Characterization, breeding and selection of PANELS OF rice germplasm under low and high soil phosphorous (P) and nitrogen (N) environments in kenya

## Soil nitrogen (N) and phosphorus (P) deficiencies are among the major constraints constrictive to rice productivity globally, especially in resource-poor farming systems. This study aimed to develop and evaluate rice genotypes with enhanced tolerance to low N and P conditions through targeted breeding approaches. A diverse panel of rice germplasm was screened under controlled and field conditions to identify traits associated with nutrient use efficiency and generate information in this discipline. A total of 389 accessions and a local cultivar *Duorado precoce* were evaluated in a simple 30 × 13 alpha lattice design with two replications under four soil experimental environments (N-P-, no N or P application; N-P+, P applied; N+P-, N applied and N+P+, both N and P applied) at the rate of 60 kg P and 90 kg N ha-1. Data was recorded on Days to heading, anthesis and maturity (days), P and N tolerance, plant height (cm), above ground biomass (g), number of panicles (absolute numbers per ten plants), days to maturity (days), 1000 grain weight (g), and grain yield (kg ha-1). The genotypes and environments were highly significant for all the traits studied. The degree of genetic determination (H2) ranged from 6.8% for P tolerance to 36.5% for above ground biomass. The phenotypic coefficient of variation of genotypes ranged from 14.3% for days to maturity to 159.7% for top biomass. The genetic advance (GA) ranged from 0.2 for phosphorous tolerance to 1080.5 for grain yield, while the genetic advance expressed as percent of the mean was 5.7% for days to maturity and 87.9% for top biomass. The top biomass seems to be a highly heritable trait and simple phenotypic selection is possible. The ten characters studied had wide variability under the four environments with days to maturity ranging from 188 for genotype ARCCU1Fa1-L4P3-HB under N+P+ to 177 for genotype CT16333(1)-CA-1-M under N-P- condition. The highest yielding genotype was CT16328-CA-18-M under N-P- with 5916 kg ha-1. The germplasm showed variability for low soil N and P adaptation, and hence improvement was possible to take advantage of the vast unexploited both rainfed lowland and upland environments for increased rice productivity to meet food-feed and nutritional households and national security in Kenya. There was high variability in the genotypes to warrant rice improvement for yield. Field trials conducted at African Rice research fields in Senegal have revealed significant yield improvements in the newly developed lines under nutrient deficient, elements toxic and problem soils environment conditions. This study underscores the potential of breeding for nutrient-efficient rice varieties as a sustainable. economic solution without much application of fertilizers to enhance productivity in nutrient poor soils, contributing to food security in sub-Saharan Africa.

Key words: Genetic advance, genotypes, heritability, Kenya, Low soil nitrogen.,Low soil phosphorous, nutrient use efficiency, rice, root architecture, slatch and burn, sustainable agriculture,

# INTRODUCTION

The global world has a strong interplay of economies, cultures and populations as a product of globalization. There are therefore many challenges of which the United Nations’ second Sustainable Development Goal (SDG 2, UN 2015) aim to attain zero hunger and achieve food and nutrition sovereignty while promoting sustainable agriculture. The government of Kenya in it’s pursuit to achieve that has put up measures registrated through various policies, regulations and strategies towards this goal. For example, article 43 of the Constitution of Kenya (2010) declares that “Every person has the right to be free from hunger, and to have adequate food of acceptable quality”. The government has the onerous task of ensuring food and nutrition security to all Kenyans and therefore it’s it national mandate. The Kenya Vision 2030 seeks to achieve an economic growth rate of 10% from the agricultural sector through transformation from small scale holder’s agriculture to an industrious innovative commercially oriented modern sector. This policy direction is strongly embedded in the devolved government structure, the United Nations’ SDGs and the Comprehensive Africa Agriculture Development Programme (CAADP) towards agriculture growth and transformation in Kenya, rice is third most important staple food crop after maize and wheat, but it is grown under low fertility conditions resulting in low yields. Rice forms part of the diet and source of employment and income for both urban and rural populations. The domestic production oscillates between 250,000 to 300,000 MT, while total national consumption is well above 904,000 MT which is expected to hit 1,290,000mt by 2030 (IRRI Kenya, 2024). This creates a deficit of more than 854,000 MT per annum which has to be imported to fill the gap between production and consumption. In 2023, Kenya in order to meet the deficit, made an import of 937,098 costing the country over USD 95 million in imports from Pakistan, China, India, neighboring countries and Vietnam (Economic survey, 2024). The current state of low productivity of the rice sector is worri- some, given that the rate of consumption is growing at 12% per annum while the domestic production has experienced slow growth for the last couple of years (MoA, 2023).

Rice breeding efforts in Kenya have slowly been taking place to develop locally adapted high yielding varieties with desirable eating qualities. These breeding initiatives supported by the development partners such as Alliance for a Green Revolution in Africa (AGRA), Japan International Cooperation Agency (JICA) through Science and Technology Research Partnership for sustainable development (SATREPS) project, International Center for Research and Education in Agriculture (ICREA), AfricaRice through Korea-Africa Food and Agriculture Cooperation Initiative (KAFACI), Shanghai Agrobiological Gene Center (SAGC), International Rice Research Institute (IRRI), Biotechnology and Biological Sciences Council (BBSRC), African Agricultural Technology Foundation (AATF) Internation Foundation for Science (IFS) and recently Korea Program on International Agriculture (KOPIA) through Korean Rural Development Administration (RDA), among others have led to development of new varieties and lines with better performance in yield and thus slowly replacing the over 40 years old cultivars. The current varieties and lines are from accessions from other parts of the world, that include Korea, India, Japan, Cote d’Ivoire of which the production condition is different to the local production environments in most instances having inherently poor soils. There are now attempts being made to breed for local genotypes for adaptation to perform under the prevailing poor soil fertility and climate change conditions. The existing materials or cultivars were acquired many years ago, and their acquisition criteria have since changed thus rendering them unsuitable for emerging issues and thus they are less relevant. Therefore, it is needed to come up with breeding methodologies that embrace and take into consideration participation of end users of the technology being developed, use of the appropriate germplasm with the desirable genes that contribute to the traits of interest and with robust climate change and emerging challenges. Further, the application and use of breeding methodologies in terms of appropriate mating designs and evaluation or environmental or field designs coupled with the use of appropriate data analytical software and correct interpretation of the results is very crucial if the desired result are to be realized (Kimani etal., 2020; Atlin et al., 2006a; Christiansen and Lewis, 1982; De-Datta et al., 2002; Fasoula and Fasoula, 1997; Fasoula and Fasoula, 2000; Fukai et al., 1999; Kwanchai, A.G., 1972).

The concerted deliberate efforts geared towards the development of resilient rainfed lowland and upland rice varieties that possess the end user traits can greatly contribute to higher adoption rate (Poussin et al., 2006). This, coupled by the fact that rainfed upland rice is unexploited despite the gigantic potential it has in terms of land availability, enhancement of paddy yield and ease of cultivation, can unlock the current status of deficit rice production (MoA, 2023; Mo, 2009). However, the cultivars lack low soil nitrogen (N) and phosphorous (P) tolerance. The genetics and variances contributing to the traits of interest should be determined and to make correct decisions regarding the varieties being used as parents and the progenies (Allard, 1960; Borojevi'c, 1990; Falconer, 1989; Simmonds and Smartt, 1999). If the genes conferring a sought trait are not present in the breeding materials used in a programme, even if all the other steps are correct; this is a total waste of time and resources as no positive results can be realized (Kimani et al., 2020; Ceccarelli, 1994; Presterl et al., 2003). Efforts should be made to ensure that evaluation stress is present in a strong way to avoid escapes and that the ‘cooking pot’ should have all the desirable ingredients (genetics) for the sought end product technology to be useful to the consumers or users (Banziger et al., 2006; Edmeades et al., 1997). In some instances the materials with genetic materials of interest may not be available locally. Genetic materials in most instances may possess undesirable traits like low yield, lodging, susceptible to diseases and pests, undesirable colour and so on. It is therefore necessary to acquire germplasm from either from local populations or accessions from other countries, especially international rice research institutes that has huge number of stored acessions. The seed is first evaluated in a quarantine facility for biosecurity run by Kenya plant health inspectorate service (KEPHIS) since rice is schedule II crop and of quarantine importance to protect the country from entry of obnoxious diseases or pests. They include freedom from the following pests: Seed-borne nematodes: Ditylenchus angustus, Aphelenchoides besseyi, bacterial diseases: Burkholderia glumae, Xanthomonas oryzae pv. oryzae, Pseudomonas fuscovaginae:- Trichoconiella padwickii (Ganguly), Alternaria padwickii (Ganguly), Tilletia barclayana, Sclerophthora macrospora (Sacc.), Monographella nivalis, Schaffnit, Cochliobolus sativus, Thanatephorus cucumeris; and viral diseases of rice. Seed treatment with appropriate chemical and /or hot water treatment could address some of the diseases.

After satisfactorily confirming the materials to be free from any biosecurity threats, the materials were released for use and characterization to find out the data especially for flowering in order to be able to synchronize hybridization during the breeding program to generate progenies with desirable gene combinations that confer the trait of interest. The rationale of the study was to evaluate and select adapted promising genotypes with desirable genes for low soil P and N efficiency from the broad based germplasm accession architecture from CIAT, KAFACI, IRRI, SAGC, KALRO, AATF, Nagoya unibersity, Tanzania Agricultural Research Institute (TARI), Namulonge Agricultural Research Organization (NARO) among other regional centres for hybridization with the local cultivars. The specific objectives were then to characterize the accessions for various agronomic traits under local conditions and different soil P and N conditions; determine variation and genetic parameters responsible for performance under low and high soil P and N conditions; and identify adapted lines from the accessions to be used as parents and cultivars in the breeding programme.

The need for genetic base broadening germplasm lead to the acquisition of 390 lines that had tolerance to low soil N and P, good grain quality, good level of pest and diseases resistance, and drought tolerance. These lines provided gene systems missing in the local cultivars and hence from their adaptation and characterization data, potential donors for desirable genes were selected for the hybridization programme. The early maturing, well adapted lines to low soil N and P, pest and diseases tolerance, and with desirable grain qualities were the main traits sought.

**METHODOLOGY**

This section will explain how the process was conducted to undertake hybridization to generate materials with great divesity of porogenies possessing various combinations of genes controlling certain trai combinations.

**Study location**

The research was conducted at the Kenya Agricultural and Livestock Research Organization (KALRO) - Industrial Crops Research Centre (ICRC), Mwea Tebere (National Rice and Fiber Research Centre (NRFRC)) which is located in Mwea Consituency, Kirinyaga county, in Central region, Kenya. It lies at Latitude 00° 37’ S and Longitude 37° 20’ E at an elevation of 1159 m above sea level (MASL). The average rainfall is about 850 mm with a range of 500 to 1250 mm divided into long rains (March to June with an average of 450 mm) and short rains (Mid-October to December with an average of 350 mm). The rainfall is characterized by uneven distribution in total amounts, time and space. The temperature ranges from 15.6 to 28.6°C with a mean of about 22°C. The area is in agro-climatic zones (ACZ) III and IV which have mean annual evaporation to mean annual rainfall ratio of 0.5-0.65 and 0.4-0.5, respectively (Sombroek et al., 1982). The soils are nitosol, deep, well drained dusky-red to dark reddish-brown, friable clay with low fertility (Kimani et al., 2020; Sikuku et al., 2019; Kimani, 2010). The soils of the uplands conditions where rice was sown are developed on intermediate igneous rocks which include phonolites and trachytic or rhyolitic phonolites. According to Wanjogu et al. (2006) these uplands have a very gently to gently undulating relief with slopes of between 1 and 5%. Soils are well drained, very deep, dark reddish brown to dark brown, very friable to friable, gravelly clay loam to clay. The colour of the topsoil is very dark greyish brown while that of the subsoil is dark reddish brown to dark brown. Topsoil interms of structure range from weak to moderate, fine to medium, crumby to weak, medium, subangular blocky. The structure of the subsoil ranges from weak, very fine to medium, subangular blocky in the upper part to porous massive near the weathering parent material. The consistency of the topsoil is slightly hard to hard when dry, friable when moist, sticky and plastic when wet while that of the subsoil is slightly hard when dry, very friable to friable when moist, slightly sticky to sticky and slightly plastic to plastic when wet. The texture of the topsoil is clay loam to clay and that of the subsoil is gravelly clay loam to clay. The soils are highly weathered. The soils indicate high erodibility and are thus susceptible to surface sealing and crusting due to occurrence of weak to moderate, 1-2 cm thick crusts on the soil surface. A compact plough pan occurs between 15-45 cm depth as a result of continuous ploughing using a tractor or oxen-plough. The soils are classified as Haplic Ferralsols.

**Germplasm, environmental layout and trial management**

Germplasm was obtained from different countries, regions and it consisted of 314 lines from CIAT Columbia, 75 lines from AfricaRice Centre and the local check *Dourado precoce*. The four experimental environments were blocks that had no P and N applied (N-&P-), P applied only (N-P+), N applied only (N+P-) and both N and P applied (N+P+). The source of N and P were inorganic fertilizers calcium ammonium nitrate (CAN) and triple super phosphate (TSP-(CaHPO4)-32.5%) respectively. The P and N were applied as basal applications in the designated block at the rate of 60 kg P ha-1 and 90 kg N ha-1. The P was applied as basal during sowing to ensure due to its immobility, it get mixed with soil and thus close to root zone for good root development for robust plant health. Nitrogen was applied in two splits each 45 kg N ha-1 at maximum tillering and at booting stage. The soil was sampled in the 0 to 30 cm topsoil layer from the experimental blocks. The sampling was in both diagonals at the four corners of the block, at the middle, between the corners, and between the middle of diagonals and corners making a total of 17 samples. These samples were analyzed separately and since they had almost the same values, these were composed and averaged. The soil analysis was carried out at JomoKenyatta University of Agriculture and Technology (JKCUAT) and had the properties indicated in Table 1.

The three hundred and ninety accessions were planted in an alpha lattice design arrangement as 30 x 13 replicated twice on 29th November 2007. Inorganic fertilizer was applied to the block, while genotypes were sown in the block. The experimental plot was 0.75 m2 consisting of a population of 34 plants. The row to row and plant to plant spacing was 15 cm. Two seeds were sown per hill and later thinned to one. Normal cultural practices like thinning, weeding, undertaking supplementary irrigation, spraying against sucking pests, birds scaring and harvesting were carried out manually.

**Data collection**

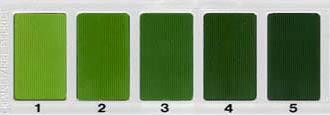
Data collection followed the established standards for rice (IRRI, 2002) on the following traits; days to heading (days), days to anthesis (flowering) (days), P tolerance (scale, 1 to 5), N tolerance (scale, 1 to 5), plant height (cm), top biomass (g), number of panicles for 10 plants (absolute numbers), days to maturity (days), 1000 grain wt (g), and grain weight ha-1 (kg). The nitrogen tolerance scale of 1 to 5 was used to measure leaf colour intensity which is a good indicator of leaf N status (Shukla et al., 2004) (Figure 1). The value on leaf colour chart (LCC) that matched the leaf colour was recorded and if the leaf colour fell between two LCC shades, the mean value was calculated and adpted. This is non-destructive method and readings were taken under the shade to shield the sunlight for correct colour readings. Plants that were N tolerant (had quality green leaf colour) were given a score of one (but in LCC its 5) and those that were least tolerant (looked more yellowish) were given a score of five (but in LCC its 1).

The P tolerant scale was developed based on the following visual parameters of P deficiency that include; stunted growth, dull-green or blue-green colour, possible purple coloration on some part of the plant, reduced flowering, delayed maturity, leaf tips look burnt, followed by older leaves turning into a dark green, and reddish-purple colour. The most P tolerant plants were rated one and these had normal vigorous and robust growth without deficiency symptoms, while the least tolerant ones were rated five and these had high rate of deficiency symptoms.

For the agronomic traits, ten plants were randomly selected for data collection and the early maturing lines were tagged using different colour code of the netting string, one colour per week for three weeks. The top biomass was taken from an area of 0.75 m2 in grams (g) by cutting the culms at the ground level with a sickle. The harvested culms without panicles were dried to constant moisture (14% MC) and then weighed and data recorded. Plant height was measured from soil surface to the tip of the tallest panicle (awns excluded) (IRRI, 2002). Days to maturity were counted as number of days from seeding to grain ripening when over 85% of the spikelets turned golden yellow or brown and white for some lines. One thousand seeds were counted with a grain counter and weighed at 14% moisture content using a precision scale. The yield was weighed as unhulled grains (paddy) harvested from an area of 0.75 m2 and then converted into kg ha-1 at 14% moisture content.

**Table 1.** Soil properties at KARI Mwea-Tebere location indicating the soil characteristics.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Parameter** | **Value** | **High** | **Medium** | **Low** | **Very low** |
| pH1:1 | 5.53 |  |  |  |  |
| ECe (Electrical conductivity) | 0.11 |  |  |  |  |
| % N | 0.16 | > 0.25 | 0.12 - 0.25 | 0.05 - 0.12 | < 0.05 |
| Available P (ppm) | 1.35 | > 18 | 10 - 17 | 5 - 9 | < 5 |
| Extractable-Zn (ppm) | 1.65 |  |  |  |  |
| Extractable-Cu (ppm) | 8.52 |  |  |  |  |
| Extractable-Mn (ppm) | 360 |  |  |  |  |
| Extractable-Fe (ppm) | 379 |  |  |  |  |



**Figure 1.** A leaf colour chart used to evaluate genotypes for nitrogen tolerance.

**Data analysis**

The analysis of variance (ANOVA) was performed according to Gomez and Gomez (1884) using GenStat statistical package version 12 (Payne et al., 2009). The statistical model was Yijk = μ + αi +βj +εk +αεik +Єijk; where the term Yijk is the observed value of ith genotype (I = 1 to 390) in jth replicate (j=1 to 2) for the kth experimental environment, μ is the grand mean of the variable; αi is the treatment effect for the ith genotype, βj is the block effect for jth block; εk is the experimental effect for the kth experimental environment, αεik is the interaction term of ith genotype in kth experimental environment and Єijk is the random error associated with the Yijk experimental unit.

The genetic variances for the various traits were calculated following the method of Johnson et al. (1955) and Karim et al. (2007). Genetic parameters were calculated as follows:

1. Genetic variance (Vg) = (genotypic mean squares – error mean squares)/number of replicates.
2. Phenotypic variance (Vp) = genotypic mean squares + error mean squares.
3. The genotypic coefficient of variation (CVG) = (√vg/grand mean)\*100.
4. Genetic advance (GA) estimates = (√Vp\*H2)\*k; where k = 2.06 and it is the selection differential expressed in standard deviations (Karim et al., 2007), that assumed that 5% of the individual plants were selected from the population (Kearsey and Pooni, 1996).

**Table 2.** Mean squares and genetic parameters for ten rice traits across the four soil experimental environments.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Traits** |  | **Days to heading (days)** | **Days to anthesis (days)** | **Phosphorous tolerance (scale 1-5)** | **Nitrogen tolerance (scale 1-5)** | **Plant height (cm)** | **Top biomass**  **(g)** | **Number of panicles (numbers)** | **Days to maturity (day)** | **1000 grain weight**  **(g)** | **Yield (kg ha-1)** |
| Source | DF |  |  |  |  |  |  |  |  |  |  |
| Replication | 1 | 752.6 | 435 | 4.313 | 86.0013 | 5215.5 | 169945 | 37773 | 435 | 183.51 | 9483000.0 |
| Genotype | 389 | 507\*\*\* | 494.1\*\*\* | 1.469\*\*\* | 1.959\*\*\* | 454.6\*\*\* | 1002130\*\*\* | 3989\*\*\* | 494.1\*\*\* | 57.25\*\*\* | 4346000\*\*\* |
| Experimental environment | 3 | 20595.9\*\*\* | 18058.2\*\*\* | 138.066\*\*\* | 74.7436\*\*\* | 3481.9\*\*\* | 1674391\*\*\* | 39612\*\*\* | 18058.2\*\*\* | 5022.78\*\*\* | 17000000\*\*\* |
| Genotype experimental environment | 1167 | 216.1\*\*\* | 214.6\*\*\* | 1.028ns | 0.702ns | 133.4ns | 181403\*\*\* | 960 | 214.6\*\*\* | 31.21ns | 1305000ns |
| Residual | 1559 | 178.4 | 174.7 | 1.119 | 0.6902 | 133.7 | 157061 | 1051 | 174.7 | 40.24 | 1173000.0 |
| Mean |  | 132.4 | 137.5 | 2.0 | 3.1 | 81.5 | 674.1 | 54.5 | 180.5 | 16.4 | 3639.0 |
| Genotypic variance (Vg) |  | 164.3 | 159.7 | 0.2 | 0.6 | 160.5 | 422534.5 | 1469.0 | 159.7 | 8.5 | 1586500.0 |
| Phenotypic variance (Vp) |  | 685.4 | 668.8 | 2.6 | 2.6 | 588.3 | 1159191.0 | 5040.0 | 668.8 | 97.5 | 5519000.0 |
| Coeficient of variation of genotypes (CVG) |  | 17.0 | 16.2 | 60.6 | 45.5 | 26.2 | 148.5 | 115.9 | 12.3 | 46.1 | 57.3 |
| Coeficient of variation of phenotypes (CVP) |  | 19.8 | 18.8 | 80.5 | 52.9 | 29.8 | 159.7 | 130.3 | 14.3 | 60.2 | 64.6 |
| Broadsense heritability (H2) |  | 23.9 | 23.9 | 6.8 | 23.9 | 27.3 | 36.5 | 29.1 | 23.9 | 8.7 | 28.7 |
| Genetic advance (GA) |  | 10.4 | 10.3 | 0.2 | 0.6 | 10.7 | 592.5 | 33.0 | 10.3 | 1.6 | 1080.5 |
| Genetic advance as % of mean (GAM) |  | 7.9 | 7.5 | 10.5 | 21.1 | 13.1 | 87.9 | 60.6 | 5.7 | 10.0 | 29.7 |

\*\*\*Significant at p < 0.001, ns Non significant at p < 0.05.

(vii) The percent genetic advance of the mean (GAM) = (GA/grand mean)\*100.

# RESULTS

## Genetic components

The results of analysis of variance components showed that genotypic differences were very highly significant (p < 0.001) for all the traits stu- died. This was also the case with experimental environments (Table 2). However, the interaction of genotypes by environments was not significant (p>0.05) except for days to heading (DH), days to anthesis (DA), top biomass (TB) and days to maturity (DM).

The lowest Vg was for phosphorous tolerance (PT) and the highest for yield and this was also

the case for Vp, except that nitrogen tolerance (NT) had the same Vp (Table 2). The CVG was lowest for days to maturity and highest for top biomass (TB), this was the same case for CVP. The ranges for CVG and CVP were 12.3 to 148.5 and 14.3 to 159.7%, respectively. Broad sense heritability (H2) estimates were highest for TB (36.5%) and lowest for PT (6.8%). The days to heading, days to anthesis, days to maturity and NT had a H2 value of 23.9%. The genetic advance (GA) had the lowest value for phosphorous tolerance (PT) of 0.2 but the value was large for yield at 1080.5. The genetic advance as a percentage of mean (GAM) was lowest for days to maturity (DM) but highest for top biomass (TB). The values for H2, GA and GAM were generally low except for top biomass and yield.

## Genotypic performance under the four field experimental environments

Different genotypes performed differently and their ranks varied under the four experimental environ- ments. The earliest line to head was 39 (Caiapo) under N-P+ fertility condition (Table 3). It was the earliest in the other soil N and P fertility conditions except under N-P-. Some genotypes however, were poorly adapted like 272 (CT16345-CA-12-M) and 303 (CT16350-CA-27-M) which headed in 167 and 160 days, respectively.

Two lines 362 (WAB 450-I-B-P-38-HB – NERICA1) and 96 (CT16317-CA-4-M) were selected as parents for crossing block appeared among the top ten in days to heading, anthesis and maturity. Caiapo (39) still was the earliest in days to anthesis at 73 days under the N-P+ condition. The genotypes ranked differently for days to heading, anthesis and maturity. Two parents 362 (WAB 450-I-B-P-38-HB) and 96 (CT16317-CA-4-M) appeared among the top ten best genotypes. Line 272 (CT16345-CA-12-M) had its anthesis period being the latest at 172 days under N+P+. The earliest line 39 (Caiapo) matured in 116 days under N-P+ experimental condition, but under N+P- it flowered in 136 days but still the earliest under this condition. The top ten lines in maturity displayed change of ranks under the four fertility conditions. Line 272 (CT16345-CA-12-M) matured latest in 215 days under N+P+ condition. Line 159 (CT16329-CA-10-M) ranked top for number of panicles for 10 plants with 150 and 178 panicles under N+P- and N+P+ fertility conditions, respectively. However, it did not appear among top ten under N-P- and N-P+ conditions, where line 242 (CT16340-CA-13-M) and 225 (CT16337-CA-7-M) were ranked at the top, respectively. Line 17 (ARCCU3Fa12-L 11 P82-HB) had the lowest number of panicles.

Line 6 (ARCCU1 Fa5-L4P1-HB) was ranked among the top 3 under N-P- and N-P+ fertility condition, while two lines, 96 (CT16317-CA-4-M) and 195 (CT16333(2)-CA-18-M) were among the top ten in phosphorous tolerance under N+P- and N+P+ fertility conditions (Table 4). Line 168 (CT16330(1)-CA-2-M) was the worst in terms of phosphorous tolerance under N-P- fertility condition. Line 170 (CT16330(1)-CA-4-M) had consistent nitrogen tolerance except under N-P+ where it was not among the top ten lines. Lines 6 (ARCCU1 Fa5-L4P1-HB) and 167 (CT16330(1)-CA-15-M) showed consistent performance by appearing top ten under N-P+ and N+P- fertility con- ditions. Line 27 (ARCCU3Fa3-L7P1-HB) consistently dis- played superior nitrogen tolerance ranking top under N+P+ and top three under N-P+ and N+P- experimental conditions. However, there was great variability in nitro- gen tolerance as indicated by varied genotypes appea- rance or rankings for both top 10 best and worst cases. Lines 39 (Caiapo) and 267 (CT16344-CA-3-M) had the worst nitrogen tolerance under N-P+ fertility condition. The 1000 seed weight had extreme variability in that no single line appeared to be consistent in performance across the four fertility experimental conditions (Table 4). Only one parent 76 (CT16313-CA-19-M) appeared among the top ten lines for best performers under N+P- condition. Line 362 (WAB 450-I-B-P-38-HB-NERICA1) appeared among the worst performers under soil N+P+ environmental

condition.

Lines 182 (CT16333(1)-CA-20-M) and 76 (CT16313-CA-

19-M) selected as parents were among the best ten yielders under N-P- and N-P+ fertility condition. Line 222 (CT16337-CA-3-M) was ranked top under N+P- and also appeared among the best ten under N+P+ fertility environments. Line 360 (WAB 450-I-B-P-20-HB) ranked number 3 under N-P+ and N+P+ fertility conditions thus showing some consistency. This was also the case for line 378 (WAB 905-B-4A 1.1). Line 370 had superior performance under N-P- and N+P+ experimental fertility environments thus indicating adaptability and responsiveness to fertility environments. Line 39 (Caiapo) and 314 (CT16350-CA-7-M) had poor performance, especially for Caiapo that was early maturing and thus used as parent for its earliness to be introgressed into the segregating progenies.

The plant height had varied performance under the four soil fertility conditions with many of the lines not showing consistency (Table 5). The line 76 (CT16313-CA-19-M) that was selected as parent appeared among the top ten lines under N+P- soil fertility condition. Line 221 (CT16337-CA-3-M) had consistency in its performance under N+P- and N+P+ soil fertility condition, a case displayed by line 175 (CT16331- CA-8-M) under N-P+ and N+P- condition. Line 195 (CT16333(2)-CA-18-M) selected as parent appeared among the worst ten in height under N+P+ condition.

Genotypes performance for plant biomass were also widely varied with line 96 (CT16317-CA-4-M) appearing among the best top ten under N+P- condition. Genotype 175 (CT16331-CA-8-M) had consistent performance under three experimental soil fertility conditions, ranking top under N-P+ and N+P+ soil conditions. The highest plant biomass (3,888.5g) was associated with line 272 (CT16345-CA-12-M) under N-P- fertility condition, which also appeared under N-P+ soil condition. The worst line was 345 (CT16356(1)-CA-7-M) having 12.5 g under N-P- soil fertility condition.

## Scatter plots and histograms for days to maturity and yield

From the display of scatter plot for yield versus days to maturity, Figure 2, line 378 (WAB 905-B-4A 1.1) was the best in terms of yield and earliness among the 25 earliest lines under N-P- soil conditions. It was followed by 368 (WAB 880-1-38-20-15-P2-HB) and 381 (WAB 919-72-4-1-HB).

Line 291 (CT16346-CA-8-M) was the most undesirable as it had low yields and very late in maturity. The scatter plot under soil N-P+ had genotypes 245 (CT16340-CA-9- M), 277 (CT16345-CA-4-M) and 364 (WAB 450-I-B-P-91-HB) being early and high yielding (Fig. 3). Genotype 74 (CT16313-CA-15-M) was the latest among the best twenty five genotypes and its yield was around the mean. Genotype 361 (WAB 450-I-B-P-28-HB) although was around the mean in maturity, it had the lowest yield. Line 340 although it was the earliest its yield potential was around the mean. Figure 4 displays the scattering of the best twenty five genotypes of which line 222 (CT16337- CA-3-M) was the highest yielding and also its maturity was below the mean. However, line 353 (*O. glaberrima*) although high yielding, it was late second to line 81 (CT16315(1)-CA-1-M) which was the second lowest in terms of yield. The earliest line was 96 (CT16317-CA-4- M) which was within the early and high yielding quadrant. Line 102 (CT16319-CA-13-M) was the lowest yielder but it was early hence not a desirable genotype. The majority of the genotypes tended to be late but were high yielding. The scatter plot of genotypes under N+P+ experimental fertility conditions by days to maturity versus yield displayed line 356 (WAB 450-11-1-P31-1-HB) as the most

**Table 3.** The mean values of DH, DA, DM and NP traits for the 10 best and worst genotypes under four environments (N-P-, N-P+, N+P- and N+P+).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Parameter** | **Days to heading (days)** | | | | | | | | **Days to maturity (days)** | | | | | | | |
| **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** |
|  | 368 | 92.5 | 39 | 68.5 | 39 | 88.0 | 39 | 76.5 | 378 | 139.5 | 39 | 116.0 | 39 | 135.5 | 39 | 126.0 |
|  | 378 | 92.5 | 362 | 83.0 | 356 | 90.0 | 355 | 90.0 | 368 | 142.0 | 362 | 129.5 | 356 | 137.5 | 355 | 136.5 |
|  | 43 | 96.0 | 356 | 93.5 | 96 | 100.0 | 374 | 95.5 | 381 | 144.0 | 285 | 142.0 | 96 | 149.5 | 374 | 144.5 |
|  | 381 | 96.5 | 285 | 94.0 | 362 | 101.5 | 356 | 98.0 | 43 | 145.0 | 356 | 142.5 | 362 | 150.0 | 356 | 148.5 |
| Top ten lines | 45 | 99.5 | 382 | 96.0 | 212 | 109.0 | 68 | 104.5 | 45 | 151.0 | 382 | 142.5 | 212 | 156.0 | 388 | 152.5 |
| 49 | 101.0 | 328 | 98.0 | 355 | 109.5 | 388 | 104.5 | 212 | 151.0 | 328 | 144.5 | 355 | 156.0 | 68 | 153.5 |
|  | 356 | 102.0 | 291 | 98.5 | 371 | 110.0 | 362 | 109.0 | 44 | 151.5 | 371 | 146.5 | 371 | 157.5 | 362 | 155.5 |
|  | 212 | 103.5 | 160 | 99.5 | 242 | 111.5 | 314 | 111.5 | 92 | 151.5 | 41 | 148.5 | 388 | 159.0 | 16 | 159.0 |
|  | 58 | 105.0 | 371 | 99.5 | 388 | 112.0 | 16 | 112.0 | 49 | 153.0 | 376 | 148.5 | 2 | 159.5 | 314 | 159.5 |
|  | 277 | 105.0 | 376 | 99.5 | 2 | 112.5 | 15 | 114.5 | 194 | 153.5 | 291 | 149.0 | 54 | 160.0 | 385 | 161.5 |
|  | 33 | 148.5 | 37 | 151.5 | 83 | 154.0 | 104 | 162.0 | 68 | 195.5 | 309 | 199.5 | 83 | 202.0 | 89 | 210.0 |
|  | 68 | 148.5 | 62 | 151.5 | 7 | 154.5 | 185 | 162.0 | 24 | 196.0 | 37 | 200.0 | 155 | 202.0 | 124 | 210.0 |
|  | 138 | 148.5 | 133 | 152.0 | 243 | 155.0 | 253 | 162.0 | 33 | 196.0 | 133 | 200.0 | 7 | 202.5 | 155 | 210.0 |
|  | 297 | 148.5 | 24 | 156.0 | 342 | 155.5 | 259 | 162.0 | 297 | 196.5 | 24 | 204.0 | 58 | 204.0 | 253 | 210.0 |
| Bottom ten lines | 307 | 149.3 | 82 | 159.0 | 58 | 156.5 | 329 | 162.0 | 32 | 197.5 | 253 | 206.5 | 342 | 204.0 | 255 | 210.0 |
| 12 | 149.5 | 196 | 159.0 | 169 | 157.0 | 86 | 162.5 | 307 | 197.5 | 82 | 207.0 | 169 | 205.0 | 259 | 210.0 |
|  | 24 | 149.5 | 253 | 159.0 | 82 | 159.0 | 89 | 162.5 | 12 | 198.5 | 332 | 207.0 | 82 | 206.0 | 329 | 210.0 |
|  | 32 | 150.0 | 294 | 159.0 | 192 | 159.0 | 186 | 162.5 | 298 | 199.0 | 303 | 207.0 | 192 | 206.5 | 104 | 210.5 |
|  | 301 | 151.5 | 387 | 159.0 | 260 | 159.0 | 255 | 163.0 | 301 | 199.0 | 196 | 207.5 | 260 | 206.5 | 186 | 210.5 |
|  | 10 | 153.0 | 303 | 159.5 | 271 | 159.0 | 272 | 166.5 | 10 | 201.5 | 387 | 207.5 | 271 | 207.5 | 272 | 215.0 |
|  | | | | | | | | | | | | | | |  | |
| Mean |  | 128.2 |  | 139.0 |  | 128.5 |  | 133.9 |  | 176.9 |  | 176.8 |  | 181.4 |  | 187.0 |
|  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  |
| Genotype | 6.68 | 13.1 |  |  |  |  |  |  | 6.61 | 13.0 |  |  |  |  |  |  |
| Experimental environment | 0.68 | 1.3 |  |  |  |  |  |  | 0.67 | 1.3 |  |  |  |  |  |  |
| Genotype\*experimental environment | 13.36 | 26.2 |  |  |  |  |  |  | 13.22 | 25.9 |  |  |  |  |  |  |
| CV% | 10.10 |  |  |  |  |  |  |  | 7.30 |  |  |  |  |  |  |  |
|  | **Days to anthesis (days)** | | | | | | | | **Number of panicles (numbers)** | | | | | | | |
|  | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** |
| Top ten lines | 378 | 96.5 | 39 | 73.0 | 39 | 92.5 | 39 | 83.0 | 242 | 133.0 | 225 | 263.0 | 159 | 149.5 | 159 | 177.5 |
| 368 | 99.0 | 362 | 86.5 | 356 | 94.5 | 355 | 93.5 | 69 | 121.5 | 157 | 215.5 | 341 | 142.5 | 54 | 155.0 |
| 381 | 101.0 | 285 | 99.0 | 96 | 106.5 | 374 | 101.5 | 212 | 119.0 | 106 | 175.0 | 328 | 142.0 | 357 | 145.0 |
| 43 | 102.0 | 356 | 99.5 | 362 | 107.0 | 356 | 105.5 | 223 | 118.5 | 54 | 172.0 | 96 | 141.5 | 74 | 126.0 |

**Table 3.** Contd.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Bottom ten lines | 45 | 108.0 | 382 | 99.5 | 212 | 113.0 | 388 | 109.5 | 214 | 114.0 | 352 | 172.0 | 50 | 136.5 | 136 | 124.0 |
| 212 | 108.0 | 328 | 101.5 | 355 | 113.0 | 68 | 110.5 | 54 | 113.5 | 281 | 164.0 | 212 | 128.5 | 79 | 121.0 |
| 44 | 108.5 | 371 | 103.5 | 371 | 114.5 | 362 | 112.5 |  | 112.5 | 328 | 158.0 | 254 | 127.5 | 78 | 120.5 |
| 92 | 108.5 | 41 | 105.5 | 388 | 116.0 | 16 | 116.0 | 185 | 110.5 | 336 | 146.0 | 54 | 126.5 | 354 | 120.0 |
| 49 | 110.0 | 376 | 105.5 | 2 | 116.5 | 314 | 116.5 | 211 | 108.5 | 212 | 144.5 | 205 | 117.5 | 222 | 119.5 |
| 194 | 110.5 | 291 | 106.0 | 54 | 117.0 | 385 | 118.5 | 292 | 107.0 | 239 | 139.0 | 140 | 116.0 | 96 | 119.0 |
| 68 | 152.5 | 309 | 156.5 | 83 | 159.0 | 89 | 167.0 | 28 | 7.0 | 14 | 23.5 | 129 | 11.5 | 19 | 11.0 |
| 24 | 153.0 | 15 | 157.0 | 155 | 159.0 | 124 | 167.0 | 33 | 7.0 | 167 | 27.0 | 180 | 11.5 | 32 | 10.0 |
| 33 | 153.0 | 133 | 157.0 | 7 | 159.5 | 155 | 167.0 | 18 | 6.5 | 180 | 16.5 | 275 | 11.5 | 4 | 9.5 |
| 294 | 153.5 | 24 | 161.0 | 58 | 161.0 | 253 | 167.0 | 20 | 6.5 | 338 | 16.0 | 11 | 11.0 | 26 | 9.0 |
| 32 | 154.5 | 253 | 163.5 | 342 | 161.0 | 255 | 167.0 | 24 | 6.5 | 307 | 25.0 | 344 | 10.5 | 37 | 9.0 |
| 307 | 154.5 | 82 | 164.0 | 169 | 162.0 | 259 | 167.0 | 5 | 6.0 | 310 | 12.5 | 20 | 9.5 | 1 | 6.0 |
| 12 | 155.5 | 294 | 164.0 | 82 | 163.0 | 329 | 167.0 | 11 | 6.0 | 13 | 13.0 | 24 | 9.0 | 8 | 6.0 |
| 298 | 156.0 | 303 | 164.0 | 192 | 163.5 | 104 | 167.5 | 17 | 6.0 | 18 | 6.5 | 38 | 8.5 | 17 | 6.0 |
| 301 | 156.0 | 196 | 164.5 | 260 | 163.5 | 186 | 167.5 | 12 | 5.0 | 12 | 5.0 | 25 | 4.5 | 18 | 6.0 |
| 10 | 158.5 | 387 | 164.5 | 271 | 164.5 | 272 | 172.0 | 32 | 4.0 | 177 | 15.5 | 17 | 3.5 | 28 | 4.5 |
|  | | | | | | | | | | |  | | | | | |
| Mean |  | 133.9 |  | 133.8 |  | 138.4 |  | 144.0 |  | 51.8 |  | 65.1 |  | 51.3 |  | 49.8 |
|  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  |
| Genotype | 6.61 | 13.0 |  |  |  |  |  |  | 16.21 | 31.8 |  |  |  |  |  |  |
| Experimental environment | 0.67 | 1.3 |  |  |  |  |  |  | 1.64 | 3.2 |  |  |  |  |  |  |
| Genotype\*experimental environment | 13.22 | 25.9 |  |  |  |  |  |  | 32.42 | 63.6 |  |  |  |  |  |  |
| CV% | 9.60 |  |  |  |  |  |  |  | 59.50 |  |  |  |  |  |  |  |

desirable (Figure 5). Line 39 (Caiapo) although it was early it had low yields a case observed also for line 355 (WAB 450-11-1-1-P41-HB).

## The scattering pattern of the 25 best rice genotypes for grain yield against different soil N and P fertility conditions

When the genotypes were displayed in a scatter plot for yield versus soil nitrogen (N) and phosphorous (P) level, majority of the twenty five lines were skewed towards less N tolerance two quadrants (Figure 6). The best genotype was 151 (CT16328-CA-18- M) because it was the highest yielding and tolerant, although it was not the most tolerant. The most tolerant lines were 340 (CT16355-CA-9-M), 7 (ARCCU1Fa1-L4P3-HB), 260 (CT16342-CA-4-M) and 251 (CT16342-CA-13-M), but these were below the mean yield. The least favourable genotype was 382 (WAB 952-B-47AB.1) as it was least tolerant and had the lowest yield among the group. The majority of the lines scattered towards the left showing more tolerance under soil N-P+ condition (Figure 7). The best genotype was 277 (CT16345-CA-4-M) although line 245 (CT16340- CA-9-M) had the highest yield, it was less tolerant than 277. Lines 255 (CT16342-CA-2-M) and 361 (WAB 450-I-B-P-28-HB) were the least adapted in terms of yield but were tolerant. The best tolerant lines had yields just slightly above the mean yield. The best adapted lines were 222 (CT16337-CA-3- M) and 29 (ARCCU3Fa6-L3P9) in terms of both yield and tolerance, but they were at the

**Table 4.** The mean values of PT, NT, 1000 SDWT and yield traits for the 10 best and worst genotypes under four environments (N-P-, N-P+, N+P- and N+P+).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Parameter Phosphorous tolerance (scale 1-5)** | | | | | | | | | **Nitrogen tolerance (scale 1-5)** | | | | | | | |
|  | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** |
|  | 3 | 1.0 | 2 | 1.0 | 14 | 1.0 | 21 | 1.0 | 12 | 1.0 | 6 | 1 | 3 | 1 | 27 | 1 |
|  | 4 | 1.0 | 5 | 1.0 | 91 | 1.0 | 27 | 1.0 | 32 | 1.0 | 20 | 1 | 6 | 1 | 303 | 1 |
|  | 6 | 1.0 | 6 | 1.0 | 96 | 1.0 | 40 | 1.0 | 68 | 1.0 | 27 | 1 | 27 | 1 | 21 | 1 |
|  | 7 | 1.0 | 8 | 1.0 | 98 | 1.0 | 47 | 1.0 | 170 | 1.0 | 30 | 1 | 167 | 1 | 316 | 1 |
| Top ten lines | 8 | 1.0 | 9 | 1.0 | 99 | 1.0 | 118 | 1.0 | 177 | 1.0 | 167 | 1 | 170 | 1 | 170 | 1.5 |
| 9 | 1.0 | 14 | 1.0 | 100 | 1.0 | 121 | 1.0 | 180 | 1.0 | 307 | 1 | 247 | 1 | 247 | 1.5 |
|  | 15 | 1.0 | 17 | 1.0 | 113 | 1.0 | 187 | 1.0 | 352 | 1.0 | 13 | 1.5 | 250 | 1 | 282 | 1.5 |
|  | 16 | 1.0 | 18 | 1.0 | 116 | 1.0 | 195 | 1.0 | 1 | 1.5 | 272 | 1.5 | 256 | 1 | 300 | 1.5 |
|  | 22 | 1.0 | 19 | 1.0 | 117 | 1.0 | 245 | 1.0 | 3 | 1.5 | 280 | 1.5 | 282 | 1 | 332 | 1.5 |
|  | 29 | 1.0 | 20 | 1.0 | 122 | 1.0 | 315 | 1.0 | 4 | 1.5 | 294 | 1.5 | 294 | 1 | 338 | 1.5 |
|  | 247 | 4.0 | 339 | 3.5 | 189 | 3.0 | 10 | 4.5 | 381 | 3.5 | 380 | 4 | 316 | 4 | 13 | 4.5 |
|  | 288 | 4.0 | 348 | 3.5 | 196 | 3.0 | 39 | 4.5 | 383 | 3.5 | 384 | 4 | 322 | 4 | 16 | 4.5 |
|  | 299 | 4.0 | 352 | 3.5 | 259 | 3.0 | 77 | 4.5 | 388 | 3.5 | 386 | 4 | 327 | 4 | 60 | 4.5 |
|  | 345 | 4.0 | 357 | 3.5 | 268 | 3.0 | 79 | 4.5 | 213 | 4.0 | 107 | 4.5 | 333 | 4 | 197 | 4.5 |
| Bottom ten lines | 362 | 4.0 | 362 | 3.5 | 298 | 3.0 | 216 | 4.5 | 238 | 4.0 | 150 | 4.5 | 335 | 4 | 355 | 4.5 |
| 374 | 4.0 | 15 | 4.0 | 312 | 3.0 | 268 | 4.5 | 240 | 4.0 | 263 | 4.5 | 340 | 4 | 75 | 4.5 |
|  | 270 | 4.5 | 75 | 4.0 | 314 | 3.0 | 270 | 4.5 | 283 | 4.0 | 301 | 4.5 | 344 | 4 | 270 | 4.5 |
|  | 300 | 4.5 | 249 | 4.0 | 28 | 3.5 | 332 | 4.5 | 291 | 4.0 | 358 | 4.5 | 343 | 4.5 | 281 | 4.5 |
|  | 375 | 4.5 | 263 | 4.0 | 34 | 3.5 | 375 | 4.5 | 342 | 4.0 | 267 | 5 | 240 | 5 | 42 | 5 |
|  | 168 | 5.0 | 346 | 4.0 | 352 | 3.5 | 379 | 4.5 | 382 | 4.0 | 39 | 5 | 39 | 4.5 | 39 | 4.5 |
|  | | | | | | | | |  | | | | | | | |
| Mean |  | 1.9 |  | 1.8 |  | 1.7 |  | 2.6 |  | 2.7 |  | 3.391 |  | 3.058 |  | 3.199 |
|  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  |
| Genotype | 0.529 | 1.0 |  |  |  |  |  |  | 0.42 | 0.8 |  |  |  |  |  |  |
| Experimental environment | 0.054 | 0.1 |  |  |  |  |  |  | 0.04 | 0.1 |  |  |  |  |  |  |
| Genotype\*experimental environment | 1.058 | 2.1 |  |  |  |  |  |  | 0.83 | 1.6 |  |  |  |  |  |  |
| CV% | 52.900 |  |  |  |  |  |  |  | 27.00 |  |  |  |  |  |  |  |
| **1000 seed weight (g)** | | | | | | | | | **Yield (kgha-1)** | | | | | | | |
|  | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** |
|  | 163 | 27.9 | 55 | 25.8 | 325 | 28.9 | 140 | 29.2 | 151 | 5916.0 | 245 | 4948.0 | 222 | 4967.0 | 370 | 4970.0 |
| Top ten lines | 238 | 26.8 | 330 | 25.7 | 76 | 28.1 | 370 | 29.0 | 370 | 5911.0 | 277 | 4939.0 | 19 | 4964.0 | 251 | 4954.0 |
| 171 | 26.4 | 16 | 24.8 | 138 | 27.3 | 23 | 27.8 | 259 | 5904.0 | 360 | 4916.0 | 29 | 4944.0 | 360 | 4940.0 |
|  | 165 | 26.2 | 165 | 24.5 | 54 | 27.1 | 29 | 27.7 | 253 | 5884.0 | 364 | 4912.0 | 54 | 4944.0 | 378 | 4937.0 |

**Table 4.** Contd.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Bottom ten lines | 126 | 25.9 | 38 | 24.3 | 279 | 26.6 | 384 | 27.5 | 163 | 5877.0 | 55 | 4902.0 | 378 | 4943.0 | 387 | 4936.0 |
| 385 | 25.7 | 153 | 23.6 | 249 | 26.4 | 119 | 27.5 | 354 | 5875.0 | 76 | 4892.0 | 181 | 4936.0 | 212 | 4933.0 |
| 372 | 25.2 | 186 | 22.9 | 175 | 26.1 | 259 | 27.4 | 74 | 5871.0 | 134 | 4867.0 | 353 | 4934.0 | 222 | 4927.0 |
| 9 | 25.0 | 289 | 22.9 | 380 | 25.9 | 163 | 27.4 | 182 | 5869.0 | 293 | 4852.0 | 273 | 4930.0 | 186 | 4925.0 |
| 383 | 24.3 | 385 | 22.8 | 351 | 25.9 | 236 | 27.3 | 77 | 5864.0 | 63 | 4848.0 | 104 | 4922.0 | 353 | 4925.0 |
| 307 | 24.3 | 191 | 22.4 | 388 | 25.8 | 151 | 27.2 | 54 | 5862.0 | 127 | 4847.0 | 117 | 4918.0 | 141 | 4921.0 |
| 344 | 6.3 | 363 | 5.5 | 39 | 7.1 | 347 | 12.9 | 125 | 990.0 | 363 | 1480.0 | 129 | 1757.0 | 179 | 1560.0 |
| 218 | 6.0 | 291 | 5.5 | 87 | 7.0 | 362 | 12.9 | 270 | 984.0 | 180 | 1471.0 | 339 | 1753.0 | 247 | 1517.0 |
| 243 | 6.0 | 314 | 5.4 | 134 | 6.9 | 101 | 12.8 | 152 | 949.0 | 257 | 1457.0 | 313 | 1750.0 | 324 | 1500.0 |
| 390 | 5.9 | 105 | 5.4 | 209 | 6.8 | 125 | 12.6 | 363 | 948.0 | 216 | 1410.0 | 85 | 1725.0 | 124 | 1450.0 |
| 346 | 5.7 | 274 | 5.2 | 83 | 6.6 | 43 | 12.5 | 263 | 914.0 | 264 | 1407.0 | 267 | 1725.0 | 203 | 1413.0 |
| 61 | 5.6 | 124 | 4.8 | 269 | 6.5 | 176 | 12.4 | 168 | 912.0 | 291 | 1350.0 | 270 | 1700.0 | 10 | 1400.0 |
| 168 | 5.3 | 344 | 4.6 | 198 | 6.5 | 246 | 12.2 | 225 | 848.0 | 270 | 1300.0 | 216 | 1635.0 | 320 | 1234.0 |
| 92 | 5.3 | 229 | 4.2 | 45 | 6.1 | 320 | 11.8 | 344 | 715.0 | 310 | 1200.0 | 363 | 1471.0 | 75 | 1114.0 |
| 177 | 4.9 | 292 | 4.1 | 141 | 5.5 | 187 | 11.5 | 345 | 549.0 | 249 | 1020.0 | 218 | 1150.0 | 263 | 1065.0 |
| 263 | 3.8 | 100 | 4.0 | 246 | 5.0 | 261 | 10.2 | 314 | 509.0 | 301 | 850.0 | 269 | 800.0 | 39 | 567.0 |
|  | | | | | | | | | | | | | | | | |
| Mean |  | 14.7 |  | 14.2 |  | 17.1 |  | 19.7 |  | 3828.0 |  | 3676.0 |  | 3491.0 |  | 3559.0 |
|  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  |
| Genotype | 3.17 | 6.2 |  |  |  |  |  |  | 541.40 | 1062.0 |  |  |  |  |  |  |
| Experimental environment | 0.32 | 0.6 |  |  |  |  |  |  | 54.80 | 107.6 |  |  |  |  |  |  |
| Genotype\*experimental environment | 6.34 | 12.4 |  |  |  |  |  |  | 1082.80 | 2124.0 |  |  |  |  |  |  |
| CV% | 38.70 |  |  |  |  |  |  |  | 29.80 |  |  |  |  |  |  |  |

demarcation line for tolerance (Figure 8). The least adapted lines were 102 (CT16319-CA-13-M) and 81 (CT16315(1)-CA-1-M) because they were low yielding although tolerant to soil N and P condition. The majority of the lines were at the medium tolerance line but many were above the mean yield. The best line 370 (WAB 880-1-38-20- 28-P1 HB) in terms of yield was less adapted to soil N and P condition, while the best tolerant lines 94 (CT16316-CA-8-M), 342 (CT16356(1)-CA-2-M) and 334 (CT16355-CA-15-M) had yields below the average (Figure 9). The majority of the lines congregated towards high yielding but less tolerant and low yielding but more tolerant quadrants.

# DISCUSSION

The germplasm under study showed wide genetic variability for all the traits studied partly because these were accessions from diverse origins. Majority of the germplasm was also well adapted to the local conditions and this might have been contributed by the use of *Oryza glaberrima* as a parent in the development of some of these materials. This species is native to western Africa and is known to be tolerant to a wide range of both abiotic and biotic factors (Sarla and Swamy, 2005; WARDA, 2006). The H2, GA and GAM had positive values indicating that breeding for the traits is feasible (Karim et al., 2007).

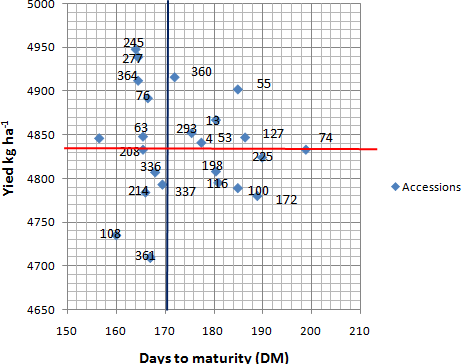
It means that selection of the parents with the desirable traits of interest (as guided by genotypic variance) to farmers and use of these in

**Table 5.** The mean values of plant height and top biomass traits for the 10 best and worst genotypes under four environments (N-P-, N-P+, N+P- and N+P+).

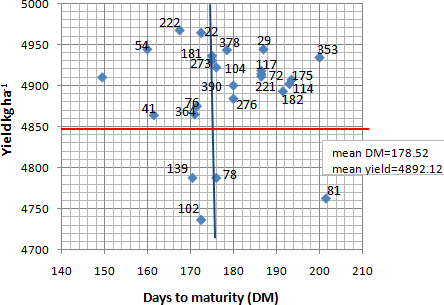
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Parameter** | **Plant height (cm)** | | | | | | | | **Top biomass (g)** | | | | | | | |
| **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** | **Lines** | **N-P-** | **Lines** | **N-P+** | **Lines** | **N+P-** | **Lines** | **N+P+** |
|  | 77 | 107.5 | 272 | 110.9 | 175 | 114.7 | 221 | 115.2 | 272 | 3888.5 | 175 | 3088.5 | 254 | 2690.0 | 175 | 2495.0 |
|  | 34 | 103.4 | 175 | 106.8 | 254 | 112.1 | 259 | 112.9 | 259 | 2406.5 | 272 | 2882.0 | 341 | 2616.0 | 159 | 2378.0 |
|  | 74 | 101.3 | 289 | 105.9 | 337 | 110 | 176 | 112.8 | 254 | 2271.5 | 54 | 2810.5 | 175 | 2582.0 | 149 | 2154.5 |
|  | 171 | 99.4 | 269 | 105.5 | 119 | 109.1 | 116 | 110.2 | 131 | 2249.0 | 159 | 2121.0 | 159 | 2490.5 | 221 | 1867.0 |
| Top ten lines | 319 | 97.8 | 94 | 103.5 | 272 | 108.7 | 78 | 109.4 | 341 | 2170.0 | 176 | 2093.0 | 96 | 2349.5 | 167 | 1842.8 |
| 88 | 96.7 | 254 | 103.0 | 76 | 108.6 | 226 | 108.2 | 54 | 2075.0 | 212 | 2024.5 | 94 | 2346.4 | 142 | 1842.0 |
|  | 134 | 96.7 | 335 | 102.6 | 221 | 106.9 | 285 | 107.9 | 74 | 2031.0 | 277 | 1999.5 | 372 | 2106.5 | 255 | 1823.5 |
|  | 89 | 96.2 | 22 | 102.5 | 342 | 105.4 | 80 | 107.7 | 242 | 2031.0 | 341 | 1965.0 | 50 | 2049.5 | 170 | 1815.5 |
|  | 272 | 95.6 | 91 | 102.5 | 183 | 103.7 | 142 | 107.1 | 212 | 1810.5 | 148 | 1916.0 | 54 | 2004.5 | 254 | 1617.0 |
|  | 155 | 95.2 | 63 | 101.6 | 336 | 102.6 | 62 | 107.0 | 305 | 1750.5 | 254 | 1901.5 | 63 | 1973.0 | 166 | 1598.0 |
|  | 362 | 62.4 | 185 | 86.0 | 321 | 62 | 173 | 58.2 | 31 | 50.5 | 3 | 124.5 | 297 | 146.5 | 32 | 94.5 |
|  | 33 | 62.0 | 297 | 71.5 | 216 | 61.6 | 232 | 58.0 | 310 | 50.5 | 332 | 124.0 | 130 | 144.5 | 31 | 88.5 |
|  | 36 | 61.8 | 249 | 60.9 | 320 | 57.5 | 228 | 57.8 | 330 | 45.0 | 344 | 112.5 | 352 | 142.5 | 234 | 85.5 |
|  | 190 | 61.6 | 343 | 66.6 | 345 | 57 | 195 | 57.5 | 247 | 38.0 | 180 | 112.0 | 8 | 125.5 | 97 | 72.5 |
| Bottom ten lines | 275 | 61.5 | 225 | 93.3 | 340 | 56.8 | 216 | 57.5 | 250 | 37.0 | 34 | 110.0 | 36 | 124.0 | 19 | 59.5 |
| 350 | 61.2 | 339 | 65.7 | 386 | 56.2 | 287 | 56.5 | 17 | 33.0 | 14 | 103.5 | 269 | 123.5 | 28 | 53.0 |
|  | 28 | 61.1 | 224 | 78.5 | 75 | 55.32 | 344 | 56.5 | 32 | 31.0 | 12 | 87.5 | 20 | 107.0 | 10 | 48.0 |
|  | 249 | 60.9 | 301 | 72.3 | 343 | 52 | 306 | 55.8 | 36 | 28.0 | 338 | 84.5 | 4 | 105.5 | 18 | 48.0 |
|  | 73 | 60.3 | 263 | 68.9 | 39 | 46.5 | 39 | 55.2 | 16 | 23.5 | 39 | 51.0 | 32 | 101.0 | 17 | 35.5 |
|  | 173 | 58.2 | 273 | 79.0 | 344 | 46 | 320 | 55.2 | 345 | 12.5 | 13 | 45.0 | 25 | 25.0 | 8 | 23.0 |
|  |  | | | | | | | | | | | | | | | |
| Mean |  | 78.4 |  | 82.7 |  | 82.98 |  | 81.9 |  | 674.9 |  | 719.5 |  | 691.8 |  | 610.4 |
|  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  | **s.e.d.** | **l.s.d.** |  |  |  |  |  |  |
| Genotype | 5.78 | 11.3 |  |  |  |  |  |  | 198.15 | 388.7 |  |  |  |  |  |  |
| Experimental environment | 0.59 | 1.1 |  |  |  |  |  |  | 20.07 | 39.4 |  |  |  |  |  |  |
| Genotype\*experimental environment | 11.56 | 22.7 |  |  |  |  |  |  | 396.31 | 777.4 |  |  |  |  |  |  |
| CV% | 14.20 |  |  |  |  |  |  |  | 58.80 |  |  |  |  |  |  |  |

a breeding programme can enhance traits such as drought and late stage nutrient deficiency tolerance, especially the one resulting from water stress. In rice, genotypes that have anthesis within a narrow range should be selected to reduce prolonged maturity and thus escape terminal drought. In maize, the anthesis-silking interval has been exploited to develop drought and nitrogen use efficient varieties (Bolanos and Edmeades, 1996; Gupta and O’toole 1986). Rice, although it is a self pollinated crop, the wide gap between heading and anthesis is variable and this is not a desirable trait. This heading-anthesis gap can lead to differential maturity with consequent problems such as grain shattering for the earliest panicles, grain discolouration and loss of quality due to over drying in the field and in case of late drought, materials with later anthesis may not have good grains set. Generally this gap should be between 1 to 5 days for uniform crop maturity that results in good grain quality, because crop harvesting can be done at the right physiological

**Figure 3.** Yield against days to maturity of the best rice genotypes under Soil N-P+ conditions.



**Figure 4.** Yield against days to maturity of the best rice genotypes under soil N+P- conditions.

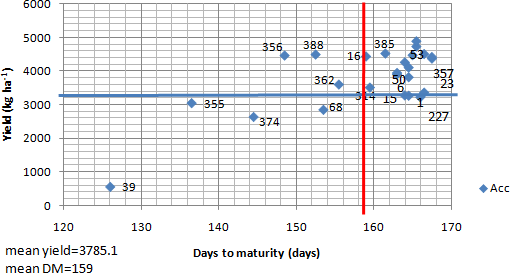


stage. The uniform maturity implies that the paddy can be harvested at closely the same MC and allow paddy to have uniform drying as opposed to wider maturity gap that results in early matured paddy cracking due to differential exposure to sunlight on different paddy sides thus encouraging differential expansion and contraction of paddy thus developing microscopic fissures that led to low head rice after milling.

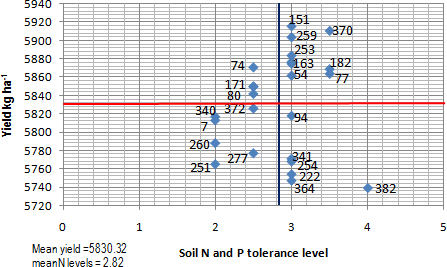
**Yield (kg ha-1)**

**Yield (kg ha-1)**

The maturity period varied greatly with a range of 116 days for 39 (Caiapo) and 140 days for 378 (WAB 905-B- 4A 1.1) and this was under N-P+ and N-P- experimental environments, respectively for earliest selected genotypes. The range of 24 days can be exploited by breeding varieties that mature early and thus escape terminal drought (Atlin et al., 2006b; Bing et al., 2005; Blum, 2000; Boonjung and Fukai, 1996).



**Figure 5.** Analysis of yield and days to maturity of the best rice genotypes under soil N+P+ conditions.



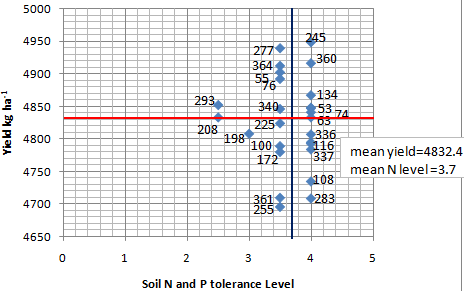
**Figure 6.** Head to head plot of the best 25 rice lines for yield versus soil N- and P- condition.

Since H2 was low at 23.9% for days to maturity, modified bulk method without selection until the materials are fairly homozygousat about F5 to F6 generation, should be emphasized as simple mass selection cannot be efficient in this case. Heritability is used to establish the expected improvement or progress after selection of genotypes from a given population (Nyquist, 1991).

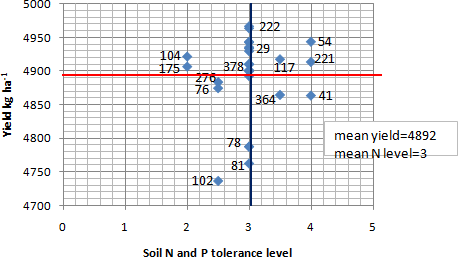
**Yield (kg ha-1)**

From the display of scatter plot of yield versus days to maturity under soil N-P- condition (Figure 2) among the best high yielding genotypes, a number of them were in the desired quadrant of high yielding and early maturing (lines 378, 212, 381 and 368). However, majority of the genotypes congregated in the high yielding but late genotypes confirming that late genotypes tend to be high yielding. The performance under soil N-P+ condition had different genotypes in the early and high yielding quadrant from those obtained under soil N-P- condition (Figure 3). Probably the reason for this behaviour is that different gene system or quantitative trait loci (QTL) are

**Figure 7.** Head to head plot of the best 25 rice lines for yield versus soil N- and P+ condition.



**Figure 8.** Head to head plot of the best 25 rice lines for yield versus soil N+ and P- condition.



**Yield (kg ha )**

operating for each of the two soils N and P conditions, thus the need to breed specific or genotypes with narrow adaptation for each soil N and P condition. The performance under soil N+P- had two genotype (76,364) occurring in the desired quadrant just as under soil N-P+ condition, but was under soil N-P+ condition. The two lines may be having the same soil environmental adaptation mechanism because the rest of the 23 genotypes were in different quadrants. The quadrant for early and high yielding lines under soil N+P+ condition (Figure 5) had different genotypes from all the other three soil condition cases. This indicates that different adaptation

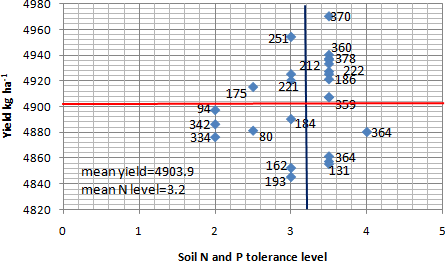
**Yield (kg ha-1)**

mechanisms are in operation for each of the four soil N and P conditions. The worst genotype was 39 as it was poorly adapted as indicated by its low yield although it was quite early. The foregoing clearly indicates the preference and need to breed different genotypes for different soil N and P conditions.

## Plant height and above ground biomass production

Farmers indicated their preference for tall plants. The top genotypes had a range of 108 to 115 cm under N-P- and

**Figure 9.** Head to head plot of the best 25 rice lines for yield versus soil N+ and P+ condition.



**Yield (kg ha-1)**

N+P- experimental soil conditions. This is in contrast to the shortest rice plants, which had a range of 46 to 79 cm under N+P- and N-P+ conditions (Table 5). This diversity can be harnessed through breeding to produce the preferred height by farmers. Farmers, in a participatory plant breeding trial, had pointed out during focus group discussion and key informants, that tall plants were easy to; harvest, a finding also observed in West Africa (Efisue et al., 2008); collect their culms and use them for livestock feed, making farm yard manure and thatching sheds. They also argued that short rice plants are normally prone to damage from flooding, splash water, rodents, ground birds and termites. They also indicated that short varieties are tiresome due to excessive bending during harvesting, cutting and threshing, views that were also found in West Africa (Efisue et al., 2008). The H2 value for this trait was 27.3% and since it is selected visually, this trait can be improved easily provided the various sources of the height and yield genes are present in the parents used for crossing (Simmonds and Smartt, 1999). This kind of materials have been observed in tongil types of rice from AfricaRice KAFACI lines that have been developed form African lines being crossed with Tongil types. Apart from high rich biomass due to broader leaves with staygreen traits, these line had high paddy yield of good quality as indicated by high head rice. The common challenge observed from these upland materials from SAGC, IRRI, BBSRC, SATREPS, AATF, KAFACI brown spot (*Cochliobolus miyabeanus* or *Bipolaris oryzae*; that affects leaves, glumes, grains, sheath plus other plant parts) was more common as they were grown under upland environment with temperatures between 16 - 360C and high relative humidity (Manibhushan, 2001; IRRI, 2024; Swaminath, 1983).

The values for TB for the top genotypes ranged from 2495 to 3889 g under N+P+ and N-P- conditions. The difference was 1394 g thus exhibiting wide variation among the genotypes for this trait. The lowest TB weight values observed for experimental environments had a range of 12.5 g under N-P- to 45 g under N-P+ condition (Table 5). Comparison of these two groups reveals that the genetic diversity for culm biomass was high. The general trend appeared to be that the CT series materials from CIAT Columbia tended to have more biomass and occupied much of the top ten (Table 5), while Africa Rice Centre germplasm (ARC and WAB series) occupied the bottom ten band. It therefore implies that the CT series materials were more adapted to varying conditions of P and N. Selection for this trait may not be difficult, since visual observation can partly be used to carry out selection and thus in a quantitative manner enhance the trait. The degree of genetic determination (H2) (Falconer and Mackay, 1996) was highest (36.5%) for TB among all the other characters, further backing up the fact that, the trait is fairly heritable and its breeding may not pose much challenge as both major and minor genes may be contributing to the trait with major genes dorminating. The genotypes that tended to have high biomass also had generally high yields indicating positive correlation, and indicating high possibility of breeding varieties that combine the two traits. The grain yield is a function of HI and biomass and therefore improvement of biomass or HI can increase paddy yield (Jianchang and Jianhua, 2023).

## The tolerance of genotypes under different soil P and N condition

The phosphorous tolerance (PT) values ranged from an overall mean of 1.703 (N+P-) and 2.62 (N+P+), while that of nitrogen tolerance (NT) was 2.7 (N-P-) and 3.391 (N- P+). Generally the top ten genotypes had a value of 1.0 for PT, but those of NT ranged from 1.0 to 1.5. This diversity in tolerance range can be utilized to develop genotypes with high nutrient use efficiency under the prevailing production environments and take advantage of applied nutrients without wastage from inability to absorb and utilize for photosynthate accumulation in the economic parts like grains, tubers and so on . This could entail breeding for narrow or specific adaptation instead of or wider adaptation (Ceccarelli, 1994; Christiansen and Lewis, 1982; Dudal, 1976; Fukai et al., 1999; Kimani and Derera, 2009; Kimani et al., 2007; Pinheiro et al., 2006; Yoji et al., 1992). The majority of the modern cultivars have been bred for high input environments, but the cost of the inputs is prohibitive to the majority of the smallholder farmers. Further, the farming systems that encourage soil replenishment or regenerative agricultural practices have been abandoned or proved inapplicable mainly because of the population pressure putting strain on agricutural units through fragmentation, infrastructure development that take away crop land and climate change that may result in frequent droughts thus impacting negatively on agricultural land (Roder et al., 1995; Saito et al., 2006; **Parker & Gillingham,** 2017); thus aggravating the problem of low soil N and P and therefore, the need for development of input efficient genotypes. These systems were slash and burn, shifting cultivation or swidden agriculture and crop rotation (**Fernandes & Alavalapati,** 2003). They are rarely possible to practice today and thus the fallow periods allowed soil to regenerate through vegetation regrowth while ash from burning vegetation improved soil fertility thus no need for inputs while sustainable biodiversity was perfect. These elementary and subsistence systems have been replaced by highly commercial farming systems because of land pressure and government policies that prohibit them because of deforestation and environmental degradation as well as air pollution, health impacts, greenhouse gas emissions through carbon dioxide, methane and nitrous oxide into the atmosphere (**Ghazoul & Sheil,** 2010; **Mertz et al.** 2009; **Mann** 2005; Kirk et al., 1998; **Barbier** 2000; **Guthman** 2004; Smaling et al., 1997). The fields nowadays are rarely left fallow or rotated with other crops as part of an effort to maintain soil health (Donovan et al., 1999; Fukai et al., 1999; Kirk et al., 1998; Wonprasaid et al., 1996). The fallow periods may be long and thus unrealistic, the uplands that are poorly managed can be eroded resulting in poor soil fertility (**Hecht,** 1985; Kirk et al., 1998). It is now imperative that the crop improvement programmes should undergo a paradigm shift from concentrating on high input dependent varieties (Wang et al., 2020). This call breeders to screening for adaptation and selecting the efficient varieties for development or improving the cultivars in order to exploit the vast unexploited problematic soil areas. Apart from soils, other stresses, varieties can be bred for to exploit may enamit from climate change resulting to frequent early mid or late droughts, cold weather, increased incidences of pests and diseases, emergence of weeds, salinity, increased presence of golden apple snails, quelea quelea birds and rodents that can rake havoc to rice and other crops (**Coomes & Barham,** 2004).

Upland rice has enormous potential in Kenya as much of the land remain unexploited especially in the coastal region counties of Kwale, Taita Taveta, Kilifi, Lamu, and Tana River. This therefore, calls for a shift from high input dependent varieties to nutrient and water use efficient varieties targeted to the prevailing specific environments used by farmers for rice production.

The scatter plots of yield versus soil N and P tolerance levels had varied results (Figures 6 to 9). Under soil N-P+, line 74 was the most desirable because it was tolerant to low soil N and P and had the highest yield in the high yielding and tolerant quadrant. This means it is easy to select genotypes according to their adaptability. Under N- P+ soil condition, line 277 was the highest yielding although not the most adapted. The line 104 was the best but it was not the highest yielding under soil N+P- condition. Under the optimum soil condition the best genotype was 251 as it was the most adapted (Figure 9). It is clear that different lines are specifically adapted to certain soil N and P conditions, and that breeding for a super variety with broad adaptation is not quite easy since many genes with small additive effects are involved. Jin et al. (2019) observed that development of varieties should aim for specific adaptation although it is possible given the nature of gene action to get varieties with general or broad adaptation (Ceccarelli, 1994; Fukai et al., 1999).

## Yield under varying soil N and P conditions

The number of panicles per plant is an important yield parameter as grain yield is a function of panicles area-1\*spikelets panicle-1 \*fertility of spikelets \*weight of grains. Farmers are quite aware of the panicle characteristic and in a participatory plant breeding (PPB) trial; they indicated preference for long well filled clean or shiny panicles with moderate grain shattering. The best genotypes had number of panicle range of 133 (N-P-) to 263 (N-P+), while the worst had 4 (N+P-) to 16 (N-P+) panicles under experi- mental environments in parenthesis. This diversity of number of panicle can be exploited visually in a breeding programme. The H2 for this trait was 29.1% being second from that of top biomass, thus indicating fairly good degree of genetic determination (Falconer, 1989).

The materials that had superior yields under low soil fertility conditions can be used for improvement of the local cultivar. The overall mean yield was 3639 kg ha-1. However, some materials gave low yield as they were poorly adapted to some of the experimental environments, but the majority of the materials having been bred for drought tolerance and problem soils had high yield, though their performance varied depending on the experi- mental environments (Table 4). The top yielding genotypes and their experimental environments were 151 (CT16328-CA-18-M) (N-P-) at 5916 kg ha-1, 245 (CT16340-CA-9-M) (N-P+) 4948 kg ha-1, 222 (CT16337- CA-3-M) (N+P-) 4967 kg ha-1, 370 (WAB880-1-38-20-28-P1 HB) (N+P+) 4970 kg ha-1. The materials from CIAT Columbia (CT series) dominated four top slots across the soil N and P conditions, while Africa Rice Centre materials (WAB) were represented by only one under high fertility condition. The best overall high yielding genotype was under low soil fertility conditions (N-P-), indicating the fact that breeding rice for problem soil adaptation is a reality as observed also by Gregorio (2002) and Saito et al. (2006). Boonchuay et al. (2017) had reported that root morphology characteristics were major determinants in rice for absorbtion of phosphorous and that different varieties were adapted differently under different P regimes. **Khan & Rahman (2012) have reported t**hat adaptation mechanisms for different soil P environments include root architecture where roots under low soil P develop deeper more branched roots thus enabling them to scavage for P in larger soil volumes and they become more efficient in limited P uptake, root hairs and lateral roots increase surface area for P absorption, rice roots can exudate organic acids mainly citric and malic acid into the soil thus assisting solubilization of inorganic P through acidification of the rhizosphere thus converting insoluble forms of P into bioavailable forms. Kumar & Singh (2013) from their study have concluded that rice has evolved in its roots and shoots phosphorous transporters (PHT1 group) and enzymes that increase P uptake efficiency from the soil; the enzymes mainly acid phosphatases help in hydrolyzing organic phosphorous elements in the soil making P available for absorption by plant. Some rice plants roots have ability to form positive mycorrhizal fungi symbiosis relationships that enhances soil P uptake, but this relationship is not strong like in legumes and other crops (Yuan & Zhang 2015). Rice has some ability to undertake P allocation through metabolic processes adjustment to conserve P and prioritize it allocation to essential functions like DNA synthesis, energy metabolism by reducing it use in ;less critical processes (Sinclair & Vadez, 2012).

From the study, the lowest yielders were 314 (CT16350-CA- 7-M) (N-P-) 509 kg ha-1, 301 (CT16350-CA-2-M) (N-P+) 850 kg ha-1, 269 (CT16344-CA-8-M) (N+P-) 800 kg ha-1, and 39 (Caiapo) (N+P+) 567 kg ha-1. Caiapo seems to be poorly adapted to low soil fertility, unlike the other parent *O*. *glaberrima* (line 353) that appeared twice in the top ten yielders under N-P+ and N+P+ optimum experimental environment and had yield above 4925 kg ha-1. Problem soils are widespread throughout the world and breeding rice varieties that are capable of extracting the most fixed nutrients like phosphorous is very important, cost effective and environmentally friendly (Yuan, & Zhang, 2015; Wissuwa and Ae, 2001). The fact that the progenies of these two materials were far above their parents in yield is a clear manifesttation that breeding for higher yields may be met with high success (Daljit V., Katherine S. and Witcombe JR. 2007). This can be fairly easy if heritability for yield under low soil P and N is high as mass selection can be applied (Mohammed A. and Hayat W. 2021; Borojevi'c, 1990). However, if heritabilities are low, other methods of handling segregating populations that include pedigree, bulk, backcross, single seed descent and modified bulk method can be used for progress in breeding work (Fasoula et al., 1993; Fawole et al., 1982; Holland et al., 2003; Li et al., 1997; Nyquist, 1991; Verma and Srivastava, 2004).

The 1000 grain weight (paddy or unhulled) is another important trait that indicates seed size and yield, where weight is used to sell the produce. Alek et al. (2023) and Mahadeva et al. (2020) reported that key advancement in increasing 1000 seed weight was the identification and utilization of the Pup1 quantitative trait locus (QTL) that is known to enhances tolerance to low soil P. The gene OsPSTOL1 (Phosphorus-Starvation Tolerance 1) within this QTL has been shown to induce vigorous root growth leading to better phosphorus uptake. The Introgression of Pup1 into sensitive rice varieties has been reported to improved grain yield and 1000 grain weight under P-deficient soil conditions.

In our study, the best top genotype had a weight range of 25.79 g (N-P+) to 29.2 g (N+P+), while the lowest performers had a range of 3.83 g (N-P-) to 10.2 g (N+P+) under the conditions in parenthesis (Table 4). The H2 was low at 8.7% indicating that bulk breeding method where lines are advanced without selection until they become more homogeneous, may be the procedure to use (Allard, 1960; Chahal and Gosal, 2002; Hallauer and Miranda FO, 1989; Holland et al., 2003; Li et al., 1997; Nyquist, 1991; Rabiei et al., 2004; Smith and Kinman, 1965; Verma and Srivastava, 2004; Wu, 2003). The grain types preferred by Kenyan consumer markets are the slender long white with medium amylose content and absence of the white belly types characteristic of the basmati rice.

Aroma is another key attribute as aromatic grains fetch premium prices in the market. However, these aromatic types have low yields and the trait seems to be strongly linked to low yield (Karim et al., 2007; Singh, 2005). Despite the strong preference for long slender white basmati aromatic grain types, the aroma it’s self is just fragrance without known nutritional value (Kimani, 2020). Aroma comes from basically volatile substances and compounds and the primary function is to enhance flavour and appetite control especially when taste come into play, these thus determine marketing. The performance of the genotypes was observed to generally have high yields for those lines with poorer grain quality. Lines such as Duorado and NERICA1 that have high grain quality tended to have low yields, a clear indication yield is inversely correlated to aroma.

Generally, the notion that development of plants with high extracting ability of nutrients such as P can be detrimental especially with no external P supply because they may deplete soil reserves is farfetched. A part from these plants benefiting from applied nutrients, the soil reservoirs for an element like P can be available for centuries, assuming that the plants are able to extract it. Kirk et al. (1998) have argued on the complex intricacies involved in nutrients dynamics and concluded that development of efficient varieties is the best option available, not only on environmental concerns but also it is economically most feasible.

# CONCLUSION AND IMPLICATION

The accessions were found to be well adapted to the local conditions as indicated by their characterization data of traits like days to maturity, plant height and yield. The variability found in the traits studied like biomass and it’s high values of H2 obtained is an indication that their heritability was under mainly the heritable additive genetic effects compared to non-additive effects. The combined use of H2 estimates, CVP, GA and GAM can be utilized to improve low soil phosphorous, nitrogen tolerance and other yield related components from the population by selecting promising genotypes under the prevailing farmers production soil envirnments. The high CVP values or phenotypic variability for traits like TB, NP, PT, yield and 1000 seed weight implies that visual assessment can be utilized during the breeding efforts. This is widely during the selections from the segregating progenies from crosses made for their introgression to develop material improvement. The high GAM values for TB, NP and yield is an indicator of their heritability in the progenies from the parents. Very few genotypes performed well across the soil N and P experimental environments. Thus indicating that different genotypes are adapted differently to the environments and that different gene or quantitative trait loci may be involved singly or in groups. This is a clear case of narrow adaptation. One of the genotype, Caiapo, which was one of the parents in the CIAT materials ranked number one for days to heading, anthesis and maturity in terms of earliness. This is an indication and a confirmation that it is possessing genes for earliness and it is therefore, a good choice for parent, where earliness is the breeding objective. The N-P- soil environment was found to discriminate well the genes for yield better than N+P+ condition. These materials therefore, can be used to develop varieties adapted to low soil fertility and with the end user desired traits. The two way biplots have shown that genotypes are adapted differently in different soil N and P environments. Rice breeding for low soil nitrogen (N) and phosphorus (P) conditions is essential for enhancing sustainable agricultural practices, particularly in resource-limited environments. By developing rice varieties that exhibit improved nutrient use efficiency, tolerance to low nutrient availability, and enhanced ability to mobilize nutrients from the soil, breeders can contribute to increased yields without the over-reliance on chemical fertilizers. Such efforts can lead to improved food security, reduced environmental impact, and greater resilience for farmers facing challenging soil conditions. Future breeding programs should incorporate advanced molecular techniques and phenotyping methods to accelerate the development of these resilient rice varieties for food-fed and nutritional security.

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