

Evaluation Genetic Variation and Diversity of Grain Yield and Quality Traits in Rice (*Oryza sativa* L.) Genotypes for Low Input NPK Fertilizers

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Abstract

Determination of genetic variance in a large number of rice genotypes is an effective strategy for increasing yield. The goal of this research was to determine the genetic variability, phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad-sense heritability, expected genetic advance and multivariate analysis for eight rice grain quality and yield traits, in twenty Egyptian and exotic genotypes under low NPK fertilizer input levels at RRTC, Sakha, Kafr El-Sheikh, Egypt and evaluated across two successive seasons. Results revealed highly significant mean squares for all traits. High estimates of both PCV and GCV were detected for grain elongation followed by gelatinization temperature and head rice. High estimates of heritability were noted for grain length, grain shape, hulling, milling, head rice, amylose content, grain elongation and grain yield. Results revealed that highly significant differences among different genotypes were observed for studied characteristics under different NPK levels. Cluster results revealed that genotypes from the same origin or taxonomy type were clustered together. Diversity analysis showed four clusters. Cluster I and III had maximum genotypes (70%) and Cluster IV showed the highest mean values for studied traits. The results revealed that PC1 and PC2 accounted for 65.6% of the diversity between genotypes investigated. These findings show that some genotypes have a lot of diversity, indicating an opportunity to breed for low-input genotypes without sacrificing grain production and quality. GZ10590-1-3-3-2 and IET1444, both of which have high grain yield, can be employed as hybrid parents and could help with further genetic research for reduced NPK input.

Introduction

Rice is one of the staple food crops for about half of the world's population. Therefore, rice production should be significantly increased to meet the needs of a growing world population. The global demand for rice is expected to increase from 439 million tons in 2010 to 496 million tons by 2020 and 553 million tons by 2035 (FAO 2013). The nutritional imbalance causes a decrease in grain yield and marginal net returns (Wattoo et al. 2018; Zafar et al. 2018). Samonte et al. (2006) reported that nitrogen is one of the most essential macronutrients for rice production. Fertilizers with appropriate management practice help to increase the productivity of rice in farmers' fields (Gairhe et al. 2018; Timsina et al. 2012). The N, P and K are macro elements. Many studies have shown that the appropriate use of NPK fertilizers has enhanced the yield and substantially improved rice quality (Oikeh et al. 2008). The recommendation of chemical fertilizers should be based on soil analysis and crop response. A good fertilization strategy should be developed that combines the use of organic and chemical fertilizers, as well as improving crop productivity and environmental quality (Devkota et al. 2019). Nitrogen plays a vital role in determining the growth and yield potential of crops. The best mineral fertilizer rate is one that yields the highest economic return at the lowest expense (Ananthi et al. 2010).

Grain quality is defined as a major factor that decides market values of agricultural products and foods in each phase from production through consumption. Rice grain quality has always been an important consideration in variety selection and development. Cooking and eating quality traits are a part of the factors in assessing the grain quality of rice. Grain quality will become even more essential in the future

for many of whom rely heavily on rice as a staple diet, become better off and want higher quality rice (Lampe 1993). Rice has different cooking and eating properties depending on the variety and grain type. The dry-flaky cooking characteristic of rice is found in varieties with a high percentage of amylose, a medium gelatinization temperature and relatively low water absorption. The varieties with low amylose and low gelatinization temperature tend to be sticky and cohesive when cooked, absorb more water, and thus have long grain elongation after cooking.

Genetic parameters such as GCV and PCV measure the amount of genetic diversity in genetic resources as well as the degree to which genotype is modified by the environment. While the selection is made primarily on yield contributing characters, heritability and genetic advance are key selection factors. Heritability estimates combined with genetic improvements are usually more useful than heritability estimates alone in estimating the gain under selection (Paul et al. 2006). We apply cluster analysis when we need to categorize crop genotypes, in which the resulted clusters are important for selecting the best parents for breeders (Sanni et al. 2012). The main objectives of the present investigation are to evaluate the performance of grain quality and yield traits in twenty rice genotypes at low fertilizer input levels to i) estimate genotypic (GCV) and phenotypic (PCV) coefficients of variability, broad-sense heritability and genetic advance for grain quality and yield traits, ii) utilize multivariate analysis to better understand the relationships and patterns between genotypes and iii) examine the connections between grain yield and grain quality attributes.

Materials And Methods

Plant materials

In total, twenty Egyptian and exotic rice genotypes were chosen at random and employed in this investigation. The genotypes were provided by the Genetic Stock of Rice Breeding Program, Agricultural Research Center (ARC, Giza, Egypt). The name, origins and subspecies group of these rice genotypes have illustrated in Table 1.

Experimental layout

The present investigation was carried out at Research Farm of the Rice Research and Training Center (RRTC), Sakha, Kafr El-Sheikh, Egypt, during the 2019 and 2020 planting seasons. The selected genotypes were evaluated under four levels of NPK fertilizers i.e., full dose, two-third, one-third and zero of the recommended dose of NPK. The recommended doses of NPK are 165, 36 and 58 kg N, P₂O₅ and K₂O per hectare, respectively. At the depth of 0-30 cm from the soil surface, representational soil samples had been selected. The method of soil interpretation followed the procedure of Black et al. (1965). The results of soil analysis in the studied seasons are presented in Table 2.

The nursery was well prepared and fertilized with four kg/m calcium superphosphate (15.5 % P₂O₅) before plowing and three kg urea (46.5% N) was applied after plowing as well as, one kg zinc sulfate (22% Zn) immediately applied before sowing and after puddling. Rice seeds at the rate of 60 kg/ha were soaked in freshwater for 24 hours and incubated for 48 hours to improve germination. The pre-germinated seeds were broadcast on May 15th in both seasons. The current investigation was applied in a split-plot design with three replications. NPK treatments were distributed over main plots and the genotypes were allocated in sub plots. The permanent field was plowed and then well dry leveled. Phosphorus fertilizer in the form of calcium superphosphate (15.5% P₂O₅) was applied before land preparation according to the treatment schedule in this hypothesis. Potassium fertilizer in the form of potassium sulfate (48 % K₂O) was incorporated in the dry soil before planting according to the treatments used in this study. Nitrogen fertilizer was added according to the treatments in the form of urea (46.5 % N). Two splits (2/3) were applied and incorporated in dry soil before planting as well as (1/3) has applied after thirty days from transplanting as topdressing. The permanent field was immediately irrigated. Thirty days old seedling of each genotype was individually transplanted in 10-row per replicate with a spacing of 20 cm between rows and 20 cm between plants.

Data collection

All rice grain quality and grain yield traits were calculated according to the standard evaluation system for rice (IRRI 1996). At harvest, grain yield (t/ha) from randomly 10 square meters was measured. Moreover, the laboratory analysis was conducted for grain quality traits, the grain samples were milled and analyzed for physicochemical properties. Milled rice out turn was determined by husking 200 g rough rice and milled in Satake Rice Mill. Head rice recovery was determined by separating broken parts from milled rice. Milling % and head rice % were expressed as a percentage of rough rice and milled rice, respectively. Rough grain length and breadth were measured by slide calipers (IRRI 1996). In determining the rough grain shape, rough rice was first classified into four classes based on length, very long (more than 7.5 mm in length), long (6.61 to 7.5 mm in length), medium (5.51 to 6.6 mm in length) and short (5.5 mm or less in length). The grain was again classified into four classes considering length to breadth ratio; long (ratio above 4), slender (ratio from 3.1 to 4), medium or (ratio from 2.1 to 3.0), bold (ratio 1.1 to 2.0) and round (ratio less than 1.1). Based on amylose content, milled rice was classified as waxy (1-2% amylose), very low (>2-9% amylose), low (>9-20% amylose), intermediate (>20-25% amylose) and high (25-33% amylose).

For measurement of grain elongation ratio, 10 measured (length and width) grains were taken into a 20 ml glass test tube and soaked for 20 minutes with 5 ml of tap water. The test tubes were then immersed in boiling water for around 30 minutes after soaking. When the grain was fully cooked, the water inside them was drained. The cooked grains were then placed on a glass sheet for a few minutes to drain excess moisture before being measured in length and width. The relative change in rice grain length after cooking is referred to as the grain elongation ratio. Six whole milled grains of rice from each plant were

spaced evenly in small transparent plastic boxes containing 10 ml of 1.70% potassium hydroxide solution to determine gelatinization temperature (GT). In an incubator set to 30°C, the boxes are covered and left undisturbed for 23 hours. The GT, which was visually rated on a seven-point numerical scale, was represented by such alkali spreading and clearing of starchy endosperm (Table 3).

Statistical analysis

The data obtained for each trait was statistically evaluated over the two seasons according to Le Clerg et al. (1962), then it was subjected to analysis of variance, which was used to partition the gross phenotypic variability into the components due to genetic (hereditary) and non-genetic (environmental) factors. Genotypic variance is the part of the phenotypic variance that can be attributed to genotypic differences among the phenotypes. Similarly, phenotypic variance refers to the total variation among phenotypes when they are produced in a variety of conditions (Dudley and Moll 1969).

Hence, variance components, genotypic (V_g), phenotypic (V_p) and error (V_e) variances were estimated using the formula of Prasad et al. (1981) and Wricke and Weber (1986) as follows:

$$V_g = [MSG - MSE / r] \quad V_{ph} = [MSG / r] \quad \text{and} \quad V_e = [MSE / r]$$

where MSG, MSE and r are the mean squares of genotypes, mean squares of error and number of replications, respectively. Phenotypic (PCV) and genotypic (GCV) coefficient of variation were evaluated according to the methods of (Burton 1952; Johnson et al. 1955; Kumar et al. 1985) as follows:

$$PCV = [\sqrt{V_p / X}] \times 100 \quad \text{and} \quad GCV = [\sqrt{V_g / X}] \times 100$$

where V_p , V_g and X are the phenotypic variances, genotypic variances and grand mean per season, respectively, for the traits under consideration. Broad sense heritability (h^2B) expressed as the percentage of the ratio of the genotypic variance (V_g) to the phenotypic variance (V_{ph}) was estimated on the genotypic mean basis as described by Allard (1999). Genetic advance (GA) expected and GA as a percent of the mean assuming selection of the superior 5% of the genotypes were estimated by the methods illustrated by Fehr (1987) as follows:

$$GA = K (S_{ph}) h^2 B \quad \text{and} \quad GA \text{ (as \% of the mean)} = (GA / x) \times 100$$

where k is a constant (which varies depending upon the selection intensity and, if the latter is 5%, it stands at 2.06), S_{ph} is the phenotypic standard deviation ($\sqrt{V_{ph}}$), h^2B is the heritability ratio and x refers to the season mean of the trait.

To create the dendrogram depending on squared Euclidean distance, the unweighted pair group method of arithmetic average linkage (UPGMA) was applied using SPSS version 15 (IBM Corporation 2010). The initial cluster distances in Ward's minimum variance method are therefore defined to be the squared Euclidean distance between points: $d_{ij} = d(\{X_i\}, \{X_j\}) = \|X_i - X_j\|^2$. The principal component analysis (PCA) was subsequently investigated using Genstat version 12.0 software.

Result

Genetic variability between rice genotypes

The grand mean, genotypic and phenotypic coefficient of variability, broad-sense heritability and genetic advance as percentages of the mean are illustrated in Table 4. Low estimates of phenotypic and genotypic variances were recorded for all the studied traits except head rice % and grain elongation traits. The environmental variance was very low for all traits especially for grain shape and grain yield. The phenotypic coefficient of variability (PCV) was higher than the GCV for all the characters studied. PCV was ranged between 2.572 and hulling to 19.956 for grain elongation. PCV and GCV were lower than (10 %) for grain length, grain shape, hulling percentage, milling percentage, amylose content and grain yield (t/ha). Otherwise, high estimates of both PCV and GCV were detected for grain elongation followed by gelatinization temperature and head rice. Negligible values of the difference between PCV and GCV were recorded for grain length, grain shape, hulling, milling, head rice recovery, amylose, grain elongation and grain yield. In general, PCV values were higher than GCV for various characters studied. Among the desirable traits, low GCV and PCV were observed for grain length. High estimates of broad-sense heritability were noted for grain length, grain shape, hulling, milling, head rice, amylose content, grain elongation and grain yield. Their estimated values were ranged between 71.25% for grain length and 99.55% for both grain elongation and grain yield traits, while almost moderate estimates were exhibited for gelatinization temperature (67.78 %). However, high estimates of expected genetic advances were found for grain elongation (40.924 %), head rice recovery (27.336 %) and gelatinization temperature (25.603 %). Grain elongation, gelatinization temperature and head rice had shown high PCV and GCV along with high to moderate heritability (h^2) and genetic advance. The additive gene action governed the above-mentioned three traits. High heritability with high genetic advance as percent mean was observed for all the grain quality traits except for hulling percent and milling percent.

Genotypes Performance under different NPK treatments

Data pointed out that there were highly significant differences among different genotypes in the studied characteristics under different NPK levels. Grain yield, grain quality and cooking quality traits were affected significantly by NPK treatments. The studied characteristics were increased gradually by increasing NPK levels from 0 up to the full dose of recommended doses of NPK fertilizers. The results

revealed that the GZ10590-1-3-3-2 rice genotype produced the highest grain yield followed by IET1444, while Nerica1 came in the last rank and gave the lowest value in this aspect (Fig. 1). Grain length was higher in IRAT170 which came in the first rank and recorded the highest value of grain length while Giza178 recorded the shortest grains (Fig. 2). Grain shape was higher in IRAT170 and came in the first rank followed by Giza182 (Fig. 3). Milyang 109 produced the lowest values of grain shape. Giza177 recorded the highest values of hulling percentage followed by Giza179. Korea1, Nerica1 and Milyang109 came in the last rank and recorded the lowest hulling percentage and recorded nearly the same value of hulling percentage (Fig. 4). The highest percentage of milling was observed by the rice genotypes Giza177, GZ10991-5-18-5-1, GZ10333-9-1-1-3 and GZ10101-5-1-1-1. While the lowest value of milling rice was observed with Nerica1 (Fig. 5). GZ10333-9-1-1-3 recorded the highest values of head rice while GZ10598-9-1-5-5 recorded the lowest value of head rice under this study (Fig. 6). Amylose content was high in Nerica 1, it came in the first rank and recorded the highest value of amylose content, while, GZ10598-9-1-5-5 recorded the lowest value of amylose content (Fig. 7). The highest value of grain elongation was recorded by IET1444. While IRAT170 and GZ10590-1-3-3-2 recorded the lowest grain elongation (Fig. 8). Gelatinization temperature (GT) in IET1444 came in the first rank and recorded the highest value while IRAT170 and GZ10590-1-3-3-2 recorded the lowest values (Fig. 9).

Diversity analysis

Principal component analyses

Principal component analysis (PCA) is used to generalize the variation in different explaining factors. Our PCA was done for different grain quality traits of the twenty rice genotypes. Eigenvalues and a fraction of variation in each principal component are shown in Table 5. PC1 explained 37.6 % of total variations observed among the genotypes while it was 28.0% for PC2. The total diversity was explained by nine principal components (Table 5). The results showed that only the first three principal components jointly accounted for 80.9% of the total variation among the genotypes, while these three exhibited eigenvalues above unity. However, the large fraction of the divergence (88.2% variation) was explained by the first four components. Hulling was correlated with Milling, in addition, gelatinization temperature was closely associated with grain elongation, as well as grain shape was found to be correlated with grain length. All Egyptian genotypes and promising lines were features with the high yielding ability and high milling and hulling relearn. IET 1444 was greater in gelatinization temperature and grain elongation compared with other rice genotypes. Both Nerica 1 and IRAT 170 were unique to grain length and grain shape traits (Fig. 10). The Principle components for grain yield and grain quality traits in twenty rice genotypes and their distribution of priority in resulting PCA were reported in Tables 6 and 7, respectively. The results demonstrated that grain length, milling and amylose content were classified in PC1, while, head rice, gelatinization temperature and grain elongation were located in PC2. On the other hand, grain yield and hulling were distributed in PC3.

Cluster analysis

Clustering analysis was performed to look for similarities between rice accessions and assess the possibility of hybridization. Mean performance of different clusters for the characters manifested that genotypes with maximum grain yield, high milling output, good grain shape and low amylose content were accumulated in cluster I, whereas genotypes with maximum hulling were grouped in cluster II. Moreover, genotypes that took minimum head rice were clubbed into cluster III. Whereas low yielding genotypes with soft gelatinization temperature and long grain elongation were grouped into cluster IV (Table 8).

Among twenty rice genotypes, cluster analysis resulted in four clusters following Ward's method (Fig. 11). Genotypes from the same origin or taxonomic type were found to be clustered together in the cluster results. Four distinct clusters emerged from the diversity analysis. Clusters I (7 genotypes) and III (7 genotypes) had the most genotypes (70%) while Cluster IV (one genotype) had the highest mean values for the qualities being evaluated. In cluster I, out of 7 rice genotypes, 5 of them were Egyptian japonica type, with high yielding, shortest grains, bold grain shape, highest milling and head rice recovery and low amylose content, namely, Giza 177, Sakha 107, Gz 10101-5-1-1-1, Gz 10598 -9-1-1-5-5 and Gz10590 – 1-1-3-9-1, while the other two genotypes Giza 178 and Korea 1 were (indica/japonica) type. With regarding cluster III, 7 genotypes were aggregated, out of them, 4 genotypes were Egyptian japonica type, namely, Sakha 108, Sakha 109, Gz 10333-9-1-1-3 and Gz 10590-1-3-3-2 with high hulling. However, the other three genotypes were exotic, namely Milyang 109 (Indica/japonica type), IRAT 170 (Indica type) and Nerica 1 (Indica type). On the other hand, 5 rice genotypes were grouped into cluster II, Out Of them, 2 genotypes, Giza 179 and Suweon 375 were (Indica/Japonica) type and 2 genotypes, Fukunishiki and Gz 10991-5-18-5-1 were (japonica type) as well as only one genotype Giza 182 was (Indica type). Finally, only one rice genotype namely, IET 1444 tolerant to water stress and suitable to cultivate under drought conditions (Indica type) was located in cluster IV. The distribution of 20 rice genotypes in different clusters is illustrated in (Table 9) and the dissimilarity matrix according to Euclidean square based on studied traits in the tested rice genotypes were observed in Table 10.

Discussion

Low estimates of phenotypic and genotypic variances were recorded for all the studied traits except head rice and grain elongation traits. The environmental variance was very low for all traits especially for grain shape and grain yield, indicating less influence of environment in the expiration of these traits. The PCV was higher than the GCV for all the characters studied. PCV and GCV were low for grain length, grain shape, hulling, milling, amylose content and grain yield indicating limited scope for further genetic improvement of these traits through selection. Otherwise, high estimates of both PCV and GCV were detected for grain elongation followed by gelatinization temperature and head rice indicating wide variability among the varieties studied for these traits and the possibility of genetic improvement of these

traits through selection. Negligible values of the difference between PCV and GCV were recorded for grain length, grain shape, hulling, milling, head rice recovery, amylose, grain elongation and grain yield suggesting a lower environmental influence on the expression of these traits. Furthermore, Bharath et al. (2018) reported that quantitative characters had shown less difference between PCV and GCV. Also, they recorded that single plant yield and gelatinization temperature had shown high PCV and GCV. Moreover, Archana et al. (2018) exhibited that PCV values, in general, were higher than GCV for various characters studied. Grain elongation, gelatinization temperature and head rice had shown high PCV and GCV along with high to moderate heritability (h^2) and genetic advance, these traits are less influenced by the environment. High heritability accompanied with high genetic advance as percent mean were recorded for grain yield per plant (Archana et al., 2018). This signifies that these characteristics are governed by additive gene action and selection for these traits would be effective. Similar findings were recorded previously (Hammoud et al. 2006a; Sahu et al. 2017). It had been observed that the coefficient of variation ranges from 8.61% for hulling percentage to 45.01% for gelatinization temperature.

There were highly significant differences among different genotypes in the studied characteristics under different NPK levels. Grain yield, grain quality and cooking characteristics were affected significantly by NPK treatments. The studied characteristics were increased gradually by increasing NPK levels from 0 up to the full dose of recommended doses of NPK fertilizers. The advantageous impacts of NPK on rice productivity and quality were noted by several previous investigations. The favorable effect of NPK fertilizer application on rice grain yield might be due to the increase in NPK availability in soil and subsequently content in rice plants leading to produce more energy which enhances the photosynthetic rate that improved grain filling process (Biswas and Dravid 2001; Ibrahim 2001). The effect of NPK fertilizer application on hulling percentage was mainly due to the maximum storing of starch in the endosperm of grains which caused a reduction in the hull components such as palea, lemma, pericarp, aleurone layers and rachilla. The increase in milling percentage due to increasing NPK levels may be due to the increase in metabolite substances in grains (Asif et al. 1999; Metwally 2007; 2011; 2012; Naeem et al. 2010). Data revealed that the GZ10590-1-3-3-2 rice genotype produced the highest grain yield followed by IET1444, while Nerica1 came in the last rank and gave the lowest value in this aspect. These results could be attributed to the superiority of GZ10590-1-3-3-2 in growth vigor as well as yield attributes. The differences among rice genotypes may be due to the genetically inherited variants. The differences among rice genotypes in yield and grain quality characteristics may be due to the genetically inherited variants. Ebaid and El-Rewainy (2005) and Metwally et al. (2020) reported that hulling, milling, head rice, gelatinization temperature, grain elongation, amylose content traits were varied among different Egyptian rice genotypes. Singh et al. (2011) indicated that rice grain quality characteristics variations among rice genotypes are dominated by the genetic background of those genotypes. Zhao et al. (2018) reported that the GS9 gene regulates grain shape and hull thickness by altering cell division. It means rice grain shape is mainly controlled by the genetic background. The variations among the studied genotypes in cooking qualities may be due to the differences in their shape and thickness. Mohapatra and Bal (2006) suggested that the thickness of the rice grain is an important factor in deciding the diffusion of water during cooking. The differences among rice genotypes may be due to the genetically inherited variants.

(Hammoud et al. 2006b; Taha Hanan 2008; Sorour et al. 2016; Zhao et al. 2018) reported that rice grain milling and physical characteristics are commanded by the genetic backdrop of rice genotypes.

PCA is used to generalize the variation in different explaining factors. The results showed that only the first three principal components jointly accounted for 80.9% of the total variation among the genotypes, while these three exhibited eigenvalues above unity. While a large fraction of the divergence (88.2% variation) was explained by the first four components. The results demonstrated that grain length, milling and amylose content were classified in PC1, while, head rice, gelatinization temperature and grain elongation were located in PC2. On the other hand, grain yield and hulling were distributed in PC3. Similarly, PCA was reported (Acevedo-Siaca et al. 2021; Anandan et al. 2011; Latif et al. 2011; Sanni et al. 2012). Mean performance of different clusters for the characters manifested that genotypes with maximum grain yield, high milling output, good grain shape and low amylose content were accumulated in cluster I. Whereas, genotypes with maximum hulling were in grouped cluster II. Moreover, genotypes that took minimum head rice were clubbed into cluster III. Whereas, low yielding genotypes with soft gelatinization temperature and long grain elongation were grouped into cluster IV.

Conclusions

High heritability of grain quality and yield traits suggests that the environment has only minor influence, implying that simple breeding methods based on selection will be efficient in genetic improvement. Low-input fertilizers in agricultural production will be considered one of the necessary agricultural production inputs in the next years allowing us to feed a growing population while keeping low costs. This study dealt with the possibility of using different rates of the necessary elements such as nitrogen (N), phosphorous (P) and potassium (K) to rice fertilize. Results exhibited highly significant mean squares for all characteristics suggesting the presence of genetic difference among rice genotypes for all traits. Low estimates of PCV and GCV were recorded for all traits except head rice and grain elongation. Grain yield, grain quality and cooking traits were influenced significantly by NPK treatments. The studied characteristics were improved progressively by rising NPK levels from 0 up to the full dose of recommended NPK fertilizers. There were highly significant variations among genotypes in studied traits. GZ10590-1-3-3-2 rice genotype exhibited the highest grain yield followed by IET1444. Also, it was concluded that origin and taxonomy were both responsible for clustering genotypes.

Declarations

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Authors' contributions

SGHRS contributed to supervision, encouragement, suggesting the problem, design, data analysis and writing up the manuscript. TFM contributed to support, design, performance field experiments, data analysis and writing up the manuscript. SHAT contributed to designing, preparing, and scientific advice, data analysis and writing up the manuscript. MMS contributed to design, data analysis and writing up the manuscript. KFMS design, data analysis and writing up the manuscript and following up the publication with the journal (correspondence). MABE design, performance field experiments, data analysis and writing up the manuscript. All authors read and approved the final version.

Code availability

Not applicable.

Availability of data and materials

All data generated or analyzed during this study already exist in this published article.

Conflict of interest

Not applicable.

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Tables

Table 1 Name, origin and subspecies group of the rice genotypes used in this study

Number of genotype	Name of genotype	Origin	Subspecies group
1	Giza177	Egypt	Japonica
2	Giza178	Egypt	Japonica/Indica
3	Giza179	Egypt	Japonica/Indica
4	Giza182	Egypt	Indica
5	Sakha107	Egypt	Japonica
6	Sakha108	Egypt	Japonica
7	Sakha109	Egypt	Japonica
8	IET1444	India	Indica
9	Nerica1	Africa Rice	Indica
10	Milyang109	Korea	Japonica/Indica
11	IRAT170	Ivory varieties	Indica
12	Suweon375	Korea	Japonica/Indica
13	Fukunishiki	Japan	Japonica
14	Korea 1	Korea	Japonica/Indica
15	GZ10101-5-1-1-1	Egypt	Japonica
16	GZ10333-9-1-1-3	Egypt	Japonica
17	GZ10590-1-1-3-9-1	Egypt	Japonica
18	GZ10590-1-3-3-2	Egypt	Japonica
19	GZ10598-9-1-5-5	Egypt	Japonica
20	GZ10991-5-18-5-1	Egypt	Japonica

Table 2 Physical and chemicals analysis of the soil at the experimental sites during two contrasting environments (2019 and 2020)

Soil Properties	Sakha		Soil Properties	Sakha	
	2019	2020		2019	2020
Clay %	57.2	54.0	Soluble cations, mg/L		
Silt %	31.9	35.3	Ca++	7.2	7.0
Sand %	10.9	11.7	Mg++	1.6	1.5
Texture	Clayey	Clayey	K+	0.5	0.5
			Na+	13.0	12.0
Organic matter%	1.56	1.45	Soluble anions, mg/L		
Available P, mg/Kg	13.50	12.70	CO3- -	0.00	0.00
Available NH4, mg/Kg	13.5	12.9	H CO3- -	5.3	5.0
Available NO3, mg/Kg	10.6	11.7	CL-	15.0	14.0
Available K, mg/Kg	341	332	SO4- -	2.0	2.0
pH (1:2.5 soil suspension)	8.35	8.26	EC dS/m (soil paste)	2.54	2.22

Table 3 Kernel elongation scale

Scale	Description	Class
1	Kernel not affected	Very high
2	Kernel swollen	High
3	Kernel swollen, collar incomplete or narrow	High-intermediate
4	Kernel swollen collar complete and wide	Intermediate
5	Kernel split or segmented, collar complete and wide	Low- intermediate
6	Kernel dispersed, merging with collar	Low
7	Kernel completely dispersed and intermingled	Very low

Table 4 Genetic variability for grain quality and grain yield (t/ha) traits among twenty rice genotypes over two contrasting environments (2019 and 2020)

Character	Grand mean	Components of variance			PCV	GCV	H ² B%	Expected GA
		VP	VG	VE				
Grain length (mm)	5.685	0.04	0.03	0.0069	3.56	3.25	71.2	5.234
Grain shape	2.049	0.02	0.02	0.0007	8.08	7.97	94.7	15.787
Hulling %	81.51	4.39	4.26	0.1314	2.57	2.53	94.2	4.990
Milling %	71.21	5.67	5.23	0.4157	3.34	3.22	86.3	5.951
Head rice %	56.20	56.9	56.6	0.3363	13.4	13.3	98.8	27.336
Amylose content %	18.00	3.08	3.04	0.0385	8.74	8.69	97.5	17.574
Grain elongation	49.30	96.8	96.6	0.2178	19.9	19.9	99.5	40.926
Gelatinization Temperature	3.661	0.45	0.36	0.0872	18.3	16.4	67.7	25.603
Grain yield (t/ha)	8.013	0.38	0.38	0.0009	7.71	7.70	99.5	15.816

Note: Vp phenotypic variance components, Vg genotypic variance components, Ve error variance components, PCV phenotypic coefficient of variation, GCV genotypic coefficient of variation and h²B broad-sense heritability.

Table 5 Eigenvalue and percent variance contribution of each principal component

Traits	Principal Components	Eigen Value	Proportion of Variation%	Cumulative Variation%
Grain length (mm)	PC1	3.383	0.376	37.6
Grain shape	PC2	2.5209	0.280	65.6
Hulling %	PC3	1.3736	0.153	80.9
Milling %	PC4	0.6580	0.073	88.2
Head rice %	PC5	0.4341	0.048	93
Amylose content %	PC6	0.3665	0.041	97.1
Grain elongation	PC7	0.1508	0.017	98.7
Gelatinization Temp.	PC8	0.0935	0.010	99.8
Grain yield (t/ha)	PC9	0.0194	0.002	100

Table 6 Principal component analysis loadings corresponding to each level for grain quality and grain yield (t/ha) traits evaluated over two contrasting environments (2019 and 2020)

Trait	PC1	PC2	PC3
Grain yield (t/ha)	-0.254	0.255	-0.437
Grain length (mm)	0.432	-0.209	0.324
Grain shape	0.467	-0.014	0.107
Hulling %	-0.240	-0.023	0.678
Milling %	-0.434	0.028	0.364
Head rice %	-0.294	-0.385	-0.232
Amylose content %	0.439	0.268	-0.088
Gelatinization Temperature	-0.063	0.587	0.014
Grain elongation %	-0.045	0.570	0.196

Note: PC1 first principle component; PC2 second principle component and PC3 third principle component.

Table 7 Traits distribution of priority in resulted principal components analysis

PC1	PC2	PC3
Grain length (mm)	Head rice %	Grain yield (t/ha)
Milling %	Gelatinization Temp.	Hulling %
Amylose content %	Grain elongation %	

Table 8 Cluster means for nine agronomic traits among twenty rice genotypes evaluated over two contrasting environments (2019 and 2020)

Traits	Cluster number			
	I	II	III	IV
Grain yield (t/ha.)	8.26	7.57	7.79	10.05
Grain length (mm)	5.46	5.78	5.85	5.65
Grain shape	1.95	2.10	2.06	2.37
Hulling %	81.71	82.29	80.91	80.34
Milling %	72.08	71.25	70.46	70.24
Head rice %:	59.11	50.33	59.14	44.75
Amylose content %	17.37	18.63	17.66	21.72
Gelatinization Temperature	3.74	3.97	3.04	6.00
Grain elongation %	52.85	52.01	41.20	67.84

Table 9 Distribution of twenty rice genotypes in different clusters

Cluster	No. of genotypes	Genotypes
I	7	Giza 177, Sakha 107, Gz 10101-5-1-1-1, Gz 10598 -9-1-1-5-5, Gz10590 - 1-1-3-9-1, Giza 178 and Korea 1
II	5	Giza 179, Suweon 375, Fukunishiki, Gz 10991-5-18-5-1 and Giza 182
III	7	Sakha 108, Sakha 109, Gz 10333-9-1-1-3 and Gz 10590-1-3-3-2, Milyang 109, IRAT 170 and Nerica 1
IV	1	IET 1444

Table 10 Dissimilarity matrix according to Euclidean square based on studied traits in the tested rice genotypes

Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	0																			
2	79	0																		
3	80	138	0																	
4	151	205	44	0																
5	14	39	58	121	0															
6	210	86	205	344	140	0														
7	185	109	103	219	116	35.2	0													
8	376	570	409	280	423	1005	847	0												
9	350	244	177	166	261	213	135	808	0											
10	264	138	154	238	169	50.3	18	921	93	0										
11	415	308	244	366	317	114	65	1230	128	54	0									
12	68	130	20	40	47	247	145	311	216	186	325	0								
13	71	152	36	27	64	298	198	262	203	238	375	17	0							
14	69	56	56	72	82	209	155	324	203	185	365	41	44	0						
15	74	36	36	88	199	36.8	45	664	208	78	180	99	138	80	0					
16	152	58	200	353	107	16.4	61	916	277	103	190	233	277	178	29	0				
17	47	22	170	248	35	152	182	501	373	237	434	141	160	71	61	94	0			
18	410	282	236	387	307	103	49	1214	185	52	32	317	398	350	163	167	408	0		
19	54	17	83	155	17	86.7	74	523	221	107	258	68	101	39	15	66	32.1	239	0	
20	62	174	25	61	61	280	171	331	249	233	337	15	18	74	117	255	170	350	101	0

Code of genotypes: 1= Giza177, 2= Giza178, 3= Giza179, 4= Giza182, 5= Sakha107, 6= Sakha108, 7= Sakha109, 8= IET1444, 9= Nerica1, 10= Milyang109, 11= IRAT170, 12= Suweon375, 13= Fukunishici, 14= Korea 1, 15= GZ10101-5-1-1-1, 16= GZ10333-9-1-1-3, 17= GZ10590-1-1-3-9-1, 18= GZ10590-1-3-3-2, 19= GZ10598-9-1-5-5 and 20= GZ10991-5-18-5-1.

Figures

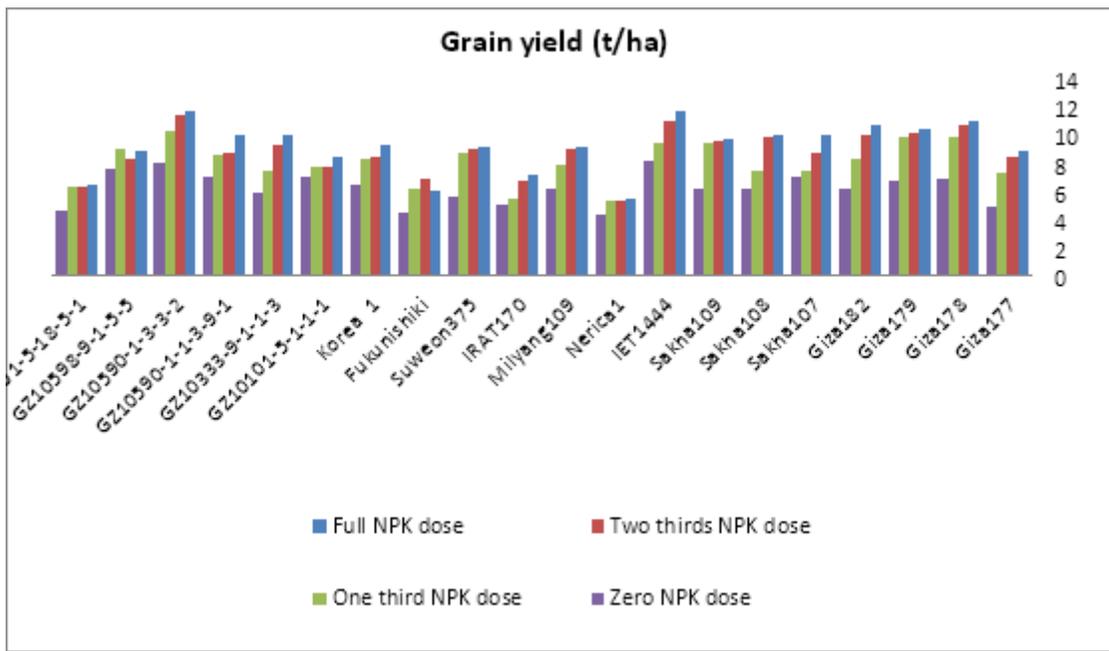


Figure 1

Mean performance of grain yield (t/ha) trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

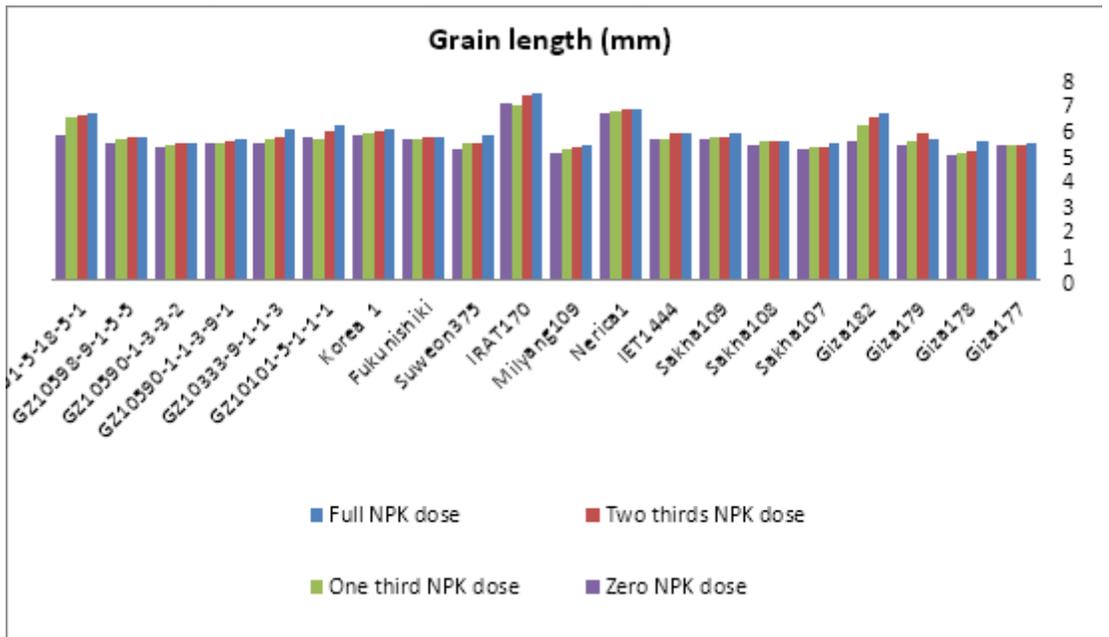


Figure 2

Mean performance of grain length trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

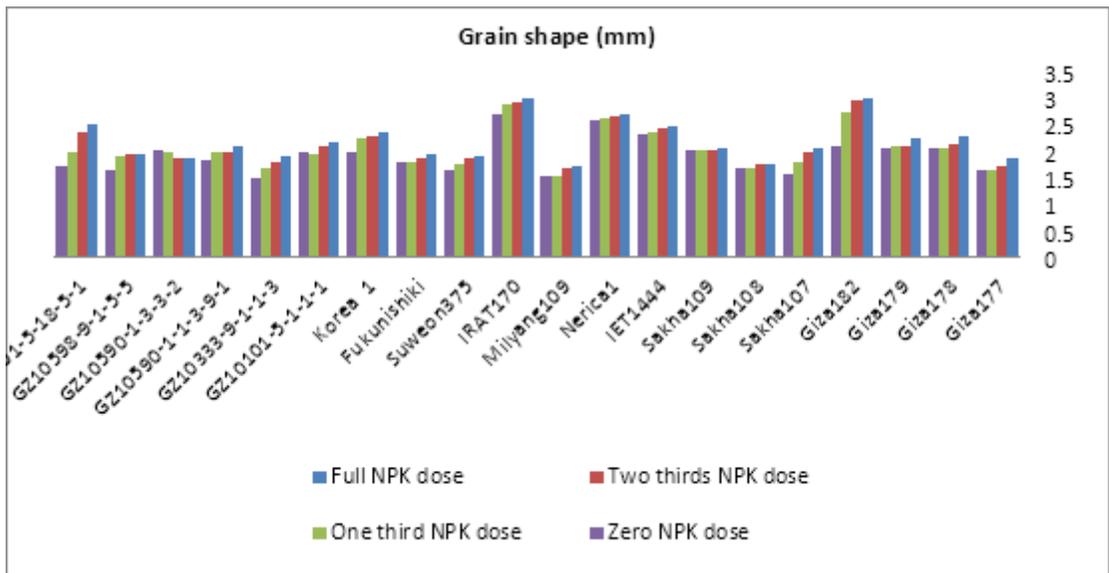


Figure 3

Mean performance of grain shape trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

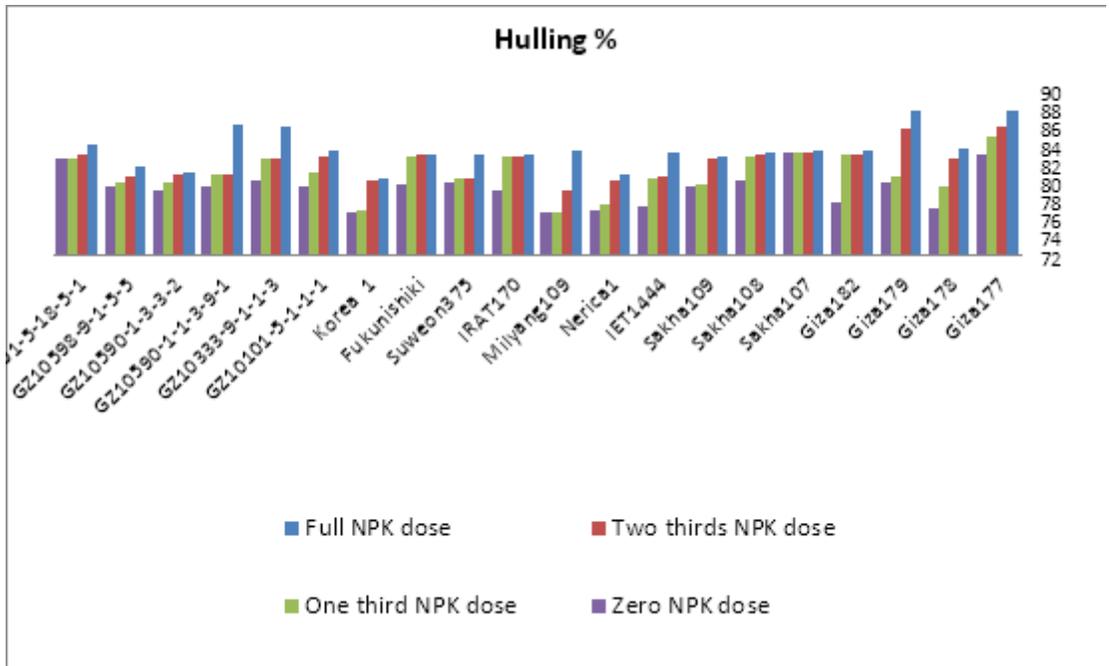


Figure 4

Mean performance of hulling % trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

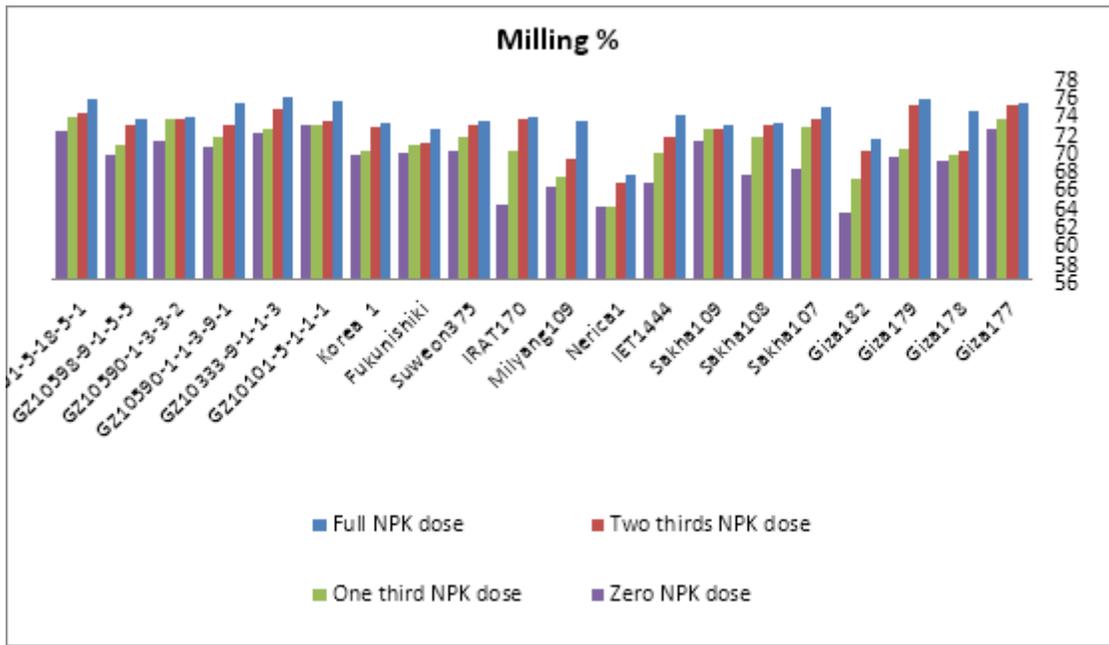


Figure 5

Mean performance of milling rice % trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

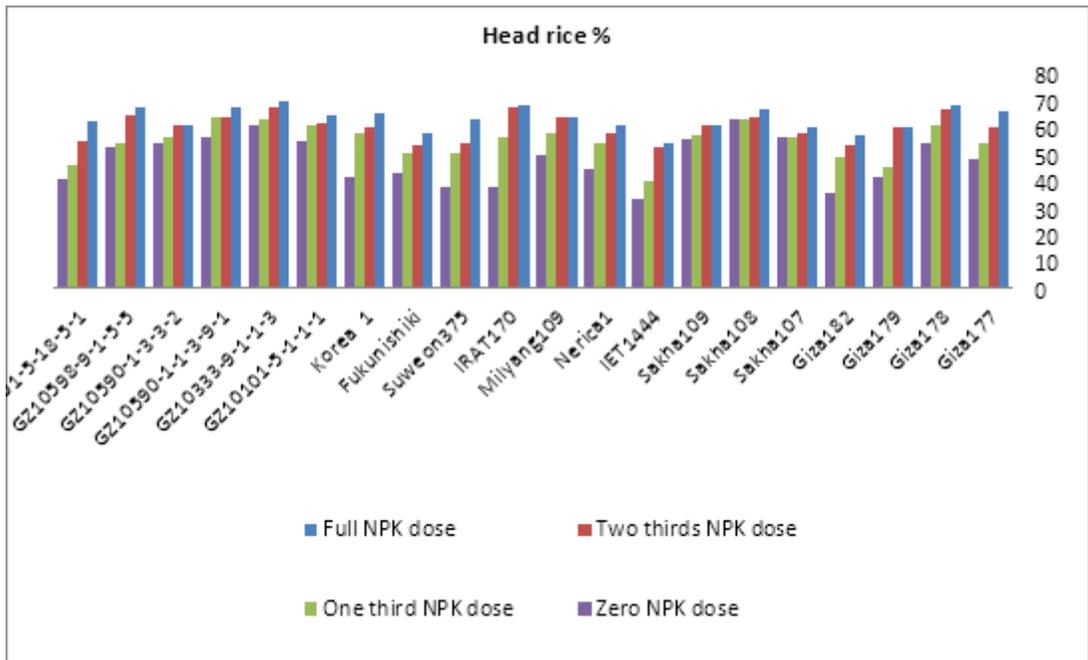


Figure 6

Mean performance of head rice % trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

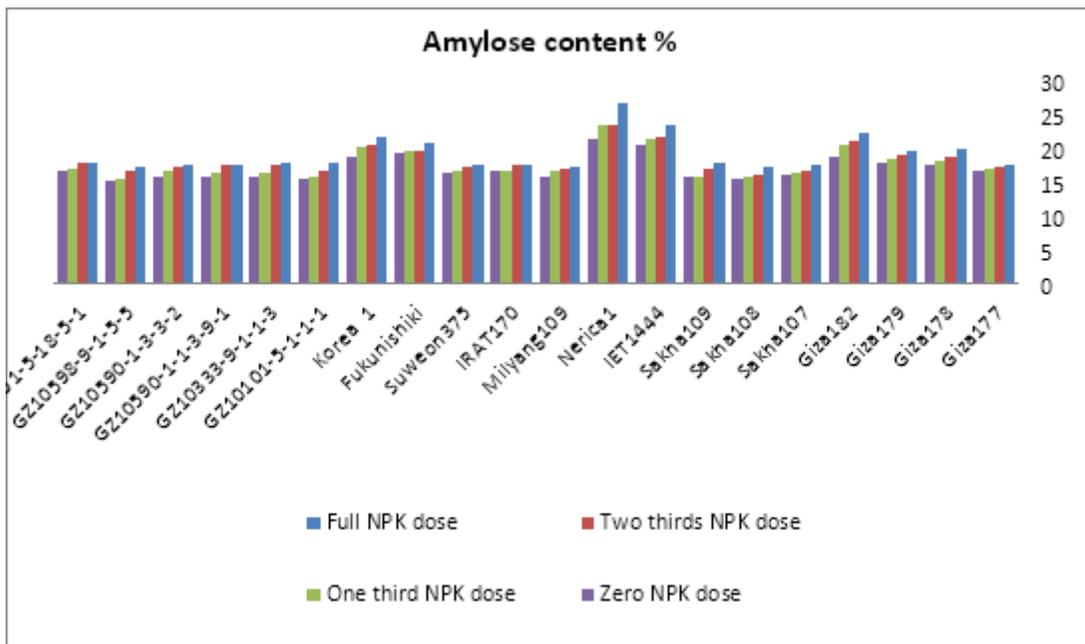


Figure 7

Mean performance of amylose content % trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

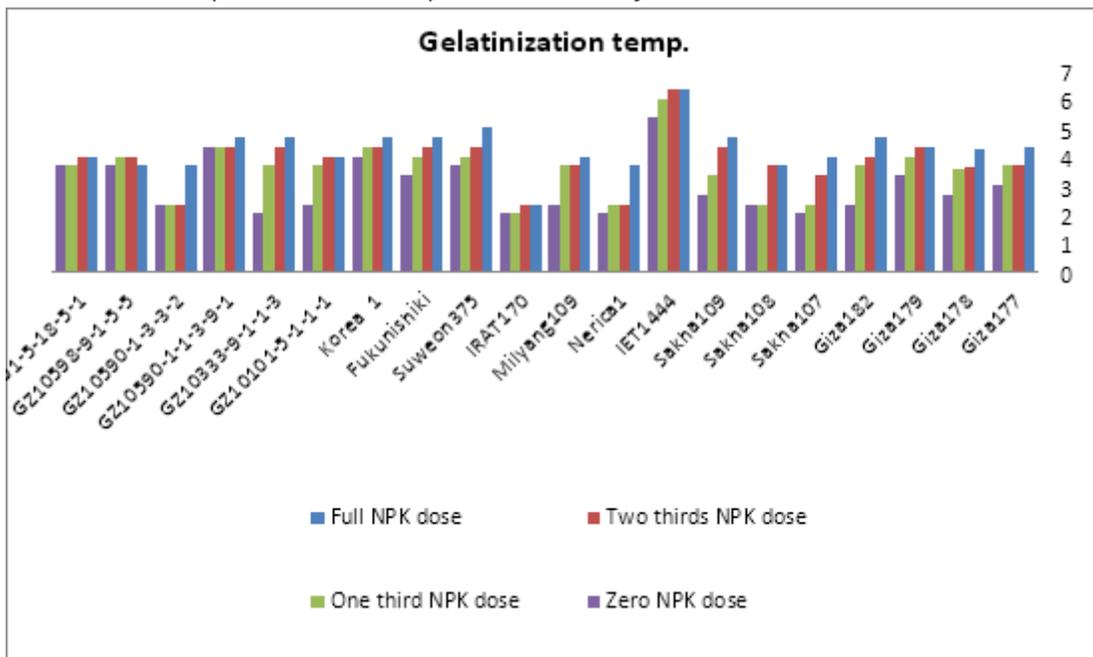


Figure 8

Mean performance of gelatinization temperature trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

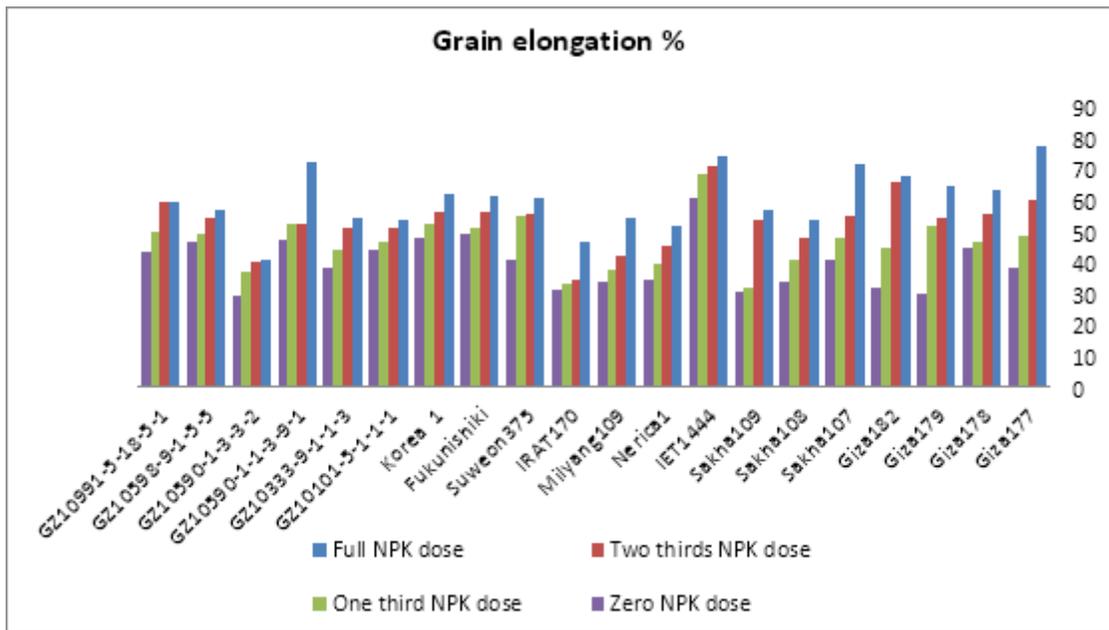


Figure 9

Mean performance of grain elongation % trait among twenty rice genotypes over two contrasting environments (2019 and 2020) as affected by NPK treatments

Dendrogram using Average Linkage (Between Groups)

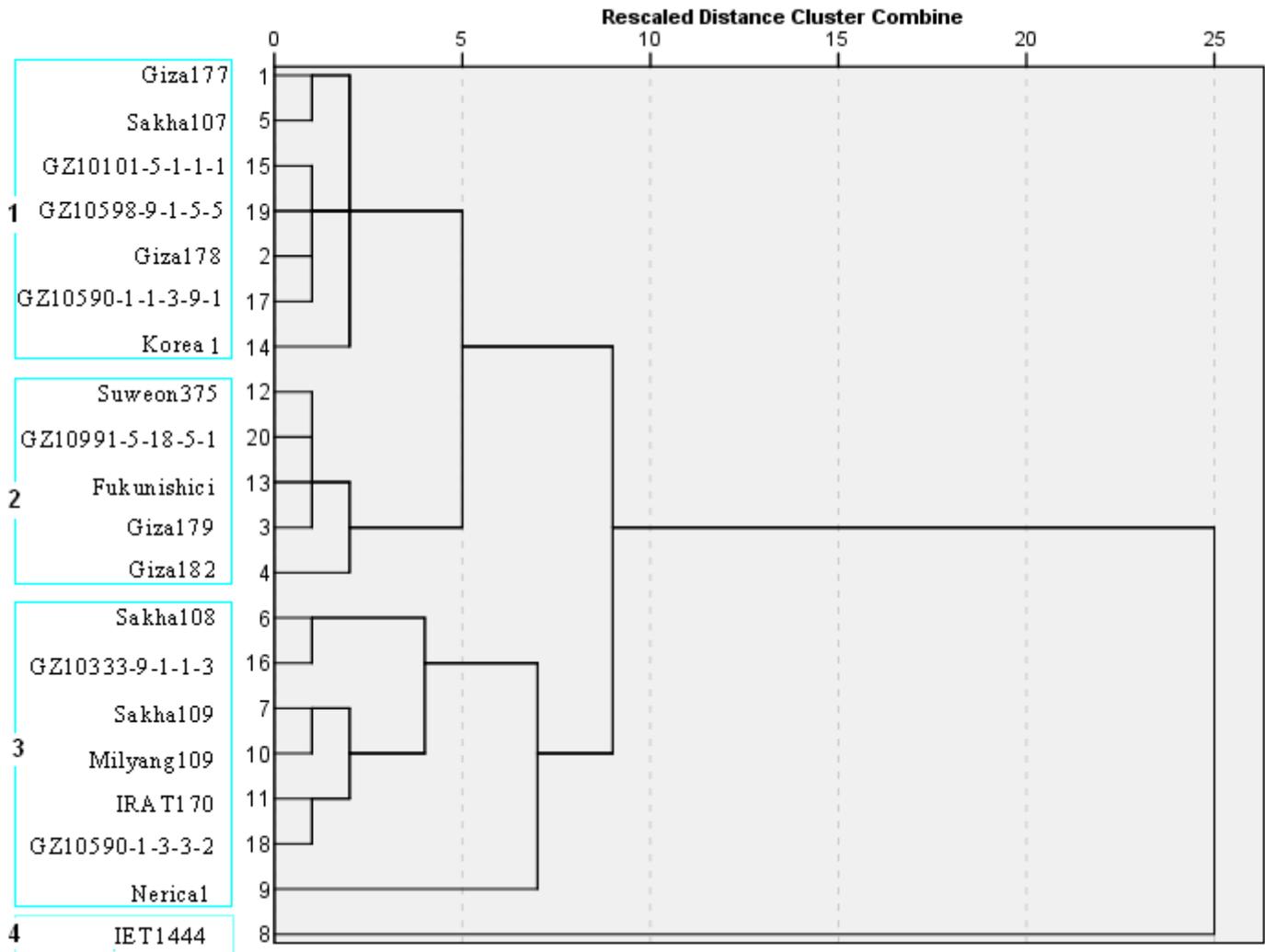


Figure 11

Clustering pattern (pooled over 2019 and 2020 seasons, RRTC, Sakha, Egypt) of the twenty Egyptian and exotic rice genotypes using Ward`s method based on grain yield and quality traits