materials studied in 2009 and 2010

Variety	**Origin**	**Land Race/Cross**	Growth duration (128.36±7.21 $_{\text{day}}$)	Grain length (9.26±1.17$_{\text{mm}}$)	Grain yield per plant (6.72±2.32$_{\text{gr}}$)
IR60	IRRI	IR4432-53-33/PTB 33//IR 36 ARIKARAI///IR 24/TKM 6//IR 20*4/O NIVARA/4/ IR 1561-228-1-2/IR	140	8	5.9
IR64	IRRI	IR5657-33-2-1/IR 2061-465-1-5-5	137.3	10.03	4.08
Khazar	Iran	IR36 sister sel./TNAU 7456	135.5	9.23	5.324
Lebonnet	USA	Blue Belle/Belle Patna Dawn	128.8	9.03	4.204
Mazand	Iran	Local Land Race	133	10.83	12.058
Neda	Iran	Amol3/Sange Tarom/ Hassan Saraei	139.8	10.9	10.926
Nemat	Iran	Amol3/Sange Tarom	138	11.03	10.048
Norin22	Japan	Kinki 15/Norin6	124	7.98	8.382
Salari	Iran	Local Land Race	130.3	10.2	5.178
Sange Jo	Iran	Local Land Race	121.5	8.95	5.97
Shah Pasand	Iran	Local Land Race	128.3	11.55	5.744
Strella	Portugal	R82/STG55861	120.8	7.98	9.322
Taichung Native 1	Taiwan	Dee geo woo gen/Tsai-Yuan-Chan	133	7.18	6.378
Tarom Pakotah	Iran	Local Land Race	132	10.18	7.336
Usen	Japan	IRGC11116/GID336137	132.5	7.13	6.096
Zenith	USA	AR, Blue Rose (selection)	125.5	10.08	7.768
Zireh	Iran	Local Land Race	121.3	9.5	9.718

Statistical analyses

The normality of the distribution of the data was evaluated and non-normal traits were transformed using the power (Box-Cox) transformation using Minitab software release 15.1. The homogeneity of variances was tested using the Bartlett test. The analysis of the data was performed using Proc GLM in SAS statistical software, according to the following statistical model:

$$Y_{il(j)(g)} = \mu + t_i + (r|a)_{j(g)} + (b|r|a)_{l(j)(g)} + a_g + (ta)_{ig} + e_{il(j)(g)}$$

where: $Y_{il(j)(g)}$ is the observation of the genotype i(i = 1,..., 49= 7^2) in the block l(l = 1,..., 7) of the replication j(j =1,..., 2), in the year g(g = 1,..., 2); μ is a constant common to all observations; t_i is the effect of the genotype i; $(r|a)_{j(g)}$ is the effect of the replication j in the year g; $(b|r|a)_{l(j)(g)}$ is the effect of the block l of the replication j in the year g; a_g is the effect of the year g; $(ta)_{ig}$ is the effect of the interaction between the genotype i and the year g; $e_{il(j)(g)}$ is the error associated with the observation $Y_{il(j)(g)}$ (10).

Selection indices were calculated as described by Smith (11) and Hazel (12). In this method, the indices and the total genetic worth are defined as follows:

$$\text{Index: } I = \sum_{i=1}^{m} b_i x_i = x^T b$$

Total genetic worth: $H = \sum_{i=\backslash}^{n} a_i g_i = g^T a$

where $x^T = (x_1 x_2 \ldots x_m)$ is the row vector of m known phenotypic values (transpose of the *x* vector), $g^T = (g_1 g_2 \ldots g_n)$ is a row vector of n unknown genetic values (transpose of the *g* vector); $a = (a_1 a_2 \ldots a_n)$ is a column vector of n known relative economic weights, and $b = (b_1 b_2 \ldots b_m)$ is a column vector of m index coefficients to be computed (13). The correlation between *I* and *H* is highest when $b=P^{-1}Ga$ where *G* and *P*are the genotypic and phenotypic variance-covariance matrices, respectively.

The alternative indices were compared based on the magnitude of the following two criteria:

$$\Delta G_i \% = \frac{\frac{KGb}{\sqrt{b^T Pb}} + m_i}{m_i} \times 100$$

This criterion measures the average percentage of advance in each trait through an index relative to its mean. In this equation, ΔG_i is the percentage of the expected genetic advance in trait *i* via the given index, *K* is the selection differential (with 10 % selection intensity, *K* is equal to 1.76), b^T is the transpose of *b* vector and m_i is the arithmetic average of trait *i* (13).

$$R_{HI} = \sqrt{\frac{b^T Pb}{a^T Ga}}$$

where $R_{HI}$is the correlation coefficient between index and total genetic worth, a^T is the transpose of the vector *a*, and *a*, *b*, b^T, *P* and *G* are as defined before (13).

Phenotypic and genotypic variance covariances and phenotypic and genotypic correlation coefficients were estimated using the SAS code assumed by Holland (14).

Broad-sense heritability (h^2_{bi}) was estimated using equation:

$$h^2_{bi} = \frac{\sigma^2_{gi}}{\sigma^2_{pi}}$$

where σ^2_{gi} and σ^2_{pi} are the genotypic and phenotypic variances of trait *i*.

To identify which traits have the strongest influence on GY, stepwise multiple linear regression (SMLR) analysis was applied using likelihood-based methodology (15). For path analysis, the correlation coefficients between response (GY) and predictor variables were partitioned into direct and indirect effects using the following procedure:

$$r_{iy} = p_{iy} + \Sigma_{ij} r_{ij} p_{jy}$$

where r_{iy} is the correlation coefficient between grain yield (y) and predictor variable *i*, p_{iy} and p_{jy} are the direct effects of predictor variables *i* and *j* on grain yield, respectively, and r_{ij} is the correlation coefficient between predictor variables *i* and *j* (16).

The stability of indices were assessed using the technique suggested by Finlay and Wilkinson (17). In this method, stability of index was described with linear regression of index mean over year mean. The more stable indices are those that have regression coefficients close to one.

Results

Analysis of variance and correlation coefficients between traits

Analysis of variance showed that variation due to genotypes was significant for all studied traits (Table 2).

Table 2. Combined analysis of 2009 and 2010 data on 13 agronomic traits measured over 49 rice genotypes

		Mean squares												
Source	df	DH	DM	GP	GL	GB	LU	PL	PH	GW	NT	FW	FL	GY
Model	123	106.46**	81.52**	3216.23**	2.18 **	0.32	43.50	16.048**	630.66**	0.224**	24.15**	0.054**	42.67**	211.79**
Y	1	28.70**	27.94**	1669.31**	0.04 ^{ns}	0.037 *	0.823 ^{ns}	10.19**	2.42 ^{ns}	0.052**	200.75**	0.029**	25.21**	115.22 **
R(Y)	2	7.597*	15.2**	44.133 ^{ns}	0.01 ^{ns}	0.056 ^{ns}	0.69 ^{ns}	2.71 ^{ns}	126.65**	0.009 ^{ns}	5.98*	0.004 ^{ns}	2.79 ^{ns}	0.56 ^{ns}
IB(Y×R)	24	3.133*	3.79**	62.01 ^{ns}	0.02 ^{ns}	0.062 ^{ns}	2.57 ^{ns}	1.45 ^{ns}	21.90*	0.006 ^{ns}	1.78 ^{ns}	0.002 ^{ns}	2.10 ^{ns}	2.95 ^{ns}
G	48	200.58**	162.54**	7369.51**	5.30 **	0.584 **	93.17**	27.87**	1159.17**	0.479**	48.32**	0.106**	83.29**	448.03**
G×Y	48	13.88**	2.51 ^{ns}	155.74**	0.26 **	0.014**	6.91**	3.11**	108.14**	0.024**	2.72 ^{ns}	0.008**	3.23**	31.63**
Error	72	1.78	1.66	43.73	0.02	0.01	2.23	1.45	14.66	0.004	1.86	0.003	1.39	2.62
R^2		0.990	0.988	0.992	0.995	0.988	0.971	0.950	0.987	0.989	0.957	0.970	0.981	0.993
C.V%		1.30	1.01	4.25	1.47	2.92	3.94	4.67	3.28	2.68	9.81	4.40	4.31	4.82
h_b^2		87.10	95.72	95.06	89.58	92.53	83.21	78.60	82.90	89.63	85.14	82.06	91.31	80.67

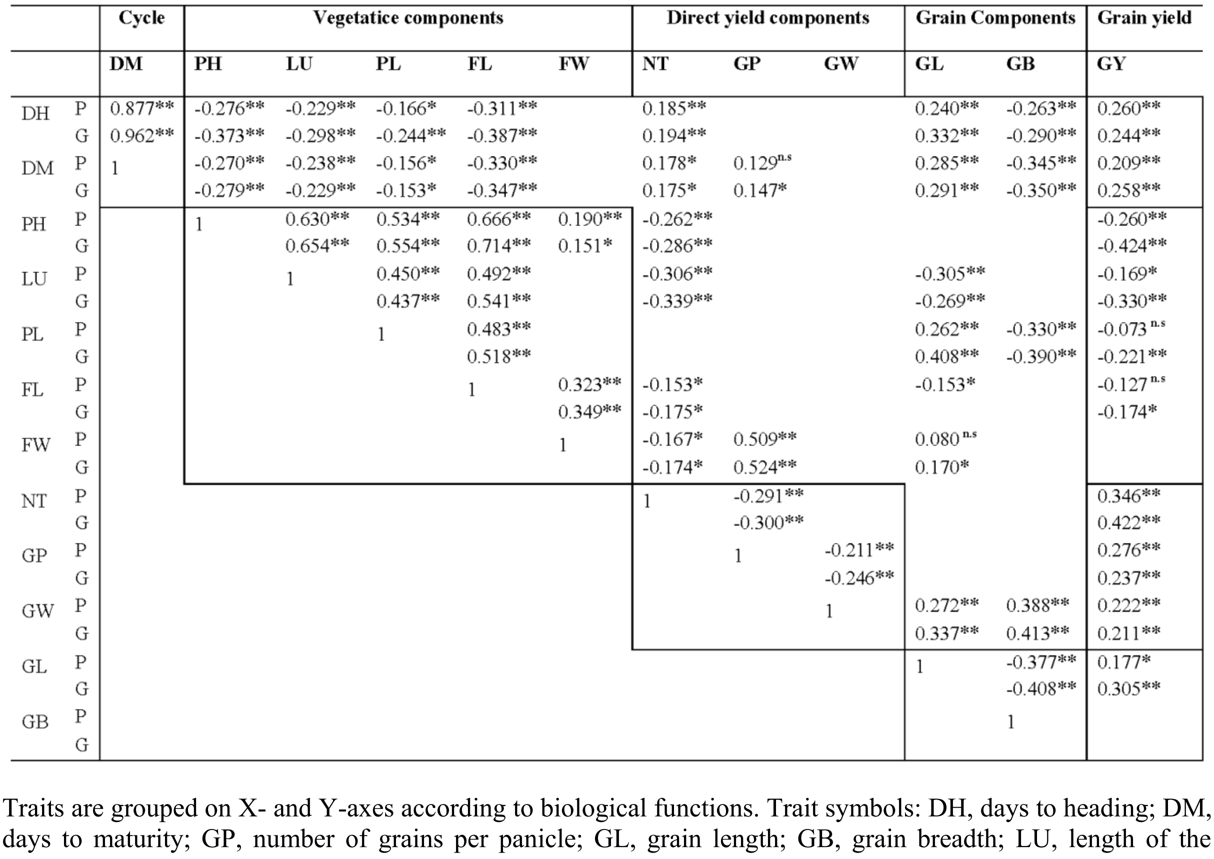
Trait symbols: DH, days to heading; DM, days to maturity; GP, number of grains per panicle; GL, grain length; GB, grain breadth; LU, the length of the uppermost inter-node; PL, panicle length; PH, plant height; GW, 100-grain weight; TP, tillers for each plant; FW, flag leaf width; FL, flag leaf length; GY, grain yield; Y, Year; R(Y), replication within year; IB(Y×R), incomplete block within interaction of year by replication; G, genotype; G×Y, genotype by year interaction; R2, coefficient of determination; CV%, coefficient of variation; h_b^2, broad-sense heritability; * , ** mean squares are significant at the 0.05 and 0.01 levels, respectively.

Year had significant effect on all traits except GL, LU and PH. Genotype by year interaction had no significant effect on DM and on TP. Days to maturity (DM) and PL had the highest and lowest heritability, respectively (Table 2).

Table 3 shows significant phenotypic (r_p) and genotypic (r_g) correlation coefficients according to the typology of traits (cycle, vegetative, reproductive and final target trait). The absolute values of the genotypic correlations ($|r_g|$) were higher than the respective phenotypic correlations ($|r_p|$).

Negative significant correlations ($P<0.001$) were observed between PH and traits GY (r_p= -0.260; r_g= -0.424), DH (r_p= -0.276; r_g= -0.373), DM (r_p= -0.270; r_g= -0.279) and TP (r_p = -0.262; r_g = -0.286). Furthermore, late maturing varieties had higher grain length with regard to the positive correlation ($P<0.001$) between GL and DM (Table 3). Grain yield showed a significant positive correlation with DH, DM, GL, GW, TP and GP, while it was negatively correlated with both LU and PH. Cycle traits (DH and DM) were positively correlated with most of the reproductive traits (five out of seven), while they were negatively correlated with all vegetative traits (eight out of eight).

Table 3. Significant phenotypic (P) and genotypic (G) correlation coefficients between 13 agronomic traits among 49 rice genotypes evaluated in 2009 and 2010



		Cycle	Vegetatice components					Direct yield components			Grain Components		Grain yield
		DM	**PH**	**LU**	**PL**	**FL**	**FW**	**NT**	**GP**	**GW**	**GL**	**GB**	**GY**
DH	P	0.877**	-0.276**	-0.229**	-0.166*	-0.311**		0.185**			0.240**	-0.263**	0.260**
	G	0.962**	-0.373**	-0.298**	-0.244**	-0.387**		0.194**			0.332**	-0.290**	0.244**
DM	P	1	-0.270**	-0.238**	-0.156*	-0.330**		0.178*	0.129$^{\text{n.s}}$		0.285**	-0.345**	0.209**
	G		-0.279**	-0.229**	-0.153*	-0.347**		0.175*	0.147*		0.291**	-0.350**	0.258**
PH	P		1	0.630**	0.534**	0.666**	0.190**	-0.262**					-0.260**
	G			0.654**	0.554**	0.714**	0.151*	-0.286**					-0.424**
LU	P			1	0.450**	0.492**		-0.306**			-0.305**		-0.169*
	G				0.437**	0.541**		-0.339**			-0.269**		-0.330**
PL	P				1	0.483**					0.262**	-0.330**	-0.073$^{\text{n.s}}$
	G					0.518**					0.408**	-0.390**	-0.221**
FL	P					1	0.323**	-0.153*			-0.153*		-0.127$^{\text{n.s}}$
	G						0.349**	-0.175*					-0.174*
FW	P						1	-0.167*	0.509**		0.080$^{\text{n.s}}$		
	G							-0.174*	0.524**		0.170*		
NT	P							1	-0.291**				0.346**
	G								-0.300**				0.422**
GP	P								1	-0.211**			0.276**
	G									-0.246**			0.237**
GW	P									1	0.272**	0.388**	0.222**
	G										0.337**	0.413**	0.211**
GL	P										1	-0.377**	0.177*
	G											-0.408**	0.305**
GB	P											1	
	G												

Traits are grouped on X- and Y-axes according to biological functions. Trait symbols: DH, days to heading; DM, days to maturity; GP, number of grains per panicle; GL, grain length; GB, grain breadth; LU, length of the uppermost inter-node; PL, panicle length; PH, plant height; GW, 100-grain weight; TP, tillers for each plant; FW, flag leaf width; FL, flag leaf length; GY, grain yield. * , ** correlation is significant at the 0.05 and 0.01 level, respectively, n.s non-significant.

SMLR and path coefficients

According to SMLR and path analysis, some traits, namely TP, GP and GW, had the highest direct effects on GY (Figure 1 and Tables 4 and 5).

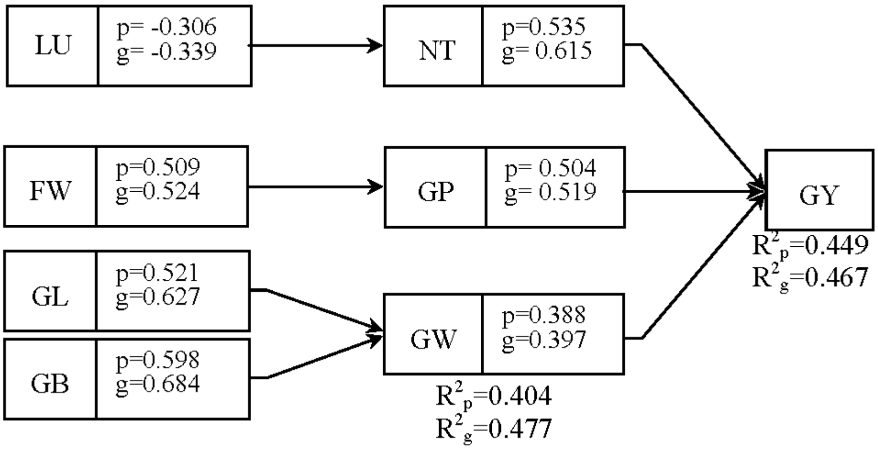


Figure 1. Phenotypic (p) and genotypic (g) path coefficients for the path analysis of eight effective traits that influence grain yield derived from evaluation of 13 agronomic traits among 49 rice genotypes during 2009 and 2010. The phenotypic (R_p^2) and genotypic (R_g^2) coefficients of determination for each component of path analysis affected by more than one trait are located below the respective component. Trait symbols: TP, tillers for each plan; GP, number of grains per panicle; GW, 100-grain weight; FW, flag leaf width; LU, the length of the uppermost inter-node; GL, grain length; GB, grain breadth; PH, plant height; and GY, grain yield

Table 4. Phenotypic (P) and genotypic (G) direct effects (bold) and indirect effects (not bold) of first- and second-order predictor variables on rice grain yield studied over 49 rice genotypes in 2009 and 2010

Traits		Direct and indirect effects on GY			Direct effect on NT	Direct effect on GP	Direct and indirect effects on GW	
		NT	GP	GW	LU	FW	GL	GB
NT	P	**0.535**	-0.147	-0.044				
	G	**0.615**	-0.156	-0.038				
GP	P	-0.156	**0.504**	-0.082				
	G	-0.185	**0.519**	-0.098				
GW	P	-0.060	-0.107	**0.388**				
	G	-0.059	-0.128	**0.397**				
LU	P				**-0.306**			
	G				**-0.339**			
FW	P					**0.509**		
	G					**0.524**		
GL	P						**0.487**	-0.184
	G						**0.606**	-0.248
GB	P						-0.216	**0.571**
	G						-0.270	**0.660**

Trait symbols: TP, tillers for each plant; GP, number of grains per panicle; GW, 100-grain weight; LU, the length of the uppermost inter-node; FW, flag leaf width; GL, grain length; GB, grain breadth.

Table 5. Results of stepwise multiple linear regression analysis carried out over traits in 49 rice genotypes evaluated in 2009 and 2010

S.O.V	df	Sum of squares	Mean square	Partial R^2	Model R^2	Parameter estimate (b)
Model	3	2703.405	901.135***			
Intercept	1	727.59	727.59**			-42.009
GP	1	1440.59	1440.59**	0.144	0.144	0.134
GW	1	879.27	879.27**	0.159	0.303	12.140
NT	1	1820.61	1820.61**	0.146	0449	1.802
Error	45	3320.830	73.80			

Dependent variable = grain yield.

* , ** significant at the 0.05 and 0.01 level, respectively.
Trait symbols: GP, number of grains per panicle; GW, 100-grain weight; TP, tillers for each plant.
Coefficient of variation = 19.22%

The R^2 values show that these traits explained about 45% and 47% of the phenotypic and genotypic variability in GY, respectively. Path analysis also revealed that a positive direct effect due to each of the predictors was concurrently associated with some negative indirect effects due to other predictors (Table 4). The length of the uppermost inter-node (LU) had a negative direct effect on TP. GL and GB also showed positive direct effects on GW, while FW had a positive direct effect on GP (Figure 1 and Table 4).

The genetic worth and stability of indices

With regard to SMLR results and path analysis, three yield components (i.e., TP, GP and GW) had the highest impact on GY. Besides these, as shown in Table 3, GY was correlated with DH, DM, GL and PH.

First, all possible combinations in relation to yield components and yield correlated traits were evaluated. Results showed that a combination comprising yield components plus two yield-correlated traits, namely GL and PH, had more effect on GY compared to other combinations of traits (Tables 6 and 7).

The economic weights assigned to the traits are presented in Table 6. Table 7, in addition, shows the expected genetic advance (EGA) for each trait through indices (ΔG%), the correlation coefficient between index and total genetic worth (R_{HI}) and the stability measures of indices. Based on the results, indices 13, 14 and 15 had the highest advances with 42.19%, 42.10% and 42.04%, respectively (Table 7). These indices showed a positive advance for GW and a suitable advance for TP with 22.31%, 22.24% and 22.31%, respectively. Moreover, these indices (13, 14 and 15) had a similar impact on GL (8.53%), which was higher compared to other indices. However, the highest EGA for GP belonged to indices 7, 9 and 8 with 48.67%, 48.66% and 48.62%, respectively. Cycle traits, i.e., DH and DM, showed the highest advance through indices 6 and 11 (Table 7). The high value of R_{HI} showed that all indices were highly correlated with total genetic worth.

Table 6. The combinations of traits and relative economic weights used for developing selection indices ($\vec{a}$ vectors)

	Relative economic weights															
	PCC			GCC			PPC			GPC			SMLRP			h^2_b
Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
DH	0.260	0.260	0.260	0.244	0	0.871	0	0	-0.016	-0.060	-0.089	-1.129	0	0	0.054	0.871
DM	0	0.209	0.209	0	0.258	0.957	0	0.045	0.06	0	0.889	1.032	0	0.071	0	0.957
GP	0.276	0.276	0.276	0.237	0.237	0.951	0.484	0.4795	0.479	0.424	0.408	0.335	0.121	0.120	0.120	0.951
GL	0.177	0	0.177	0.305	0.305	0.896	0.087	0.740	0.074	0.163	0	0.258	0.847	0.719	0.753	0.896
GB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LU	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PH	-0.260	-0.260	-0.260	-0.424	-0.424	0	-0.164	-0.156	-0.157	-0.260	-0.352	-0.422	-0.096	-0.091	-0.090	0
GW	0.222	0.222	0.222	0.211	0.211	0.896	0.366	0.370	0.372	0.336	0.455	0.367	11.134	11.247	11.120	0.896
NT	0.346	0.346	0.346	0.422	0.422	0.851	0.533	0.527	0.527	0.527	0.506	0.490	1.628	1.608	1.610	0.851
FW	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
FL	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GY	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Trait symbols: DH, days to heading; DM, days to maturity; GP, number of grains per panicle; GL, grain length; GB, grain breadth; LU, the length of the uppermost inter-node; PL, panicle length; PH, plant height; GW, 100-grain weight; TP, tillers for each plant; FW, flag leaf width; FL, flag leaf length; GY, grain yield; PCC, phenotypic correlation coefficient; GCC, genotypic correlation coefficient; PPC, phenotypic path coefficient; GPC, genotypic path coefficient; SMLRP, stepwise multiple linear regression parameter; h^2_b, broad-sense heritability.

Table 7. Expected genetic advance in each trait with 10% selection intensity (ΔG%), and correlation coefficient between genetic worth and each index (R_{HI}) based on optimum (Smith-Hazel) index along with stability parameter of Finlay and Wilkinson (bi)

	Index	ΔG %													R_{HI}	bi
		DH	DM	PH	GL	GP	GW	NT	GB	LU	PL	FW	FL	GY		
PCC	1	4.88	3.61	-14.37	4.64	44.57	-6.14	-2.52	-3.91	-6.97	-4.50	9.84	-7.78	23.86	0.988	0.026
	2	5.89	4.38	-14.58	4.75	43.47	-6.14	-1.66	-4.62	-7.10	-4.74	9.84	-8.58	24.13	0.988	0.200
	3	5.93	4.40	-14.56	5.07	43.44	-6.14	-1.66	-4.62	-7.18	-4.62	9.84	-8.62	24.31	0.988	0.742
GCC	4	5.57	3.91	-18.89	4.43	38.97	-5.73	2.45	-3.20	-9.87	-6.60	7.38	-12.67	27.52	0.983	0.071
	5	5.51	3.92	-18.64	4.32	39.35	-6.14	2.30	-3.20	-9.71	-6.44	7.38	-12.49	27.52	0.984	0.266
	6	6.75	4.81	-18.81	4.97	37.73	-5.73	3.17	-4.27	-9.92	-6.60	7.38	-13.33	27.73	0.984	0.744
PPC	7	2.27	1.93	-8.44	3.56	48.67	-6.55	-7.84	-3.56	-3.25	-1.79	11.48	-1.10	18.30	0.988	0.386
	8	2.56	2.14	-8.41	4.32	48.62	-6.14	-7.84	-3.91	-3.41	-1.48	11.48	-1.28	18.86	0.988	0.470
	9	2.42	2.05	-8.41	3.67	48.66	-6.55	-7.77	-3.56	-3.22	-1.79	11.48	-1.13	18.36	0.988	0.663
GPC	10	2.47	1.99	-10.82	3.56	47.64	-6.55	-5.97	-3.20	-4.67	-2.79	10.66	-3.32	20.47	0.988	0.876
	11	5.98	4.54	-13.71	4.75	43.88	-6.14	-2.01	-4.98	-6.60	-4.31	9.84	-7.96	23.77	0.988	0.668
	12	2.49	2.00	-14.22	2.91	44.93	-7.37	-2.52	-2.49	-6.73	-4.19	9.02	-6.98	23.77	0.983	1.249
SMLRP	13	4.74	3.05	-13.85	8.53	20.16	7.37	22.31	1.78	-10.77	-4.27	4.92	-8.00	42.19	0.959	2.787
	14	5.39	3.55	-13.87	8.53	20.12	7.37	22.24	1.42	-10.72	-4.46	4.92	-8.33	42.10	0.960	2.483
	15	5.28	3.45	-13.90	8.53	20.05	7.37	22.31	1.42	-10.74	-4.43	4.92	-8.29	42.04	0.960	2.801
h^2_b	16	5.31	4.25	-7.15	5.61	46.90	-5.73	-7.41	-6.40	-2.82	-1.16	12.30	-1.64	18.18	0.988	0.909

Trait symbols: DH, days to heading; DM, days to maturity; GP, number of grains per panicle; GL, grain length; GB, grain breadth; LU, the length of the uppermost inter-node; PL, panicle length; PH, plant height; GW, 100-grain weight; TP, tillers for each plant; FW, flag leaf width; FL, flag leaf length; GY, grain yield.

PCC, phenotypic correlation coefficient; GCC, genotypic correlation coefficient; PPC, phenotypic path coefficient; GPC, genotypic path coefficient; SMLRP, stepwise multiple linear regression parameter; h^2_b, broad-sense heritability.

The stability parameters of indices are shown in Table 7. Index 16, developed based on heritability of traits, was the most stable index (bi= 0.909). Indices 10 and 12 (developed based on genotypic path coefficients) also had a high stability with regression coefficients 0.876 and 1.249, respectively (Table 7).

Despite high stability, indices 16, 10 and 12 had low EGA for GY. The lowest stabilities were observed for indices 13, 14 and 15.

Discussion

Correlation coefficients between traits

According to Table 3, negative correlations between PH and some traits such as GY, DH, DM and TP showed competition between the vegetative and reproductive functions. Most of the correlations between vegetative and reproductive traits, such as the negative correlation between GY and traits LU and PH", were negative showing competition in the partitioning of the plant resources between vegetative and reproductive functions. The reproductive traits were positively correlated with GY, while vegetative traits were correlated negatively. There was more antagonism between traits (TP-GP, GP-GW and GB-GL) than associations. In the vegetative component, traits were highly and positively correlated. The positive correlation between GY and DM also showed that longer maturity duration may raise the amount of GY. Accordingly, direct selection for GY can raise DM, negative correlation between GP and TP, as well as between GP and GW, showed a compensatory relationship between these traits (Table 3).

Most of the correlations were consistent with other reports, such as those of Sarawgi *et al*. (18), Surek and Beser (19) and Rabiei *et al*. (4).

SMLR and path coefficients

Path analysis showed that LU had a negative direct effect on TP, which shows the existence of competition between vegetative and reproductive functions.

Although Rabiei *et al*. (4) and Sabouri *et al*. (5) recommended indices developed based on path coefficients, however, in this research the highest genetic worth was observed using SMLR coefficients as economic weights (indices 13, 14 and 15 in Tables 6 and 7). We suggest the following reasons for the observed superiority of SMLR coefficients over path coefficients and other parameters.

(i) Path coefficients and correlation coefficients vary from -1 to +1. Heritability of traits is also varied from 0 to +1. These coefficients are limited between two constant values, while SMLR coefficients are not constrained by minimum and maximum values. (ii) In fact, the associated weight assigned to each trait acts as a slope of regression line; therefore indices developed based on SMLR coefficients had more genetic advance.

The genetic worth and stability of indices

In this research, index 16 (developed based on heritability of traits) was the most stable index, followed by indices 10 and 12, which are developed based on genotypic path coefficients. The result shows that, compared to other indices, the index developed based on the use of genetic components of variance had more stability. However, as shown in Table 7, such indices (16, 12 and 10) had low genetic advance for important traits such as GY. On the other hand, indices 13, 14 and 15, which showed the highest EGA for GY were the most unstable indices. Based on these results, there was an inverse relationship between the stability and genetic worth of indices and, thus, in agreement with Singh and Bellman (9) report, there is no possibility of developing an index with a high level of both genetic worth and stability. Therefore, an index developed for a given plant population with a good genetic worth may not be useful for the same populations, and the corresponding economic values should be recalculated.

The results of this study showed that selecting for higher TP, GW, GP and GL and decreased PH by using SMLR coefficients as economic weights would be an effective criterion for improving rice grain yield based on the Smith-Hazel index. On the other hand, the heritability of traits and genotypic path coefficients may be used to develop indices with more stability.

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