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Genetic Variability, Heritability and Genetic Advancefor Quantitative Traits in Ginger

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ABSTRACT

Genetic variability, heritability and genetic advance were studied in twenty five ginger accessions for eight quantitative traits during the rainy season of 2015 at the Research Farm of School of Agricultural Technology, Nuhu Bamalli Polytechnic, Zaria, SamaruKataf Campus. The experiment was laid out using 5 x 5 simple lattice design with three replications. Wide genetic variation was observed for all accessions for plant height, leaf length, number of tillers per plant, number of primary fingers per rhizome and number of secondary fingers per rhizome and fresh rhizome yield. The accession Kch-Zo4 recorded the highest number of primary and secondary fingers per rhizome. It also produced the highest fresh rhizome yield of 19.59 tons/ha than all the other accessions tested. Considering genetic parameters, genotypic coefficient of variation and phenotypic coefficient of variation were of high (>20%) for fresh rhizome yield (22.98%, 28.30%) and moderate (10-20%) for number of tillers per plant (13.46%, 15.75%), leaf length (10.07%, 10.84%) and number of primary fingers per rhizome (12.96%, 14.41%). In all cases, phenotypic variances and phenotypic coefficient of variation were higher than the corresponding genotypic variances and genotypic coefficient of variation. Based on high heritability coupled with high genetic advance as percentage of mean, the traits number of tillers per plant (73.10%, 23.71%), number of primary fingers per rhizome (80.79%, 23.99) and fresh rhizome yield (65.92%, 38.44%) were found as superior and representing additive gene action. Effective selection would be made considering these traits.

Keyword: Ginger, Genetic variability, Heritability, Genetic advance, Characters

1.0 INTRODUCTION

Ginger (*Zingiberofficinale* Roscoe) belongs to the family Zingiberaceae. It is believed to have originated in Southeast Asia and now occurs only under cultivation (Bailey 1949). India is one of the world's leading ginger-producing countries. Ginger is also grown in almost all tropical countries such as southern China, Taiwan, Philippines, Sierra Leone, Jamaica, Nigeria, Indonesia, Malaysia (Ravindran*et al*., 1994). Production of Ginger in Nigeria started in 1927 (Enrile, 1988) around Kwoi, Kubacha, Kafanchan and Kagoro of Southern Kaduna and around the Plateau and Nasarawa States. In recent times, ginger cultivation has been introduced into the South East and South-Western agricultural zones of Nigeria (NAERLS, 2004). According to the report of a national survey on exportable agricultural commodities in Nigeria (2007-2009), 23 states were listed including FCT as producers of ginger in 2009. However five states namely; Kaduna, Nasarawa, Imo, Benue, Niger are the major producers with Kaduna a distant highest producer. Ten percent of production is locally consumed as fresh ginger while 90% is dried primarily for the export markets (Ewuziem*et al*., 2009).
According to FAO (2011) the average ginger yield in Nigeria was about 3-4 tonnes/ha in 2009 which is far short of yield

currently obtained in most parts of the world. This is attributed to several factors; of which shortage of improved varieties, poor agronomic practices and poor soil fertility are the most important ones (Hailemichea*et al*., 2008). Due to the numerous uses of this important crop, its demand is always increasing all over the world and in Nigeria. Studies on genetic variability which is a first step in any crop improvement programme are either scanty or not available on ginger so far from Nigeria.

Studies on genetic variability for yield and associated characters in ginger from other countries indicated the existence of moderate to high variability in ginger. According to Tiwari (2003), Phenotypic Coefficient of Variation (PCV)was more than Genotypic Coefficient of Variation (GCV). A narrow range of GCV and PCV was observed for almost all the characters. The same author reported that leaf length had comparatively high estimates of GCV, heritability and genetic advance. Rajyalakshmi and Umajyoti (2014) reported number of tillers per plant, number of mother and finger rhizomes per plant and fresh rhizome yield showed high GCV, PCV, heritability and genetic advance as per cent mean. Islam *et al*. (2008) reported genetic advance in percentage of mean along with heritability was very high for tillers per plant, plant height, leaf length, leaf breadth, leaves per tiller, number of primary fingers per rhizome, number of secondary fingers per rhizome and number of tertiary fingers per rhizome. Ravinshanker *et al*. (2013) reported wide genetic variation for yield per plant, plant height and days taken to harvest. They found phenotypic variances were higher than the genotypic variances. They also found high heritability coefficient coupled with high genetic advance as % of mean for most of the traits they studied representing additive genetic variance.

The success of any crop improvement programme is 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 to progress that can be made through selection. Genetic variability for agronomic characters therefore is a key component of breeding programmes for broadening the gene pool of crops while heritability provides information on the extent to which a particular 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. Therefore, the findings in this study may help boost the ginger productivity beyond its present level in Nigeria. The objectives of the study were to estimate genetic variability, heritability and genetic advance of ginger rhizome yield and other quantitative traits.

2.0 MATERIALS AND METHODS

The research was conducted during the 2015 rainy season at the Research Farm of School of Agricultural Technology, NuhuBamalli Polytechnic, Zaria, Samaru Kataf Campus situated in the southern Guinea savannah ecological zone of Nigeria. It is located between latitude 25ºN and 10º 20'N and longitude 7º 45'E and 8º 40'E. The treatments consisted of 25 accessions of ginger, of which 14 were acquired from local farmers' collection and the remaining 11 from local markets. The collections were made mainly from Southern part of Kaduna State which is a major growing region of ginger in Nigeria. Details of the accessions that were used in the experiment are given in Table 1.

The treatments were laid down in 5 x 5 Lattice Design with three replications. The

experimental field was cleared and ploughed with hand hoeing followed by leveling. Cow dung at the rate of 5 tonnes per hectare was incorporated during the time of land preparation. Each gross plot consisted of one row of 3m long and 0.75m width giving a plot size of 2.25m^2. The ginger rhizomes were cut into smaller sets each having at least two good buds. One set was sown manually per hole at a depth of 5cm on seed bed. Each accession was planted on 1 row plot of 3m long with inter and intra row spacing of 0.40m and 0.20m, respectively. Mulching was carried out immediately after planting with green leaves. Hand weeding was done three times at 4, 8 and 12 weeks after sowing (WAS). Fertilizer (NPK 15:15:15) was applied at 300kg/ha at 4 and 8 WAP. Top dressing with 120kg/ha of Urea was carried out at 12 WAS.Data were collected on tillers per plant (no.),plant height (cm),number of leaves per plant, leaf length (cm),leaf breadth (cm),number of primary fingers per rhizome (no.), number of secondary fingers per rhizome (no.) and fresh rhizome yield (kg/ha).

The data collected were subjected to analysis of variance (ANOVA) using individual plot means. All statistical analyses were computed using the generalized linear model (GLM) procedure of the Statistical Analysis System (SAS Institute, 2004). Mean comparison was done using Duncan Multiple Range Test (DMRT) according to Gomez and Gomez (1984). Variance components, phenotypic and genotypic coefficients of variationas well as heritability were estimated according to Singh and Chaudhary (1985).GCV and PCV values were classified as low (<10%), moderate (10-20%) and high (>20%) as suggested by Siva-Subramanian and Menon (1973).The heritability values were classified as low (<30%), moderate (30-60%) and high (>60%) according to Johnson *et al*. (1955).Genetic advance was estimated according to Falconer and Mackey (1996) and expressed as a percentage of mean. Genetic advance as percent of mean was classified as low (<10%), moderate (10-20%) and high (>20%) according to Johnson *et al.* (1955).

3.0 RESULTS AND DISCUSSIONS

Analysis of variance for eight quantitative traits in ginger is presented in table 2. The genotype mean squares were highly significant (P≤0.01) for plant height, leaf length and fresh rhizome yield. The genotype mean squares were also significant (P≤0.05) for number of tillers per plant, number of primary fingers per rhizome, number of secondary fingers per rhizome and dry rhizome yield and were not significant for number of leaves per plant and leaf breadth. The significant differences observed for most of the traits indicate the presence of sufficient amount of variability in the accessions under study. Such wide variation indicated the scope for improving the accessions for these traits. Similar results were also reported in ginger by Islam *et al*. (2008) and Rajyalakshmi and Umajyothi (2014).

Mean performance for eight quantitative traits in ginger are presented in Table 3. Number of tillers per plant showed significant difference among the accessions. Kgk-Zo2 produced highest number of tillers per plant which was statistically the same with Kjr-Zo1, whereas Kch-Zo1 produced the least number of tillers per plant which was statistically the same with Zkf-Zo4. Statistically significant difference existed for plant height and the tallest plant was Kgk-Zo1, while the shortest was Zkf-Zo4. Statistical significant difference did not exist for number of leaves per plant. However, the accession with highest number of leaves per plant was Jem-Zo2, while the least was Kjr-Zo2 and were statistically the same with the

rest. Leaf length showed significant difference among the ginger accessions. The accession with the highest leaf length was Kgk-Zo1 while Zkf-Zo4 had the lowest leaf length.

Leaf breadth did not showed statistical difference among the accessions. However, the accession with the largest leaf breadth was Jab-Zo2while the lowest was Zkf-Zo4 and were statistically the same with the rest.Number of primary fingers per rhizome showed statistically significant differences among the accessions. The accession with the highest number of primary fingers per rhizome was Kch-Zo4 and the lowest was Kjr-Zo2. Number of secondary fingers per rhizome also showed significant difference among the ginger accessions. The accession with the highest number of secondary fingers per rhizome was Kch-Zo4 while the lowest was Kjr-Zo2.The results showedhighly significant variation among the ginger accessions with regard to the fresh rhizome yield.The accession Kch-Zo4produced significantly higher fresh rhizome yield, whereas, the accession Zkf-Zo4 recorded significantly lower fresh rhizome yield which was statistically the same with Kgk-Zo4.

Genetic variability parameters, heritability and genetic advance for eight quantitative traits in ginger are presented in Table 4. The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) (were of high magnitude (>20%) for fresh rhizome yield (22.98%, 28.30%). This indicates the presence of maximum amount of genetic variability which emphasized the wide scope of selection for the improvement of this trait. Islam *et al*. (2008) and Monima*et al*. (2011) also reported high GCV and PCV for fresh rhizome yield in ginger. The estimates of GCV and PCV were of moderate magnitude (10-20%) for number of tillers per plant (13.46%, 15.75%), leaf length (10.07%, 10.84%) and number of primary fingers per rhizome (12.96%, 14.41%), and of low magnitude (<10%) for leaf breadth (2.22%, 5.82%) and number of secondary fingers per rhizome (7.65%, 9.68%). Plant height had low GCV (9.45%) and moderate PCV (10.62%). Phenotypic variances were higher than the corresponding genotypic variances. PCVs were slightly higher than the corresponding GCVs for all these traits indicating that environment played a very little role in the expression of these traits. Similar result was reported by Rajyalakshmi and Umajyothi (2014).

High heritability along with high genetic advance as percent of mean were observed for number of tillers per plant (73.10%, 23.71%), number of primary fingers per rhizome (80.79%, 23.99) and fresh rhizome yield (65.92%, 38.44%). These traitswere found superior traits and representing additive gene action. Therefore, effective selection can be made for these traits. Similar result was reported by Baranwal*et al.* (2012).Hence, improvement of fresh rhizome yield in ginger would be effective through phenotypic selection for these traits. Low heritability and low genetic advance as percent of mean values were observed for the traits number of leaves per plant (13.29%, 1.17%) and leaf breadth (14.59%, 1.75%). This indicates these traits are highly influenced by environmental effects and selection would be ineffective.

4.0 CONCLUSIONS

In conclusion, the study revealed that the greater the genetic variability, the higher would be the broad sense heritability, hence the better the chances of success to be achieved through proper selection. The traits number of tillers per plant, number of primary fingers per rhizome and fresh rhizome yield had high estimates of heritability coupled with high genetic

advance as percent of mean. Hence, these traits need to be given more emphasis in selection as these are expected to be controlled by additive genes. The higher values of both genotypic coefficient of variation and phenotypic coefficient of variation obtained for fresh rhizome yield indicates that selection based on this trait would be possible. Continuous selection for yield and other traits is known for fixing of genetic variability in crop plants. The study indicated a broad genetic base in the ginger accessions studied.

Table 1 Ginger accessions, origin and collection source

Serial Number	Accession	Origin	Collection source
1	Kgk-Zo1	Kagarko	Local farm
2	Kgk-Zo2	Kagarko	Market
3	Kgk-Zo3	Kagarko	Market
4	Kgk-Zo4	Kagarko	Local farm
5	Zkf-Zo1	ZangoKataf	Market
6	Zkf-Zo2	ZangoKataf	Market
7	Zkf-Zo3	ZangoKataf	Local farm
8	Zkf-Zo4	ZangoKataf	Local farm
9	Jab-Zo1	Jaba	Market
10	Jab-Zo2	Jaba	Market
11	Jab-Zo3	Jaba	Local farm
12	Kch-Zo1	Kachia	Market
13	Kch-Zo2	Kachia	Local farm
14	Kch-Zo3	Kachia	Local farm
15	Kch-Zo4	Kachia	Market
16	Kau-Zo1	Kaura	Market
17	Kau-Zo2	Kaura	Market
18	Kau-Zo3	Kaura	Local farm
19	Kjr-Zo1	Kajuru	Local farm
20	Kjr-Zo2	Kajuru	Local farm
21	Jem-Zo1	Jema’a	Local farm
22	Jem-Zo2	Jema’a	Local farm
23	Jem-Zo3	Jema’a.	Local farm
24	San-Zo1	Sanga	Local farm
25	San-Zo1	Sanga	Market

Table 2 Analysis of variance for eight quantitative traits in ginger

Source	DF	NTPP	PLHT	NLPP	LFLT	LFBT	NPFR	NSFR	FRYD
Block(Rep)	12	1.41	42.91	4.36	4.26	0.05	0.46	21.72	12.14
Replication	2	4.45	52.93	17.67	3.73	0.72	0.11	101.45	45.93
Genotypes	24	4.60*	99.30**	2.02	19.95**	0.07	0.86*	10.95*	49.71**
Error	36	1.24	20.59	1.75	2.72	0.06	0.16	4.11	16.94

*, ** Significant at 0.05 and 0.01 probability level respectively; NTPP= number of tillers per plant: PLHT=plant height; NLPP=number of leaves per plant; LFLT=leaf length; LFBT=leaf breadth; NPFR=number of primary fingers per rhizome; NSFP=number of secondary fingers per rhizome; FRYD=fresh rhizome yield

Table 3 Mean performance for eight quantitative traits in ginger

Accession	NTPP (no)	PLHT (cm)	NLPP (no)	LFLT (cm)	LFBT (cm)	NPFR (no)	NSFR (no)	FRYD (tons/ha)
Kgk-Zo1	7.68^{a-d}	61.45^{a}	19.90	26.67^{a}	2.76	3.90^{abc}	18.49^{ghi}	17.06^{ab}
Kgk-Zo2	9.38^{a}	58.29^{ab}	20.01	24.63^{abc}	2.76	4.05^{ab}	17.90^{hi}	15.04^{abc}
Kgk-Zo3	7.83^{a-d}	55.17^{abc}	19.80	23.49^{bc}	2.63	3.13^{bcd}	22.15^{ab}	18.64^{ab}
Kgk-Zo4	7.71^{a-d}	53.76^{a-d}	20.91	24.83^{abc}	2.77	3.75^{a-d}	20.50^{a-g}	9.96^{c}
Zkf-Zo1	7.03^{cd}	48.02^{cd}	19.94	23.59^{bc}	2.72	3.98^{abc}	18.01^{ghi}	10.43^{bc}
Zkf-Zo2	8.89^{ab}	54.79^{a-d}	20.00	23.26^{bc}	2.62	3.57^{a-d}	21.09^{a-d}	15.07^{abc}
Zkf-Zo3	8.52^{ab}	55.39^{abc}	19.49	24.92^{abc}	2.75	3.52^{a-d}	19.80^{b-i}	13.53^{abc}
Zkf-Zo4	6.53^{d}	45.25^{d}	19.20	20.83^{c}	2.34	3.75^{a-d}	18.93^{e-i}	8.34^{c}
Jab-Zo1	8.67^{ab}	54.09^{a-d}	18.39	23.35^{bc}	2.68	3.96^{abc}	19.20^{c-i}	13.63^{abc}
Jab-Zo2	6.88^{cd}	55.68^{abc}	20.89	24.91^{abc}	2.95	3.81^{a-d}	21.53^{abc}	10.52^{bc}
Jab-Zo3	8.48^{abc}	53.43^{a-d}	17.79	22.09^{bc}	2.56	3.90^{abc}	19.76^{b-i}	14.27^{abc}
Kch-Zo1	6.34^{d}	53.52^{a-d}	19.88	23.45^{bc}	2.59	3.93^{abc}	17.56^{hi}	11.66^{bc}
Kch-Zo2	8.59^{ab}	50.29^{bcd}	18.55	22.95^{bc}	2.47	3.64^{a-d}	19.94^{a-h}	17.89^{ab}
Kch-Zo3	7.95^{a-d}	55.10^{abc}	20.41	24.06^{abc}	2.77	3.79^{a-d}	21.51^{abc}	16.93^{ab}
Kch-Zo4	7.97^{a-d}	55.74^{abc}	19.78	23.84^{bc}	2.72	4.33^{a}	23.43^{a}	19.59^{a}
Kau-Zo1	7.74^{a-d}	57.30^{abc}	17.68	24.58^{abc}	2.77	3.83^{a-d}	21.05^{a-e}	16.71^{ab}
Kau-Zo2	7.89^{a-d}	56.03^{abc}	18.92	23.68^{bc}	2.71	3.51^{a-d}	18.54^{f-i}	17.77^{ab}
Kau-Zo3	8.27^{abc}	50.70^{bcd}	17.91	22.74^{bc}	2.69	3.75^{a-d}	18.33^{f-i}	15.62^{abc}
Kjr-Zo1	9.20^{a}	53.89^{a-d}	18.48	23.01^{bc}	2.78	3.13^{bcd}	18.31^{ghi}	13.87^{abc}
Kjr-Zo2	7.60^{a-d}	52.29^{a-d}	16.99	22.77^{bc}	2.69	2.94^{d}	16.03^{i}	14.73^{abc}
Jem-Zo1	6.50^{d}	54.17^{a-d}	18.88	24.56^{abc}	2.80	4.10^{ab}	19.92^{a-i}	11.17^{bc}
Jem-Zo2	7.99^{a-d}	57.72^{ab}	20.93	25.71^{ab}	2.82	3.86^{a-d}	19.03^{d-i}	14.55^{abc}
Jem-Zo3	8.06^{abc}	56.10^{abc}	19.40	22.50^{bc}	2.62	3.85^{a-d}	22.15^{ab}	17.58^{ab}
San-Zo1	7.34^{bcd}	53.49^{a-d}	18.48	24.42^{abc}	2.65	3.41^{bcd}	20.64^{a-f}	14.18^{abc}
San-Zo2	7.46^{bcd}	52.83^{a-d}	18.89	23.85^{bc}	2.66	3.30^{cd}	19.93^{a-h}	10.83^{bc}
Mean	7.86	54.18	19.26	23.79	2.69	3.71	19.75	14.38
CV (%)	14.15	8.96	6.87	6.93	9.32	10.94	10.26	28.62

Means with same letter(s) in a column are not significantly different according to DMRT at 5% level of probability. NTPP= number of tillers per plant; PLHT=plant height; NLPP=number of leaves per plant; LFLT=leaf length; LFBT=leaf breadth; NPFR=number of primary fingers per rhizome; NSFP=number of secondary fingers per rhizome; FRYD=fresh rhizome yield

Table 4 Genetic variability parameters, heritability and genetic advance for eight quantitative traits in ginger

Traits	σ_g^2	σ_e^2	σ_{ph}^2	GCV	PCV	h_b^2	GA	GAM
NTPP	1.12	0.41	1.53	13.46	15.75	73.10	1.86	23.71
PLHT	26.24	6.86	33.10	9.45	10.62	79.27	9.39	17.34
NLPP	0.09	0.58	0.67	1.55	4.26	13.29	0.22	1.17
LFLT	5.74	0.91	6.65	10.07	10.84	86.36	4.59	19.29
LFBT	0.00	0.02	0.02	2.22	5.82	14.59	0.05	1.75
NPFR	0.23	0.05	0.29	12.96	14.41	80.79	0.89	23.99
NSFR	2.28	1.37	3.65	7.65	9.68	62.50	2.46	12.46
FRYD	10.92	5.65	16.57	22.98	28.30	65.92	5.53	38.44

σ_g^2=genotypic variance; σ_e^2=error variance; σ_{ph}^2=phenotypic variance;GCV=genotypic coefficient of variation; PCV=phenotypic coefficient of variation; h_b^2=broad sense heritability; GA=genetic advance; GAM=genetic advance as % of mean; NTPP= number of tillers per plant: PLHT=plant height; NLPP=number of leaves per plant; LFLT=leaf length; LFBT=leaf breadth; NPFR=number of primary fingers per rhizome; NSFP=number of secondary fingers per rhizome; FRYD=fresh rhizome yield

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