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Association of Agronomic Traits with Grain Yield of Lowland Rice (*Oryza Sativa* L.) Genotypes

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Abstract – **Rice is a versatile crop globally, though it has relatively short history of production and research in Ethiopia. Hence, genetic improvement is highly important to increase the production and productivity of the crop, which needs understanding of traits association. The study was conducted during 2017/2018 main cropping season at Fogera, Ethiopia, to determine the magnitude of association of yield and yield attributed traits in 30 lowland rice genotypes. The experiment was laid out using randomized block design with three replications. Data were collected for 17 agronomic characters and significant differences were found among the genotypes for all studied characters. Grain yield ha^{-1} had positive and highly significant phenotypic and genotypic correlations with filled grains panicle^{-1}, panicle weight, biomass yield and harvest index, but it had negative genotypic and phenotypic correlation with unfilled grains panicle^{-1} and thousand-grain weight; only the phenotypic correlations being significant. Biomass yield, harvest index, number of filled grains panicle^{-1} and panicle plant^{-1} exerted the highest positive direct effect on grain yield while days to flowering exerted negative direct effect on grain yield at both genotypic and phenotypic levels. These traits can be used as selection indices to grain yield of lowland rice.**

Keywords – **Correlation, Direct Effect, Genotypic, Oryza Sativa (Rice), Phenotypic.**

I. INTRODUCTION

Rice is one of the most important food crops in the world. According to the 2019 data, China, India and Indonesia are the largest rice producing countries in the world, with percentage share of 28.0%, 23.7% and 7.2 %, respectively (FAOSTAT, 2021). Worldwide the area covered by rice exceeds 162 million ha with a production of 755 million tons (FAOSTAT, 2021). The world's average productivity (kg/ha) has doubled during the last 25 years, largely due to the use of improved technologies such as high yielding varieties (Rahman *et al.*, 2012).

Rice was introduced in to Ethiopia during the 1970s and fast distribution of the crop within the country has been achieved (Beakal *et al.*, 2016). In Ethiopia, rice covered about 48,418.09 hectares of land, and 136,000.726 tons of grain was produced per annum in 2016/17 (CSA, 2017). However, the average rice productivity is estimated at 2.81 t ha^{-1} (CSA, 2017), which is much lower than the world's average of 4.7t ha^{-1} (FAOSTAT, 2019). Despite the fact that rice has been recognized by government as "the new millennium crop of Ethiopia" to attain food security, lack of improved varieties, lack of recommended crop management, lack of pre and postharvest management coupled with biotic and abiotic stresses limit the production and productivity of the crop in the country (EIAR/ FRG II, 2011). Among these problems, lack of improved varieties suitable for different agro-ecologies of the country is the most critical one (Dejen *et al.*, 2021)

In order to maximize the productivity of rice in the country, research has been conducted mainly at Fogera National Rice Research and Training Center (FNRRTC). The center introduced a bulk of genotypes, which are sources of variability for future rice improvement in Ethiopia, from International Rice Research Institute (IRRI) and African Rice Center (WARDA).

The success of plant breeding research depends on the availability of genetic variation. However, sufficient information is lacking on the character association of grain yield and yield related traits available within recently introduced low land rice genotypes in the study area. Variability in genotypes for yield and yield component traits forms the basic factor to be considered while making selection (Dejen *et al.*, 2021). The yield obtained reflects the performance of all plant components and might be considered as the final result of many other traits. i.e. every plant contains an inherent physiological production capacity that operates on energy required for normal plant performance. Not all genotypes have the same inherent physiological capacity to yield (Welsh, 1981).

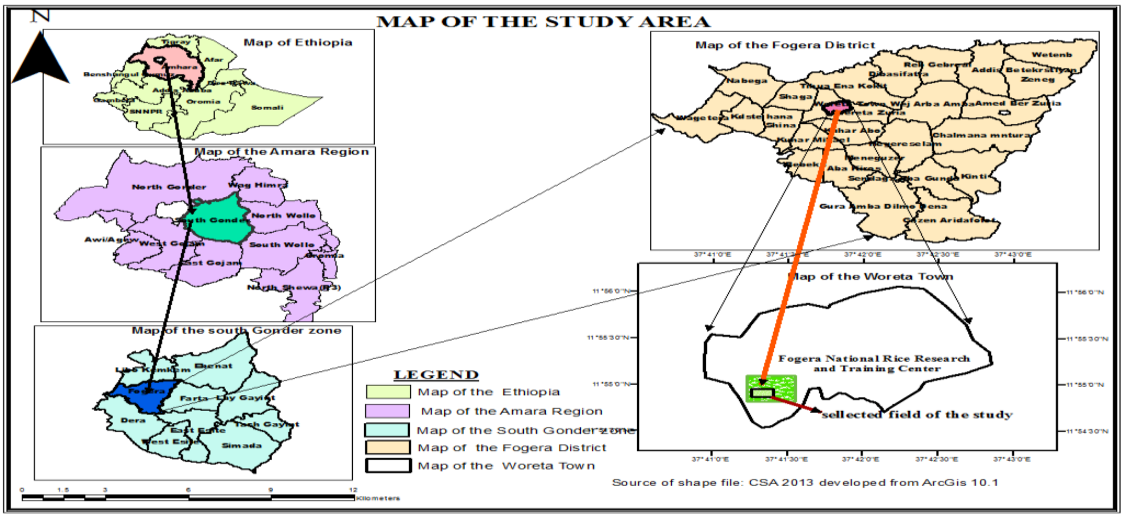
The knowledge regarding relative contribution of individual traits to yield may be accomplished by correlation studies (Habibullah *et al.*, 2015). However, simple correlation does not provide the adequate information about the contribution of each factor towards yield (Hakim, 2008). Therefore, it is essential to understand the association among yield and its component characters of recently introduced lowland rice genotypes along with the nature and extent of direct and indirect effects of components through correlation and path analysis.

Therefore, the present investigation has been undertaken to find out the association between yield and yield attributed traits through correlation studies and path coefficient analysis.

II. MATERIALS AND METHODS

Experimental Site Description

The experiment was conducted in the North-Western part of Ethiopia at Fogera National Rice Research and Training Center (FNRRTC) during the rainy season (June-December) of 2017/18. FNRRTC is located at $11^{0}58'$ N, 37° 41’ E and at 1810 m above sea level in Amhara Regional state, Ethiopia. It is 607 km far from Addis Ababa (Figure 1). According to the average meteorological data, the annual rainfall and average air temperatures are 1300mm and 18.3°C, respectively. The soil type is black *Vertisol* with pH of 5.90 (Dejen *et al.*, 2021). The main water source for rice production in the study area is rain-fall. Irrigation water from rivers, Rib and Gumara, was also used in the off season for production of vegetables as the second crop after rice.



Source of shape file: CSA 2013 developed from ArcGis 10.1

Fig. 1. Diagrammatic descriptions of experimental site.

Experimental Materials and Design

Thirty genotypes consisting of 27 lowland rice genotypes introduced in 2015 from African Rice Center (Formerly called WARDA), two released lowland varieties (Ediget and Hibir) and one locally available genotype (X-Jigna), obtained from FNRRTC, were used for this study. The experiment was laid out in randomized complete block design with three replications. Each plot had six rows each 4m long, with a spacing of 25 cm between rows and 15cm between plants. The plot size was 4 x 1.5m = 6m^2. Net plot size was 1 m x 4m = 4m^2. Spacing between plots and replications was 0.3 m and 1 m, respectively. Three healthy and uniform sized seeds were drilled per hill on date 5 July 2017, and thinning was conducted after germination to ensure single plant per hill.

Fertilizer in the form of N and P_2O_5 was applied at a rate of 69/23 Kg/ha, Urea and NPS, respectively. All the NPS was applied at sowing. Urea was applied as split three times, 1/3 at sowing, 1/3 at tillering and the remaining at panicle initiation stage. All other agronomic practices were applied as recommended for rice production in the study area.

Data Collection

Based on the standard evaluation system developed by International Rice Research Institute (IRRI, 2002), seventeen quantitative traits were recorded at appropriate growth stage on plot and plant basis. Number of tillers per plant (TP), number of panicles per plant (PP), culm length (CL) (cm), panicle length (PL) (cm), plant height (PH) (cm), flag-leaf length (FL) (cm), flag-leaf width (FW) (cm), number of filled grains per panicle (FGPP), number of unfilled grains per panicle (UGPP) and Panicle weight (PW) (g) were recorded from pre-tagged ten randomly sampled plants in the four central harvestable rows of each experimental unit/plot. However, yield per plot and phenological traits were taken on plot basis.

Statistical Analysis

Phenotypic and Genotypic Correlations

Phenotypic correlation (rp), the observable correlation between two variables, which includes both genotypic and environmental association between two traits, were estimated using the formula suggested by Johnson *et al.* (1955) and Singh and Chaudhary (1985).

Table 1. Analysis of Covariance (ANCOVA) for RCB design.

Source of Variation	**DF**	**MSCP**	**EMSP**
Replication	r-1	MSCPrxy	
Genotype	g-1	MCSPgxy	σ^2exy+ r σ^2gxy
Error	(r-1) (g-1)	MCSPexy	σ^2exy

Where, DF = degrees of freedom, r and g = numbers of replications and genotypes, respectively; MSCPrxy = mean sum of cross products of replications for traits x and y, MSCPgxy = mean sum of cross products of genotypes for traits x and y, MSCPexy = mean sum of cross products of environments for traits x and y, MSCP = Mean sum of cross products, σ^2exy = environmental covariance between traits x and y and σ^2gxy = genotypic covariance between traits x and y, EMSP = Expected mean sum of products.

Gcov(xy) = $\frac{MSCPgxy-MSCPexy}{r}$, Pcov (xy) = gcov(xy) + Cov(exy)

Where, gcov(xy) = genotypic covariance between traits x and y; pcov(x,y) = phenotypic covariance between character x and y ; Cov(exy) = environmental covariance between character x and y.

rpxy = $\frac{\sigma\, 2\ pxy}{\sqrt{(\sigma\, 2\ px.)(\sigma\, 2\ py)}}$, rgxy = $\frac{\sigma\, 2\ gxy}{\sqrt{((\sigma^2 gx)(\sigma^2 gy)}}$

Where, rp_{xy} and rg_{xy} are phenotypic and genotypic correlation coefficients, respectively; σ_{gxy} and σ_{pxy} = the genotypic and phenotypic covariance between trait x and y; $\sigma^2 gx$ and $\sigma^2 px$ = the genotypic and phenotypic variance for trait x, and σ^2_{gy} and $\sigma^2 py$ = the genotypic and phenotypic variance for trait y.

The phenotypic correlation value was tested for its significance using t-test: t = $\frac{rp}{SE(rp)}$

Where, r^p = Phenotypic correlation; SE (r^p) = Standard error of phenotypic correlation obtained using in the following procedure (Sharma, 1998).

SE (r^p) = $\sqrt{\frac{(1-r2p)}{(n-2)}}$, Where, n is the number of genotypes, r_p is phenotypic correlation coefficient.

The coefficients of correlations at genotypic level were tested for their significance using the formula described by Robertson (1959) as indicated below: t = $\frac{rgxy}{SErgxy}$

The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n = number of genotypes.

SEr_{gxy} = $\sqrt{\frac{1-r2gxy}{2Hx.Hy}}$, Where, Hx = heritability of trait x; Hy = heritability of trait y.

Path Coefficient Analysis

The direct and indirect effects of yield related traits on yield per hectare were worked out through path coefficient analysis. The analysis was made following the method suggested by Dewey and Lu (1959). The formula is described as follows.

$r_{ij} = P_{ij} + \Sigma r_{ik} p_{kj}$, Where : - rij = Mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient; Pij = Component of direct effects of the independent trait (i) on the dependent variable (j) as measured by the path coefficient and Σrikpkj = Summation of components of indirect effects of a given independent trait (i) on the given dependent trait (j) via all other independent traits (k).

Residual effect was estimated by the formula: h = $\sqrt{1-R2}$ where: - R^2 =Σpijrij

R^2 is the residual factor, Pij = Components of direct effects of the independent character (i) and dependent character (j) as measured by the path coefficient. rij = Mutual association between the dependent and independent character (i) and dependent character (j) as measured by the correlation coefficient.

III. RESULTS AND DISCUSSION

Phenotypic and Genotypic Associations of Traits

In this study, the genotypic and phenotypic correlation coefficients between yield and yield contributing traits are discussed below (Table 2). It appears that most of the genotypic correlation values were higher than their corresponding phenotypic values. This indicated greater genetic association of the genotypes rather than environmental for the traits under consideration.

Association of Grain Yield with Other Traits

Grain yield, which is the major economic character in rice, depends on several component traits which are mutually related. The correlation coefficient analysis exhibited that grain yield ha^{-1} had positive and significant associations ($p \leq 0.01$) with number of filled grains per panicle^{-} (rp = 0.75**; rg = 0.77**), panicle weight (rp = 0.54**; rg = 0.58**), biomass yield (rp = 0.59**; rg = 0.61**), harvest index (rp = 0.57**; rg = 0.59**), panicle length (rp = 0.37**; rg = 0.40*) and flag-leaf length (rp = 0.41**; rg = 0.43*). Culm length (rp = 0.30**) and plant height (rp = 0.33**) had a positive and significant association with grain yield at phenotypic level. Thus, indicated that the increase in grain yield of rice mainly because of the increase of these traits. Therefore, the indirect selection for higher yield based on these characters would be reliable.

This study agrees with the findings of Karim *et al.* (2014) who observed positive association between harvest index and grain yield. Kishore *et al.* (2015) stated positive association of number of filled grains per panicle with grain yield. If tekharuddaula *et al.* (2002) also reported the positive correlation of grain yield with panicle length and harvest index. Abarshahr *et al.* (2011) found a significant positive correlation among grain yield with panicle length, flag leaf length, flag leaf width and filled grain per panicle.

In contrast, grain yield ha^{-1} exhibited negative correlation with number of unfilled grains panicle^{-1} (rp = -0.25* and rg = - 0.23), and thousand grain weight (rp = - 0.21* and rg = - 0.29) at both phenotypic and genotypic level. This indicated, as number of unfilled grains increase, number of filled grains decrease and subsequently highly associated economical trait grain yield declined. However, a seed size increase due to low in numbers for competition of assimilate partitioning to filled grain. The breeder must be very careful while selecting of these traits which may result in grain yield decline. Because of these traits had negatively correlated with grain yield and cannot be used as positive selection traits to increase grain yield per unit area. These results were consistent with findings of Idris *et al.* (2012) who found that thousand grains weight had negative correlation with grain yield.

Generally, in this study, all studied characters except for UGPP and TGW had positive correlation with grain yield at genotypic and phenotypic level, which is considerably significant to breeders because component breeding would be very effective under such situation. Selection for these traits may be essential for improvement of grain yield in lowland rice ecology. However, it is always important to validate the result by partitioning the correlation coefficients into direct and indirect effects through component traits; by performing path coefficient analysis.

Genotypic and Phenotypic Correlation among Yield Related Traits

Days to heading was correlated positively and significantly with days to flowering, days to maturity, panicle length, flag-leaf length, flag-leaf width, filled grain per panicle and biomass yield; while negatively and significantly correlated with thousand grain weight and harvest index at both phenotypic and genotypic levels. However, non-significantly correlated with tillers per plant, panicles per plant and grain yield ha^{-1}. Similar results were confirmed in which days to heading correlated positively and significantly with days to maturity, p-

-anicle length, number of filled grains per panicle and biomass yield (Tefera *et al*, 2017).

Days to 50% flowering was correlated positively and significantly with days to maturity, panicle length, flag-leaf length, flag-leaf width, filled grain per panicle and biomass yield, but was negatively and significantly correlated with thousand grain weight and harvest index at both phenotypic and genotypic levels. Whereas, culm length, plant height, unfilled grains panicle^{-1} and panicle weight had significant and positive correlation with days to flowering at the phenotypic level while non-significant correlation at genotypic level. Tillers per plant, panicles per plant and grain yield had non-significant correlation with days to flowering at both levels.

Similar results were reported by Nandan *et al*. (2010), for correlation of days to flowering with days to maturity, number of grains per panicle and biomass yield. Kalyan *et al.* (2017) found similar findings for correlation between days to flowering and days to maturity. Similar result explained by Bhadru *et al*. (2012) that thousand grain weight negatively correlated with days to flowering. Days to maturity showed significant and positive correlation with panicle length, flag leaf length, flag-leaf width, filled grain per panicle, unfilled grains per panicle and biomass yield, but significant and negative correlation with thousand grain weight and harvest index at both phenotypic and genotypic level. This may indicated as days to maturity increase in ideal condition, panicle prolonged its length and thickness that cause for increment of total grains per panicle. Beside of this, number of unfilled grains probably increases due to terminal moisture stress in rice. Panicle weight had significant and positive correlation with days to maturity at the phenotypic level, while non-significant correlation at genotypic level. Tillers per plant was significantly and negatively correlated at phenotypic level, but non-significantly correlated at genotypic level. Culm length, plant height, panicle per plant and grain yield had non-significant correlation with days to maturity at both levels. This study agreed with the findings of Nandan *et al.* (2010) for thousand grain weight.

Tillers per plant had significant and positive correlation with panicles per plant, but significant and negative correlation with culm length, plant height, panicle length, flag leaf length, flag leaf width, panicle weight at both levels. However, tillers per plant had non-significantly correlated with the rest of the traits. Binod *et al.* (2016) also stated that tillers per plant showed a negative association with plant height, panicle length, number of grains per panicle and filled grain per panicle.

Panicles per plant had significant and negative correlation with flag-leaf width and panicle weight at both levels. Culm length, panicle length, plant height and flag leaf length had significant and negative correlation with panicles per plant at phenotypic level. Culm length was correlated significantly and positively with panicle length, plant height, flag-leaf length, flag-leaf width, number of filled grains per panicle and panicle weight. Panicle length had significant and positive correlation with plant height, flag-leaf length, flag-leaf width, filled grains per panicle, panicle weight and biomass yield and grain yield, but significant and negative correlation with thousand grain weight. On the other hand, plant height had significant and positive correlation with flag leaf length, flag leaf width, filled grains per panicle, panicle weight and biomass yield both at phenotypic and genotypic levels. Similar results were found by Tefera *et al. (*2016).

Flag-leaf length had significant and positive correlation with flag-leaf width, filled grains per panicle, panicle weight, biomass yield and grain yield, but significant negative correlations with thousand grains weight both at phenotypic and genotypic levels. Flag-leaf width had significant and positive correlation with filled grains per panicle and panicle weight at both levels, in contrast significant negative correlation with harvest index at phenotypic level. Filled grains per panicle had significant and positive correlation with panicle weight, biomass yield and grain yield, while significant negative correlation with thousand grain weight at both levels.

Unfilled grains per panicle had significant and negative correlation with thousand grain weight and harvest index at both levels, while significant positive correlation with biomass yield at phenotypic level. Panicle weight had significant and positive correlation with biomass and grain yield, whereas thousand grains weight had significant and negative correlation with biomass yield at both levels. Biomass yield had significant and positive correlation with grain yield at both levels, but significantly negatively correlated with harvest index at phenotypic level. Harvest index had significant and positive correlation with grain yield at both phenotypic and genotypic levels.

Table 2. Genotypic (rg) above diagonal and phenotypic (rp) below diagonal correlation coefficient for 17 traits of 30 low land rice genotypes.

Traits	**DH**	**DF**	**DM**	**TP**	**PP**	**CL**	**PL**	**PH**	**FL**	**FW**	**FGPP**	**UGPP**	**PW**	**TGW**	**BY**	**HI**	**GY**
DH		0.99**	0.93**	-0.25	-0.09	0.23	0.62**	0.31	0.67**	0.56**	0.48**	0.30	0.34	-0.60**	0.74**	-0.48**	0.21
DF	0.99**		0.93**	-0.26	-0.09	0.22	0.62**	0.30	0.67**	0.55**	0.48**	0.31	0.35	-0.61**	0.74**	-0.49**	0.21
DM	0.91**	0.91**		-0.30	-0.15	0.13	0.52**	0.21	0.67**	0.57**	0.39*	0.44*	0.30	-0.48**	0.70**	-0.55**	0.12
TP	-0.20	-0.20	-0.24*		0.98**	-0.40*	-0.41*	-0.42*	-0.40*	-0.54**	-0.29	-0.11	-0.61**	-0.15	-0.10	0.17	0.07
PP	-0.05	-0.05	-0.10	0.96**		-0.34	-0.31	-0.35	-0.28	-0.42*	-0.14	-0.12	-0.51**	-0.23	0.04	0.18	0.19
CL	0.23*	0.22*	0.13	-0.33**	-0.27*		0.70**	0.99**	0.55**	0.56**	0.46*	-0.20	0.51**	-0.04	0.34	0.00	0.31
PL	0.58**	0.58**	0.47**	-0.33**	-0.25*	0.67**		0.79**	0.82**	0.44*	0.60**	0.12	0.67**	-0.45*	0.61**	-0.14	0.40*
PH	0.31**	0.30**	0.20	-0.35**	-0.28*	0.99**	0.77**		0.63**	0.56**	0.51**	-0.15	0.56**	-0.12	0.41*	-0.03	0.34
FL	0.65**	0.65**	0.64**	-0.32**	-0.23*	0.54**	0.78**	0.62**		0.51**	0.70**	0.17	0.68**	-0.40*	0.67**	-0.16	0.43*
FW	0.52**	0.51**	0.51**	-0.45**	-0.34**	0.52**	0.43**	0.53**	0.50**		0.50**	0.00	0.46*	-0.10	0.35	-0.27	0.08
FGPP	0.44**	0.44**	0.34**	-0.19	-0.06	0.43**	0.55**	0.47**	0.63**	0.45**		-0.10	0.81**	-0.39*	0.58**	0.32	0.77**
UGPP	0.29**	0.29**	0.42**	-0.13	-0.14	-0.20	0.09	-0.15	0.15	-0.01	-0.15		-0.17	-0.39*	0.31	-0.57**	-0.23
PW	0.32**	0.33**	0.27*	-0.53**	-0.43**	0.48**	0.64**	0.54**	0.64**	0.44**	0.73**	-0.15		-0.11	0.39*	0.32	0.58**
TGW	-0.51**	-0.51**	-0.41**	-0.10	-0.16	-0.04	-0.34**	-0.10	-0.33**	-0.06	-0.28**	-0.35**	-0.09		-0.66**	0.32	-0.29
BY	0.68**	0.68**	0.63**	-0.04	0.06	0.32**	0.54**	0.38**	0.60**	0.30**	0.54**	0.23*	0.34**	-0.53**		-0.26	0.61**
HI	-0.45**	-0.45**	-0.52**	0.13	0.14	0.00	-0.11	-0.02	-0.15	-0.22*	0.30**	-0.51**	0.28**	0.31**	-0.31*		0.59**
GY	0.20	0.20	0.10	0.07	0.18	0.30**	0.37**	0.33**	0.41**	0.09	0.75**	-0.25*	0.54**	-0.21*	0.59**	0.57**	

* and ** = significance levels of p-value at 5%, and 1% respectively, DH = days to heading, DF = days to Flowering, DM = days to maturity, TP = tillers plant $^{-1}$, PP = panicles plant $^{-1}$, CL = culm length, PL = panicle length, PH = plant height, FL = flag leaf length, FW = flag leaf width, FGPP = filled grain panicle^{-1} , UGPP = unfilled grain panicle^{-1}, PW = panicle weight, TGW = 1000 grain weight, BY = Biomass yield per ha in Kg, HI = harvest index, GY = paddy yield per ha in Kg.

Path Coefficient Analysis

The genotypic and phenotypic correlations were partitioned in to direct and indirect effects using grain yield as a dependent variable and results are presented in Tables 3 and 4 respectively. In the present study, based on step wise selection methods of regression, 10 traits were selected as casual variables for grain yield. The selected independent traits were: days to flowering, days to maturity, number of panicles per plant, panicle length, plant height, filled grains per panicle, unfilled grain per panicle, thousand grain weight, biomass yield and harvest index.

Phenotypic Path Coefficient Analysis

Path coefficient analysis of the phenotypic correlations revealed that biomass yield (0.77) had the highest direct effect followed by harvest index (0.764) and filled grains per panicle (0.108) on grain yield (Table 3). These traits also had highly significant and positive phenotypic correlation (0.59**, 0.57** and 0.75**) with rice grain yield. Plant height, panicles per plant and days to maturity also showed positive phenotypic direct effect on grain yield with values of 0.044, 0.026 and 0.018, respectively.

These results are in harmony with the findings of Kalyan *et al.* (2017) for plant height and Kampe *et al*. (2018) for days to maturity and number of panicles per plant that showed positive direct effect on grain yield but, contrary to the findings of Kampe *et al*. (2018) for panicle length and thousand grain weight which showed positive direct effect on grain yield at phenotypic level. Although days to flowering (-0.048), panicle length (-0.033), thousand grain weight (-0.028) and unfilled grains panicle^{-1} (-0.007) had negative direct effect on grain yield, their contribution in explaining the variability in grain yield was negligible. Therefore, it is evident from the result of this study that high consideration should be given for the traits with highest positive direct effect on grain yield such as BY, HI and FGPP. The indirect effect of BY on grain yield via all traits except TGW (-0.41) and HI (-0.24) was also positive. Selecting genotypes with the highest biomass yield will lead to the identification of genotypes with high grain yield, but care should be taken about the negative indirect effect on grain yield of BY via traits such as TGW and HI. Biomass yield also had highly significant negative correlation with thousand grain weight (-0.53**), while selecting plants with high biomass, care should be taken not to select plants with heavier (bigger) seeds.

The highest positive indirect effect on grain yield via biomass yield was exerted by filled grains per panicle (0.059) followed by plant height (0.017) and TGW (0.015), although the indirect effects of DM (0.011) and PP (0.002) were also positive, but negligible. Plants with large number of filled grains per panicle can be emphasized since filled grains per panicle had relatively high positive indirect effect (0.059) on grain yield via biomass yield. HI (-0.28) had the largest negative indirect effect on grain yield via BY. Other traits such as DF (-0.03), PL (-0.018) and UGPP (-0.002) also had small but negative indirect effect on grain yield via BY. Surek and Beser (2003) carried out path coefficient analysis for some yield related traits and pointed out that most traits had positive indirect effect via each other except between biological yield and harvest index and between the number of panicles plant^{-1} and the number of filled grains panicle^{-1}.

The variable that exerted the second highest positive direct effect on grain yield was harvest index (0.764); it also had a highly positive phenotypic correlation (0.57**) with grain yield. DF (0.022), PP (0.004), PL (0.004) and FGPP (0.033) had positive indirect effect on grain yield via harvest index. Whereas, DM (-0.009), PH (-0.001), TGW (-0.009) and BY (-0.237) had negative indirect effect via harvest index. The highest positive indirect effect on grain yield via harvest index was that of filled grains per panicle. Therefore, genotypes with high harvest index and high biomass yield with large number of filled grains per panicle, but with short duration for days to flowering and moderate plant height and maturity date should be selected. However, the indirect effect of HI on grain yield via DF (-0.347), DM (-0.399), UGPP (-0.392), BY (-0.236), PL (-0.087) and PH (-

0.016) were negative. It also had negative phenotypic correlation with these traits. Although selecting genotypes with high HI leads to the identification of high yielding genotypes, care should be taken not to select very early and short genotypes with low BY and PL.

Filled grains panicle^{-1} exerted relatively high phenotypic direct effect (0.108) on grain yield. It also had a strong positive phenotypic correlation (0.77**) with grain yield which resulted from the positive large indirect effects of BY (0.419) and HI (0.23). FGPP also had a highly significant positive correlation with these two traits (0.54** and 0.30**), respectively. However, the indirect effect of DF (-0.021), PL (-0.018) and PP (-0.002) was negative on grain yield via FGPP. PH had direct effect of (0.044) on grain yield which resulted from the positive indirect effects of BY (0.291), DM (0.004), FGPP (0.051), UGPP (0.001) and TGW(0.003), but the indirect effect of DF,PP, PL and HI were negative and low in absolute value.

The indirect effects of biomass yield (0.291) being very large and positive. PH also had a significant positive correlation with this trait (0.60**). The phenotypic correlation of PH on grain yield was positive (0.33**), selection of genotypes with the highest BY and FGPP of moderate PH should be selected to identify genotypes with the highest grain yield.

Number of panicles plant^{-1} (0.026) and days to maturity (0.018) had positive phenotypic direct effect on grain yield. The indirect effect of BY (0.048) and HI (0.107) was positive on grain yield via panicle per plant, but negative for plant height (-0.012). However, the remaining traits showed negligible indirect effect through panicle plant^{-1}. The indirect effect of BY (0.489), FGPP (0.0.037) and TGW (0.011) was positive on grain yield via days to maturity, but negative for HI (-0.399), DF (-0.044) and PL (-0.016). However, the remaining traits showed negligible indirect effect through days to maturity on grain yield.

Moreover, 80% of the traits in phenotypic path analysis had positive total effect on grain yield, while the remaining 20% of the traits showed negative total effect through number of unfilled grain paicle^{-1} (-0.249) and thousand grain weight (-0.209). Generally, the direct effect of traits at phenotypic path analyses (Table3) was lower than at genotypic direct path analyses. The residual effect was (0.15) indicating that 85% of the phenotypic variability in grain yield was contributed by ten traits considered in this path analysis study.

Table 3. Estimates of direct (bold and diagonal) and indirect effect (off diagonal) of ten traits on grain yield of 30 low land rice genotypes at phenotypic level at Fogera in 2017/18.

Traits	DF	DM	PP	PL	PH	FGPP	UGPP	TGW	BY	HI	r^{ph}
DF	**-0.048**	0.016	-0.001	-0.019	0.013	0.048	-0.002	0.014	0.525	-0.347	0.197
DM	-0.044	**0.018**	-0.003	-0.016	0.009	0.037	-0.003	0.011	0.489	-0.399	0.099
PP	0.002	-0.002	**0.026**	0.008	-0.012	-0.007	0.001	0.004	0.048	0.107	0.176
PL	-0.028	0.009	-0.006	**-0.033**	0.033	0.060	-0.001	0.009	0.417	-0.087	0.372
PH	-0.015	0.004	-0.007	-0.026	**0.044**	0.051	0.001	0.003	0.291	-0.016	0.331
FGPP	-0.021	0.006	-0.002	-0.018	0.021	**0.108**	0.001	0.008	0.419	0.230	0.752
UGPP	-0.014	0.008	-0.004	-0.003	-0.007	-0.017	**-0.007**	0.010	0.177	-0.392	-0.249
TGW	0.025	-0.007	-0.004	0.011	-0.005	-0.030	0.002	**-0.028**	-0.410	0.236	-0.209
BY	-0.033	0.011	0.002	-0.018	0.017	0.059	-0.002	0.015	**0.770**	-0.236	0.585

Traits	DF	DM	PP	PL	PH	FGPP	UGPP	TGW	BY	HI	r^{ph}
HI	0.022	-0.009	0.004	0.004	-0.001	0.033	0.003	-0.009	-0.237	**0.764**	0.573

Residual = 0.154 DF = days to flowering, DM = days to maturity, PP = panicles plant $^{-1}$, PL = panicle length, PH = plant height, FGPP = filled grain panicle^{-1}, UGPP = unfilled grain panicle^{-1}, TGW = thousand grains weight, BY = Biomass yield ha^{-1} in Kg, HI = harvest index, GY = paddy yield ha^{-1} in Kg.

Genotypic Path Coefficient Analysis

A similar trend as in path coefficient analysis of the phenotypic correlations was observed in path coefficient analysis at the genotypic level. Except for PL, PH and TGW, the sign of the direct effects of each independent trait on grain yield was similar in both analyses. Thus, PL and TGW had negative sign in phenotypic but positive sign in genotypic path coefficient analysis, while PH had negative sign at genotypic but positive sign at phenotypic level.

DM, PP, FGPP, BY and HI had positive direct effects while DF and UGPP had negative direct effects on grain yield in both analyses. None of the direct effects were negligible in path analysis of genotypic correlations, the difference between them being wider than those at the phenotypic level. They varied between -0.138 (DF) to (0.787**)** (BY). Both BY (0.787) and HI (0.644) still had the highest positive direct effect on grain yield. Surek and Beser (2003) pointed out similar results for some yield related traits that biological yield, harvest index, number of filled grains per panicle and number of panicles plant^{-1} recorded a positive direct effect on grain yield. Tefera (2016) found that biomass yield (1.052) followed by harvest index (0.722) and number of total grains per panicle (0.643) had the highest direct effect on grain yield.

The highest and positive indirect effect on grain yield was exhibited by days to flowering through biomass yield (0.58), days to maturity via biomass yield (0.548), panicle length through biomass yield (0.484), number of filled grains per panicle through biomass yield (0.456), plant height via biomass yield (0.322), number of unfilled grains per panicle by biomass yield (0.244), thousand grain weight via harvest index (0.206), number of filled grains panicle^{-1} through harvest index (0.205), number of panicles plant^{-1} through harvest index (0.116) and biomass yield via number of filled grains per panicle (0.101). Tefera (2016) found similar results that the highest and positive indirect effect on grain yield was exhibited by days to maturity through biomass yield (0.796), days to heading via biomass yield (0.769), panicle length through biomass yield per plot (0.767), number of filled grains panicle^{-1} by biomass yield (0.611), number of total grains panicle^{-1} by biomass yield (0.559) and number of panicles plant^{-1} through harvest index (0.457).

The positive direct effect of biomass yield with grain yield was assisted by days to maturity, panicles plant^{-1}, panicle length and filled grains panicle^{-1}. Biomass yield showed the highest positive indirect effect on grain yield via days to flowering (0.58). However, the fifth negative indirect effects were also recorded for this trait via harvest index (-0.204). The second maximum positive direct effect was observed for HI (0.644) on grain yield. The positive indirect effect was manifested via DF, PP, FGPP, UGPP and TGW. Harvest index showed the second highest negative indirect effect on grain yield via UGPP (-0.369). These results confirmed with reports of Sravan *et al*. (2012), a maximum direct effect of biological yield on grain yield followed by harvest index in upland rice.

The third maximum positive direct effect was observed on FGPP (0.175) on grain yield. The positive direct e-

-ffect of FGPP with grain yield was assisted through days to maturity, panicle length, unfilled grains panicle^{-1}, biomass yield and harvest index. These results are in conformity with that of Mulugeta *et al*. (2012) that number of grains panicle^{-1} exhibited high positive direct effect on grain yield and panicle length had positive indirect effect on grain yield through number of grains per panicle. The fourth maximum positive direct effect was observed on number of panicles per plant (0.058) on grain yield. The positive direct effect of panicle per plant with grain yield was assisted through days to flowering, plant height, number of unfilled grains panicle^{-1}, biomass yield and harvest index.

The fifth maximum positive direct effect was observed on thousand grain weight (0.023) on grain yield. The indirect effect of DF, PH, UGPP and HI was positive on grain yield via TGW, but negative for remaining traits. The sixth highest positive direct effect was observed on DM (0.019) on grain yield. Panicle length had the last positive direct effect (0.014) on grain yield. Positive direct effect of most traits on grain yield indicated true relationship between traits and should be given prior attention in practicing selection aimed at the improvement of grain yield, because of major influence on grain yield.

The character that exerted the highest negative genotypic direct effect on grain yield were recorded for DF (-0.138) followed by UGPP (-0.037) and PH (-0.010). Kampe *et al*. (2018) noticed similar results that days to 50% heading (-0.24) and plant height (-0.99) exerted negative direct effect on grain yield ha^{-1}. In such situations, the indirect causal factors are to be considered simultaneously for selection. The negative direct effect of days to flowering indicated that selection for early to medium flowering genotypes might lead to high grain yield in rice genotypes that helps increase grain filling period and escaping terminal moisture stress.

Therefore, it is evident from the result of this study that high consideration should be given for biomass yield, harvest index, filled grain per panicle, panicle per plant and days to maturity, indicating the importance of these traits in improving yield of the crop through selection. Forward and stepwise selection methods of regression have both identified FGPP, BY, HI, DF and PP as the most influential variables that determine grain yield. FGPP, BY, HI, DF and PP alone explained almost all of the variability in grain yield. The residual effect was (0.12), indicating that 88% of the variability in grain yield was contributed by traits considered in the genotypic path analysis.

Table 4. Estimates of direct (bold and diagonal) and indirect effect (off diagonal) of ten traits on grain yield of 30 lowland rice genotypes at genotypic level at Fogera in 2017/2018.

Traits	DF	DM	PP	PL	PH	FGPP	UGPP	TGW	BY	HI	rg
DF	**-0.138**	0.018	-0.005	0.009	-0.003	0.084	-0.011	-0.014	0.580	-0.314	0.205
DM	-0.129	**0.019**	-0.009	0.008	-0.002	0.067	-0.016	-0.011	0.548	-0.357	0.118
PP	0.013	-0.003	**0.058**	-0.004	0.004	-0.024	0.005	-0.005	0.028	0.116	0.187
PL	-0.085	0.010	-0.018	**0.014**	-0.008	0.106	-0.004	-0.010	0.484	-0.089	0.399
PH	-0.042	0.004	-0.020	0.011	**-0.010**	0.088	0.005	-0.003	0.322	-0.018	0.339
FGPP	-0.066	0.007	-0.008	0.009	-0.005	**0.175**	0.004	-0.009	0.456	0.205	0.767
UGPP	-0.043	0.008	-0.007	0.002	0.001	-0.018	**-0.037**	-0.009	0.244	-0.369	-0.227
TGW	0.084	-0.009	-0.013	-0.006	0.001	-0.067	0.014	**0.023**	-0.523	0.206	-0.292

Traits	DF	DM	PP	PL	PH	FGPP	UGPP	TGW	BY	HI	rg
BY	-0.102	0.013	0.002	0.009	-0.004	0.101	-0.011	-0.015	**0.787**	-0.167	0.613
HI	0.067	-0.011	0.010	-0.002	0.000	0.056	0.021	0.007	-0.204	**0.644**	0.590

Residual = 0.11884DF = days to Flowering, DM = days to maturity, PP = number of panicles plant $^{-1}$, PL = panicle length, PH = plant height, FGPP = number of filled grain panicle^{-1}, UGPP = number of unfilled grain panicle^{-1}, TGW = thousand grains weight, BY = Biomass yield ha^{-1} in Kg, HI = harvest index, GY = paddy grain yield ha^{-1} in Kg.

Comparison of Elite Genotypes with the Overall Mean

Though, regression identified FGPP, BY, HI, DF and PP as the most influential traits that explained almost all of the variability in grain yield, supportive index is required to strength the evidence. Six highest yielding genotypes by grain yield were selected to advance the prediction of explanatory traits from the regression. The mean of the original population (all 30 genotypes) and the mean of these elite genotypes (G26, G14, G8, G27, G29 and G30) are given below in table 5.

Table 5. Mean of 17 traits for 30 genotypes and six highest yielding low land rice genotypes.

Traits	Mean of 30 Genotypes	Mean of Six Selected Lines	Difference	Change (%)
DH	95.70	102.94	7.24	7.57
DF	99.78	106.94	7.17	7.18
DM	136.81	141.28	4.47	3.26
TP	9.57	9.71	0.13	1.37
PP	9.11	9.67	0.56	6.17
CL	69.79	80.38	10.60	15.18
PL	20.59	22.88	2.30	11.15
PH	90.38	103.27	12.89	14.26
FL	26.26	31.86	5.60	21.31
FW	1.16	1.23	0.07	5.91
FGPP	108.44	134.16	25.72	23.72
UGPP	10.27	8.53	-1.74	-16.94
PW	2.64	3.61	0.97	36.85
TGW	28.52	26.79	-1.73	-6.07
BY	10457.13	12823.83	2366.70	22.63
GY	4736.13	6629.28	1893.16	39.97
HI	46.11	52.57	6.46	14.01

DH = days to heading , DF = days to Flowering, DM = days to maturity, TP = tillers plant $^{-1}$, PP = panicles plant $^{-1}$,CL = culm length, PL = panicle length, PH = plant height, FL = flag leaf length, FW = flag leaf width, FGPP = filled grain panicle^{-1}, UGPP = unfilled grain panicle^{-1}, PW = panicle weight, TGW = thousand grain weight, BY = biomass yield ha^{-1} in Kg, HI = harvest index, GY = paddy yield ha^{-1} in Kg.

Except, UGPP & TGW the mean of the selected genotypes has increased positively by 1.37% in TP to 39.97% in grain yield (Table 5). Biomass yield had the highest direct effect on grain yield followed by HI and

FGPP both at phenotypic and genotypic levels of path analysis (Tables 3 and 4). These traits had positive correlation with grain yield at both genotypic and phenotypic levels (Table 2) and the mean of the selected genotypes was higher than the mean of the original population by 22.63%, 14.01% and 23.72%, respectively, in these traits. This selection index has also increased DF by 7.18%, PH by 14.26% and PL by 11.15%. The direct effect of DF on grain yield was negative at both phenotypic and genotypic levels of path analysis. PL and PH exerted positive and negative direct effects on grain yield respectively during path analysis of genotypic correlations. The signs are opposite during path analysis of phenotypic correlations. However, these traits had positive correlation with grain yield at both genotypic and phenotypic levels (Table 2).

The mean UGPP and TGW of the selected lines were lower than the mean of the original population as expected. The direct effect of these traits on grain yield was negative at phenotypic level. The indirect effect of UGPP and TGW via most traits was negative at both levels. Both UGPP and TGW had negative correlation with grain yield at both phenotypic and genotypic levels and a selection index designed to increase grain yield will of course reduce the two traits.

Although the indirect effect of DF and HI via BY and the indirect effect of DM and BY via HI on grain yield were negative at both genotypic and phenotypic levels, the mean of the selected lines was higher than the mean of the original population by 7.2% in DF by14.26% in HI and by 22.63% in BY. This is because these traits had positive correlation with grain yield at both phenotypic and genotypic levels. DH, DM, CL, PL, PH, FL, FW and PW also had positive correlation with grain yield through FGPP and BY, which is supported by this index. The negative direct effect of PH on grain yield and the indirect effects of PH via other trait were also not large enough in absolute value in phenotypic path analysis. Therefore, an index based on regression has identified FGPP, BY, HI, DF and PP as the most influential traits that determine grain yield of low land rice.

Figure 2 below also supported the overall associations of dependent and independent traits and also clearly showed the positive association of influential traits to the elite lowland rice genotypes. The genotypes were distributed throughout the quadrant demonstrating large genetic variability in these traits.

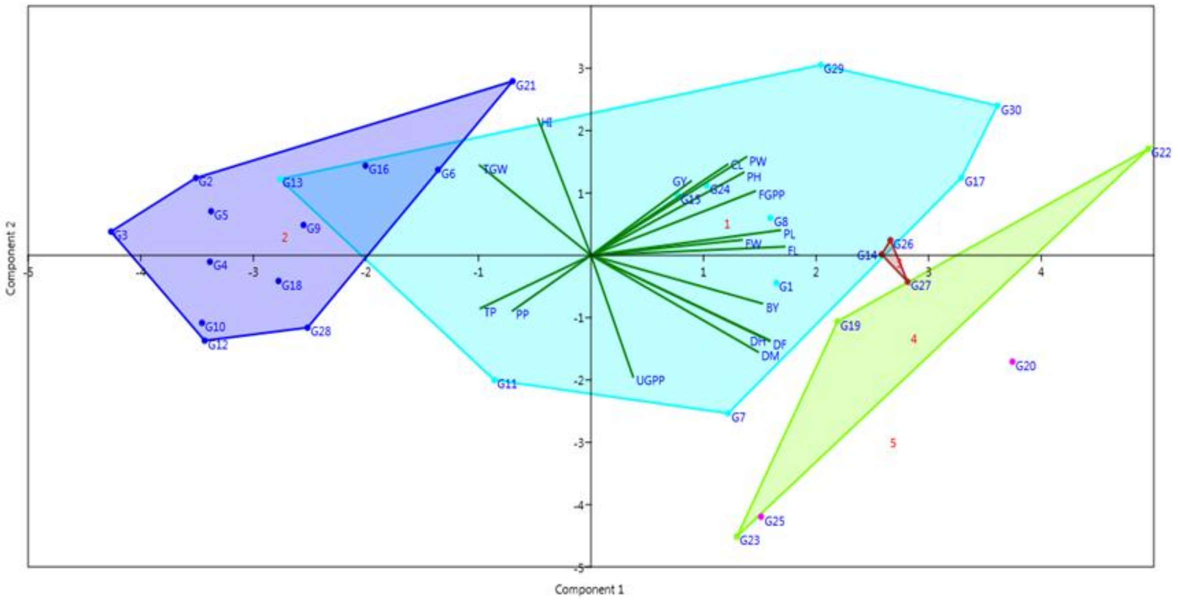


Fig. 2. Graphical representations (biplot) of the contribution of the first two principal components to the total variation in low land rice genotypes.

IV. CONCLUSION

The genotypic correlation coefficients were higher than the phenotypic correlation coefficients demonstrating that, the observed relation-ships among the various traits were due to genetic causes. The correlation coefficient analysis exhibited that grain yield ha^{-1} had positive and highly significant associations with number of filled grains panicle^{-1}, panicle weight, biomass yield, harvest index, panicle length and flag-leaf length both at phenotypic and genotypic levels. In contrast, grain yield had negative association with number of unfilled grains per panicle, and thousand grain weight at both phenotypic and genotypic levels.

Path coefficient analysis revealed that biomass yield, harvest index, number of filled grains per panicle, panicles per plant and days to maturity had the highest direct effect on grain yield with positive correlation at both phenotypic and genotypic levels, indicates the direct selection through these traits will be effective. Thus, selection of genotypes with large biomass yield, harvest index, number of filled grains per panicle, panicles per plant and days to maturity should be given an emphasis for variety development. The residual effect for both phenotypic and genotypic path analysis was not exceeded 0.15 indicating that the major variability in grain yield ha^{-1} was accounted for by 10 traits included in the present study. Generally, traits viz. biomass yield, harvest index and number of filled grains per panicle which have strong positive correlation and high positive direct effects on grain yield should be used for selection aimed at improving grain yield.

CONFLICT OF INTERESTS

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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