



## **Ranking Rice (*Oryza sativa* L.) Genotypes Using Multi-Criteria Decision Making, Correlation and Path Coefficient Analysis**

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### **Authors' contributions**

*This work was carried out in collaboration between all authors. All authors read and approved the final manuscript.*

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### **ABSTRACT**

The evaluation of selection criteria using correlation coefficients, multiple regression and path analysis was carried out for a period of two years on sixteen genotypes of rice (*Oryza sativa* L.). These genotypes were studied during 2008 and 2009 summer seasons at EDduim and Kosti locations in randomized complete block design with three replications per each location. The field experiment is directed to study character association; contribution of various yield influencing traits on rice for establishment of appropriate plant attributes to select and improve the grain yield, and accordingly select the most suitable genotype.

Combined analysis of variance revealed highly significant effects of locations, seasons, genotypes and their interactions for most of the studied traits indicating that these genotypes are highly variable. Genotypes differed significantly in grain yield, (NERICA 4, NERICA 14, NERICA 15, YUNLU 33 and WAB-1-38-19-14-P2-HB) were higher yielding genotypes giving 3.78, 4.03, 3.24, 3.55 and 3.51 t/ha respectively. These genotypes presented a valuable source of diversity which can be used for breeding programs.

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Correlation analysis in both seasons indicated that grain yield was positively and significantly correlated with plant height, number filled grains/ panicle and 1000-grain weight, while it was negatively correlated with percentage of unfilled grains/panicle. Path coefficient analysis indicated that among yield components number of filled grains/ panicle, number of panicles/m<sup>2</sup> and 1000-grain weight showed a positive direct effect on grain yield and therefore, may be considered as selection criteria for the improvement of grain yield.

Multi-objective decision-making model was employed to rank the studied genotypes according to the measured various yield influencing traits and the degree of association of each trait on yield. For determination of criteria weight this article considers the analysis of correlation that is used frequently in to quantify the degree of association between a response variable, and some explanatory variable. Consequently, we propose new weighted information criteria to be used to guide the selection of the “best” genotype based on determining correlation coefficient. As a result, compromise programming analysis is in agreement with analysis of variance and indicated that genotypes can be ranked in a descending order as: N12, N14, Y30, WAB8, WAB19, N4, Y33, Y26, N15, N17 and Y24.

*Keywords: Rice genotypes; Multi-criteria decision making; path coefficient analysis; correlation coefficient.*

## 1. INTRODUCTION

Worldwide Rice (*Oryza sativa* L.) is the second most important cereal crop, grain production of rice being exceeded only by that of wheat. It provides 20 percent of the world's dietary energy supply [1]. Rice in Sudan has been grown since 1905 on very limited acreage, but there is a plenty of land suitable for its production, and was estimated to be 300000 hectares in White Nile, Bahr Elgazel, South Darfour, Gadarif and Blue Nile States. Recently, in (2005) different genotypes from WARDA and IRRI are being evaluated for yield and earliness although, 82 aerobic rice varieties and lines were introduced in an attempt to save irrigation water and to reduce human diseases risks in the irrigated schemes. Also FAO is planning to rehabilitate the White Nile research farm to improve rice production [2].

Since grain yield is a complex trait, indirect selection through correlated, less complex and easier measurable traits would be an advisable strategy to increase the grain yield. Efficiency of indirect selection depends on the magnitude of correlations between yield and target yield components [3,4,5,6]. Breeding strategy in rice mainly depends upon the degree of associated characters as well as its magnitude and nature of variation [7,8]. Path coefficient analysis furnishes information of influence of each contributing traits to yield directly as well as indirectly and also enables breeders to rank the genetic attributes according to their contribution [9]. In rice, selection of high yielding cultivars via specific traits requires knowledge of not only final yield but also the many compensation mechanisms among yield components resulting from changing genotypic, environmental and management factors. Grain yield of rice is a quantitative trait which is affected by many genetic and environmental factors [10,11,12]. For selection in rice, information on correlation coefficient always has been helpful as a basis for selection in a breeding program[13]. Path coefficient analysis partitions into direct and indirect matrix presenting correlation in a more meaningful way [14]. The path analysis has been used by plant breeders [15,16,17] to support in identifying traits that are promising as selection criteria to improve crop yield and to detect the amount of direct and indirect effect of the causal components on the effect

component [6]. Multiple regression and path coefficient analyses are particularly useful for the study of cause-and-effect relationships because they simultaneously consider several variables in the data set to obtain the coefficients. Determination of correlation and path coefficients between yield and yield criteria is important for the selection of promising rice genotypes to be used in any meaningful breeding program. Surek and Beser [18] studied correlation and path coefficient analysis between yield and some agronomical characters in rice. They reported positive direct effect on grain yield and number of productive tillers/m<sup>2</sup>, biological yield and harvest index.

The relationship between rice yield and yield components has been studied extensively at phenotypic level. Nuruzzaman et al. [19] studied variability for eight quantitative characters in 14 rice genotypes. They found significant mean squares indicating strong variability among the genotypes for the traits studied. Researchers [20,21] studied variability on yield and its components in 15 and 8 rice genotypes, respectively. They found significant differences among genotypes for most of the traits, indicating genetic diversity and hence selection was effective. Maximum variability was recorded in grain yield/plant, followed by productive tillers/plant, and total number of tillers/plant. Zahid et al. [7] studied correlation and path analysis in 14 genotypes of Basmati rice. They found that number of grains per panicle had the highest positive direct effect (0.1486) on grain yield followed by 1000 grain weight (0.1064). Genetic diversity is pre-requisite for any crop improvement program, as it helps in the development of superior recombinants [22]. Genetic divergence among the genotypes plays an important role in selection of parents having wider variability for different characters [23].

Variety selection is one of the most important management decisions. This choice is generally based upon agronomic traits and variety yield potential. Selection of rice varieties with wide adaptability over diverse farming environments is important, prior to varietal recommendation in order to achieve a high rate of varietal adoption. [2] evaluated sixteen exotic genotypes of rice (*Oryza sativa* L.) across two locations for their grain yield and stability performance to identify high yielding and stable genotypes. Two genotypes (NERICA 14 and YUNLU 33) were classified as high yielding and stable genotypes across environments (locations and years) because of their high grain yield, with a regression coefficient close to unity. Rice breeders are interested in selecting high yielding cultivars with improved yield and other desirable agronomic characters. However, [24] analyzed employed compromise programming techniques and criteria weight specified by various decision makers to select the best rice genotype. They concluded that NERICA 4, NERICA 14, NERICA 15, YUNLU 33 and WAB-1-38-19-14-P2-HB were higher yielding genotypes, and recommend cultivating NERICA 14 and YUNLU 33 as first priority in the field according to breeder judgments.

To achieve this goal, a modified multi-criteria analysis needs to be used as a tool to screen and rank alternative rice genotypes. Modification stems from the problem of judgment of the relative impact of each trait on final yield. In multi-criteria analysis several criteria are simultaneously optimized in the feasible set of alternatives (genotypes). In the general case there does not exist one alternative (genotype), which optimizes all the criteria. There is a set of alternatives however, characterized by the following: each improvement in the value of one criterion leads to deterioration in the value of at least one other criterion. This set of alternatives is called a set of the non-dominating or Pareto optimal alternatives (solutions). Each alternative in this set could be a solution of the multi-criteria problem. In order to select one alternative, it is necessary to have additional information set by the so-called decision

maker (DM). The information that the DM provides reflects his/her global preferences with respect to the quality of the alternative sought.

The multi-criteria analysis problems can be divided into three types: problems of multi-criteria choice, problems of multi-criteria ranking and problems of multi-criteria sorting.

Different methods have been developed to solve multi-criteria analysis problems. These methods can be grouped in three separate classes [25]. The first class of methods [26] includes the multi-attribute utility (value) theory methods (value tradeoff method [27,28,29] and direct weighting method [30] etc.. There are differences in the way in which the DM's global preferences are aggregated in the two subclasses of these methods. In the first one a generalized functional criterion is directly synthesized, whereas in the second subclass (weighting methods) it could be said that such a criterion (additive form) is indirectly synthesized.

The second class of methods are called outranking methods (ELECTRE methods) [31]; (PROMETHEE methods) [32]; (TACTIC method) [33] ... etc. and they are based on the assumption that there exists limited comparability among the alternatives. While the inter-criteria information is expressed in the form of weights and veto thresholds, the intra-criteria information is usually expressed in the form of indifference and preference thresholds.

The third group include: The interactive algorithms (VIMDA method) [34]; (aspiration- level method) [35]; (InterQuad method) [36]; (LBS method) [37]; (RNIM method) [38] etc. The first and the second methods use the first type of DM's preference model and the DM must define the desired or acceptable values of the criteria at every iteration. The fourth and the fifth methods use the second DM's preference model and the DM has to give not only the desired or acceptable values of the criteria but also inter-and intra-criteria information at every iteration.

From this review [39], it can be deduced that the main problem in applying all classes of MCDM is specification of weights. As such we propose in this study to use a screening approach based on correlation coefficients, multiple regression and path analysis.

Analysis of correlation is used frequently in to quantify the degree of association between a response variable, and some explanatory variable [40,41]. Crop yield is said to be correlated with the factors of agronomic traits and variety yield potential. In agriculture, path analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve crop yield [42]. Use of path analysis permits the partitioning of correlation coefficient into its components, one component being the path coefficient that measures the direct effect of predictor variable upon its response variable; the second component being the indirect effect(s) of a predictor variable on the response variable through another predictor variable. However, no specific literature was found to specify weights and subsequently the overall index to rank the genotypes according to these factors. This paper proposes a ranking of the selected factors associated with genotype performance using the correlation analysis and Multi Criteria Decision Making.

[43] developed an evaluation model based on the analytic hierarchy process (AHP) and reviewed the technique for order performance by similarity to ideal solution, to help the decision-maker for the selection of optimal alternative in a fuzzy environment. They used AHP to analyze the structure of the selection problem and to determine weights of the criteria, and fuzzy method was used to obtain final ranking. To develop a strategic water management plan, Stewart and Scott [44] also proposed a group decision-making method

which is based on the principle of MCDM. They applied an MCDM technique to evaluate a number of scenarios to be included in a regional water management plan in South Africa. Netto et al. [45] applied an MCDM technique to develop a long-term water supply plan which involves many interest groups. It is a regional development plan in the south-western part of France to develop more water resources. They set a model that consists of four actor groups, 13 criteria and 38 alternatives, to determine the location of a large reservoir in the plan. They reduced the number of alternatives to eight by using the ELECTRE III technique and then expanded the ELECTRE III to simulate the multi-actor multi-criterion decision process. Their evaluation procedures involve several objectives, and it is hence, necessary to compromise among possibly conflicting tangible and intangible factors. For these reasons, multiple criteria decision making (MCDM) has been found to be a useful approach to solve this kind of problem. Taken together, the ranking in the present paper can be seen as a bivariate analysis using secondary source of statistical data and also a multi criteria decision making (MCDM) problem using correlation coefficient rather than the traditionally used linguistic judgments of experts. Consequently, the ranks can be drawn using the strength of correlation coefficients and the magnitude of closeness coefficients to the idea point.

Path coefficient analysis shows the extent of direct and indirect effects of the causal components on the response component. In most studies involving path analysis, researchers considered the predictor characters as first-order variables to analyze their effects over a dependent or response variable such as yield. This approach might result in multicollinearity for variables, particularly when correlations among some of the characters are high [46]. There may be difficulties in interpretation of the actual contribution of each variable, as the effects are mixed or confounded because of collinearity. Samonte et al. [46] adopted a sequential path analysis for determining the relationships between yield and related characters in rice (*Oryza sativa* L.) by organizing and analyzing various predictor variables in first, second and third order paths. The objectives of the present study are two folds: to describe character association and contribution of various yield influencing traits to establish appropriate plant attributes for selection to improve the grain yield; and to select rank rice genotypes using a multi-attribute decision making scheme.

## 2. MATERIALS AND METHODS

### 2.1 Data Collection

The study was conducted at the Faculty of Agriculture and Natural Resources, University of Bakht Alruda, EDduim (long. 32°20'E, lat. 13°39' N) and 380 msl, and Kosti Research Station (long 32°46,' lat 13°6' N), ARC, Sudan during 2008 and 2009. The experimental material was composed of 16 rice genotypes introduced from West African Rice Development Association (WARDA), International Rice Research Institute (IRRI) and China. They include: JM 49, JM 25, JM 21, JM 44, JM 45, JM 48, JM /97, JM 3 JM 30, JM 24, and JM 23, from Darfur Sudan, BS/Sh94 from Shambat, Ugandi from Uganda (adapted) and JM 38 from Madelkawiya.

The seed was sown directly in field on 15 of July in 2008 and 16 of June 2009. The experiment was laid out in a randomized complete block design with three replications. The row to row and plant to plant distance was 20 x 20 cm. Phosphorus fertilizer in form of triple super phosphate ( $P_2O_5$ ) was applied as basal dose before sowing at the rate of 43 Kg ha<sup>-1</sup>. Nitrogen, in the form of urea (46% N), was applied in two equal split doses one after three

weeks from sowing and the second after one month from the first one at the rate of 86 Kg ha<sup>-1</sup> of N in each location.

Data was recorded for days to 50% flowering at each plot and at the time of maturity the rest of the data on five plants from each plot were recorded for plant height (cm), days to 50% maturity, panicle length (cm), number of tillers per plant, number of grains/panicle, number of filled grains/panicle, percentage of unfilled grains/panicle, 1000-grain weight, number of panicles/m<sup>2</sup> and grain yield t/ha. Analysis of variance for the data was carried out by using computer program Statistical Analysis System [47]. DMRT was used as mean separation method. The combined data means over locations were used to calculate the simple linear correlation coefficients between 9 pairs of traits by using the Statistical Package for the Social Sciences, (SPSS) version 16. The traits included in the model were: Number of grains/panicle (NGP), number of filled grains/panicle (NFG), percentage of unfilled grains/panicle (PUG), number of panicle/m<sup>2</sup> (NP/m<sup>2</sup>), 1000- grain weight (TGW) and grain yield (GY). Correlation coefficients between these traits were used to calculate the path coefficients.

## 2.2 Correlation Coefficient (r): Phenotypic Correlation

The observable correlation between two variables, which includes both genotypic and environmental effects and genotypic correlation, the inherent association between two variables were estimated using the standard procedure suggested by [48,13]. Covariance analysis between all pairs of the variables followed the same form as the variance. Thus, estimates of genetic covariance component between two traits ( $\sigma^2_{g_{xy}}$ ) and the phenotypic covariance component ( $\sigma^2_{p_{xy}}$ ) were derived in the same fashion as for the corresponding variance components.

$$r_{g_{xy}} = \sigma^2_{g_{xy}} / ([\sigma^2_{g_x} * X * \sigma^2_{g_y}]^{0.5})$$

$$r_{p_{xy}} = \sigma^2_{p_{xy}} / ([\sigma^2_{p_x} * X * \sigma^2_{p_y}]^{0.5})$$

Where:  $\sigma^2_{g_{xy}}$  = genotypic covariance of two variables x and y;  $\sigma^2_{p_{xy}}$  = phenotypic covariance of two variables x and y;

## 2.3 Path Coefficient Analysis

Path coefficient analysis is a statistical technique of partitioning the correlation coefficients into its direct and indirect effects, so that the contribution of each character to yield could be estimated. 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. The goal of the path analysis is to accept descriptions of the correlation between the traits, based on a model of cause and effect relationship and to estimate the importance of the affecting traits on a specific trait. If the cause and effect relationship is well defined, it is possible to present the whole system of variables in the form of the diagram, known as path-diagram. Direct effects tell how a one unit change in X will affect Y, holding all other variables constant. However, it may be that other variables are not likely to remain constant if X changes, e.g. a change in X can produce a change in Z which in turn produces a change in Y. Putting another way, both the direct and indirect effects of X on Y must be considered if we want to know what effect a change in X will have on Y, i.e. we want to know the total effects (direct + indirect).

Path coefficient analysis was carried out using the phenotypic correlation coefficients as well as genotypic correlation coefficients to determine the direct and indirect effects of the

yield components and other morphological characters on grain yield using the general formula of Singh and Chaudhary [3].

Path coefficient:  $r_{ij} = p_{ij} + r_{ik} * p_{kj}$

Where,  $r_{ij}$  = mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficients.

$p_{ij}$  = components of direct effects of the independent character (i) on the dependent variable (j) as measured by the path coefficients and  $\sum r_{ik}p_{kj}$  = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent characters (k). The residual effects were estimated using the formula:

$$(1 - R^2)^{0.5} \text{ where } R^2 = p_{ij}$$

## 2.4 Multi-objective Optimization

The adopted model to rank various genotypes is based on compromise programming technique. Compromise programming was initially proposed by [49] and subsequently used by many researchers to determine the optimal solution as the one that has the shortest distance to an ideal point where the multiple objectives simultaneously reach their minimal values e.g., [50, 51, 52]. The ideal point is not practically achievable but may be used as a base point. The algorithm for multi-objective optimization includes a stochastic generating process and a choosing process. The former specify scores of each alternative obtained for each evaluating criterion, estimate maximum and minimum points for each criterion, searches weight vectors in the whole weighting space using correlation coefficients, and in the latter analytic hierarchy process evaluation model chooses the best Pareto solution and rank alternatives on basis of minimum relative distance to the ideal point (The compromise solution). Hence, the screening and ranking approach: It involves the following steps (Fig. 1):

- 1- Select alternative genotypes and quantify performance of each one with respect to evaluation criteria (to determine the nature of the relationships between yield and yield components)
- 2- Run regression and correlation coefficient on the collected data to estimate relative weight of each criterion.
- 3- Run Path coefficient analysis for partitioning the correlation coefficients into its direct and indirect effects, so that the contribution of each character to yield could be estimated. Consequently, estimate the traits of most impacts on improving the crop yield.
- 4- Conduct compromise programming technique as shown below:

The total value of the alternative was calculated based on the weighted sum method given in the following equation [49]:

$$V(A) = \sum_i w_i v_i(a_i)$$

Where,  $w_i$  is the weight of the criterion  $i$ ,  $v_i(a_i)$  is the score of the alternative with respect to criterion  $i$  and  $V(A)$  is the value of the alternative  $A$ . As the scores have different unit (cardinal or ordinal), standardization is necessary to convert all scores in the same unit. Standardization means that the score of a strategy 'with respect to a criterion' is expressed as a function of the score of the other strategies. In this study, standardization was performed. The difference between the individual and the minimum score is divided by the difference between the maximum and the minimum score. The best strategy has a standardized score of one and the worst strategy has a standardized score of zero. Mathematically, the method is expressed for alternative  $k$  with respect to criterion  $j$  below:

For the case of minimization:

$$STD_{k,j} = \frac{|(ACT_{k,j} - WORST_{k,j})|}{|(BEST_{k,j} - WORST_{k,j})|}, \dots, \text{ else}$$

For the case of maximization:

$$STD_{k,j} = \frac{|(BEST_{k,j} - ACT_{k,j})|}{|(BEST_{k,j} - WORST_{k,j})|}$$

where, STD is the standardized score, ACT is the  $k,j$  actual score,  $WORST_{k,j}$  is the worst (minimum) score and  $BEST_{k,j}$  is the best (maximum) score.

Finally, the sensitivity analysis was carried out by changing weights of different criteria so that the role of each criterion on the selection of alternatives can be understood.

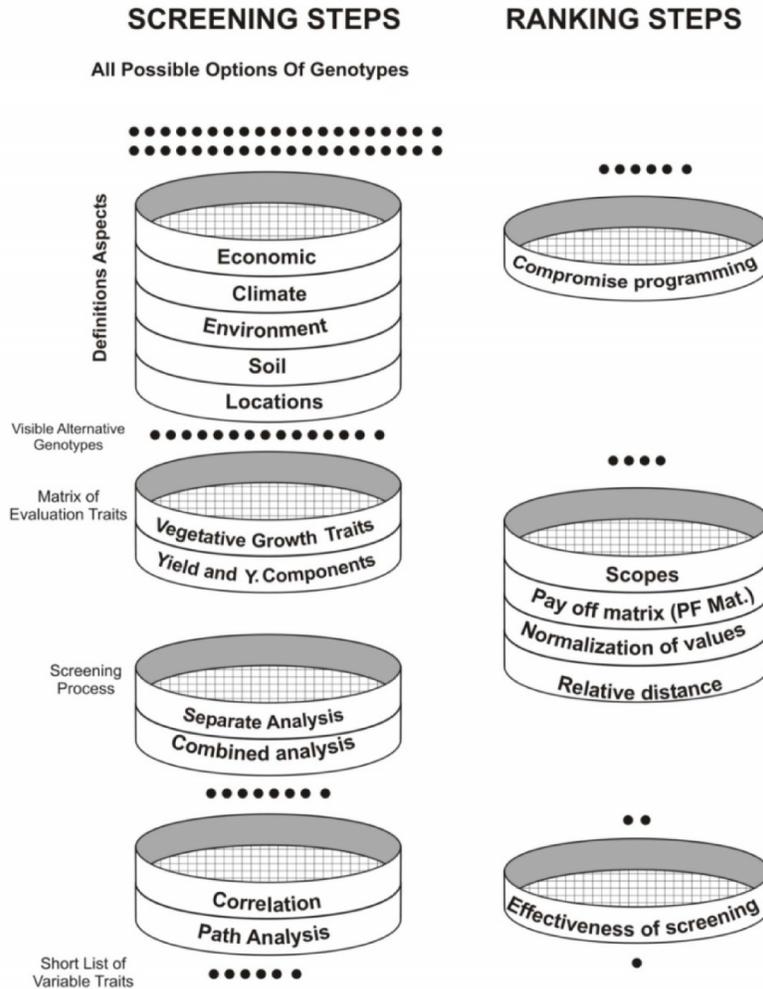


Fig. 1. Considerations when screening alternative treatment processes (adapted from [53].)

### 3. RESULTS AND DISCUSSION

#### 3.1 Characters Association

Simple linear correlation coefficients among yield and yield contributing traits for 16 rice genotypes were calculated from data pooled over locations for the two seasons (Table, 1).

**Table 1. Simple linear correlation coefficients (r) among various pairs in rice genotypes at two locations combined 2008 upper diagonal and 2009 lower diagonal.**

Trait	PH	NTP	PL	NGP	NFG	PUG	NP/m <sup>2</sup>	TGW	GY
PH	-	0.433**	0.671**	0.545**	0.517**	0.070	0.313**	0.435**	0.437**
NTP	0.021	-	0.316**	0.290**	0.241*	0.104	0.248**	0.214*	0.419**
PL	0.435**	0.495**	-	0.523**	0.496**	0.041	0.289**	0.544**	0.412**
NGP	0.287**	0.112	0.397**	-	0.763**	0.205*	0.260**	0.379**	0.454**
NFG	0.512**	-0.079	0.313**	0.748**	-	-0.267**	0.073	0.450**	0.538**
PUG	-0.281**	0.481**	0.203*	0.092	-0.449**	-	0.183	-0.030	-0.131
NP/m <sup>2</sup>	0.524**	-0.445**	-0.004	-0.088	0.269**	-0.519**	-	0.165	0.185
TGW	0.437**	0.016	0.351**	0.061	0.178	-0.153	0.347**	-	0.334**
<b>GY</b>	<b>0.490**</b>	<b>-0.285**</b>	<b>0.098</b>	<b>0.066</b>	<b>0.466**</b>	<b>-0.574**</b>	<b>0.675**</b>	<b>0.315**</b>	-

PH=Plant height (cm), NTP=Number of tillers/plant, PL=Panicle length(cm), NGP=Number of grains/panicle, NFG=Number of filled grains/panicle, PUG=Percentage of unfilled grains/panicle, NP/m<sup>2</sup>=Number of panicles/m<sup>2</sup>, TGW= 1000-grain weight, GY=Grain yield t/ha.

\*, \*\* Significant at the 0.05 and 0.01 probability levels, respectively.

Grain yield was positively and significantly correlated with plant height, number of filled grains/panicle and 1000-grain weight. It was positively and significantly correlated with number of tillers/plant, panicle length and number of grains/panicle in 2008, while negatively and weakly correlated with these three characters in 2009. Grain yield was negatively and not significantly associated with percentage of unfilled grains/panicle in 2008 and significantly correlated with the same character in 2009. It was positively and significantly associated with number of panicles/m<sup>2</sup> in 2009, but positively and not significantly correlated with character in 2008. Researchers [20,54,55] reported positive association of plant height with grain yield. Bhatti et al. [6] reported that number of grains per panicle and 1000-grain weight has positive genotypic and phenotypic correlation with grain yield. The negative association between yield and percentage of unfilled grains/panicle was expected since filled grains/panicle has a high significant correlation with grain yield [56]. The negative correlation between number of tillers per plant and grain yield in 2009 might be due to increased frequency of barren tillers. These findings are in agreement with the work done by Zahid et al. [7]. The results obtained in this study were in agreement with the findings of Soundrapandian [57] for the number of panicles per square meter and [58] for the number of filled grains per panicle.

Plant height was positively and significantly correlated with panicle length, number of grains/panicle, number of filled grains/panicle, number of panicles/m<sup>2</sup> and 1000-grain weight in both seasons. It was positively and significantly related with number of tillers/plant in 2008, but weakly and positively correlated with the same character in 2009. These results agreed with that of [20], though the present findings do not coincide with the findings of [59], who reported negative correlation between plant height and tillers per plant.

A positive and significant correlation was presented between panicle length and number of grains/panicle, number of filled grains/panicle and 1000-grain weight in both seasons, while it was positively related but not significantly with percentage of unfilled grains/panicle in 2008 and positively and significantly related with such character in 2009. A non-significant and negative association was observed between panicle length and number of panicles/m<sup>2</sup> in 2009, but positive and significant in 2008. The differences in correlation between these traits it could be due to environmental conditions prevailing in both seasons.

Number of grains/panicle was positively and significantly correlated with number of filled grains/panicle in both seasons. It was positively and significantly associated with percentage of unfilled grains/panicle, number of panicles/m<sup>2</sup> and 1000-grain weight in 2008, but positively and significantly associated with percentage of unfilled grains/panicle and 1000-grain weight in 2009, although it was negatively and non-significantly correlated with number of panicles/m<sup>2</sup> in the same season.

For number of filled grains/panicle negatively and significantly correlation was observed with percentage of unfilled grains/panicle in both seasons. The strong negative association between number of filled grains/panicle and percentage of unfilled grains/panicle is expected, the increase in one of them is resulted in decrease in the other. In 2008 it was positively, non significantly correlated with number of panicles/m<sup>2</sup>, but positively and significantly associated with 1000-grain weight. Different results were observed in 2009 with these two traits. Filled grains/panicle was positively and significantly correlated with number of panicles/m<sup>2</sup>, while positively, non-significant with 1000-grain weight. These variations in correlation coefficients between traits can be explained by the genetic makeup of the genotypes and the climatic or edaphic conditions in which they were evaluated.

Percentage of unfilled grains/panicle had negative and non- significant correlation with 1000-grain weight in both seasons. It had positive and non- significant correlation with number of panicles/m<sup>2</sup> in 2008, while negatively and significantly associated with the same character in 2009. Negative correlation between percentage of unfilled grains/panicle with 1000-grain weight and number of panicles/m<sup>2</sup> may be due to the highest correlation with grain yield.

A positive and significant correlation was observed between number of panicles/m<sup>2</sup> and 1000-grain weight in 2009, but positive and non-significant association was observed between these two traits in 2008. In both seasons it was observed that grain yield was positively and significantly correlated with plant height, number filled grains/ panicle and 1000-grain weight, while it was negatively correlated with percentage of unfilled grains/panicle.

### **3.2 Path Coefficient Analysis for Screening Traits**

Tables 2 and 3 revealed the results of direct and indirect effects of various grain yield components on grain yield.

Among yield components, path coefficient analysis showed that number of filled grains per panicle and number of panicles/m<sup>2</sup> had the highest positive direct effect on grain yield in both seasons, indicating that selection based on this character would be effective.

In general, the direct effects of the other characters on grain yield were small, weak though in most cases positive, in both seasons, except number of grains per panicle in 2009 which showed the highest negative direct effect on grain yield (Table, 2) this trait also exhibited positive weak association with grain yield in the same season. In 2009, number of filled grains per panicle and number of panicles/m<sup>2</sup>, were highly and positively correlated with grain yield.

The positive association of grain yield with number of filled grains per panicle and number of panicles/m<sup>2</sup> was due mainly to their direct effect with negligible indirect effects through other characters in both seasons. This suggested the direct use of these two characters as selection criteria.

Unfilled grain percentage, showed negative direct effect on grain yield in 2008, but positive and weak direct effect in 2009, negative correlation with grain yield in both seasons was noticed in unfilled grain percentage. It had negative weak, indirect effect on grain yield in both seasons via number of filled grains/ panicle and 1000-grain weight.

Thousand grain weights, showed positive weak direct effect on grain yield in both seasons, although it exhibited, positive indirect effect on grain yield via all traits in both seasons with the exception of number grains per panicle and percentage of unfilled grains per panicle in 2009, it showed negative indirect effect on grain yield via these traits. Cheng et al. [60] reported positive direct effect of 1000-grain weight on grain yield while Babu et al. [61] stated positive direct effect for productive tillers per plant on yield.

The present study indicated that among yield components number of filled grains/ panicle, number of panicles/m<sup>2</sup> and 1000-grain weight had the highest correlation coefficients with grain yield. These traits also showed a positive direct effect on grain yield and therefore, may be considered as selection criteria for the improvement of grain yield.

**Table 2. Path coefficients of some traits in rice using simple linear correlation coefficients for season (2008) combined at EDduim and Kosti locations.**

Trait	NGP	NFG	PUG	NP/m <sup>2</sup>	TGW	Pij
NGP	0.060	0.325	-0.010	0.034	0.036	0.445**
NFG	0.045	0.426	0.013	0.009	0.043	0.538**
PUG	0.012	-0.113	-0.050	0.024	-0.002	0.131
NP/m <sup>2</sup>	0.015	0.031	-0.009	0.131	0.015	0.185
TGW	0.022	0.191	0.001	0.021	0.096	0.334**

*Pij*= Genotypic correlations with yield. NGP =Number of grains/panicle.  
 NFG=Number of filled grains/panicle. PUG=Percentage of unfilled grains/panicle.  
 NP/m<sup>2</sup>=Number of panicles/m<sup>2</sup>. TGW=1000 grain weight/g.  
 Direct effects are in bold.

**Table 3. Path coefficients of some traits in rice using simple linear correlation coefficients for season (2009) combined at EDduim and Kosti locations.**

Trait	NGP	NFG	PUG	NP/m <sup>2</sup>	TGW	Pij
NGP	-0.438	0.497	0.001	-0.038	0.044	0.066
NFG	-0.328	0.664	-0.001	0.116	0.013	0.466**
PUG	-0.040	-0.298	-0.001	-0.224	-0.011	-0.574**
NP/m <sup>2</sup>	0.038	0.178	-0.001	0.432	0.025	0.675**
TGW	-0.026	0.118	-0.001	0.150	0.073	0.315**

*Pij*: Genotypic correlations with yield. NGP=Number of grains/panicle.  
 NFG=Number of filled grains/panicle. PUG=Percentage of unfilled grains/panicle.  
 NP/m<sup>2</sup>=Number of panicles/m<sup>2</sup>. TGW=1000 grain weight/g.  
 Direct effects are in bold.

### 3.3 Ranking of Genotypes using Compromise Programming Technique

The outcome of applying the screening and ranking procedure outlined above revealed that:

- 1- From Path coefficient analysis the important traits with high impact on crop final yield are: NFG=Number of filled grains/panicle, NP/m<sup>2</sup>=Number of panicles/m<sup>2</sup>, TGW=1000-grain weight and GY=Grain yield t/ha. In contrast other traits may be neglected (PH=Plant height (cm), NTP=Number of tillers/plant, PL=Panicle length (cm), NGP=Number of grains/panicle, and PUG=Percentage of unfilled grains/panicle).
- 2- Using characters association study it is possible to take correlation coefficients for the identified traits as criteria weights namely: 0.43, 0.35, 0.50 and 1.00 for NFG/P, NP/m<sup>2</sup>, TGW, and GY t/ha respectively.
- 3- The performance of each genotype with respect each one of the four identified traits is quantified from data collected in the field and depicted in (Table 4).
- 4- The scores obtained by each genotype with respect to the most influential traits (Table 4) were used to normalize and non-dimension the data for purpose of developing the payoff matrix (Table 5).
- 5- Normalized distance to ideal point is quantified for each genotype by considering criteria weights and relative scores and given in Table 6.

- 6- Final ranking of various genotypes and their respective distance is shown in Table 7. This result indicated that NERICA genotypes 12 and 14 are the most preferred alternative to grow in farmer fields.

**Table 4. Performance of genotypes with respect to the most influential traits**

Genotypes	NFG/P	NP/m <sup>2</sup>	TGW	GY t/ha
N 2	17.30	443.30	20.80	2.66
N 4	31.80	405.00	23.00	2.90
N 5	20.00	382.50	20.00	1.93
N 12	37.80	405.80	31.60	3.05
N14	28.70	377.50	25.00	3.73
N 15	27.20	312.50	29.10	2.65
N17	23.20	447.50	32.00	1.93
Y 22	22.80	398.30	23.30	2.38
Y 24	25.80	405.00	24.30	2.26
Y 26	33.70	380.80	26.60	2.30
Y 30	30.30	425.80	24.00	3.26
Y 33	29.30	377.50	28.30	2.70
Y 34	30.80	340.80	25.00	2.28
WAB8	31.30	394.10	25.70	3.22
WAB12	26.40	372.00	25.60	2.08
WAB19	26.80	416.60	28.60	2.70

*NFG=Number of filled grains/panicle, NP/m<sup>2</sup>=Number of panicles/m<sup>2</sup>, TGW= 1000-grain weight, GY=Grain yield t/ha.*

**Table 5. Payoff matrix of relative scores estimated for each genotype**

Genotypes	NFG/P	NP/m <sup>2</sup>	TGW	GY t/ha
N 2	1.00	0.03	0.93	0.59
N 4	0.29	0.31	0.75	0.46
N 5	0.87	0.48	1.00	1.00
N 12	0.00	0.31	0.03	0.38
N14	0.44	0.52	0.58	0.00
N 15	0.52	1.00	0.24	0.60
N17	0.71	0.00	0.00	1.00
Y 22	0.73	0.36	0.73	0.75
Y 24	0.59	0.31	0.64	0.82
Y 26	0.20	0.49	0.45	0.79
Y 30	0.37	0.16	0.67	0.26
Y 33	0.41	0.52	0.31	0.57
Y 34	0.34	0.79	0.58	0.81
WAB8	0.32	0.40	0.53	0.28
WAB12	0.56	0.56	0.53	0.92
WAB19	0.54	0.23	0.28	0.57

*NFG=Number of filled grains/panicle, NP/m<sup>2</sup>=Number of panicles/m<sup>2</sup>, TGW= 1000-grain weight, GY=Grain yield t/ha.*

**Table 6. Normalized distance calculated for each genotype by considering criteria weights and relative scores**

Genotypes	Relative scores				Lj
	NFG/P	NP/m <sup>2</sup>	TGW	GY t/ha	
N 2	0.43	0.01	0.47	0.59	1.50
N 4	0.13	0.11	0.38	0.46	1.07
N 5	0.37	0.17	0.50	1.00	2.05
N 12	0.00	0.11	0.02	0.38	0.50
N14	0.19	0.18	0.29	0.00	0.67
N 15	0.22	0.35	0.12	0.60	1.30
N17	0.31	0.00	0.00	1.00	1.31
Y 22	0.31	0.13	0.36	0.75	1.56
Y 24	0.25	0.11	0.32	0.82	1.50
Y 26	0.09	0.17	0.23	0.79	1.28
Y 30	0.16	0.06	0.33	0.26	0.81
Y 33	0.18	0.18	0.15	0.57	1.09
Y 34	0.15	0.28	0.29	0.81	1.52
WAB8	0.14	0.14	0.26	0.28	0.82
WAB12	0.24	0.20	0.27	0.92	1.62
WAB19	0.23	0.08	0.14	0.57	1.03

*NFG=Number of filled grains/panicle, NP/m<sup>2</sup>=Number of panicles/m<sup>2</sup>, TGW= 1000-grain weight, GY=Grain yield t/ha.*

**Table 7. Minimum distances to ideal point and rank of genotypes**

Genotypes	Lj Distance	Rank
N 12	0.503	1
N14	0.666	2
Y 30	0.810	3
WAB8	0.823	4
WAB19	1.026	5
N 4	1.074	6
Y 33	1.088	7
Y 26	1.281	8
N 15	1.296	9
N17	1.306	10
Y 24	1.501	11
N 2	1.504	12
Y 34	1.524	13
Y 22	1.557	14
WAB12	1.621	15
N 5	2.045	16

Mohamed [2] and Idris et al. [24] ranked NERICA 14 and YUNLU 33 as top priority. However, using the modified Multi-criteria analysis adopted in this study the genotypes reported by these investigators ranked second and seven (Table 7). This because the former researchers based their decision on mean yield only without considering the impacts of other traits ;while the later judged their ranks by the relative impact of each trait (criteria weight) made according to the preference of the interviewed decision maker and it is possible that judgments of breeders are not identical and differ greatly.

#### 4. CONCLUSIONS

In this study, correlation analysis in both seasons indicated that grain yield was positively and significantly correlated with plant height, number filled grains/ panicle and 1000-grain weight. Path coefficient analysis indicated that among yield components number of filled grains/ panicle, number of panicles/m<sup>2</sup> and 1000-grain weight showed a positive direct effect on grain yield and therefore, may be considered as selection criteria for the improvement of grain yield. To arrive to sound selection of most preferred genotype to grow the ranks of alternative ones can be drawn using the strength of correlation coefficients, path analyses (screening step) and the magnitude of closeness coefficients to the idea point (ranking step). Hence, the adopted procedure can be taken as improvement to compromise programming technique. Thus, the results of the study indicate that (NERICA 12 and NERICA 14) yielded the highest ranking followed by YUNLU 30 and WAB8. This ranking gives rise to concerns about the relevance of the factors affecting crop final yield for future breeding programs.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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