Genotypic and phenotypic associations of yield related traits in barley genotypes

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Abstract

The knowledge of the nature of associations existing among different component traits is basic to conduct effective selection. Thus, a field experiment was conducted on 28 barley genotypes in randomized block design arrangement with three replications at Holeta in the 2015 season to examine the existing interrelationship between desirable characters including yield barley. The data was recorded on heading date, maturity date, seed filling period, height, effective or tillers plant^{-1}, flag leaf area, spike length, kernel number per spike, seed weight, biomass weight plant^{-1}, grain yield plant^{-1} and harvest index plant^{-1}. Thus, the result indicated most of the relationships in phenotypic and genotypic terms between the desirable characters were positive and significant showing the need to examine the most yield influencing characters for selection. The relationship among every character also showed most of the quantitative characters were influenced by the interaction of several characters. Moreover, the path analysis result of biomass yield and harvest index characters showed a direct strong influence on yield in the positive direction and at the same time, these characters had a highly positive association with grain yield indicating as major contributors of yield. Thus, in general, the finding reveals that both biomass yield and harvest index plant^{-1} characters had a true relationship with barley grain yield implying some amount of improvement in one or both characters will directly contribute to an increased yield. While increased biomass provides additional animal feed. © 2021 Department of Agricultural Sciences, AIOU

Keywords: Barley, Correlations, Direct effect, Path analysis

Introduction

Yield is a complex trait controlled by many genes with a small cumulative effect and highly influenced by the environment (Dyulgerova, 2012) and grain yield has resulted from many quantitative traits interacting with each other (Akhtar et al., 2011). Thus, depending on component traits of higher heritability which is associated with grain yield has more genetic potential for genetic improvement of quantitative traits (Falconer, 1998). Hence, the knowledge of the existing interrelationship among component characters is essential to determine selection criteria for improving new varieties. Correlation analysis depicts the pair-wise relations between different pairs of characters without regarding the nature of cause-and-effect association (Mohammadi, 2015). The correlation coefficient reveals the degree of correlation and whether it is the heritable or non-heritable relationship between several characters. The interaction of genes such as linkage or pleiotropic effect of genes or environmental effect or a combination of all is supposed to be the cause of association (Oad et al., 2002).

In this regard, path analysis is an important tool to disentangle the effect of various independent variables into direct and indirect association on yield (Dewey and Lu, 1959; Shrimali et al., 2017). Moreover, path analysis is a statistical tool that is helpful to the breeders for a better understanding of the causes involved in the associations between traits and to partition the existing correlation into direct and indirect effects, through the main variable (Lorencetti et al., 2006). Understanding the correlation existing between desirable traits can facilitate the interpretation of results obtained and provide the basis for planning a more efficient breeding program (Mrtintell et al., 2005). Association studies among morphological characters of barley have been reported by Mohammadi (2015); Tofiq et al. (2015); Azeb et al. (2016); Amardeep & Vishwanath (2017).

Selection is a basic activity of plant breeders following the creation of genetic variability and selection is applied to genetically variable populations. However, effective selection is crucial to achieving successful improvement. Therefore, the present study was conducted on diverse cross barley populations. Understanding the extent of interrelationship existing among the different characters is helpful to design better breeding strategies to achieve successful improvement in yield. Thus, the study was initiated to explore the extent of phenotypic and genetic correlation existing among yield and related characters as well as estimate the direct and indirect influences on grain yield.

Materials and Methods

Experimental site

The experimental site was Holetta Agricultural Research Center which is about 30 km west of Addis Ababa, Ethiopia, in 2015 main season which is located at an altitude of 2390 m above sea level (m.a.s.l) and with the geographical latitude of

$09^0 04'$ N and longitude of 38^0 30'E. The highest and lowest temperature of Holetta is 22.2 °C and 6.13 °C, respectively while average rainfall is about 1100 mm and the soil types are vertisol and nitosol

Planting materials and design

Twenty-eight barley genotypes were tested at Holetta Research station in 2015 in the main planting season. Seeds of each genotype were planted in a plot of size with two rows of 2.5 m length and 0.20 m width at 0.15 m spacing between plants in a random complete block design in three replications.

Data collection

Plot basis data on heading date (at 40 growth stage) and maturity date (when plant reaches 95% physiological maturity). While ten random selected plants were tagged at tillering growth stage and the data was recorded on height, tillers plant^{-1}, flag leaf area, spike length, kernels per spike, seed weight, biomass weight plant^{-1}, grain yield plant^{-1} and harvest index plant^{-1}

Data analysis

The extent of variation among barley genotypes was estimated from analysis of variance using GLM procedures of SAS (2004) software. The magnitude of genetic (r_g) and phenotypic (r_p) correlation coefficient was calculated using the CANDISC Procedure of SAS (2004) and genetic and phenotypic variances and covariances were determined as described by Singh and Chaudhary (1985). Tabulated value of 't' at n-2 degrees of freedom using n as the number of genotypes was applied to test the correlation coefficients at 5% and 1% probability levels.

Path coefficient analysis

Direct and indirect influence of each character on grain yield was computed using partial regression coefficient. The direct and indirect influences of the independent characters on grain yield were calculated using the formula: $r_{ij} = P_{ij} + \Box r_{ik} P_{kj}$ where r_{ij} is a mutual association between the independent variable ($_i$) and dependent variable ($_j$) as measured by correlation coefficient (phenotypic and genotypic); P_{ij} is component of the direct effect of the independent variable (i) on the dependent variable ($_j$) as measured by path coefficient, and $\Box r_{ik} P_{kj}$ is the summation of components of indirect effects of a given independent variable ($_i$) on a given dependent variable ($_j$) *via* all other independent variables (k). The residual factor ($P^2 R$) was calculated by the formula; $1 = P^2 R + \Box P_{ij} r_{ij}$ (Dewey and Lu, 1959),

Results and Discussion

The information on the existing associations among yield and component traits is useful to identify which character is mainly contributing to yield increment. The existing relationships between agro-morphological characters are influenced by the association resulting from genetic, genetic x environment interaction, and the environment. The phenotypic correlation between traits is an association which is resulted from genetic and environmental effects. While the genotypic correlation is caused due to the genetic system of the traits which is controlling heritable characters for the next generation is useful in breeding programs (Falconer, 1989). In the present study, the analysis result indicated high variability among all barley genotypes for all characters studied (Zerihun et al., 2019) which is a prerequisite for crop improvement.

Correlation characters with grain yield

Important characters such as heading date (0.100, 0.105), seed filling period (0.232*, 0.366), maturity date(0.291**, 0.381), height of plant (0.425**, 0.579**), flag leaf area (0.421**, 0.566**), tillers plant^{-1}(0.374**,0.363*), the seed number spike^{-1}(0.297**,0.445*), thousand kernel weight (0.172, 0.226) biomass yield plant^{-1}(0.897**, 0.873**) and harvest index plant^{-1}(0.226,0.282**) at phenotypic (r_p) and genotypic (rg) levels, respectively with grain yield (Table 1) indicating the association is in the desirable direction for yield for most characters. In contrary to this, spike length showed negative phenotypic association (-0.009) while positive genetic relation with seed yield (Table 1). Similarly, positive associations were obtained for grain yield with all other yield-related characters in barley (Carpici and Celik, 2012).

Correlation among characters

Phenotypic correlation (r_p)

There was a negative correlation of heading date with seed filling period (-0.495**), the height of plant (-0.018), tiller/plant (-0.226*), and harvest index (-0.055) (Table 1) requiring some caution during selection as these may lead to some undesirable. However, the relationship of the same character was positive with the rest of the characters studied; and its association with maturity period (0.741**) and kernel number spike^{-1} (0.217*) was highly significant. Besides this, the phenotypic correlation between seed filling period and maturity date (-0.495*), spike length (-0.162), and harvest index (-0.034) was negative.

Moreover, the phenotypic association between seed filling period and height of plant (0.414**), flag leaf area (0.263**), tillers plant^{-1}(0.265**) was significant and positive (Table 1). The positive and significant phenotypic association was recorded among maturity date and height of plant (0.300**), leaf area of the flag (0.336**), kernel number spike^{-1} (0.331**) and biomass yield plant^{-1} (0.329**). Except for the heading date (-0.018) and harvest index plant^{-1} (-0.265**). In addition to this, the height of the plant had a positive association with

the rest of the characters. There was also a significant phenotypic association of leaf area of the flag with thousand kernel weight (0.218*), kernel number spike[-1] (0.554**), and biomass yield plant[-1] (0.521**).

Furthermore, the relationship between tillers plant[-1] and length of the spike (0.264**), thousand kernels weight (0.356**), biomass yield plant[-1] (0.491**), between kernel number spike[-1] (0.478**) and length of the spike, thousand kernel weight (0.604**, among thousand kernel weight and biomass yield (0.352**) was highly significant and positive. Generally, biomass yield showed a positive association with all characters studied except with harvest index. In contrast, the harvest index had a negative phenotypic association with all the characters measured except for kernel number at phenotypic level (Table 1). In another study, at the phenotypic level, seed yield was associated positively with biomass yield, tillers of the plant, harvest index, and kernel number spike[-1] in barley (Amardeep and Vishwanath, 2017). In addition, a positive phenotypic association of grain yield with spike length (0.46**), biomass yield (0.44**), the height of plant (0.26*) and thousand-grain weight (0.25*) was reported in barley (Adhikari et al. 2018) and a similar report was indicated by Carpici and Celik (2012) for kernel number per spike, and harvest index (r = +0.474) with grain yield.

Genotypic correlation (r$_g$)

In this study, above-ground biomass yield of a plant exhibited positive correlation all characters considered except harvest index while the same character had a significant association with thousand kernel weight (0.507**), effective tillers plant[-1] (0.507**), leaf area of the flag (0.700**), the height of plant (0.766**) and maturity date (0.466**). On other hand, all characters except for kernel number spike[-1] showed negative genotypic and phenotypic association with harvest index plant[-1] (Table 1) this may be due to genetic linkage drag. Similarly, some negative but significant correlations among some yield components; especially that involving harvest index was reported in barley (Carpici and Celik, 2012) and there was also a significant and positive association between thousand kernel weight and height if the plant (0.721**), spike length (0.660**) and tillers plant[-1] (0.555**) (Table 1). Similarly, Amardeep and Vishwanath (2017) reported in barley, at a genotypic level, grain yield plant[-1] was associated positively with biological yield, effective tillers plant[-1], harvest index, grains per spike, days to maturity, and plant height. Besides this, the genotypic association between different desirable characters like between kernel number spike[-1] and maturity date (0.378*), area of flag leaf (0.617**), between spike length and tillers plant[-1] (0.418*), between flag leaf area and days to maturity (0.410*), height of plant (0.669**), between height of the plant and seed filling period (0.512**), maturity date and seed filling time (0.058*) positive and significant (Table 1). The

negative genotypic association between kernel number spike[-1] and spike length, tillers plant[-1] (Table 1) may be because two-row barleys tend to have more spike length but less kernel number spike[-1] than six-row barleys. The result of genetic association was greater than their respective values of phenotypic correlation coefficients for most characters which may be attributed to the association being more of the genetic and small effect of environment on the character expression. Another study on barley showed grain yield had positive and highly significant phenotypic and genotypic correlation with thousand kernel weight and biological yield (Azeb et al., 2016).

Path coefficient analysis

The only result of simple correlation between the characters doesn't fully express the nature of the association. Thus, the importance of path analyses is to divide the association into direct and indirect causes which is useful to examine the various forces involved to produce a given correlation.

Phenotypic path

he phenotypic path analysis result showed some characters had positive direct force on grain yield. Hence, biomass yield (0.951) exerted a directly higher effect upon grain yield plant[-1] positively followed by harvest index (0.406), seed filling period (0.059), the maturity date(0.075), and kernel number spike[-1] (0.012) (Table 2). And the same characters have shown a positively significant phenotypic correlation with grain yield showing the traits are less influenced by the environment which is useful for effective selection. In addition, higher magnitude of the positive indirect effect exerted by all characters except harvest index on yield *via* biomass yield. And this could have exerted a high direct influence of biomass yield per plant on yield resulting in high total phenotypic correlation. The relationship between biomass yield and all the rest studied characters except for harvest index was positive and most of them were phenotypically significant, but there were negative indirect effects exerted on grain yield by most of the characters via harvest index in phenotypic terms indicating harvest index has a true association with yield. Moreover, negative indirect effect via all characters except for kernel number spike[-1] and harvest index on grain yield. The indirect effect via other characters was negligible. Thousand kernel weight, flag leaf area, and heading date had a negative phenotypic direct effect and positive correlation coefficients (Table 2). Spike length had a negative correlation with grain yield (Table 1) and its phenotypic direct influence on grain yield was also negative and smaller than its correlation value. On the other hand, maturity date and kernel number spike[-1] had positive strongly correlated with grain yield while the magnitude of the direct influence is also positive and less than that of correlation coefficient (Table 2).

Table 1 Estimation of phenotypic (r_p) (above diagonal) and genotypic (r_g) (below diagonal) correlation coefficients of barley agronomic characters at Holeta

Characters	HD	SFP	MD	PH	FLA	ETL	SPKL	KNSP	TKW	BMP	HI	GYP
HD		-0.495**	0.741**	-0.018	0.118	-0.226*	0.198	0.217*	0.013	0.127	-0.055	0.100
SFP	-0.539**		-0.495*	0.414**	0.263**	0.265**	-0.162	0.113	0.193	0.241*	-0.034	0.232*
MD	0.810**	0.058*		0.300**	0.336**	-0.050	0.097	0.331**	0.164	0.329**	-0.088	0.291**
PH	-0.013	0.512 **	0.342		0.583**	0.454**	0.249	0.131	0.680	0.563**	-0.265**	0.425**
FLA	0.150	0.332	0.410*	0.669**		0.304	0.003	0.554**	0.218*	0.521**	-0.182	0.421**
ETL	-0.260	0.295	-0.103	0.563**	0.348		0.264**	-0.196	0.356**	0.491**	-0.195	0.374**
SPKL	0.231	-0.258	0.094	0.275	-0.059	0.418*		0.478**	0.604**	0.087	-0.150	-0.009
KNSP	0.239	0.136	0.378 *	0.129	0.617**	-0.257	-0.576**		-0.425**	0.206	0.167	0.297**
TKW	0.022	0.232	0.188	0.721**	0.242	0.555**	0.660**	-0.488**		0.352**	-0.318**	0.172
BMP	0.153	0.407 *	0.466**	0.766**	0.700**	0.507**	0.187	0.324	0.507**		-0.143	0.897**
HI	-0.109	-0.114	-0.208	-0.371*	-0.296	-0.269	-0.274	0.190	-0.505*	-0.258		0.226
GYP	0.105	0.366	0.381	0.579**	0.566**	0.363*	0.030	0.445*	0.226	0.873**	0.282**	

Where * = Significant; ** = Highly significant at 5 and 1% probability levels, respectively; HD = Heading date; SFP = Seed filling period; MD = Maturity date; PH = Plant height; FLA = Leaf area of the flag; ETL = Tillers plant[-1]; SPKL = Spike length; KNSP = Kernel number spike[-1]; TKW = Thousand seed weight; BMP = Biomass yield plant[-1]; HI = Harvest index; GYP = Grain yield plant[-1]

Table 2 The effect of phenotypic direct (bold diagonal) and indirect influence (off-diagonal) of agronomic characters on yield plant^{-1} in barley.

Characters	HD	SFP	MD	HP	FLA	ETL	SPKL	KNSP	TKW	BMP	HI	Total r_p
HD	**-0.022**	-0.029	0.055	0.000	-0.004	0.000	-0.001	0.003	-0.001	0.121	-0.022	0.100ns
SFP	0.011	**0.059**	-0.037	-0.001	-0.009	0.000	0.001	0.001	-0.008	0.229	-0.014	0.232ns
MD	-0.016	-0.029	**0.075**	-0.001	-0.011	0.000	0.000	0.004	-0.006	0.313	-0.036	0.291ns
HP	0.000	0.024	0.022	**-0.003**	-0.020	-0.001	-0.001	0.002	-0.027	0.536	-0.108	0.425*
FLA	-0.003	0.015	0.025	-0.002	**-0.034**	0.000	0.000	0.006	-0.009	0.496	-0.074	0.421*
ETL	0.005	0.016	-0.004	-0.002	-0.010	**-0.001**	-0.001	-0.002	-0.014	0.467	-0.079	0.374ns
SPKL	-0.004	-0.010	0.007	-0.001	0.000	0.000	**-0.005**	0.006	-0.024	0.083	-0.061	-0.009ns
KNSP	-0.005	0.007	0.025	0.000	-0.019	0.000	-0.002	**0.012**	0.017	0.196	0.068	0.297ns
TKW	0.000	0.011	0.012	-0.002	-0.007	-0.001	-0.003	-0.005	**-0.039**	0.335	-0.129	0.172ns
BMP	-0.003	0.014	0.025	-0.002	-0.018	-0.001	0.000	0.002	-0.014	**0.951**	-0.058	0.897**
HI	0.001	-0.002	-0.007	-0.002	0.006	0.000	0.001	0.002	0.012	-0.136	**0.406**	0.282ns

Where * = Significant; ** = Highly significant at 5 and 1% probability levels, respectively; HD = Heading date; SFP = Seed filling period; MD = Maturity date; HP = Plant height, FLA = Leaf area of a flag; ETL = Tillers/plant^{-1}; SPKL = Spike length; KNSP = Kernels number/spike; TKW = Thousand seed weight; BMP = Biomass yield plant^{-1}; HI = Harvest index; GYP = Seed yield plant^{-1}; Residual effect: 0.1414

Genotypic path

In this study, the genotypic path exerted a positive and high direct influence on grain yield plant[-1] by biomass plant[-1] (1.020) followed by harvest index plant[-1] (0.463), heading date (0.158), and seed filling period (0.110) (Table 3). Besides this, grain yield has a positive genotypic association with most of these traits suggesting the existence of a true relationship, and direct selection through these characters is effective. Positive and high indirect effects were exhibited by all the characters except harvest index plant[-1] via biomass yield on grain yield. Whereas negative indirect effects of all characters except maturity date and thousand seed weight via harvest index were observed (Table 3) reveals that significant direct influence on seed yield was exerted on biomass yield and harvest index plant[-1]. Therefore, this suggests that an increment of biomass plant[-1] had a positive influence on grain yield through an enhanced rate of photosynthesis or increases overall crop assimilation, more dry matter partitioning to reproductive parts and enhanced plant development and increased biomass yield potential of barley has additional benefits to be utilized as animal feed in Ethiopian.

Relatively maximum negative direct effects were exhibited via thousand seed weight (-0.181) followed by maturity date (-0.105) and kernels spike[-1] on grain yield (Table 1). Moreover, a negative indirect effect of most of the characters through harvest index, several kernel spike[-1,] and seed weight on yield was recorded (Table 3) and the indirect influence of most of the characters was negligible. Both heights of the plant and flag leaf area were positively strongly correlated with grain yield at the genotypic level while the magnitude of their genotypic direct effect was also positive and less than that of a correlation coefficient. Heading date, seed filling period, and spike length had a positive genotypic direct effect and their indirect effects via other characters were mostly positive and negligible (Table 1 and 3). Furthermore, there were also positive and high indirect effects exhibited by all the characters on seed yield plant[-1] via biomass yield plant[-1] except harvest index in genotypic and phenotypic path analyses. This study conforms to Shrimali1 et al., (2017) report who indicated that the relation of seed yield plant[-1] with plant height, biomass yield plant[-1], and spike length was positively and significantly while they stated that both biomass yield plant[-1] t and harvest index caused a direct high positive effect on seed yield.

Biomass yield exerted a maximum positive direct effect on grain yield across locations followed by harvest index (Azeb et al., 2016). Moreover, it partly coincides with the path coefficient report of Amardeep and Vishwanath (2017) grain yield plant[-1] with biomass yield and harvest index. In this study, a strongly positive correlation of height of plant and flag leaf area with yield plant[-1] was recorded at a genotypic level and the same characters had positive direct effect but less than that of their correlation coefficient indicating the importance of other characters *via* which flag leaf area, and plant height, contributed to grain yield. Heading date, seed filling period, and spike length had a positive genotypic direct effect as well as the indirect effects of these characters via other characters were mostly positive but negligible (Table 1 and 3). While there were negative indirect influences exerted on seed yield at phenotypic and genotypic levels by all characters *via* harvest index plant[-1] except for kernel number spike[-1] (Table 2; Table 3) indicating that the correlation coefficients of harvest index with grain yield had been largely due to its direct effect resulting high total phenotypic and genotypic correlation suggesting that there is a true relationship and direct selection through this character is effective.

Moreover, thousand kernel weight, leaf area of the flag, and heading date had a negative phenotypic direct effect and positive correlation coefficients (Table 2; Table 1) which was may be largely due to its respective indirect effects. Spike length had a negative correlation with grain yield (Table 1) and its phenotypic direct effect on grain yield was also negative and smaller than its correlation value (Table 2) indicating an indirect influence of the trait via other component characters. Maturity period and kernel number spike[-1] had positive strongly correlated with grain yield while the magnitude of the phenotypic direct effect is also positive and less than that of correlation coefficient (Table 2). The relatively maximum negative genotypic direct influence was exerted on grain yield *via* thousand kernel weight (-0.181) and then maturity date (-0.105) and kernel number spike[-1] (-0.100) but their genotypic association with grain yield was positive (Table 1; Table 3). Thus, the positive genotypic association was largely due to its respective indirect influences. Therefore, to improve negative associations of the yield components with other characters, suitable recombinants may be achieved via diallel selective mating, biparental mating, and recurrent selection breeding techniques.

The characters that are associated positively and significantly as well as exerting positive direct effect with seed yield are known to affect seed yield in the desirable direction. In this study, biomass yield and harvest index of a plant caused maximum positive direct influence towards yield. On the other hand, these characters themselves are a product of the interaction of several agronomic traits and so that they could have a cumulative effect of various traits. Hence, selection progress may be enhanced through the improvement of these characters to improve grain yield as some amount of improvement in one or both characters will directly contribute to an increased yield. The causal factors expressed as the residual effect of was 0.1414 and 0.0161 have resulted in phenotypic and genotypic paths, respectively (Table 2; Table 3). This shows the characters subjected to path analysis expressed the variability in grain yield by 85.9% and 98.4%, respectively indicating most of the characters are considered.

Table 3 The effect of genotypic direct (bold diagonal) and indirect influence (off diagonal) of agronomic characters on grain yield plant^{-1} in barley genotypes.

Characters	HD	SFP	MD	HP	FLA	ETL	SPKL	KNSP	TKW	BMP	HI	Total r_g
HD	**0.158**	-0.059	-0.085	-0.001	0.005	0.005	0.004	-0.024	-0.004	0.156	-0.050	0.105ns
SFP	-0.085	**0.110**	-0.006	0.041	0.011	-0.006	-0.005	-0.014	-0.042	0.415	-0.053	0.366ns
MD	0.128	0.006	**-0.105**	0.027	0.013	0.002	0.002	-0.038	-0.034	0.475	-0.096	0.381*
HP	-0.002	0.056	-0.036	**0.079**	0.022	-0.012	0.005	-0.013	-0.131	0.781	-0.172	0.579**
FLA	0.024	0.036	-0.043	0.053	**0.033**	-0.007	-0.001	-0.062	-0.044	0.714	-0.137	0.566**
ETL	-0.041	0.032	0.011	0.045	0.011	**-0.021**	0.008	0.026	-0.101	0.517	-0.125	0.363ns
SPKL	0.036	-0.028	-0.010	0.022	-0.002	-0.009	**0.019**	0.058	-0.120	0.191	-0.127	0.030ns
KNSP	0.038	0.015	-0.040	0.010	0.020	0.005	-0.011	**-0.100**	0.089	0.331	0.088	0.445*
TKW	0.003	0.025	-0.020	0.057	0.008	-0.011	0.012	0.049	**-0.181**	0.517	-0.234	0.226ns
BMP	0.024	0.045	-0.049	0.061	0.023	-0.010	0.004	-0.032	-0.092	**1.020**	-0.120	0.873**
HI	-0.017	-0.013	0.022	-0.029	-0.010	0.006	-0.005	-0.019	0.092	-0.263	**0.463**	0.226ns

Where * = Significant; ** = Highly significant at 5 and 1% probability levels, respectively; HD = Heading date; SFP = Seed filling period; MD = Maturity date; HP = Plant height, FLA = Leaf area of a flag; ETL = Tillers/plant^{-1}; SPKL = Spike length; KNSP = Kernels number/spike; TKW = Thousand seed weight; BMP = Biomass yield plant^{-1}; HI = Harvest index; GYP = Seed yield plant^{-1}; Residual effect: 0.0161

Conclusion

The phenotypic and genotypic association among various characters showed the yield had a positive significant association with most desirable characters showing in the desired direction in increasing economic yield. Desirable yield influencing characters such as biomass yield and harvest index caused the highest positive direct influence on grain yield which had also positive phenotypic and genotypic relation with grain yield. Moreover, the interrelationship result also indicated the characters are influenced by the interaction of several characters. Besides this, increased biomass production has additional benefits especially useful as a feed for small-scale farmers. The causal factors in residual effect for phenotypic and genotypic paths were about 14.14% and 1.6%, respectively, indicating most of the characters responsible for the variability of the grain yield were considered. In general, the result suggests that biomass yield and harvest index plant[-1] characters had a true association with grain yield of barley revealing some amount of improvement in one or both characters will directly contribute to an increased yield.

Conflict of Interest: The author declares that there is no conflict of interest.

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