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RESEARCH ARTICLE

Selection response and selection efficiency for the genetic gain in rice

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Abstract

The purpose of this study was to identify superior genotypes among the ten genotypes used, as well as selection indices with as few character combinations as possible but high selection indices values. The research which took place in Jatimulyo Village, Lowokwaru District, Malang City at the Experimental Field of the Faculty of Agriculture, Universitas Brawijaya was carried out from March to June 2022. The research method used was experimental research. A randomized block design (RBD) with three replications was used to conduct the experiment. The selection indices value is searched using the R Studio Program. Six of the thirteen variables were chosen to form the selection index's constituent characters. Based on the results of the genotype research, the genotype with the highest index selection is Inpago 8, with the recommended character combinations grain yield characters, the number of grains per panicle, and panicle length.

Keywords: Rice, genetic gain, yield, selection response, variable

Introduction

The increasing population of Indonesia indicates that the demand for rice (*Oyza sativa* L.) as a main food ingredient and source of carbohydrates will continue to rise. To maintain the quantity and quality of rice as the main food source for both lowland rice and dryland rice, technology development, seed improvement, cultivation, and post-harvest techniques for sustainable rice production are required (Taufik *et al.*, 2013). Around 8,000 years ago, humans directly observed wild rice, intuitively selected the texture of the rice, and (Khush, 1987). Rice breeding in Indonesia depends on societal challenges, as well as current or future issues (Poehlman and Sleper, 1995; Syukur *et al.*, 2017). Plant breeding activities includes obtaining plants with high yields and resistant to biotic and abiotic stresses, (Syukur *et al.*, 2017). Target determination, germplasm (population) preparation, cultivar selection, evaluation, certification, and release are all stages of plant breeding (Acquaah, 2012).Selection is critical to the success of plant breeding activities. Selection will be more effective if the population under consideration has a high genetic diversity and heritability. Selection on characters with a high heritability and diversity will result in progress or an increase in the average value after selection (Yunandra *et al.*, 2017).

Selection is one of the stages of plant breeding activities in which individuals with the desired genotype will be selected to become a new cultivar. Selection can be done by focusing on one or more traits (multi-character) (Acquaah, 2012). Index selection is a type of selection that involves many plant traits at the same time. Selection indices are typically built using a variety of methods, including heritability estimation, the relative economic importance of each trait, and genetic and phenotypic correlations between the traits observed. Plant traits (characters) with the highest index will be used in future breeding activities (Acquaah, 2012). Selection by index allows you to maximise the response to selection for one or more traits. Based on the index elicits responses not only from the main trait (which is being observed), but also from other traits that correlate with the trait being observed (Geraldi, 2020). The objective of this study is to identify among the 10 genotypes utilized a genotype with a high selection index value and a limited amount of features.

Materials and methods

The study was carried out between March and July of 2022. The research was carried out at the experimental field, Faculty of Agriculture, University of Brawijaya in Jatimulyo Village, Lowokwaru District, Malang City. This study's materials included ten rice genotypes (19I-06-09-23-03; 21B-57-21-21-23; 23A-56-20-07-20; 23A-56-22-20-05; 23F-04-10-18-18; Danau Gaung; Inpago 8; Inpago 12; PBM UBB1; Rindang), alphaboard, nails, wooden/bamboo poles, envelopes, fungicides, pesticides, chemical fertilizers. The experiment was carried out with three replications of an environmental randomised block design (RBD). The treatment consisted of 10 genotypes, with each genotype planted in a separate plot measuring 4 5 m and separated by 1 m. Each plot contains 320 planting holes, with three seeds planted in each planting hole. Ten clumps will be selected at random in each plot for each genotype and repetition to be observed and data collected. The sample collected is also a clump that is not on the border (edge of the plot). The collected data is organized in a table to determine the average value using the Microsoft application. Excel, and then use the SPSS application to look for correlations between variables. Determine the variables used in index selection preparation based on the economic value of each variable. The correlation of all variables with the grain yield variable is used to calculate economic value. If the variable is positively correlated with the grain yield variable, its economic value is 1, while if it is negatively correlated, its economic value is 0. Using the R Studio programme, look for index selection variables with an economic value of 1.

Result and discussion

In our studies, grain yield (X_1) is positively correlated and has an economic value of 1 along with five other variables, dry milled grain (X_2), grain width (X_3), grain length (X_4), number of grain per panicle (X_5), and panicle length (X_6). The grain yield character is considered a stand-alone character in the selection index, with a relative efficiency value of 100%. According to Hazel (1943), when compiling index selection, it is necessary to determine the economic value of each character used. When compiling index selection, determining the economic value of each character can improve the accuracy of the index selection results. Results of relative efficiency, genetic advance, discriminant function, and index selection calculations (Table 1). Six characters are used as index selection constituent variables to form 63 combinations. As the number of characters used in combination increases, so does the relative efficiency of index selection. The average value of the relative efficiency of a single character combination is 293.8%, raising the average value of the relative efficiency of a two-character combination to 568.5%(Table2).

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Table 1: Selection index, discriminant fuction, genetic advance (GA) and relative efficiency (RE)

No	Selection Index	Discriminant function	GA (%)	RE (%)
1	X_1 (GY)	$0.970\ X_1$	7.61	100.00
2	X_2 (DMG)	$0.987\ X_2$	7.28	95.70
3	X_3 (GW)	$0.733\ X_3$	1.14	14.97
4	X_4 (GL)	$0.825\ X_4$	1.64	21.55
5	X_5 (NSP)	$0.994\ X_5$	110.27	1449.76
6	X_6 (PL)	$0.905\ X_6$	6.19	81.32
7	$X_1 + X_2$	$0.472\ X_1 + 1.540\ X_2$	15.01	197.41
8	$X_1 + X_3$	$0.977\ X_1 + 0.717\ X_3$	7.90	103.81
9	$X_1 + X_4$	$0.984\ X_1 + 0.800\ X_4$	8.36	109.93
10	$X_1 + X_5$	$1.000\ X_1 + 0.994\ X_5$	113.78	1495.95
11	$X_1 + X_6$	$0.985\ X_1 + 0.906\ X_6$	10.78	141.78
12	$X_2 + X_3$	$0.995\ X_2 + 0.764\ X_3$	7.61	100.04
13	$X_2 + X_4$	$1.002\ X_2 + 0.832\ X_4$	8.08	106.20
14	$X_2 + X_5$	$1.051\ X_2 + 0.993\ X_5$	113.82	1496.44
15	$X_2 + X_6$	$1.009\ X_2 + 0.905\ X_6$	10.70	140.68
16	$X_3 + X_4$	$0.642\ X_3 + 0.985\ X_4$	2.82	37.12
17	$X_3 + X_5$	$1.215\ X_3 + 0.994\ X_5$	110.45	1452.10
18	$X_3 + X_6$	$0.800\ X_3 + 0.910\ X_6$	6.45	84.76
19	$X_4 + X_5$	$1.081\ X_4 + 0.995\ X_5$	110.36	1450.99
20	$X_4 + X_6$	$0.828\ X_4 + 0.907\ X_6$	6.61	86.85
21	$X_5 + X_6$	$1.031\ X_5 + 0.279\ X_6$	115.88	1523.50
22	$X_1 + X_2 + X_3$	$0.393\ X_1 + 1.633\ X_2 + 0.721\ X_3$	15.29	201.02
23	$X_1 + X_2 + X_4$	$0.372\ X_1 + 1.663\ X_2 + 0.794\ X_4$	15.73	206.78
24	$X_1 + X_2 + X_5$	$-0.203\ X_1 + 2.328\ X_2 + 0.990\ X_5$	117.72	1547.78
25	$X_1 + X_2 + X_6$	$0.258\ X_1 + 1.792\ X_2 + 0.876\ X_6$	17.54	230.63
26	$X_1 + X_3 + X_4$	$0.979\ X_1 + 0.647\ X_3 + 0.963\ X_4$	8.85	116.39
27	$X_1 + X_3 + X_5$	$0.993\ X_1 + 1.186\ X_3 + 0.994\ X_5$	113.91	1498.40
28	$X_1 + X_3 + X_6$	$0.989\ X_1 + 0.775\ X_3 + 0.911\ X_6$	11.08	145.69
29	$X_1 + X_4 + X_5$	$0.992\ X_1 + 1.046\ X_4 + 0.995\ X_5$	113.91	1497.68
30	$X_1 + X_4 + X_6$	$0.999\ X_1 + 0.784\ X_4 + 0.907\ X_6$	11.45	150.52
31	$X_1 + X_5 + X_6$	$0.870\ X_1 + 1.039\ X_5 + 0.197\ X_6$	119.31	1568.69
32	$X_2 + X_3 + X_4$	$1.002\ X_2 + 0.697\ X_3 + 0.958\ X_4$	8.61	113.23
33	$X_2 + X_3 + X_5$	$1.045\ X_2 + 1.220\ X_3 + 0.993\ X_5$	114.01	1498.93
34	$X_2 + X_3 + X_6$	$1.015\ X_2 + 0.817\ X_3 + 0.909\ X_6$	11.02	144.89
35	$X_2 + X_4 + X_5$	$1.047\ X_2 + 1.037\ X_4 + 0.993\ X_5$	113.95	1498.19
36	$X_2 + X_4 + X_6$	$1.027\ X_2 + 0.806\ X_4 + 0.905\ X_6$	11.38	149.62
37	$X_2 + X_5 + X_6$	$0.929\ X_2 + 1.035\ X_5 + 0.247\ X_6$	119.36	1569.27
38	$X_3 + X_4 + X_5$	$1.257\ X_3 + 0.856\ X_4 + 0.994\ X_5$	110.56	1453.57
39	$X_3 + X_4 + X_6$	$0.826\ X_3 + 0.871\ X_4 + 0.911\ X_6$	7.14	93.81
40	$X_3 + X_5 + X_6$	$1.258\ X_3 + 1.030\ X_5 + 0.280\ X_6$	116.05	1525.86
41	$X_4 + X_5 + X_6$	$1.287\ X_4 + 1.033\ X_5 + 0.241\ X_6$	115.98	1524.86
42	$X_1 + X_2 + X_3 + X_4$	$0.287\ X_1 + 1.751\ X_2 + 0.671\ X_3 + 0.939\ X_4$	16.11	211.87
43	$X_1 + X_2 + X_3 + X_5$	$-0.276\ X_1 + 2.401\ X_2 + 1.174\ X_3 + 0.990\ X_5$	117.92	1550.38
44	$X_1 + X_2 + X_3 + X_6$	$0.181\ X_1 + 1.880\ X_2 + 0.778\ X_3 + 0.878\ X_6$	17.84	234.49
45	$X_1 + X_2 + X_4 + X_5$	$-0.313\ X_1 + 2.444\ X_2 + 0.993\ X_4 + 0.990\ X_5$	117.89	1550.02
46	$X_1 + X_2 + X_4 + X_6$	$0.156\ X_1 + 1.919\ X_2 + 0.779\ X_4 + 0.872\ X_6$	18.23	239.72
47	$X_1 + X_2 + X_5 + X_6$	$-0.502\ X_1 + 2.513\ X_2 + 1.034\ X_5 + 0.196\ X_6$	123.18	1619.47
48	$X_1 + X_3 + X_4 + X_5$	$1.009\ X_1 + 1.315\ X_3 + 0.763\ X_4 + 0.994\ X_5$	114.12	1500.36
49	$X_1 + X_3 + X_4 + X_6$	$1.000\ X_1 + 0.866\ X_3 + 0.802\ X_4 + 0.911\ X_6$	11.90	156.41
50	$X_1 + X_3 + X_5 + X_6$	$0.859\ X_1 + 1.299\ X_3 + 1.039\ X_5 + 0.192\ X_6$	119.50	1571.15
51	$X_1 + X_4 + X_5 + X_6$	$0.797X_1 + 1.536\ X_4 + 1.046\ X_5 + 0.095\ X_6$	119.45	1570.57
52	$X_2 + X_3 + X_4 + X_5$	$1.075\ X_2 + 1.455\ X_3 + 0.654\ X_4 + 0.992\ X_5$	114.16	1500.91
53	$X_2 + X_3 + X_4 + X_6$	$1.032\ X_2 + 0.925\ X_3 + 0.782\ X_4 + 0.908\ X_6$	11.85	155.81
54	$X_2 + X_3 + X_5 + X_6$	$0.920\ X_2 + 1.326\ X_3 + 1.035\ X_5 + 0.245\ X_6$	119.55	1571.76
55	$X_2 + X_4 + X_5 + X_6$	$0.863\ X_2 + 1.479\ X_4 + 1.041\ X_5 + 0.158\ X_6$	119.50	1571.15
56	$X_3 + X_4 + X_5 + X_6$	$0.773\ X_3 + 1.366\ X_4 + 1.033\ X_5 + 0.236\ X_6$	116.17	1527.42
57	$X_1 + X_2 + X_3 + X_4 + X_5$	$-0.377\ X_1 + 2.540X_2 + 1.441\ X_3 + 0.621\ X_4 + 0.989\ X_5$	118.11	1552.85
58	$X_1 + X_2 + X_3 + X_4 + X_6$	$0.080\ X_1 + 2.003X_2 + 0.882\ X_3 + 0.785\ X_4 + 0.873\ X_6$	18.62	244.85
59	$X_1 + X_2 + X_3 + X_5 + X_6$	$-0.575\ X_1 + 2.582X_2 + 1.281\ X_3 + 1.034\ X_5 + 0.191\ X_6$	123.37	1622.07
60	$X_1 + X_2 + X_4 + X_5 + X_6$	$-0.637\ X_1 + 2.591X_2 + 1.471\ X_4 + 1.040\ X_5 + 0.103\ X_6$	123.35	1621.82
61	$X_1 + X_3 + X_4 + X_5 + X_6$	$0.748\ X_1 + 0.082X_3 + 2.131\ X_4 + 1.052\ X_5 + 0.016\ X_6$	119.66	1573.24
62	$X_2 + X_3 + X_4 + X_5 + X_6$	$0.835\ X_2 + 0.394X_3 + 1.840\ X_4 + 1.045\ X_5 + 0.114\ X_6$	119.70	1573.84
63	$X_1 + X_2 + X_3 + X_4 + X_5 + X_6$	$-0.741\ X_1 + 2.663\ X_2 + 0.252\ X_3 + 1.938\ X_4 + 1.045\ X_5 + 0.042\ X_6$	123.57	1624.63

Where, GY = grain yield; FGW = dry milled grain; GW = Grain Width; GL = Grain Length; NSP = Number of Grain per panicle
PL = Panicle Length

Table 2: Average relative efficiency of different combination of characters

Number of character in Index	Average of Relative Efficiency (%)
1	293.88
2	568.51
3	836.79
4	1102.10
5	1364.78
6	1624.63

Table 3: The combination with the highest relative efficiency value

No	Combination	Genetic Advance (%)	Relative Efficiency (%)
5	Number of Grain per Panicle		1449.76
10	Grain Yield + Number of Grain per Panicle	110.27	1495.95
14	Dry Milled Grain + Number of Grain per Panicle	113.78	1496.44
21	Number of Grain per Panicle + Panicle Length	113.82	1523.50
24	Grain Yield + Dry Milled Grain + Number of Grain per Panicle	115.86	1547.78
31	Grain Yield + Number of Grain per Panicle + Panicle Length	117.72	1568.69
37	Dry Milled Grain + Number of Grain per Panicle + Panicle Length	119.31	1569.27
40	Grain Width + Number of Grain per Panicle + Panicle Length	119.36	1525.86
47	Grain Yield + Dry Milled Grain + Number of Grain per Panicle + Panicle Length	116.06	1619.47
50	Grain Yield + Grain Width + Number of Grain per Panicle + Panicle Length	123.18	1571.15
54	Dry Milled Grain + Grain Width + Number of Grain per Panicle + Panicle Length	119.50	1571.76
55	Dry Milled Grain + Grain Length + Number of Grain per Panicle + Panicle Length	119.55	1571.15
59	Grain Yield + Dry Milled Grain + Grain Width + Number of Grain per Panicle + Panicle Length	119.50	1622.07
60	Grain Yield + Dry Milled Grain + Grain Length + Number of Grain per Panicle + Panicle Length	123.37	1621.82
63	Grain Yield + Dry Milled Grain + Grain Width + Grain Length + Number of Grain per Panicle + Panicle Length	123.35	1624.63

Table 4: Selection index value for each genotype in combinations with high genetic advance an relative efficiency values

S. No	Discriminant function	Genetic advance (%)	Relative efficiency (%)	Selection Index									
				G1	G2	G3	G4	G5	G6	G7	G8	G9	G10
5	$0.994X_5$	110.27	1449.77	98.50	87.11	103.85	107.95	52.74	140.21	216.28	103.90	132.31	217.00
10	$1.000X_1 + 0.994X_5$	113.78	1495.95	109.13	100.44	113.94	115.05	58.87	144.27	232.94	110.28	139.75	227.01
14	$1.051X_2 + 0.993X_5$	113.82	1496.44	108.19	99.39	113.01	113.87	57.82	143.45	231.82	109.48	138.93	226.22
21	$1.031X_5 + 0.279X_6$	115.86	1523.50	107.91	95.70	113.57	117.28	59.47	152.14	231.37	113.50	144.49	232.09
24	$-0.203X_1 + 2.328X_2 + 0.990X_5$	117.72	1547.78	117.70	111.52	121.99	119.51	62.71	146.42	247.12	114.85	145.33	235.18
31	$0.870X_1 + 1.039X_5 + 0.197X_6$	119.31	1568.66	116.23	106.39	121.43	122.74	63.82	154.79	245.47	118.17	149.86	240.42
37	$0.929X_2 + 1.035X_5 + 0.247X_6$	119.36	1569.27	116.31	106.38	121.53	122.46	63.70	154.95	245.39	118.30	150.19	240.53
40	$1.258X_3 + 1.030X_5 + 0.280X_6$	116.06	1525.86	109.54	99.22	116.94	118.85	63.42	154.45	234.45	116.75	147.79	235.96
47	$-0.502X_1 + 2.513X_2 + 1.034X_5 + 0.196X_6$	123.18	1619.47	124.67	117.36	129.36	127.00	67.49	156.77	259.51	122.60	155.29	248.46
50	$0.859X_1 + 1.299X_3 + 1.039X_5 + 0.192X_6$	119.50	1571.15	117.75	109.83	124.74	124.23	67.76	157.07	248.46	121.40	153.11	244.30
54	$0.920X_2 + 1.326X_3 + 1.035X_5 + 0.245X_6$	119.55	1571.77	117.90	109.94	124.94	124.01	67.76	157.30	248.48	121.62	153.54	244.50
55	$0.863X_2 + 1.479X_4 + 1.041X_5 + 0.158X_6$	119.50	1571.15	125.23	118.06	133.46	130.83	75.77	165.17	256.70	128.71	161.37	251.65
59	$-0.575X_1 + 2.582X_2 + 1.281X_3 + 1.034X_5 + 0.191X_6$	123.37	1622.07	126.13	120.71	132.58	128.41	71.32	158.96	262.41	125.74	158.45	252.23
60	$-0.637X_1 + 2.591X_2 + 1.471X_4 + 1.040X_5 + 0.103X_6$	123.35	1621.82	133.35	128.77	141.03	135.11	79.30	166.75	270.53	132.78	166.22	259.33
63	$-0.741X_1 + 2.663X_2 + 0.252X_3 + 1.938X_4 + 1.045X_5 + 0.042X_6$	123.57	1624.63	135.85	132.49	144.85	137.54	83.31	169.93	274.17	136.18	169.75	263.21
	Average of Selection Index	118.55	1558.62	117.63	109.55	123.81	122.99	66.35	154.84	247.01	119.62	151.09	241.21

Where X_1 = Grain Yield; X_2 = Dry Milled Grain; X_3 = Grain Width; X_4 = Grain Length; X_5 = Number of Grain per Panicle; X_6 = Panicle Length
G1=19I-06-09-23-03; G2= 21B-57-21-21-23; G3= 23A-56-20-07-20; G4= 23A-56-22-20-05; G5= 23F-04-10-18-18; G6= Danau Gaung; G7= Inpago 8; G8= Inpago 12; G9= PBM UBB1; G10= Rindang.

The average value of the relative efficiency of the three-character combination then rises to 836.79%. When compared to the average relative efficiency values of the other combinations, the combination of six characters has the highest average relative efficiency. The relative efficiency value describes a selection's level of efficiency, greater the relative efficiency, which describes the results of a combination of several characters in index selection, the more effective and successful (Akbar *et al.*, 2016). The discriminant function with the grain yield character does not have the maximum advantage. This can be seen from the value of genetic advance and relative efficiency of grain yield (X_1) with values of 7.61 and 100%, which are still smaller than the values of genetic advance and relative efficiency of the number of grains per panicle (X_5) with values of 110.27% and 1449. 76%. Among the index selection with two characters, the discriminant function of grain quantity per panicle and panicle length (X_5+X_6) has a higher genetic advance value, namely 115.88% with a relative efficiency of 1523.50%. Index selection with three characters showed that the discriminant function with the character of dry milled grain, number of grains per panicle and panicle length (X_2+X_5+X_6) had a higher genetic advance value of 119.36% with a relative efficiency of 1569.27%. Index selection with four characters on the discriminant function of grain yield, dry milled unhulled grain, number of grains per panicle (X_1+X_2+X_5+X_6) with genetic advance of 123.18% with a relative efficiency of 1619.47%. Index selection with five characters on the discriminant function of grain yield, dry milled grain, grain width, number of grains per panicle and grain yield (X_1+X_2+X_3+X_5+X_6) with 123.37% genetic advance and 1622.07% relative efficiency. Selection of the best index to increase rice grain yield, which involves grain yield, dry milled grain, grain width, grain length, number of grain per panicle and panicle length (X_1+X_2+X_3+X_4+X_5+X_6) with genetic advance 123 .57% and a relative efficiency of 1624.63%. The degree of gain produced in selection is explained by genetic advance. The high value of genetic advance raises the prospect of added value for a character in the next generation. High genetic advance may indicate that further breeding will result in progress on these traits in the next generation (Ahmadikhah, 2010; Ibrahim *et al.*, 2012). A high value of genetic advancement indicates that this trait contains additive genes. Consequently, if a trait has a high genetic improvement value, it is suggested in plant breeding for further improvement to be reliable by selecting that trait (Ogunniyan and Olakojo, 2015).The higher the index selection value, the more characters used in the discriminant function. The value of the combination index selection increases as the number of characters used in the discriminant function in compiling the index selection increases. Furthermore, using two or more characters as selection constituents increases the value of genetic advance and relative efficiency when compared to using only one character (Bizari *et al.,* 2017; Bhuva et al., 2020). The genetic advance and relative efficiency of a single character are lower than the genetic advance and relative efficiency of two or more characters combined. Making a discriminant function in the preparation of index selection is more useful in increasing crop yields than direct selection with one character (Kachhadia *et al.,* 2014). Fifteen combinations out of the 63 had higher relative efficiency values and genetic advance than the others, namely combinations 5, 10, 14, 21, 24, 31, 37, 40, 47, 50, 54, 55, 59, 60, and 63. The 15 combinations are shown in (Table 4), the average value of the data for each character used in compiling the index is entered into the discriminant function to obtain the index selection of each discriminant function after obtaining the discriminant function with high genetic advance and relative efficiency values.

The discriminant function used in index construction aims to reference the character combination to obtain the selection index value. The discriminant function arranges the value of a character in the form of a linear function. We can determine the value of a character by employing the concept of the discriminant function. So that the data can be used as a reference for character values in future research (Smith, 1936). Smith's discriminant function is based on Fisher's discriminant function, which is used to discriminate against the values of individuals in two different populations with overlapping characteristics (Singh and Chaudary, 1979). The highest selection index values were found in genotypes G7 and G10 (Inpago 8 and Rindang varieties) based on the calculation of index selection values using the discriminant function, out of the 15 discriminant functions calculated. G7 contains the discriminant function with the highest index selection value: combinations 10, 14, 24, 31, 37, 47, 50, 54, 55, 59, 60, and 63. G10 has the discriminant function with the highest index selection value in combinations 5, 21, and 40. G7 has the highest average selection index score, with a selection index value of 247.21. Farmers can quickly adopt genotypes with a high selection index value because these genotypes have traits that appeal to farmers (Souleymane *et al.,* 2019).

Plant breeding with multiple characters will take a significant amount of time and money. Because it must take into account the time and costs of the breeding programme, the selected index selection has a high selection index value but a small number of characters (Raghuwanshi *et al.,* 2016). Breeders prefer to increase grain yields by using the fewest number of characters possible, with the goal of saving time and effort in breeding programmes (Adsul and Monpara, 2014; Kachhadia *et al.*, 2014; Bhuva *et al.*, 2020). According to (Table 4), the discriminant function 9 has a high selection index value with high genetic advance and high relative efficiency, namely the combination of grain yield characters, dry milled grain, number of grains per panicle, and panicle length with genetic advance and relative efficiency values of 123.18 and 1619.47%, respectively. Therefore, it is advised to use the Inpago 8 variety with the chosen characters, namely grain yield, milled dry grain, number of grains per panicle, and panicle length, if you want to increase grain yields.

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