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CORRELATION AND PATH ANALYSIS FOR YIELD AND RELATED TRAITS IN UPLAND RICE (*Oryza sativa L.*) VARIETIES

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Abstract: The study was carried out on twenty varieties of upland rice (oryza sativa L.) to find out the correlation and path co-efficient values among the grain yield and its' components. Genotypic and phenotypic coefficients of variation ranged from 6.44 (days to maturity) to 30.47% (yield per plant) and 6.51 (days to maturity) to 30.67% (yield per plant), respectively. High genotypic and phenotypic coefficients of variation with low magnitude of differences between the two were observed for days to maturity, yield per plant and number of filled grains per panicle. Highly significant (P<0.01) and positive phenotypic and genotypic correlations were observed between grain yield with yield per plant, number of filled grains per panicle, biomass yield in the range between 0.55 to 0.78. The highest positive and significant genotypic direct effects on grain yield were exerted by plant height, harvest index, days to maturity and biomass yield, suggesting higher chance of improving yield of upland rice through indirect selection of these traits. Grain yield was significantly and positively associated with yield per plant, number of filled grain panicle-1, and number of fertile tillers per plant and harvest index.

Keywords: Correlation coefficient, Path coefficient, Component traits, Varieties

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1. Introduction

Rice is a self-pollinated cereal crop belonging to the family Gramineae under the order Cyperales and class monocotyledon having chromosome number 2n=24 (Hossian et al., 2015). The genus Oryza is known to consist of two cultivated species i.e., Asian rice (O. sativa, 2n=24=AA) and African rice (O. glaberrima, 2n=24=AA) and 23 wild species (2n=24, 48) (Singh et al., 2015).

In Ethiopia, rice development of modern cultivars for the past nearly two decades concentrated towards high yielding plant type: short stature, erect leaves, high tillering, sturdy stems, early maturing and fertilizer responsive.

Genotypic coefficient of variation (GCV) measures the variability of any trait. The extent of the environmental influence on any trait is indicated by the magnitude of the differences between the genotypic and phenotypic coefficients of variation (Allard, 2000).

Correlation coefficient measures the relationship between two characters and does not indicate relative importance of each factor. The degree of correlation among the characters is an important factor especially in economic and complex character as yield (Cyprien and Kumar, 2011). The selection for one trait results in progress for all characters that are positively correlated and retrogress for traits that are negatively correlated.

Path coefficient analysis measures the direct influence of one variable upon the other, and permits separation of correlation coefficients into components of direct and indirect effects. Partitioning of total correlation into direct and indirect effects provide actual information on contribution of characters and thus form the basis for selection to improve the yield (Mohsin et al., 2009). It is used in plant breeding programs to determine the nature of the relationships between yield and yield components that are useful as selection criteria to improve the crop yield. If the cause and effect relationship is well defined, it is possible to present the whole system of variables in the form of a diagram, known as path-diagram (Ekka et al., 2011).

Grain yield is a complex trait, which is influenced by many independent traits and its improvement is essentially linked with deep understanding of interrelationship between them. Studies on the correlation of traits and their relative direct and indirect effect on yield are important, as they are helpful in selecting desirable traits.

2. Material and Methods

2.1. Description of the Study Area

The study was undertaken at Fogera national rice research and training center, Ethiopia. Average altitude of Fogera ranges from 1750 to 2500 meters above sea level (m.a.s.l.) with an average rain fall of 1284 millimeter and temperature ranging from 11.5 °C to 27.9 °C. The experimental site is located at 11°58'N latitude, 37°41'E longitude and at an elevation of 1810 m.a.s.l. Based on ten years' average meteorological data, the annual rainfall is 1300 mm and mean annual minimum and maximum temperatures are, 11.5° C and 27.9°C, respectively. The soil type is Vertisol with pH of 5.90.

2.2. Experimental Materials

Experimental materials were 20 upland rice varieties released by different research centers in different years. Eight of the varieties were NERICA (New Rice for Africa) types initially developed for upland ecosystem by Africa Rice. NERICA varieties were developed by interspecific hybridization of *Oryza glaberrima* and *Oryza sativa* (Samado et al., 2008). The description of the varieties is as shown in Table 1.

Table 1. List of upland rice varieties used for the study (MoANR, 2016)

No	Variety	Pedigree	Year of release
1	Pawe-1	M-55	1998
2	Kokit	IRAT-209	2000
3	Suprica-1	WAB 450	2006
4	NERICA3	WAB 450-IB-P-2B-HB	2006
5	NERICA4	WAB 450-IB-P-9/1	2006
6	NERICA2	WAB 450-1-1-P31-1-HB	2007
7	Getachew	AD-01	2007
8	Andassa	AD-012	2007
9	Tana	AD-048	2007
10	NERICA14	WAB 880-1-32-1-2-P1-HB	2010
11	Kallafo-1	FOFIFA-3737	2010
12	NERICA6	WAB 450-IBP-160-HB	2011
13	NERICA15	WAB 881-10-37-18-3-P1-HB	2011
14	Hidasse	WAB 515-B-16A1-2	2012
15	Chewaqa	YIN lu 20	2013
16	NERICA10	WAB 450-11-1-1-P41-HB	2013
17	NERICA12	WAB 880-1-38-20-17-P1-HB	2013
18	Adet	WAB 450-1-B-P-462-HB	2014
19	NERICA13	WAB 880-1-38-20-28-P1-HB	2014
20	Fogera-1	ART15-7-16-30-2-B-B	2016

2.3. Experimental Design and Management

A field experiment was conducted using 20 released upland rice varieties at Fogera national rice research and training center during 2017 main cropping season. Randomized complete block design with three replications in 14m x 39.5m total area was used. Each experimental plot had a total area of 6m^2 (1.5m x 4m) and six rows at 0.25m interval while the distance between plots and between blocks were 0.5m and 1m, respectively. Seeds have been sown in rows with manual drilling at a rate of 60kg ha^{-1}. Fertilizer application was at a rate of 60.5 kg NPS and 125 kg urea per hectare. All NPS have been applied during planting while urea application was in three splits at planting, tillering and at panicle initiation stages.

2.4. Data Collection

Observation and data recording for the traits under study were based on the standard evaluation system for rice (IRRI, 2013). The data were collected from ten randomly selected plants of each plot for traits treated on plant-basis like plant height (cm), panicle length (cm), number of panicles per plant, number of total grains per panicle, number of filled-grains per panicle, number of fertile tillers per plant, yield per plant (gm). However, days to heading, days to maturity, grain-filling period, thousand-seed weight (gm), biological yield (t ha^{-1}) and grain yield (t ha^{-1}) were taken on plot-basis; the four central rows were considered. Grain yield was adjusted at 14% moisture level.

2.5. Statistical Analysis

Correlation coefficient analysis was done using Statistical Analysis System (SAS) version 9.4 Computer software program following SAS statement (syntax) for randomized complete block design (SAS, 2013). Path coefficient analysis was done using excel.

3. Results and Discussion

3.1. Genotypic and Phenotypic Coefficients of Variation

The genotypic coefficient of variation ranged from 6.442% for days to maturity to 30.471% for yield per plant; and phenotypic coefficient of variation ranged from 6.505% for maturity date to 30.671% for yield per plant. Maximum values of genotypic coefficient of variation were recorded for yield per plant (30.471%) followed by biological yield (22.387%), number of filled grains per panicle (19.561 %) and grain filling period (19.01). Better value of phenotypic coefficient of variation were recorded for yield per plant followed by biological yield, number of filled grain per panicle, grain filling period, grain yield and harvest index with values of 30.671%, 22.805 %, 19.612%, 19.219%,19.185%, and 19.134%, respectively, in the study.

The magnitude of phenotypic coefficient of variation (PCV) is higher than the genotypic coefficient of variation (GCV) for all 16 traits. This indicates that apparent variation for the characters was not only due to genotypes but also due to influence of wide range of genotypic and environmental variance observed in all studied traits. This result is related with the findings of other similar works (Allard, 2000; Idris et al., 2012, Mulugeta Seyoum et al., 2012). However, magnitude of differences between GCV and PCV for most of the traits were low indicating that these traits were less influenced by environmental factors and the phenotypic expression of these traits are controlled more by the genetic factors.

3.2. Correlations Analysis of Quantitative Traits

A positive value of correlation (r) shows that the changes of two variables are in the same direction; high values of one variable are associated with high values of other and vice versa. Genotypic and phenotypic correlation coefficients of all possible combinations for traits under study are presented in Table 2. In most of the cases the genotypic correlation coefficient were higher than the corresponding phenotypic correlation coefficient indicating strong inherent relation between the traits but suppressing effect of the environment, which modified the phenotypic expression of these characters by reducing phenotypic coefficient values (Ekka et al., 2011).

Table 2. Genotypic correlation coefficient (rg) (below diagonal) and phenotypic correlation coefficient (rp) (upper diagonal) of 16 traits of 20 released upland rice varieties

Variable	DH	DM	GFP	PH	PL	CL	FL	NSP	NGP	NFGP	NFTP	TSW	YP	BY	GY	HI
DH		0.54**	-0.53**	0.47**	-0.32*	0.55**	-0.04	0.07	-0.05	-0.02	-0.05	0.42**	0.03	0.54**	0.01	-0.51**
DM	0.55*		0.43**	0.27*	-0.20	0.32*	0.10	0.20	0.49**	0.42**	0.33*	0.40**	0.47**	0.57**	0.30*	-0.38**
GFP	-0.54*	0.41		-0.23	0.14	-0.27*	0.14	0.13	0.54**	0.44**	0.38**	-0.05	0.44**	-0.01	0.28*	0.17
PH	0.47*	0.27	-0.25		0.43**	0.99**	-0.11	0.18	0.26*	0.26*	0.01	0.00	0.28*	0.50**	0.39**	-0.18
PL	-0.35	-0.23	0.15	0.44*		0.31*	0.14	0.23	0.24	0.20	-0.06	-0.41**	0.16	0.02	0.37**	0.33**
CL	0.56*	0.32	-0.28	0.99**	0.32*		-0.16	0.13	0.22*	0.23	0.02	0.08	0.26*	0.54**	0.36**	-0.25
FL	-0.04	0.09	0.15	-0.14	0.09	-0.19		0.48**	0.39**	0.36**	-0.02	0.00	0.28*	-0.14	0.07	0.27*
NSP	0.06	0.27	0.21	0.15	0.20	0.10	0.57**		0.45**	0.43**	0.00	-0.08	0.34**	0.15	0.17	-0.02
NGP	-0.05	0.50*	0.55*	0.25	0.25	0.22	0.42	0.53*		0.95**	0.48**	-0.18	0.81**	0.25*	0.55**	0.21
NFGP	-0.02	0.43	0.45*	0.26	0.21	0.23	0.40	0.50*	0.95**		0.49**	-0.05	0.88**	0.34**	0.64**	0.18
NFTP	-0.05	0.36	0.42	0.00	-0.09	0.02	-0.09	-0.06	0.53*	0.55*		0.05	0.56**	0.29*	0.50**	0.07
TSW	0.44	0.41	-0.07	-0.01	-0.51*	0.08	-0.08	-0.15	-0.19	-0.06	0.03		0.16	0.39**	0.04	-0.40**
YP	0.03	0.47*	0.44*	0.27*	0.15	0.26	0.28*	0.39	0.82**	0.89**	0.61**	0.15		0.39**	0.77**	0.27*
BY	0.57**	0.58**	-0.03	0.52*	-0.04	0.56**	-0.24	0.11	0.26	0.36	0.30	0.37	0.38		0.57**	-0.57**
GY	0.01	0.29	0.28	0.40	0.35	0.37	-0.03	0.15	0.58**	0.67**	0.56*	-0.02	0.78**	0.55*		0.31*
HI	-0.53*	-0.40	0.17	-0.20	0.38	-0.27	0.30*	0.00	0.22	0.19	0.10	-0.43	0.29	-0.59**	0.30	

(*, **) at 5 % and 1% probability level respectively, ns= non-significant.

DH=days to heading, DM=days to maturity, GFP=grain filling period, H=plant height, PL= panicle length, CL= culm length, FL= flag leaf length, NFTP=number of productive tillers per plant, NSP=number of spike per panicle, NGP=Number of grains per panicle, NFGP= number of fertile grain per panicle, TSW= thousand seed weight, YP= yield per plant, BY= biomass yield, GY= grain yield and HI=harvest index.

In general the magnitude of genotypic correlations (r_g) is higher than those of phenotypic correlations (r_p) except number of spikelet per plant which is (r_p) greater than (r_g) for days to heading and culm length. This revealed that association among characters is under genetic control. When value of r_p is greater than r_g, it shows apparent association of two traits is not only due to genes but also due to favorable influence of environment. By contrast, if value of r is zero or insignificant, this shows that the two traits are independent (Akhtar et al., 2011). Thus from the study, yield per plant correlated positively with all studied characters both at genotypic and phenotypic level. Yield per plant also correlated significantly with all studied characters both at genotypic and phenotypic level except days to heading, panicle length, culm length and thousand seed weight at phenotypic level and days to heading and panicle length at genotypic level was non-significant.

Days to heading had highly significant positive association at genotypic and at phenotypic levels (r_g=0.57**, r_p=0.54**) with biomass yield and significantly negative associated with harvest index at genotypic and phenotypic level (r_g=-0.53*, r_p =-0.51**). Therefore days to heading increase with increase in biomass production whereas decrease with increase in harvest index.

Days to Maturity showed significant positive association at phenotypic level with number of grain per panicle (r_p=0.49*) and grain yield per hectare (r_p=0.30*). Highly positive association with number of filled grain per panicle (r_p=0.42**), yield per plant (r_p=0.47**), biomass yield (r_g=0.58**, r_p=0.57**). This finding is in agreement with the findings of Chandra et al. (2006) and Aditya and Bhartiya (2013) reported Days to maturity was found to be significantly positively correlated with grains per panicle and fertile grains per panicle. Hairmansis et al. (2010) reported days to maturity and 1000-grain weight had negligible effect on grain yield. Days to maturity negative significant associated with harvest index at phenotypic level (r_p=-38**).

The correlation between plant height and grain yield per hectare was positive at genotypic and significantly correlated at phenotypic level (r_g=0.4, r_p=0.39**) which indicates that an increase in plant height leads to an increase grain yield. Similar results have been found (Sabesan et al., 2009; Kashif et al., 2013). However, Hairmansis et al. (2010) reported negative correlation of plant height and grain yield. Plant height had negative significant association with grain-filling period, culm length and harvest index at phenotypic level. However it was positive significant associated with yield per plant and biological yield at both correlation types.

The correlation between number of productive tillers per plant and grain yield per hectare was positive and significant at both genotypic and phenotypic levels (r_g=0.56*, r_p=0.50**). Number of productive tillers per plant was positive and significant associated with number of total grain per panicle (r_g=0.53*, r_p=0.48**), number of filled grain per panicle (r_g=0.55*, r_p=0.49**) and yield per plant (r_g=0.61**, r_p=0.56**) both at genotypic level and phenotypic level. It was positively correlated with biomass yield (r_g=0.30, r_p=0.29*) which is similar to the report of Rasheed et al. (2002). Surek and Beser (2003) and Ratna et al. (2015) study reveals grain yield significantly correlated with its component characters like the number of productive tillers.

Number of spikelet per panicle was in positive relationship at genotypic level (r_g=0.15) and at phenotypic level (r_p=0.17) with grain yield per hectare. It had a significant and positive correlation with yield per plant and flag leaf length at genotypic level. At genotypic level it was significantly correlated with total numbers of grains per panicle and filled grains per panicle and phenotypically it was highly and positively associated with these traits. Zhang and Kokubun (2004) observed number of spikelet per m2 significantly correlated with grain yield.

Number of filled grains per panicle had positive and highly significant association with grain yield per hectare at genotypic level (r_g=0.67**), and at phenotypic level (r_p=0.64**). It had highly significant positive relationship with yield per plant at genotypic (0.89**) and phenotypic (0.88**) levels. The perusal of both the correlation coefficient results suggested that number of filled grains per panicle should be given prime importance regarding its contribution to yield. These results suggest that selections should be based on number of filled grains per panicle for developing new high yielding upland rice varieties. These results are substantiated with those of Madhavilatha et al. (2005) and Elsadig and Abdalla, (2013).

Thousand-seed weight showed negative and non-significant association at genotypic and phenotypic levels (r_g=-0.02, r_p=0.04) with grain yield per hectare. This result is in contradicted with a number of works in rice (Madhavilatha et al., 2005).

Biomass yield was in positive and significant relationship at both phenotypic and genotypic levels with grain yield per hectare (r_g=0.55*, r_p=0.57**). These results are supported by the findings of Chowdhry et al. (1991). In the present study, it was highly and positively correlated with days to heading, days to maturity, culm length and plant height at both genotypic and phenotypic levels.

Harvest Index had positive at genotypic level and significantly positive relationship at phenotypic level with grain yield per hectare (r_g=0.30, r_p=0.31*). These results are supported by the findings of Chowdhry et al. (1991) and Zhang and Kokubun (2004). In this study harvest index was negatively correlated with days to heading, days to maturity, spike length and thousand-seed weight at genotypic level, and the result is supported by the findings of Moghaddam et al. (1997).

The study of correlation suggests that plant height, number of productive tillers per plant, yield per plant, harvest index and biomass yield were the most important characters which possessed highly positive association with grain yield per plant. From the study, positive and significant correlation of characters with grain yield and yield per plant both at genotypic and phenotypic levels, suggests that yield would increase with increase of those characters and vice versa. Therefore, these traits could be used as indirect selection criteria for grain yield improvement.

3.3. Path Coefficient Analysis

Estimates of path coefficients, direct and indirect effects of yield contributing characters on grain yield per hectare using genotypic correlation, which showed significant association with grain yield, were presented in Table 3 and phenotypic relations were given in Table 4. Maximum positive direct effect on grain yield per hectare was exerted by plant height (3.60) followed by harvest index (1.03). This means that increase in these traits may directly contribute to increased grain yield. Pandey et al. (2012) identified harvest index as one of the major direct contributors towards yield. On the other hand, traits like culm length (-3.23), days to heading (-1.03), total number of grains per panicle (-0.75), grain filling period (-0.68) showed negative direct effect on grain yield. Since the direct effect were negative, so the direct selection for these traits to improve yield will be undesirable.

Biomass yield had positive indirect effect on grain yield through thousand seed weight, panicle length, flag leaf length, number of fertile tillers per plant, number of filled grain per panicle, days to maturity and plant height.

Negative direct effect in case of yield per plant on grain yield was estimated by displaying a value of -0.27 on grain yield and in addition to this yield per plant positively affected grain yield indirectly through harvest index (0.29), plant height (0.97), date of maturity (0.47), number of filled grain per panicle (0.63) and biomass yield (0.38).

Biomass yield, days to maturity, number of fertile grains per panicle, number of fertile tillers per plant, number of spike per panicle and thousand-seed weight showed positive direct effect on grain yield by displaying a value of 0.99, 1.01, 0.71, 0.22, 0.12, and 0.04, respectively. Dramatic increase in the grain yield of major world cereal crops is due mainly to increases in the harvest index and to a lesser extent the biological yield (Acquaah, 2007). In this study plant height, days to maturity, harvest index and biomass yield showed high genotypic correlation and positively significant direct effect on grain yield. Thus, plant breeder should practice selection through those most favorable traits for future upland rice yield improvement programs.

On the basis of estimates of path coefficients, it could be suggested that plant height, harvest index and biological yield are the main contributors to grain yield in the present investigation. Selection for these characters will possibly improve other component characters thereby improving grain yield. Therefore, these traits can be used as selection indices in grain yield improvement in upland rice. The result agrees with Pandey et al. (2012).

The residual effect in path analysis determines how best the independent variables account for the variability of the dependent variable, grain yield per plant (Singh and Chaudhary, 1985). To this end, the genotypic and phenotypic residual effect in the present study were 0.0208 and 0.0691 showing that 97.9 % and 93.7% of the variability in grain yield was explained by the component factors. This result was related with the findings of Allard (2000), who reported residual effects 0.065. But when the amount of residual effect is high it indicates that in addition to the studied characters, there are also other factors to justify grain yield changes (El-Mohsen et al., 2012).

Table 3. Estimate of direct (diagonal) and indirect (off diagonal) effects at genotypic correlation coefficient

Variable	DH	DM	GFP	PH	PL	CL	FL	NSP	NGP	NFGP	NFTP	TSW	YP	BY	HI
DH	-1.03	0.55	0.37	1.70	0.17	-1.80	0.01	0.01	0.04	-0.01	-0.01	0.02	-0.01	0.56	-0.55
DM	-0.56	1.01	-0.28	0.96	0.11	-1.04	-0.01	0.03	-0.37	0.31	0.08	0.02	-0.13	0.58	-0.42
GFP	0.56	0.42	-0.68	-0.89	-0.07	0.91	-0.02	0.02	-0.42	0.32	0.09	0.00	-0.12	-0.03	0.18
PH	-0.49	0.27	0.17	3.60	-0.22	-3.20	0.02	0.02	-0.19	0.19	0.00	0.00	-0.07	0.51	-0.21
PL	0.36	-0.24	-0.10	1.60	-0.49	-1.03	-0.01	0.02	-0.18	0.15	-0.02	-0.02	-0.04	-0.04	0.39
CL	-0.57	0.33	0.19	3.56	-0.16	-3.23	0.02	0.01	-0.16	0.17	0.00	0.00	-0.07	0.56	-0.28
FL	0.04	0.09	-0.09	-0.51	-0.05	0.60	-0.12	0.07	-0.32	0.29	-0.02	0.00	-0.07	-0.24	0.31
NSP	-0.06	0.28	-0.14	0.53	-0.10	-0.34	-0.07	0.12	-0.40	0.36	-0.01	-0.01	-0.11	0.10	0.00
NGP	0.05	0.50	-0.38	0.92	-0.12	-0.70	-0.05	0.06	-0.75	0.67	0.12	-0.01	-0.22	0.25	0.23
NFGP	0.02	0.44	-0.31	0.95	-0.10	-0.75	-0.05	0.06	-0.71	0.71	0.12	0.00	-0.24	0.35	0.20
NFTP	0.06	0.37	-0.29	0.01	0.04	-0.07	0.01	-0.01	-0.40	0.39	0.22	0.00	-0.17	0.30	0.10
TSW	-0.45	0.41	0.05	-0.03	0.25	-0.26	0.01	-0.02	0.15	-0.04	0.01	0.04	-0.04	0.37	-0.44
YP	-0.03	0.47	-0.30	0.97	-0.07	-0.83	-0.03	0.05	-0.62	0.63	0.13	0.01	-0.27	0.38	0.29
BY	-0.58	0.59	0.02	1.87	0.02	-1.82	0.03	0.01	-0.19	0.25	0.07	0.01	-0.10	0.99	-0.61
HI	0.55	-0.41	-0.12	-0.72	-0.18	0.89	-0.04	0.00	-0.17	0.13	0.02	-0.02	-0.08	-0.59	1.03

Residual effect= 0.0208.

Table 4. Estimate of direct (diagonal) and indirect (off diagonal) effects at phenotypic correlation coefficient

Variable	DH	DM	GFP	PH	PL	CL	FL	NSP	NGP	NFGP	NFTP	TSW	YP	BY	HI
DH	-11.28	5.44	5.29	-0.07	-0.01	0.15	0.00	0.00	0.02	-0.01	-0.01	-0.01	0.00	0.53	-0.44
DM	-6.05	10.13	-4.23	-0.04	-0.01	0.09	0.00	0.01	-0.21	0.20	0.04	-0.01	-0.03	0.55	-0.33
GFP	6.02	4.32	-9.90	0.04	0.00	-0.07	0.00	0.01	-0.24	0.20	0.04	0.00	-0.03	-0.01	0.15
PH	-5.28	2.70	2.32	-0.15	0.01	0.27	0.00	0.01	-0.11	0.12	0.00	0.00	-0.02	0.49	-0.16
PL	3.56	-2.01	-1.38	-0.06	0.03	0.08	0.00	0.01	-0.11	0.09	-0.01	0.01	-0.01	0.02	0.29
CL	-6.21	3.22	2.69	-0.15	0.01	0.27	0.00	0.01	-0.10	0.11	0.00	0.00	-0.02	0.52	-0.22
FL	0.48	0.99	-1.42	0.02	0.00	-0.04	-0.03	0.02	-0.17	0.17	0.00	0.00	-0.02	-0.13	0.23
NSP	-0.75	2.07	-1.32	-0.03	0.01	0.03	-0.01	0.04	-0.20	0.20	0.00	0.00	-0.02	0.15	-0.01
NGP	0.56	4.93	-5.35	-0.04	0.01	0.06	-0.01	0.02	-0.44	0.44	0.05	0.00	-0.05	0.25	0.18
NFGP	0.20	4.30	-4.40	-0.04	0.01	0.06	-0.01	0.02	-0.42	0.46	0.05	0.00	-0.05	0.33	0.15
NFTP	0.60	3.31	-3.81	0.00	0.00	0.01	0.00	0.00	-0.21	0.23	0.11	0.00	-0.03	0.28	0.06
TSW	-4.72	4.11	0.41	0.00	-0.01	0.02	0.00	0.00	0.08	-0.02	0.01	-0.02	-0.01	0.38	-0.34
YP	-0.32	4.73	-4.33	-0.04	0.00	0.07	-0.01	0.01	-0.36	0.40	0.06	0.00	-0.06	0.38	0.24
BY	-6.11	5.78	0.08	-0.08	0.00	0.15	0.00	0.01	-0.11	0.16	0.03	-0.01	-0.02	0.97	-0.49
HI	5.78	-3.84	-1.68	0.03	0.01	-0.07	-0.01	0.00	-0.09	0.08	0.01	0.01	-0.02	-0.56	0.86

Residual effect= 0.0691.

4. Conclusion

High genotypic and phenotypic coefficient of variations with low magnitude of differences were observed for yield per plant, plant height, grain filling period, grain yield ha-1 and harvest index indicated that these traits were less influenced by environmental factors. The phenotypic expression of these traits are controlled more of by the genetic factors. The highest positive and significant genotypic direct effects on grain yield were exerted by plant height, harvest index, days to maturity and biomass yield. The results suggested the higher chance of improving yield through indirect selection of these traits.

Improved grain yield in the modern varieties appeared to be associated more with the production of a higher grain yield than with higher partitioning efficiency to the biomass yield. It can be considered that changes in number of productive tillers per plant, grain yield panicle^{-1}, number of filled grain panicle-1, harvest index and grain yield per plant had contributed to the changes in grain yield breeding of upland rice in Ethiopia

The positive and significant correlation of plant height, number of productive tillers per plant, yield per plant and biological yield traits with grain yield suggests that yield have increased with increase of those characters.

Author Contributions

BZ; initiated the research idea, developed, organized, analyzed and interpreted the data and wrote the manuscript. FW; supervised the research, suggested the research methods, structured the paper and edited the manuscript.

Conflict of Interest

The authors declared that there is no conflict of interest.

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