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# EVALUATION OF QUANTITATIVE YIELD PERFORMANCE OF PUMPKIN ACCESSIONS IN KENYA USING MOTHER TRIALS

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## ABSTRACT
Quantitative yield performance of pumpkin (*Cucurbita moschata (*Lam.) Poir.) accessions was evaluated for two seasons in 2012 and 2013. Accessions were planted on-station in KALRO Kakamega and Embu farms at a spacing of 2 m x 2 m in a replicated Completely Randomised Design. Analysis of variance indicated significant variations among accessions in all yield parameters. The number of female and male flowers ranged from 1-10 and 11-197, respectively. Fruits per accession ranged from 1-9. Accession KK-40 produced 9 fruits. Average fruit weight was 4.2 kg in NY-130 and 0.2 kg in NY-77. Total fruit weight was between 0.2 kg and 15.9 kg for NY-77 and KK-40, respectively. Kakamega trials were yielded highest in most characters, except 100-seed weight, which was 14.2 g and 12.5 g in Embu and Kakamega, respectively. The yield parameters were subjected to phenotypic, genotypic, environmental, phenotypic coefficient, genotypic coefficient, heritability, genetic advance and correlation analysis. The highest GCV and PCV resulted in fruit number and total weight per accession, respectively. PCV was higher than GCV for all yield parameters, meaning that the variations were not only due to genotype, but also due to environment. The high heritability and high genetic advance of seed number and 100-seed weight indicates that effective selection can be based on these characters. The high GCV, PCV, heritability and genetic advance values can be applied to select and isolate high yielding accessions for improvement into commercial cultivars.

**KEYWORDS:** Coefficient of Variation, Genotype, Genetic Advance, Heritability, Phenotype.

## INTRODUCTION
Pumpkin (*Cucurbita moschata* Duch) is a very popular vegetable in tropical and sub-tropical countries (Ahamed *et al*., 2011). There are many varieties and farmer variety landraces that have been selected for adaptability to local conditions (Radovich, 2010). Evaluation is an integral part of good crop management that enable researchers to learn and make adjustments, revise objectives and methods that make real contribution to solving agricultural and environmental problems (Twomlow and Lilja, 2004). Mother trials are evaluated under researcher managed recommended practices, or researcher managed farmers' practices (Baluti *et al.,* 2011). They are planted in the centre of farming communities and incorporate multiple aspects of natural resource use into sustainable crop management to meet goals such as poverty alleviation, welfare of future generations and environmental conservation, and direct uses such as food security, profitability and risk aversion (Twomlow and Lilja, 2004). Quantitative traits with agro-economical value like fruit and seed weight, fruit number, seeds and leaves and flowers are complex in nature because they confirm polygenic inheritance and are greatly influenced by minute fluctuation of environmental components (Roychowdhury and Tah, 2011). Local landraces are known to withstand adverse weather conditions (Oloyede, 2013), but their yields are influenced by growing conditions, genetics, soil and fertilization (Karklelienė *et al*., 2008). Pumpkin genotypes with all-round resistance to major pests and abiotic stresses improve yields at the farm level (Baluti *et al.,* 2011).

Pumpkins come across many problems that limit full expression of their growth and productivity (Sajjan and Prasad, 2009). In Kenya, they receive little research and development attention, compared to major crops. Pumpkins with diverse characteristics are grown in different parts of Kenya, with varied agro-climactic conditions. Their performance in attainable yield is inconsistent (Kumar *et al*., 2014). Genetic improvement of pumpkin yields depends on the analysis of variance of each mean value, phenotypic and genotypic variances, phenotypic and genotypic coefficient of variation, broad sense heritability and genetic gain (Roychowdhury and Tah, 2011). Variations due to cross-pollination (Ahamed *et al.,* 2011) and exotic introductions are high. Little information on cultivars with better plant growth (Sajjan and Prasad, 2009), fruit and seed yield performance that could be used to delineate and standardize different accessions is available (Ahamed *et al.,* 2011; Isutsa and Mallowa, 2013; Mwaura *et al*., 2014; Kiharason *et al*., 2015). In Kenya, there are no recommended pumpkin cultivars. Kenya being a secondary centre of diversity has a wide array of pumpkin genotypes that need detailed evaluation (Karuri *et al*., 2010) and genetic analysis. The present study conducted on-station evaluation and analysis of genetic variability of pumpkin accessions, collected from varied agro-ecological zones in Kakamega and Nyeri, so as to provide a basis for effective selection by breeders for improvement into standard cultivars.

## MATERIALS & METHODS

### Research Site

Mother trial accessions were planted on Kenya Agriculture and Livestock Research Organizations (KALRO) farms in Kakamega and Embu. The KALRO Embu farm is located at 00° 32' S, 37° 27' E, 1560 m above sea level, has Nitisol soils and 1000 mm average annual rainfall. The KALRO Kakamega farm is located at 00° 34' S and 34° 49' E, 1700 m asl, has loamy soils, and 1200 mm average annual rainfall (Jaetzold and Schmidt, 1983).

### Experimental Design and Planting of Accessions

A total of 72 and 79 accessions were planted in Kakamega and Embu, respectively, in a completely randomized design, with three replications for two seasons. Exotic cultivar Sugar Baby was used as control. The accessions were planted on-station at a spacing of 2 m x 2 m on 21$^{st}$ June and 29$^{th}$ September, 2012, and on 8$^{th}$ April and 13$^{th}$ April, 2013 in Embu and Kakamega, respectively, and managed by the researcher. Each accession represented a research plot. Farmers' practices were followed during entire plant management period.

Five plants per accession were tagged for evaluation and their average data values were used for analyses. Evaluation was conducted using some IPGRI descriptors for cucurbits. At maturity each accession was harvested individually and planted once more in the second season to determine stability. Fruits were harvested when 50% started changing colour from green to brown. Variables assessed per plant were number of female and male flowers, fruit and seed number, leaf number, fruit weight, length and width, and 100-seed weight. The performance of accessions was compared using matrix ranking through focus group discussions. Comparisons of local accessions to the exotic 'Sugar Baby' were also made.

### Data Analysis

Data recording was done from 20 days after planting up to harvesting. Descriptive statistics were calculated and subjected to analysis of variance using SAS program. To estimate the extent of variation, components of variance, including $\sigma^2g$ (Genotypic variance), $\sigma^2p$ (Phenotypic variance) and $\sigma^2e$ (environmental variance) were calculated using Kwon and Torrie (1964) formulae. Genotypic variance ($\sigma^2g$) = (MSA – MSE)/r; Phenotypic variance ($\sigma^2p$) = ($\sigma^2g$ + $\sigma^2e$)/r; Environmental variance ($\sigma^2e$) = MSE, where MSA, MSE and r refer to mean squares of accessions, mean squares of error and number of replications, respectively (Ahsan *et al.*, 2015). Phenotypic and genotypic coefficients of variation were calculated using the formula given by Singh and Chaudhary (1985) that PCV (%) = ($\sigma p$/X) * 100, GCV (%) = ($\sigma g$/X)*100, where $\sigma p$, $\sigma g$ and X refer to the phenotypic, genotypic standard deviations and grand mean of respective characters, respectively (Bozokalfa *et al*., 2010). Broad sense heritability ($h^2$) was estimated on genotypic mean using the formula: *Heritability* ($h^2$) = $\sigma^2g/\sigma^2p$, *w*here $h^2$ =broad sense heritability, $\sigma 2g$ = genotypic variance, $\sigma^2p$ = phenotypic variance (Allard, 1999; Bozokalfa *et al*., 2010). Expected genetic advance (GA) and percentage of GA of the mean were calculated using the formula: Expected genetic advance (GA) = $i\sigma p h^2$; GA (%) = *(GA/*X) *100, where i= standardized selection differential constant 2.06 is used at $P$ = 0.05, $\sigma p$ =phenotypic standard deviation, $h^2$ =broad sense heritability, X = grand mean (Bozokalfa *et al*., 2010). Simple correlation coefficients were obtained using Pearson correlation analysis to determine associations between different characteristics. Significance levels were determined using $P$=0.05.

## RESULTS & DISCUSSION

### Quantitative Yield Factors

Analysis of variance revealed significant differences ($P$<0.05) among the accessions, and between Kakamega and Embu mother trials for all the quantitative yield characteristics (Table 1). The female and male flowers were highest in KK-40 (Table 2) and in Kakamega (Figure 1).

**TABLE 1:** Analysis of variance of quantitative traits of accessions in Kakamega and Embu mother trial

| Characters | Minimum value | Maximum value | Accessions mean | Kakamega and Embu *P*-value | Accessions *P*-value |
|---|---|---|---|---|---|
| No. of female flowers/plant | 1 | 10 | 2.7 | 0.000 | 0.000 |
| No. of male flowers/plant | 11 | 197 | 73.5 | 0.000 | 0.000 |
| Average fruit weight (kg/plant) | 0.2 | 4.2 | 1.4 | 0.000 | 0.018 |
| Total fruit weight (kg/plant) | 0.2 | 15.9 | 3.2 | 0.000 | 0.000 |
| No. of fruits/accession | 1 | 9 | 2.3 | 0.000 | 0.000 |
| No. of leaves/accession | 84 | 392 | 190.1 | 0.000 | 0.000 |
| No. of seeds/fruit/accession | 41 | 773 | 263.2 | 0.000 | 0.000 |
| 100-seed weight (g/plant) | 5.6 | 32.9 | 13.2 | 0.000 | 0.000 |
| Fruit length (cm/plant) | 7 | 35.1 | 18.5 | 0.000 | 0.000 |
| Fruit width (cm/plant) | 7 | 24.5 | 14.6 | 0.000 | 0.000 |

The mean male and female flowers in Kakamega and Embu were 86.1 and 63, and 3.4 and 2.1 flowers, respectively (Figure 1). Most of the flowers were mostly male flowers. The number of leaves per accession was high in Kakamega (Figure 1), and in accession KK-40 (Table 2). Accessions NY-150 had the least leaves. The average leaves were 216 and 168.7 in Kakamega and Embu, respectively.

Kakamega had the highest average and total fruit weight, and number of fruits (Figure 1). The fruit number and total weight were high in accession KK-40, whereas average fruit weight was high in NY-130 (Table 2).

**TABLE 2:** Accessions giving highest and lowest performance for each highlighted character

| Code name | Character | NFF | NMF | NFA | AFW | TFW | NLA | NSA | 100-SW | FL | FW |
|---|---|---|---|---|---|---|---|---|---|---|---|
| KK-40 | NFF | 10 | 181 | 9 | 1.8 | 15.9 | 392 | 264 | 10.95 | 14 | 17 |
| KK-45 | | 10 | 169 | 7 | 1.9 | 13.2 | 211 | 488 | 13.09 | 14 | 17.1 |
| NY-85 | | 1 | 48 | 1 | 1 | 1 | 177 | 189 | 13.7 | 13 | 15 |
| NY-90 | | 1 | 17 | 1 | 1 | 1 | 142 | 268 | 12.48 | 12.9 | 13.5 |
| NY-117 | | 1 | 28 | 1 | 1 | 1 | 154 | 127 | 10.51 | 15 | 11 |
| NY-119 | | 1 | 24 | 1 | 1.3 | 1.3 | 153 | 285 | 8.09 | 11.6 | 17.7 |
| NY-129 | | 1 | 23 | 1 | 0.7 | 0.7 | 149 | 119 | 10.9 | 12 | 13.2 |
| NY-131 | | 1 | 16 | 1 | 0.25 | 0.25 | 148 | 152 | 15.54 | 11.4 | 9.2 |
| NY-137 | | 1 | 17 | 1 | 0.75 | 0.75 | 159 | 122 | 25.41 | 12.4 | 17.7 |
| NY-139 | | 1 | 23 | 1 | 0.5 | 0.5 | 163 | 98 | 5.56 | 10.8 | 9 |
| NY-145 | | 1 | 25 | 1 | 1 | 1 | 162 | 135 | 23.37 | 14 | 12 |
| NY-146 | | 1 | 28 | 1 | 0.25 | 0.25 | 158 | 55 | 22.58 | 12 | 11.4 |
| NY-155 | | 1 | 26 | 1 | 0.5 | 0.5 | 159 | 96 | 14.11 | 13.5 | 12 |
| KK-40 | NMF | 10 | 181 | 9 | 1.8 | 15.9 | 392 | 264 | 10.95 | 14 | 17 |
| NY-90 | | 1 | 17 | 1 | 1 | 1 | 142 | 268 | 12.48 | 12.9 | 13.5 |
| NY-131 | | 1 | 16 | 1 | 0.25 | 0.25 | 148 | 152 | 15.54 | 11.4 | 9.2 |
| KK-40 | NFA | 10 | 181 | 9 | 1.8 | 15.9 | 392 | 264 | 10.95 | 14 | 17 |
| KK-41 | | 1 | 38 | 1 | 1 | 1 | 180 | 134 | 14.15 | 17 | 11 |
| NY-74 | | 1 | 36 | 1 | 0.4 | 0.4 | 164 | 107 | 12.1 | 7 | 8 |
| NY-77 | | 1 | 22 | 1 | 0.2 | 0.2 | 155 | 250 | 5.64 | 19 | 13 |
| NY-78 | | 1 | 33 | 1 | 0.5 | 0.5 | 157 | 183 | 11.71 | 11.2 | 10 |
| NY-81 | | 1 | 30 | 1 | 1 | 1 | 174 | 159 | 8.41 | 18.2 | 11.6 |
| NY-83 | | 2 | 33 | 1 | 0.9 | 0.9 | 163 | 214 | 7.36 | 10.3 | 13 |
| NY-85 | | 1 | 48 | 1 | 1 | 1 | 177 | 189 | 13.7 | 13 | 15 |
| NY-91 | | 1 | 24 | 1 | 0.8 | 0.8 | 157 | 274 | 12.56 | 10 | 11 |
| NY-94 | | 2 | 27 | 1 | 1.5 | 1.5 | 160 | 381 | 10.98 | 16.2 | 15.3 |
| NY-98 | | 1 | 30 | 1 | 0.8 | 0.8 | 164 | 91 | 12.88 | 11 | 8.7 |
| NY-99 | | 1 | 32 | 1 | 0.5 | 0.5 | 164 | 78 | 5.86 | 12 | 10 |
| NY-101 | | 1 | 31 | 1 | 0.25 | 0.25 | 185 | 73 | 23.53 | 12.5 | 13.7 |
| NY-103 | | 1 | 18 | 1 | 1 | 1 | 144 | 276 | 11.94 | 10.9 | 13 |
| NY-113 | | 1 | 28 | 1 | 1 | 1 | 165 | 210 | 16.68 | 15 | 11 |
| NY-114 | | 1 | 33 | 1 | 1 | 1 | 160 | 192 | 11.71 | 14 | 12.2 |
| NY-115 | | 1 | 38 | 1 | 1 | 1 | 166 | 148 | 12.43 | 12 | 15 |
| NY-124 | | 1 | 28 | 1 | 0.5 | 0.5 | 162 | 137 | 20.14 | 12 | 10 |
| NY-127 | | 1 | 33 | 1 | 0.25 | 0.25 | 166 | 56 | 19.38 | 11 | 11 |
| NY-129 | | 1 | 23 | 1 | 0.7 | 0.7 | 149 | 119 | 10.9 | 12 | 13.2 |
| NY-133 | | 1 | 30 | 1 | 0.5 | 0.5 | 157 | 82 | 13.98 | 9 | 11 |
| NY-135 | | 1 | 27 | 1 | 2 | 2 | 163 | 162 | 24.85 | 17.5 | 16 |
| NY-140 | | 1 | 42 | 1 | 0.5 | 0.5 | 159 | 129 | 6.64 | 9.3 | 11.5 |
| NY-145 | | 1 | 25 | 1 | 1 | 1 | 162 | 135 | 23.37 | 14 | 12 |
| NY-148 | | 1 | 31 | 1 | 0.4 | 0.4 | 167 | 199 | 18.77 | 9 | 10 |
| NY-152 | | 1 | 25 | 1 | 0.9 | 0.9 | 162 | 178 | 8.89 | 13 | 8.8 |
| NY-155 | | 1 | 26 | 1 | 0.5 | 0.5 | 159 | 96 | 14.11 | 13.5 | 12 |
| NY-130 | AFW | 2 | 56 | 1 | 4.25 | 4.25 | 191 | 189 | 25.89 | 20.4 | 19.7 |
| NY-77 | | 1 | 22 | 1 | 0.2 | 0.2 | 155 | 250 | 5.64 | 19 | 13 |
| KK-40 | TFW | 10 | 181 | 9 | 1.8 | 15.9 | 392 | 264 | 10.95 | 14 | 17 |
| NY-77 | | 1 | 22 | 1 | 0.2 | 0.2 | 155 | 250 | 5.64 | 19 | 13 |
| KK-40 | NLA | 10 | 181 | 9 | 1.8 | 15.9 | 392 | 264 | 10.95 | 14 | 17 |
| NY-150 | | 1 | 41 | 0.5 | 0.5 | 1 | 84 | 104 | 10.5 | 18.4 | 11.8 |
| KK-4 | NSA | 5 | 89 | 4 | 2.9 | 6.6 | 226 | 773 | 13.56 | 21.5 | 15 |
| Exotic | | 1 | 31 | 1 | 0.3 | 0.3 | 113 | 41 | 10.09 | 9.1 | 11 |
| NY-107 | 100SW | 4 | 98 | 2 | 2.75 | 5.5 | 222 | 362 | 32.86 | 20.6 | 16.6 |
| NY-139 | | 1 | 23 | 1 | 0.5 | 0.5 | 163 | 98 | 5.56 | 10.8 | 9 |
| KK_12 | FL | 5 | 111 | 4 | 2.3 | 8.2 | 323 | 657 | 13.36 | 31.9 | 17 |
| NY-74 | | 1 | 36 | 1 | 0.4 | 0.4 | 164 | 107 | 12.1 | 7 | 8 |
| Exotic | FW | 8 | 169 | 7 | 3 | 4 | 356 | 224 | 27.87 | 14.2 | 22 |
| NY-74 | | 1 | 36 | 1 | 0.4 | 0.4 | 164 | 107 | 12.1 | 7 | 8 |

NFF = number of female flowers; NMF = number of male flowers; AFWT = average fruit weight (kg); TFW = total fruit weight (kg); NFA = number of fruits per accessions; NLA = number of leaves per accession; NSA = number of seeds per accession; 100SW = 100-seed weight (g); FL = fruit length (cm); FW = fruit width (cm).

The mean total and average fruit weight, and number of fruits was 4.0 kg and 1.5 kg, and 2.9 in Kakamega; 2.2 and 1.2 kg, and 1.7 in Embu, respectively. Fruit length and width were significantly high in Kakamega (Figure 1). The mean fruit length was 21.5 and 14.8 cm, and width 15.1 and 14 cm in Kakamega and Embu mother trials, respectively. The longest fruit was for KK-12, and the widest was for exotic ‘Sugar Baby’. Fruit length and width were short in NY-74 (Table 2).

Embu had the highest 100-seed weight, whereas the number of seeds in Kakamega was highest (Figure 1). The highest 100-seed weight was for NY-107, and the lowest was for NY-139 (Table 2). The 100-seed weight was 29.1 g in KK-15 and 7.6 g in KK-44. The 100-seed weight was 14.2 g and 12.5 g in Embu and Kakamega, respectively.

### Genetic Variability

### Genotypic and phenotypic variance

Genotypic variance varied from 0.3 for average fruit weight to 29781.8 for seeds per accession (Table 3). Phenotypic variance varied from 0.4 for average fruit weight to 32819.5 for seeds per accession.

Genotypic and phenotypic variances were more than environmental variances, except for male flowers, which were higher and average fruit weight that equaled genotypic variance. The difference in range of variability between phenotypic and genotypic variance was 0.1 in average fruit weight per accession, and highest in number of male flowers, number of leaves and seeds per accession (Table 3).

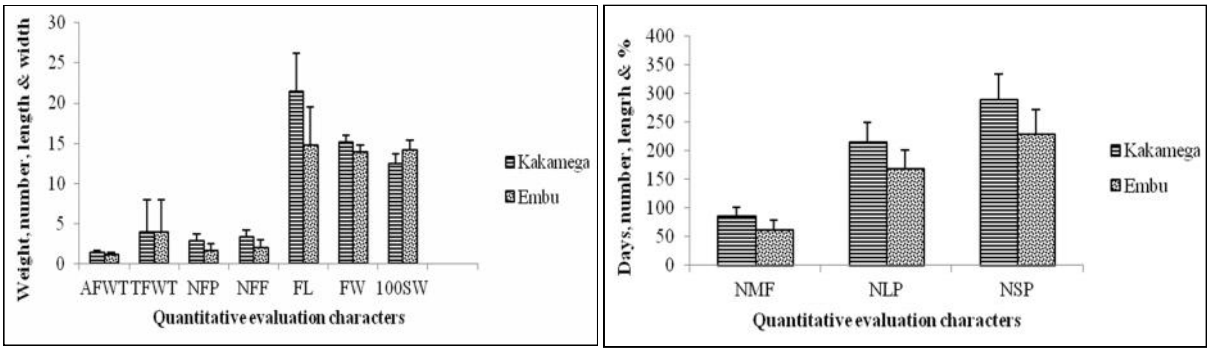


**FIGURE 1**: Yield characters (L) and yield determining characters (R). Error bars represent standard deviation.
AFWT = average fruit weight (kg); TFW = total fruit weight (kg); NFP = number of fruits per plant; NFF = number of female flowers; FL = fruit length (cm); FW = fruit width (cm); 100SW = 100-seed weight (g); NMF = number of male flowers; NLP = number of leaves per plant; NSP = number of seeds per plant

**TABLE 3:** Estimation of variance components $\sigma^2g$, $\sigma^2p$, $\sigma^2e$, phenotypic coefficients of variation, genotypic coefficients of variation, broad sense heritability and genetic advance for yield characters of pumpkin accessions

| Character | Range | Mean | GV ($\sigma^2g$) | PV ($\sigma^2p$) | EV ($\sigma^2e$) | GCV% | PCV% | $h^2B$% | GA | GA% |
|---|---|---|---|---|---|---|---|---|---|---|
| NFF | 1 - 10 | 2.7 | 3.1 | 3.8 | 2.7 | 65.5 | 72.4 | 81.9 | 3.3 | 122.0 |
| NMF | 11 - 182 | 73.5 | 869.9 | 1210.5 | 1021.7 | 40.1 | 47.3 | 71.9 | 51.5 | 70.1 |
| AFW | 0.2 - 4.2 | 1.4 | 0.3 | 0.4 | 0.3 | 40.9 | 47.2 | 74.9 | 1.0 | 72.9 |
| TFW | 0.2 - 15.9 | 3.2 | 8.7 | 10.1 | 4.3 | 92.7 | 100.0 | 85.9 | 5.6 | 176.9 |
| NFA | 1 - 9 | 2.3 | 3.1 | 3.7 | 1.7 | 75.7 | 82.2 | 84.8 | 3.4 | 143.5 |
| NLA | 84 - 392 | 190.1 | 3738.7 | 4545.4 | 2420.1 | 32.2 | 35.5 | 82.3 | 114.2 | 60.1 |
| NSA | 41-773 | 263.2 | 29781.8 | 32819.5 | 9112.9 | 65.6 | 68.8 | 90.7 | 338.7 | 128.7 |
| 100 SW | 5.6 - 32.9 | 13.2 | 66.8 | 70.1 | 9.8 | 61.8 | 63.3 | 95.3 | 16.4 | 124.2 |
| FL | 7 - 35.1 | 18.5 | 69.0 | 79.9 | 32.5 | 44.8 | 48.2 | 86.4 | 15.9 | 85.8 |
| FW | 7 - 24.5 | 14.6 | 9.8 | 12.3 | 7.4 | 21.4 | 23.9 | 79.8 | 5.8 | 39.3 |

PV($\sigma^2p$) = Phenotypic variance, GV($\sigma^2g$) = Genotypic variance, EV($\sigma^2e$) = environmental variance, PCV% = Phenotypic coefficients of variation percentage, GCV% = Genotypic coefficients of variation percentage, $h^2B$ = broad sense heritability, GA = Genetic advance, GA% = Genetic advance percentage, NFF = number of female flowers, NMF = number of male flowers, AFW = average fruit weight (kg), TFW = total fruit weight (kg), NFA = number of fruits per accessions, NLA = number of leaves per accession, NSA = number of seeds per accession, 100SW = 100-seed weight (g), FL = fruit length (cm), FW = fruit width (cm).

### Genotypic and phenotypic coefficients of variation

Genotypic coefficient of variation ranged from 21.4% for fruit width to 92.7% for total fruit weight, while phenotypic coefficient of variation ranged from 23.9% for fruit width to 100% for total fruit weight. Phenotypic coefficients of variation were higher than those of genotypic coefficients of variation. The highest GCV and PCV were for total fruit weight and number of fruits per accession. Total fruit weight had 100% PCV. The lowest GCV and PCV were for number of leaves per accession and fruit width in that order (Table 3). The difference in range of variability between PCV and GCV was above 6.0 for number of female and male flowers, average and total fruit weight, and number of fruits per accession. On the other hand, it was below 4.0 for number of leaves and seeds per accession, 100-seed weight, fruit length and width.

### Heritability and genetic advance

Heritability estimates ranged from 71.9% for number of male flowers to 95.3% for 100-seed weight. Heritability exceeding 70% was observed in all yield characters. The highest heritability was for 100-seed weight, and the lowest was for number of male flowers. Genetic advance was high for number of seeds and leaves per accession. Low genetic advance was for average fruit weight, number of female flowers, total fruit weight, number of fruits per accession and fruit width in that order. The expected genetic gain was highest for total fruit weight and lowest for fruit width. High heritability was accompanied by high expected genetic gain for all characters, except for number of leaves and fruit length. Fruit width had high heritability estimates and low expected genetic gain (Table 3).

**Correlations**

The correlations of yield characteristics were calculated using Pearson correlation (Table 4). Number of male flowers, total fruit weight and number of fruits per accession were highly positively correlated to number of female flowers. Total fruit weight was highly positively correlated with number of fruits per accession and number of male flowers. Number of female flowers was significantly positively correlated with average fruit weight and number of seeds per accession. Number of leaves per accession significantly positively correlated with number of seeds per accession and fruit width, and was significantly negatively correlated to 100-seed weight. Average fruit weight positively correlated with total fruit weight, number of seeds per accession and fruit width. The 100-seed weight was negatively correlated with all the 10 yield characters measured (Table 4).

**TABLE 4:** Pearson bivariate correlation coefficients of quantitative characters of pumpkin accessions

| Character | NFF | NMF | AFW | TFW | NFA | NLA | NSA | 100SW | FL | FW |
|---|---|---|---|---|---|---|---|---|---|---|
| NFF | 1 | | | | | | | | | |
| NMF | 0.61 | 1 | | | | | | | | |
| AFW | 0.09* | 0.11 | 1 | | | | | | | |
| TFW | 0.67 | 0.49 | 0.51 | 1 | | | | | | |
| NFA | 0.77 | 0.56 | 0.04 | 0.81 | 1 | | | | | |
| NLA | 0.44 | 0.44 | 0.04 | 0.30 | 0.35 | 1 | | | | |
| NSA | 0.09* | 0.17 | 0.50 | 0.31 | 0.11 | 0.09* | 1 | | | |
| 100SW | -0.12 | -0.21 | -0.03 | -0.20 | -0.22 | -0.10* | -0.17 | 1 | | |
| FL | 0.14 | 0.38 | 0.31 | 0.35 | 0.29 | 0.23 | 0.35 | -0.17 | 1 | |
| FW | 0.12 | 0.19 | 0.50 | 0.38 | 0.17 | 0.09* | 0.26 | -0.11 | 0.33 | 1 |

* Correlation is significant at $P = 0.05$ (2 tailed)

## DISCUSSION

**Quantitative Yield Responses**

The analysis of variance for Kakamega and Embu mother trials and for the accessions was significant for all the yield characters evaluated (Table 1). The significant differences were attributed to genetic and environmental effects. The higher the proportion of the phenotypic variation attributed to the genotypic differences, the greater the feasibility of genetic manipulation to improve crop performance (El-Hamed and Elwan, 2011). Aruah *et al*. (2012) reported significant differences in days to 50% flowering, number of fruits per plant, weight of harvested fruits, fruit diameter and number of seeds per fruit. Genotypes are able to alter their morphology and/or physiology in response to changes in environmental conditions (El-Hamed and Elwan, 2011). These variations indicate the differences among the accessions and the existence of genetic divergence (Fayeun *et al*., 2012). The variations are very important to plant breeders, when magnitude of variability in a breeding population is enough (Ahsan *et al.*, 2015).

**Flower Characteristics**

The male and female flowers in Kakamega were significantly higher than in Embu. This was attributed to the good rains experienced in Kakamega that helped lower high temperatures. In Embu, rain shortage and high temperatures were common. High day/night temperatures reduce the number of inflorescences and flowers (Hasanuzzaman *et al*., 2013). The flowers in Kakamega and Embu were mostly male, ranging from 11 to 182, and minimally female, ranging from 1 to 10. These results were similar to those of Aruah *et al*. (2010), who observed male flowers range from 34 to 66 and female flowers from 6 to 9. Similarly, Onyishi *et al*. (2013) observed male flowers range from 63 to 97, and female flowers from 1.7 to 3.7. Temperature and day length influence the ratio of male to female flowers (McCormack, 2005). Sex expression in cucurbits is influenced by hormones produced within the plant. Gibberellins promote male flowers, whereas ethylene and auxins promote pistillate flowers (Maynard, 2007).

**Leaf Characteristics**

Kakamega mother trials had the highest number of leaves, probably due to genetic and good environmental conditions. The Embu trials had many green-leafed accessions with indeterminate growth, conspicuous leaf senescence, and very minimal lateral branching. The mother trials were also planted under varying agro-ecological conditions in Kakamega and Embu. These regions have different soil types and climactic conditions that influence great variation in many agronomic characteristics (Du *et al*., 2011) through nutrients, soil characteristics, rainfall, and maximum temperature (Muungani *et al.*, 2007). The differences in genetics, soil types and climactic conditions could have caused variations in leaf number that ranged from 84 to 392 across the accessions. Aruah *et al*. (2010) reported leaves ranging from 98 to 210, similar to Gwanama *et al*. (1998) from 113 to 226. High number of leaves increases leaf surface area, which is important in plant growth, light interception, photosynthetic efficiency, evapo-transpiration, response to fertilizers and irrigation (Blanco and Folegatti, 2005).

**Fruit Yield Characteristics**

The number, total and average weight of fruits were all high in Kakamega probably due to good environmental conditions. The unreliable rains and high temperatures in Embu for most part of the growing period resulted in low number, total and average weight of fruits. Temperature and precipitation influence fruit set (Stapleton *et al*., 2000). The source and sink of assimilates are affected by a decline in photosynthesis, which ultimately reduces yields (Hasanuzzaman *et al*., 2013). Conditions that reduce the amount of assimilate available tend to decrease the weight of individual fruits. Reduced water supply tends to decrease fruit weight (Maynard, 2007). Poor environmental conditions contribute to low number of fruits (OECD, 2012), and interfere with pollination and pollinator activity (Maynard, 2007). More male flowers result on long and very hot days (OECD, 2012). The fruits depend on number of pistillate flowers and their successful pollination and fruit set (Wien *et al*., 2004).

Total fruit weight ranged from 0.2 to 15.9 kg, average fruit weight from 0.2 to 4.25 kg, and number of fruits from 1 to 10 across the accessions. Ahamed *et al.* (2011) reported fruit weight ranging from 1 to 10 kg among pumpkin varieties. Balkaya *et al*. (2010) reported average fruit weight ranging from 7.4 kg across pumpkin populations and average individual fruit weight ranging from 3 to 12 kg. Aruah *et al*. (2010) reported the number of fruits ranging from 5 to 8. Accession KK-40 produced the highest number and total weight of fruits. This was attributed to the high number of leaves produced by the accession. The number of leaves increases the source/sink strength for heat, water and $CO_2$ exchange, which translate into high photosynthetic and assimilation rates and ultimately more fruits and yields (Warren *et al*., 1998).

**Fruit Length and Width Characteristics**

The length and width of fruits were high in Kakamega. They are affected by environmental and genetic factors (OECD, 2012). High average weight of fruits produced in Kakamega mother trials (Figure 1) contributed to long and wide fruits. Chukwudi and Agbo (2014) reported higher fruit length in large-sized fruits than in medium and small-sized fruits. The 7 to 35.1 cm fruit length, averaging 18.5 cm, and 7 to 24.5 cm fruit width, averaging 14.6 cm were obtained in the present study. Aruah *et al*. (2010) observed fruit diameter range from 56.33 to 90.67 cm. Balkaya *et al*. (2010) observed fruit length range from 26 to 50 cm, averaging 39 cm and fruit diameter range from 35 to 57 cm, averaging 45 cm. Chukwudi and Agbo (2014) obtained 29.7 to 61.2 cm fruit length and 54.3 to 92.4 cm fruit circumference. Accession KK-12 had the longest fruits and NY-74 the widest, which were attributed to genotypic effects. Some accessions were elongated, while others were flattened and wide.

**Seed Yield Characteristics**

The number of seeds was high in Kakamega, whereas the 100-seed weight was high in Embu. Nerson (2007) observed large differences in seed yield among and within fruit-types. Aruah *et al*. (2010) stated that variations in seed number were genetically controlled, and they were greatly affected by environmental conditions, cultural practices, as well as pests and diseases. The many seeds in Kakamega were attributed to the high average fruit weight and number, and good environmental conditions. The seeds depend on pollination efficiency and growing conditions (OECD, 2012; McCormack, 2005). The number increases in proportion to pollen deposited on the stigma (Gavilanez-Slone, 2001). Fruits with many seeds have great size and weight (Aruah *et al*., 2010).

The 100-seed weight in Embu was high due to many green-leafed accessions that normally have higher seed size and weight than local accessions. In the present study, seed number ranged from 41 to 773, and 100-seed weight from 5.6 to 32.9 g. These were similar to 215 to 524 seeds per fruit, and 10 to 53 g 100-seed weight (Aruah *et al*., 2010), 6 to 14 g 100-seed weight (Ahamed *et al*., 2011), and 503 to 644 seeds in pumpkins without honey bees, 570 to 700 seeds in pumpkins with bees, 11 to 15 g 100-seed weight of pumpkins without honey bees, and 14 to 19 g in pumpkins with honey bees (Walters and Taylor, 2006).

**Genetic Variability**

Analysis of variance was used to evaluate the interaction between pumpkin accessions and the growing environments and the contribution of each of them to the total variation in yield factors. All the 10 quantitative characters had significant differences due to accessions, which proved that the 151 accessions evaluated were genetically divergent and provided a big sample that could be used to select promising accessions with different quantitative characters (Roychowdhury and Tah, 2011). The higher phenotypic variance than the corresponding genotypic variance suggested the presence of environmental influence to some extent in the expressions of the yield characters (Sultana *et al*., 2015). The presence of variability for all yield characters was attributed to diverse origins of accessions and environmental factors that influence phenotypes (Roychowdhury and Tah, 2011). The responses of accessions vary depending on locations, years and seasons. The accessions may exhibit superior yield in one location or environment, but this may not be stable in other environments with different agro-ecologies because the performance of a genotype mainly depends on environmental interaction (Razim, 2011).

**Genotypic and Phenotypic Variances**

The difference between genotypic and phenotypic variance for number of male flowers, number of leaves and seeds per accession, 100-seed the weight, fruit length and width were considerable high due to effects of environment on expression of the characters. Sultana *et al*. (2015) reported high genotypic variance, as well as phenotypic variance in fruit length. Khan *et al*. (2009) found maximum genotypic variance in fruits per plant followed by fruit yield and fruit weight per fruit, while high phenotypic variance resulted in fruit number, yield, weight and pulp weight per fruit in pointed gourd.

Aruah *et al*. (2012) reported high genotypic and phenotypic variance in fruit weight per plant, fruit diameter per plant, seeds per fruit and fruits per plant. In the present study, the difference between genotypic variance and phenotypic variance for female flowers, fruits per accession and total fruit weight was intermediate, meaning that the environment moderately influenced these characters (Roychowdhury and Tah, 2011). The difference between genotypic variance and phenotypic variance for average fruit weight per accession was low, indicating low influence of environment on the character. Similar results were reported by Sultana *et al*. (2015) in single fruit weight. Khan *et al.* (2009) reported low phenotypic variance in fruit length and breadth. The low variance for average fruit weight indicated stability of the character (Roychowdhury and Tah, 2011). Genotypic variances were more than environmental variances, except for number of male flowers and average fruit weight, meaning that the genetic component was the major contributor to the total variation (Aruah *et al*., 2012).

**Genotypic and Phenotypic Coefficients of Variation**

The highest genotypic and phenotypic coefficients of variation were observed for fruits per plant, fruits per accession, total fruit weight, female flowers, seeds per accession and 100-seed the weight in that order. The results indicated that the variation was due to genotype by environment interaction (Sultana *et al*., 2015). Therefore, selection can be applied on these traits for high yielding accessions (Ahsan *et al.,* 2015). Sultana *et al.* (2015) found high GCV and PCV in female and male flowers per plant, single fruit weight and fruits per plant. Khan *et al.* (2009) reported high PCV in fruit number and weight. Aruah *et al*. (2012) reported high PCV in weight of fruits per plant, number of seeds per fruit, and male flowers. Khan *et al.* (2009) obtained moderately high genotypic coefficient of variation in fruit number and weight per plant. The lowest PCV and GCV were for leaves and fruit width, indicating low scope for selection for improvement of pumpkin accessions (Aruah *et al.,* 2012).

A wide difference between PCV and GCV resulted for female and male flowers, total and average fruit weight and fruits per accession, while a narrow difference resulted for 100-seed weight, fruit length and width, leaf and seed numbers. Big PCV and GCV difference indicates high influence of environment on the characters thereby reducing the response to selection on phenotypic basis. Small PCV and GCV difference indicates great governance by genetic factors and minimal environmental influence on phenotypic expression of the characters. Thus, selection based on phenotypic values may be effective (Aruah *et al.,* 2012). Jahan *et al.* (2012) found highest difference between GCV and PCV for fruits and female flowers per plant.

**Heritability and Genetic Gain**

All the characters except fruit width showed high heritability and genetic advance, indicating additive gene effect. Selection based on this character would be effective for improvement of pumpkins (Sultana *et al*., 2015). The characters are less influenced by the environment (Ahsan *et al.,* 2015). Sultana *et al.* (2015) observed high heritability and genetic advance for single fruit weight and fruit yield per plant in pumpkins. Fayeun *et al.* (2012) obtained high heritability, exceeding 50%, and genetic advance for leaves per plant. In the present study, seven yield characters had above 80% heritability, indicating high contribution of genotypic component (Kumar *et al*., 2014). Aruah *et al*. (2012) observed high heritability for seeds per fruit, fruit diameter per plant, weight of harvested fruits per plant and number of fruits per plant.

Characters with high heritability have minimal environmental influence and can be accorded high attention in selection aimed at improving pumpkins (Aruah *et al*., 2012). In the present study, fruit width had high heritability and low genetic advance, indicating a non-additive gene effect. Thus, selection based upon phenotypic expression of fruit width would not be effective for the improving pumpkins (Sultana *et al*., 2015). The high heritability value of fruit width was due to favourable influence of environment rather than genotype, and selection of accessions based on fruit width may not be effective for improving pumpkins (Kumar *et al*., 2014). Moderate and low heritability makes selection difficult due to the environment masking expression of genotypic effects (Aruah *et al*., 2012). Better understanding of genotype and environment interaction helps to optimize yield and quality of crops (El-Hamed and Elwan, 2011).

**Correlation Coefficients**

The high positive correlation meant that increase in male and female flowers would result in high pollen production to enhance fertilization and ultimately fruit yields (Sultana *et al*., 2015). Similarly, an increase in fruits ultimately results in an increase in total fruit weight (Aruah *et al.*, 2012). The significant positive correlation between female flowers and seeds or average fruit weight, indicated that as female flowers increased or decreased, fruits also increased or decreased to similarly affect seeds and average fruit weight. Rabbani *et al*. (2012) found that fruit weight was positively and significantly correlated with fruits, average fruit weight, and female flowers, indicating close association and dependency of yield on these characters.

The leaves were significantly positively correlated with seeds and fruit width, and significantly negatively correlated with 100-seed weight. As leaves increase leaf surface area for photosynthesis increase, resulting in high photosynthate production, bigger fruits and better source–sink relationships (Isutsa and Mallowa, 2013). High number of fruits leads to large number of seeds and size quality of fruits, because of less competition for nutrients by sinks when other factors are constant. Mat *et al.* (2015) reported significant and positive correlation between fruits and seeds, female flowers and 100-seed weight. The significant and negative correlation between leaves 100-seed weight, indicated a decrease in weight as leaves increased due to competition. When partitioning assimilates, source-sinks transition changes, depending on sink strength of individual organs and the number of individual organs competing for the common pool of assimilates. Young developing plant organs which are actively growing become active sinks, while older mature fruits become inactive sinks. Photosynthates are directed toward new leaf and other organ development at the expense of being stored in fruits or seeds (Isutsa and Mallowa, 2013). Resmi and Sreelathakumary (2010) reported high negative correlations for fruit and average fruit weight or 1000-seed weight.

## CONCLUSION & RECOMMENDATIONS

The accessions had significant variations in quantitative yield characters, depending on region of growth. Good agro-ecological conditions lead to better performance of the characters. Introduced green-leafed accessions have big seeds, are susceptible to insect pests and diseases, and low yielding in Kenya. Wide genetic variability exists among accessions for all quantitative yield characters. All estimate formulae concluded that female and male flowers, average and total fruit weight, fruits, seeds and leaves, 100-seed weight, and fruit length could be used as selection criteria in pumpkin accessions for yield improvement purposes. These characters should be given the uttermost priority during selection for improvement of local pumpkins.

Naturalized pumpkin accessions in Kenya have great genetic variability, which needs to be tapped to improve local pumpkin accessions. Phenotypic and genotypic variance and coefficients of variation measure the magnitude of variability present in a population, whereas heritability indicates the reliability with which the accessions are recognized by their phenotypic expression. Therefore, PV, GV, PCV and GCV are not enough to determine the level of genetic variability among accessions to be used for selection. They should be investigated concomitantly with heritability and genetic advance to make credible selection of best performing pumpkin genotypes. Since these findings are based on pumpkin accessions collected from Kakamega and Nyeri regions only, collection and evaluation of accessions from other regions is warranted to provide more knowledge.

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