

Path Coefficient Analysis in Hull-less Barley under Rainfed Condition

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Abstract: In order to determine correlation between some traits and path analysis of grain yield in hull-less barley, fifteen genotypes were evaluated in randomized complete block design with three replication. Result of analysis of variance indicated that there were significant differences among the genotypes in the majority of traits. The results of correlation analysis showed that grain yield had positive and significant simple correlation with number spike per square meter, harvest index, biological and straw yield, and negative correlation with spike length and awn length. The highest positive correlation was obtained between biological yield and grain yield. Using stepwise regression, 1000 kernel weight, number of spike per square meter, kernel per spike and harvest index was the most important yield component. Path analysis for grain yield showed that the number of spike per square meter and harvest index had positive direct effect on grain yield.

Key words: Hull-less barley, Rainfed condition, Correlation, Path analysis.

INTRODUCTION

Barley is a member of cereals and is being used as food and feed crop. Hull-less or naked barley (*Hordeum vulgare*, L. subsp. *vulgare*) differs from hulled barley by the loose husk cover of caryopses that is easily separable upon threshing in contrast to hulled barley. The hull-less grain character is controlled by the single recessive gene 'nud' located on the long arm of chromosome 7H (Kikuchi, *et al.*, 2003). Cultivation of naked barley is less common worldwide than that of hulled barley (Takahashi, 1955; Sun and Wang, 1999). Hull-less barley is mainly used as animal feed, however, it is an important human food in Himalayas and in Ethiopia. Compared to hulled barley, hull-less barley has higher contents of protein and limiting amino acids, lysine and threonine (Baidoo and Liu, 1998; Bhatti, 1999). Zaefizadeh, *et al.*, (2011) in hull-less barley observed positive and significant correlation between total tillers with fertile tillers, chaff weight and 1000 grain weight. (Khayatnezhad, *et al.*, 2010) reported negative correlation between harvest index and plant height and (Mohammadi, 1997) also found negative correlation between plant height and grain yield, an observed most direct positive effect on yield by number of seeds per main spike and most negative direct effect were for days to heading, in hull-less barley genotypes. (Buttha and Ibrahim, 2005) in six- rowed barley genotypes conclude that there were significant positive correlation between grain yield with 1000 grain weight and number of spikelets per spike, grain yield was negatively correlation with days to heading. Path coefficient analysis revealed that positive maximum association between Peduncle length and number of spikelets with grain yield, extrusion length and spike density had maximum negatively association with grain yield. (Ataei, 2006) reported that grain number in spike with a direct effect on yield was the most important factor. The direct effect of 1000-kernel weight and number of spike on yield was positive also. Path-coefficient analysis is one of the reliable statistical techniques which allow quantifying the interrelationships of different components and their direct and indirect effects on grain yield through correlation estimates. The objective of this study was identifying attributes, relation between them and determining direct and indirect effects on grain yield in hull-less barley genotypes.

MATERIALS AND METHODS

This study was carried out in Agriculture and Natural Resources Research Center in Lorestan Province of Iran in rainfed condition. Located in 3 km west of Khoramabad. (Latitude 33°20', longitude 48°20', altitude 1220m). The experimental material consisted of 15 rainfed hulls-less barley genotypes. A randomized complete block design with three replications were used, each plot contained 4 rows 20cm apart and 6m in length. Plants were evaluated for traits including: days to heading, days to maturity, plant height, kernel per spike, number of spike per square meter, 1000 kernel weight, spike weight, spike length, awn length, peduncle length, test weight, harvest index, biological yield, straw yield and grain yield. Analysis of variance, correlation among traits, stepwise multivariate regression and path analysis were performed using *SAS*, *SPSS* and *Path2 software*, respectively.

RESULTS AND DISCUSSION

Analysis of variance showed significant differences for all traits, except plant height and spike length (Table 1). these Indicate that genetic variation exists among genotypes. Correlation analysis among grain yield and other traits showed that the number of spike per square meter, harvest index, biological and straw yield had the highest significant positive correlation with yield, $r= 0.62^{**}$, $r= 0.66^{**}$, $r= 0.85^{**}$ and $r= 0.71^{**}$, respectively (Table 2). This result was agreement with those reported by (Milomirka, *et al.*, 2005; Aghaei, 1994). Khayatnezhad, *et al.*, (2010), reported negative correlation between harvest index and plant height. Correlation between grain and biological yield was higher than other traits, thus the role of biological yield in grain yield was higher than other traits. Significant and positive correlation between grain yield and harvest index, indicated that genotypes that have higher harvest index able to use most of photosynthetic materials. This result was in agreement with those reported by (Yazdan sepas, 1998). grain and straw yield were significantly correlated. Because barley used as animal nutrition, the genotypes that have high performance are preferred. The relationship of grain yield with other characters is shown in table 2. Using stepwise regression 1000 kernel weight, number of spike per area, number of grain per spike and harvest index was the most important yield component.

Table 1: Analysis of variance of grain yield and other morphological traits in hull-less barley.

S.O.V	df	MS						
		Day to heading	Day to maturity	Plant height (cm)	Kernel Per spike	Number of spike Per square meter	1000 kernel weight(g)	Spike weight (g)
Replication	2	106.86	1.75	4.20	85.10	41672.26	6.46	0.05
Genotype	14	7.581 *	6.08 **	41.10 ns	272.60 **	47951.04 *	46.21 **	0.27 **
Error	28	3.89	0.42	34.96	45.71	62523.02	15.79	0.06
		MS						
Spike length (cm)	Awn length (cm)	Peduncle length (cm)	Test weight (kg/100lit)	Harvest index (%)	Biological yield(kg/ha)	Straw yield (kg/ha)	Grain yield (kg/ha)	
5.14	1.02	29.57	50.90	14.93	14560680.55	5775714.20	1073822.60	
4.87 ns	3.59 **	17.23 *	12494.91 **	30.11 **	4610144.84 **	1344668.14 *	1874227.41 *	
3.84	1.53	8.15	531.92	7.42	4705576.38	1721115.77	1280959.79	

* and ** : significant at 5% , 1% probability levels, respectively

Table 2: Simple correlation coefficients matrix belonging to trait

Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1 Day to heading	1														
2 Day to maturity	0.18	1													
3 Plant height (cm)	-0.15	-0.11	1												
4 Kernel Per spike	-0.23	0.32*	0.02	1											
5 Spike Per square meter	0.06	-0.17	0.04	-0.34*	1										
6 1000 Kernel weight (g)	-0.09	0.15	-0.02	0.54*	0.01	1									
7 Spike weight (g)	-0.05	0.48**	0.03	0.76**	0.45**	0.12	1								
8 Spike length (cm)	-0.14	0.01	-0.05	0.08	-0.20	-0.22	-0.21	1							
9 Awn length (cm)	0.09	0.18	-0.21	-0.25	-0.06	0.01	0.07	0.02	1						
10 Peduncle length (cm)	0.11	0.01	-0.11	0.08	-0.12	-0.21	0.17	0.22	-0.17	1					
11 Test weight (kg/100lit)	0.18	0.31*	0.10	-0.11	0.08	-0.21	0.09	0.12	-0.02	0.02	1				
12 Harvest index (%)	0.09	0.12	0.07	0.44**	0.07	-0.07	0.50**	-0.21	-0.24	0.17	-0.01	1			
13 Biological yield(kg/ha)	-0.18	0.04	-0.01	-0.01	0.68**	-0.14	0.07	0.08	-0.21	-0.02	0.22	0.37*	1		
14 Straw yield(kg/ha)	-0.21	-0.70	-0.05	-0.15	0.72**	-0.13	-0.13	0.15	-0.13	-0.03	0.24	0.10	0.96**	1	
15 Grain yield (kg/ha)	-0.08	0.01	0.03	0.18	0.62**	0.11	0.21	-0.04	-0.27	0.05	0.12	0.66**	0.85**	0.71**	1

* and ** : significant at 5% , 1% probability levels, respectively

Investigation regarding path-coefficient analysis (Table 3) showed that number of spike per square meter had the highest positive direct effect in grain yield, This indicated that with regard to constant other variables, an increase of this trait, grain yield has been increased. This result was agreement with those reported by (Ataei, 2006), but does not confirm the results (Bhutta, *et al.*,1991). According to these results can be stated with although relationship between yield and some yield components (e. g, 1000 kernel weight) were negative, but genotypes through increasing number of spike per square meter, reduced negative effect on grain yield and their effects were not significant. Then we should increase number of plant per square meter in genotypes in order to

component indirect and few effects of other traits. Furthermore the direct effect of harvest index on grain yield was positive and significant. Direct effect of other traits on grain yield was negligible. The highest positive indirect effect on grain yield was related to kernel per spike. The indirect effects of other components are in table 3.

Table 3: Direct (parenthesis) and Indirect effect of some traits in hull-less barley.

	X ₁	X ₂	X ₃	X ₄	rg	Residual
X ₁	(0.076)	0.006	0.004	0.038	0.11	
X ₂	-0.001	(0.636 ^{**})	-0.054	0.037	0.62	
X ₃	0.001	-0.217	(0.156)	0.238	0.18	
X ₄	0.005	0.044	0.068	(0.541 ^{**})	0.66	0.46
X ₁ = 1000 kernel weight(g)			X ₂ = Number of spike per square meter			
X ₃ = Kernel per spike			X ₄ = Harvest index (%)			

Conclusion:

It is evident according to the results of this study, to evolve barley genotypes with ultimate higher grain yield, attention should be focused selecting plant traits which have positive direct effect on grain yield.

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