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*Original Research Article*

# Agronomic Performance, Genetic Variability and Heritability of Yield and its Attributing Characters in Maize (*Zea mays* L.) Hybrids Grown in Northern Sudan

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## Abstract

**Two introduced Egyptian maize hybrids from Misr HyTtech Co. (HyTech2066-Yellow and HyTech1100-White) were tested against two standard checks (Pan6966 and Hudieba2) in Merowe Research Station Farm for two consecutive winter seasons (2012/13 and 2013/14) to estimate the genetic variability, broad sense heritability, genetic advance and correlation coefficient analysis. The genotypes were arranged in RCB Design with 3 replicates. Grain yield, yield components and related traits were studied. The maize hybrids showed significant differences for all the parameters studied except the 100 – grain weight. The results obtained indicated that the yellow maize hybrid HyTech2066 gave significantly out - yielded than the two standard checks in grain yield with average yield advantage over Hudieba2 and Pan6966 amounting to 22.6% and 24.1% respectively. HyTech2066 was significantly earlier than the check Pan6966. The genetic advance as percent of mean was high for plant height (16.77%), cob length (16.43%), days to 50% tasseling (6.21%), number of plants per plot (5.42%), number of cobs per plant (1.88%), and days to 90% maturity (0.75%) indicating additive gene action for these traits. High estimates of heritability were observed for cob length, plant height and days to 50% tasseling . High to moderate heritability with moderate estimates of genetic advance recorded for plant height, number of plants per plot and days to 50% tasseling where careful selection may lead towards improvement for these traits. Hence, provides better opportunities for selecting plant material for these traits in maize.**

**Keywords:** Characters, Grain Yield, Heritability, Maize, Variability

## INTRODUCTION

Maize also known as Corn (*Zea mays* L.) is a grain crop that belongs to the family *Poaceae*. The origin of this grain remains unknown, however, many historians believe that maize was first domesticated in Mexico's Tehuacan valley, then introduced to Africa by the Portuguese in the sixteenth century and has become Africa's most important staple food crop (FAO, 2005). Maize is the most important cereal crop in the world after wheat and rice. It has great yield potential and attained the leading position among cereal based on production as well as productivity and that is why it is called "queen of cereals" (Turi *et al.,* 2007). Maize is multipurpose crop, provides food for human, feed for animals and poultry, and fodder for livestock. It is rich source of raw materials for industry. Also, maize is an important source of calories and protein in human lives in many countries of the world and is the main staple food in Africa particularly in eastern Africa (Salami *et al*., 2007). The top ten maize producers in 2016/2017 (in million metric tons) were United States of America (385), China (219,5), Brazil (91,5), Argentina (37,5), Ukraine (28 ), India (26), Russia (15,5), South Africa(14,6), Canada (13,2) and Indonesia (10,2) (FAOSTAT, 2017).

In Sudan, it ranks 4th in importance as a cereal crop coming after sorghum, millets and wheat. It is grown mainly as feed crop (both grain and forage) and rarely as food crop. Recently, the demand for maize has increased dramatically due to the flourishing industry of poultry and animal fattening. Imports of corn have been doubled, rising from < 20000 ton during the 1990s to > 40000 ton during the 2000s (FAOSTAT, 2011).

The success of any crop improvement programme not only dependent on the amount of genetic variability present in the population but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Wang *et al.,* 2011). Genetic variability for agronomic characters therefore is a key component of breeding programmes for broadening the gene pool of crops (Ahmad *et al.,* 2011). Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. It provides information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of selection procedures used by the plant breeder to decide which selection methods would be most useful to improve the character, to predict gain from selection and to determine the relative importance of genetic effects (Laghari *et al.,* 2010). The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer and Mackay, 1996). Different researchers (Nelson and Somers, 1992) and (Rafique *et al.,* 2004) have reported high heritability and high genetic advance for different yield controlling traits in maize. Therefore, availability of good knowledge of these genetic parameters existing in different yield contributing characters and the relative proportion of this genetic information in various quantitative traits is a pre-requisite for effective crop improvement.

Improvements in yield can be achieved by selection for grain yield, 1000 grain weight, plant height, ear height (Prodhan and Rai, 1997). The additive genetic variance component is the most important component of genetic variability for all traits (Betran and Hallauer, 1996). All this information helps a plant breeder to ensure efficient cultivar selection and screening of available sources of maize germplasm i.e. maize hybrids and synthetics involving two or more characters simultaneously for desirable attributes..

The purpose of the present study is to assess genetic variability and heritability for yield and its attributing characters in maize hybrids. The results from this investigation would serve as a guide to plant breeders to initiate an improvement grain yield.

## MATERIALS AND METHODS

### Plant materials

Four maize genotypes (Table 1) comprising two introduced maize hybrids from Misr HyTtech Co. (HyTech2066, HyTech1100) and two standard checks (Pan6966, Hudieba2) were investigated. The two check varieties were released by the Agricultural Research Corporation (ARC) for commercial cultivation in the Sudan.

### Cultural practices

Sowing date was effected in the last week of November. The genotypes were arranged in RCB design with 3 replicates. The plot size was 5 ridges each 5 m long spaced 0.75 m**.** Two seeds were placed in holes spaced at 20 cm on one side of the ridge. Nitrogen was added as urea (46%) at the second watering at a rate of 55 Kg N/ha. The experiment was irrigated every 10- 12 days throughout the growing season. Weeds were kept to minimum by hand removal during the first month from sowing. Pests, specially stem borers, were monitored and controlled if required.

### Data collected

Grain yield was estimated by harvesting the cubs in the inner 3 ridges leaving 0.5 m from each side. Days to 50% tasseling and days 90% maturity were recorded. Number of cobs per plant, cob length (cm), number of plants/plot at harvest, 100 –grain weight (g) and plant height (cm) were recorded in two seasons.

### Phenotypic and genotypic variability

The variability present in the genotypes was estimated by simple measure, namely range, mean, standard error, phenotypic and genotypic variance and coefficient of variation. The phenotypic and genotypic variance and coefficient of variation were estimated according to the methods suggested by (Burton and Devane, 1953) as follows:

$\sigma^2 g = (Mg - Me) / r$

Where:

$\sigma^2 p$ = Phenotypic variance

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Environmental (error) variance (Error mean square)

Mg = mean square of genotypes

**Table 1.** Plant materials used in the study

| Entry | Name | Type | Seed color | Source |
|---|---|---|---|---|
| 1 | Hudieba2 (check) | Open pollinated | Yellow | ARC , Sudan |
| 2 | Pan6966 (check) | One way hybrid | Yellow | Pannar Co. South Africa |
| 3 | HyTech2066 | One way hybrid | Yellow | Misr HyTech Co. Egypt |
| 4 | HyTech1100 | Three way hybrid | White | Misr HyTech Co. Egypt |

**Table 2.** Mean squares of yield and some yield components for 4 maize hybrids grown during two seasons 2012/13, 2013/14

| Characters | Season (d.f = 1) | Genotype (d.f = 3) | Seas. X geno. (d.f = 3) | Pooled error (d.f = 4) |
|---|---|---|---|---|
| Days to 50% tasseling | 228.167*** | 51.278*** | 8.167* | 2.639 |
| Days to 90% maturity | 816.667*** | 26.778*** | 19.667*** | 0.306 |
| Plant height (cm) | 1536.00* | 3073.571*** | 331.315ns | 233.493 |
| No. of plants/Plot | 3825.375* | 303.819* | 72.375ns | 110.722 |
| No. of cobs/plant | 0.240*** | 0.036* | 0.028* | 0.013 |
| Cob length (cm) | 4.378* | 9.737*** | 0.418ns | 0.574 |
| 100-grain weight | 345.042** | 1.931ns | 4.819ns | 2.458 |
| Grain yield | 30632041.500* | 37277625.222** | 139311.611n.s | 495739.333 |

*, ** and *** Significant at 0.05, 0.01 and 0.001 levels of probability, respectively.
n.s: non-significant difference at 0.05 probability level.

Me = mean square of error,
r = Number of replication
Phenotypic coefficient of variation, PCV = ($\sqrt{\sigma^2 g} / x$) x100
Genotypic coefficient of variation, GCV = ($\sqrt{\sigma^2 p} / x$) x 100
Where x= population mean

### Estimate of heritability

Heritability ($H^2$) in broad sense for all characters was computed using the formula adopted by (Allard, 1960) as:
$H^2 = (\sigma^2 g / \sigma^2 p) \times 100$
$\sigma^2 p = \sigma^2 g + = \sigma^2 e$
Where:
$\sigma^2 g$ = genotypic variance
$\sigma^2 p$ = phenotypic variance
$\sigma^2 e$ = error variance

### Estimation of expected genetic advance

Genetic advance (GA) for each character was computed using the formula adopted from (Johnson *et al.,* 1955) and (Allard, 1960).
GA= (k) ($\sigma$ p)* ($H^2$), and
GA (as % of the mean) = (GA / $\bar{x}$) x 100
Where, k= selection differential (k = 2.06 at 5% selection intensity)
$\sigma$ p = phenotypic standard deviation
$H^2$ = heritability (Broad sense)
$\bar{x}$ = Grand mean

### Statistical analysis

Separate ANOVA for grain yield and related traits before running the combined analysis. The mean separation was done using Duncan's Multiple Range Test (DMRT) for the different characters collected from the field experiments. The statistical analysis using MSTATC program.

## RESULTS AND DISCUSSIONS

### Analysis of Variance

Mean squares of 8 traits of the four maize hybrids in the two environments (seasons) are shown in Table 2. There were significant differences among genotypes, seasons and their interaction (P ≤ 0.01) for most of the studied traits.

### Yield related traits

Table 3 and 4 shows mean squares from combined ANOVA for yield related traits. The hybrid HyTech2066 tasseled significantly earlier than the check Pan6966 and was comparable or even earlier than check Hudaieba2. As could be seen in Table 3, days to tassel shown by HyTech2066 taking 71 days whereas that of the check Pan6966 taking 76 days. The hybrid HyTech1100 was similar to the check Pan6966 taking 77 days to tassel but

**Table 3.** Average performance for days to 50% tasseling, days 90% maturity and plant height (cm) of 4 maize hybrids, combined over two seasons.

| Genotype | DT | DM | PH |
|---|---|---|---|
| Hudieba2 (check) | 72 | 114 | 202 |
| Pan6966 (check) | 76 | 119 | 251 |
| HyTech2066 | 71 | 115 | 216 |
| HyTech1100 | 77 | 116 | 243 |
| Mean | 74 | 116 | 228 |
| S.E± | 0.663*** | 0.225*** | 6.238*** |
| C.V (%) | 2.1 | 0.4 | 6.6 |

DT: Days to 50 % tasseling , DM: Days to 90 % maturity, PH: Plant height (cm).
*** Significant at 0.001 probability level

**Table 4.** Grain yield (kg/ha) and its primary components of 4 maize hybrids, combined over two seasons

| Genotype | GY | NPP | NCP | CL | HSW |
|---|---|---|---|---|---|
| **Hudieba2 (check)** | 5208 | 170 | 1.20 | 14.2 | 17.8 |
| **Pan6966 (check)** | 5111 | 167 | 1.31 | 13.2 | 18.3 |
| **HyTech2066** | 6734 | 157 | 1.13 | 16.2 | 19.0 |
| **HyTech1100** | 5160 | 156 | 1.25 | 14.7 | 19.0 |
| **Mean** | 5553 | 163 | 1.22 | 14.6 | 18.5 |
| **S.E±** | 287.44** | 4.295* | 0.046* | 0.309*** | 0.64n.s |
| **C.V (%)** | 12.6 | 6.4 | 9.2 | 5.1 | 8.4 |

GY: grain yield (kg ha-1), NPP: Number of plants per plot, NCP: Number of cobs per plant, CL: cob length (cm), HSW: hundred grain weight (g).
*, ** and *** Significant at 0.05, 0.01 and 0.001 probability level respectively.
n.s: non-significant difference at 0.05 probability level.

was later than the check Hudieba2 that took 72 days to tassel. The results might be due to high genetic variability for days to 50% tasseling existing in different maize hybrids. The results are in agreement with the findings of (Rather and Shaikh, 1999) who also reported different days to 50 % tasseling in maize.

Maximum plant height (243 cm) was observed for HyTech1100, while minimum plant height was recorded for the check Hudieba2 with a value of (202 cm). These differences for plant height might be due to genetic variations among the hybrids. These results are in line with the finding of Umakanth and Satyanarayana (2000) who reported similar results on genetic differences for plant height among different maize hybrids.

Maximum cob length (16.2 cm) was recorded for hybrid HyTech2066, whereas minimum for the check hybrid Pan6966 with a value of 13.2 cm. These divergences in cob legth may be due to the different inherited backgrounds of the various maize hybrids. These results are in harmony with (Rahman *et al.,* 1995) and (Singha and Prodhan, 2000), who also observed similar results for genetic variability in cob length of selected maize hybrids. The two hybrids recored the highest seed weight while the check Hudieba2 gave the lowest value.

The hybrid HyTech2066 had the highest mean value for cob length, 100 - grain weight and grain yield (kg ha$^{-1}$). The check Hudieba2 recorded the highest mean value for plant height and number of cobs per plant, while the check Pan6966 had the highest mean value for number of plants per plot. The check Hudieba2 had the lowest mean values for plant height and 100 - grain weight (Table 4).

## Grain Yield

Table 4 shows grain yield obtained by different genotypes in combined over two seasons. Among the maize hybrids maximum yield (6734 kg ha$^{-1}$) was obtained by hybrid HyTech2066 (yellow). It gave significantly higher than obtained by the checks, Pan6966 (5551 kg ha$^{-1}$) and Hudieba2 (5208 kg ha$^{-1}$). The increment in yields over the checks amounted to 22.6% and 24.1% respectively (Table 4), while the minimum yield was obtained by the check hybrid Pan6966 with a value of (5111 kg ha$^{-1}$). The difference in yield among different maize hybrids may be due to their different genetic background. The results are in agreement with the findings of (Drinic and Vancetovic, 1994), which obtained similar results and further confirmed by (Zhang et al., 2000).

## Genetic parameters

Estimates of phenotypic and genotypic variances,

**Table 5.** Estimation of genetic parameters for different quantitative characters of 4 maize hybrids, combined over two seasons

| **Characters** | **$\delta^2$g** | **$\delta^2$ph** | **GCV (%)** | **PCV (%)** | **$H^2$ (%)** | **GA** | **GAM (%)** |
|---|---|---|---|---|---|---|---|
| Tasseling | 7.18 | 10.33 | 66.98 | 80.35 | 69.50 | 4.60 | 6.21 |
| Maturity | 1.18 | 7.78 | 27.15 | 69.73 | 15.16 | 0.87 | 0.75 |
| Plant height | 457.04 | 606.38 | 534.46 | 615.61 | 75.37 | 38.24 | 16.77 |
| Plants/Plot | 38.75 | 81.32 | 155.62 | 225.44 | 47.65 | 8.85 | 5.42 |
| Cobs/plant | 0.0013 | 0.0127 | 0.90 | 2.81 | 10.23 | 0.023 | 1.88 |
| Cob length | 1.55 | 1.78 | 31.12 | 33.35 | 87.07 | 2.40 | 16.43 |
| 100-grain weight | - | - | - | - | - | - | - |
| Grain yield | 6189718.9 | 6318779.3 | 62197.8 | 62842.9 | 97.95 | 5072.51 | 91.34 |

$\delta^2$g = Genotypic variance, δ2ph = Phenotypic variance, PCV = Phenotypic coefficient of variance, GCV = Genotypic coefficient of variance, $H^2$ (%)= Broad sense heritability, GA = Genetic advance, GAM= Genetic advance as percent of mean.

phenotypic coefficient of variance, genotypic coefficient of variance, broad sense heritability, genetic advance and genetic advance as percent of mean are presented in Table (5).

Hence in conclusion high estimates of genotypic and phenotypic coefficient of variations were observed plant height, number of plants per plot and days to 50% tasseling suggesting sufficient variability and thus offers scope for genetic improvement through selection. High magnitude of broad sense heritability estimated in all the characters except number of cobs per plant and days to 90% maturity, (Table 5). This implied the possibility of effective selection for genetic improvement of these traits. High heritability estimates for cob length (87.07) and plant height (75.34). Similar results were reported by (Aboyi *et al.,* 2004); (Mohammad Akbar *et al.,* 2006); (Sofi and Rather 2007); (Ali *et al.,* 2010) and (Ram Reddy *et al.,* 2012). Values of genetic advance as percent of mean ranged from 91.34 for grain yield to 0.75 for days to 90% maturity. Genetic advance as percent of mean was also high for cob length and days to 50% tasseling (Table 5). Similarly (Bekele and Rao, 2014) also reported high genetic advance for plant height, cob length and grain yield per plot. The high heritability coupled with high genetic advance noticed for these traits indicate the role of additive gene action in controlling the traits.

## CONCLUSION

Preceding results and discussion revealed that different maize hybrids have performed differently for grain yield and yield components except 100 – seed weight. The hybrid HyTech2066 have resulted in a better performance for grain yield and yield components and gave significant increase in yield over the two checks Pan6966 (24.1%) and Hudieba2 (22.6%). Heritability estimates along with genetic advance is more helpful in foresee the genetic gain under selection than heritability estimates alone. High genetic advance joined with heritability was observed for cob length (cm) and plant height. Therefore selection of genotypes based on these indicated traits will be effective.

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