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ASSESSMENT OF EARLY GENERATION FAMILIES OF WHITE YAM (*DIOSCOREA ROTUNDATA*) FOR GROWTH AND YIELD PARAMETERS

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SUMMARY

Assessing the genetic potential of the early generation families of white yam (*Dioscorea rotundata*) for growth and yield traits became this study's aim. The experiment began in 2021 at the Njala Agricultural Research Centre (NARC), Njala, Sierra Leone. The results revealed the yam families significantly ($P < 0.05$) varied for days to first emergence (DAYFE), days to 50% emergence (DAYSE), germination index (GI), seedling vigor index (SVI), and the number of tubers per plant. The Family TDr190016 germinated earliest (14.5 days); however, families TDr190053 and TDr190113 exhibited the longest germination period (> 20 days). Traits with high phenotypic (PCV) and genotypic coefficient of variation (GCV) were germination index, seedling vigor index, percent seed emergence at 21 and 28 days after sowing, and pooled percent seed emergence (PSE). Broad sense heritability (HB) values ranged between 21.5% (pooled PSE) and 92.1% (SVI). Traits with the high broad sense heritability were days to 50% emergence (83.2%), germination index (74.6%), seedling vigor index (92.1%), percent seed emergence at 21 days (80.0%), and percent seed emergence at 28 days (62.8%). The yam families revealed the higher genetic advance for almost all traits except days to first emergence. In terms of various traits, the genetic effects of the early generation white yam families contributed more to the total phenotypic variability than the non-genetic effects, requiring more exploration for breeding.

Keywords: White yam (*Dioscorea rotundata*), progeny families, seed germination, growth and yield traits, genetic parameters

Key findings: Significant variation exists among the early generation families of white yam (*Dioscorea rotundata*) for growth and yield traits. Genetic effects of the early generation white yams contribute more than the non-genetic effects to the total phenotypic variability.

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INTRODUCTION

White yam (*Dioscorea* spp.) is a multi-species and multipurpose crop belonging to the family Dioscoreaceae, genus *Dioscorea,* and order Dioscoreales (Norman, 2010). Six yam species emerged as important staples, including *D. rotundata* (white yam), *D. alata* (water yam), *D. cayenensis* (yellow yam), *D. bulbifera* (aerial yam), *D. dumetorum* (trifoliate yam), and *D. esculenta* (Chinese yam) (Ng and Ng, 1994). Among these six economical yam species, *D. rotundata* and *D. cayenensis* are indigenous to West Africa, while the *D. alata* and *D. bulbifera* belong to Southeast Asia and Tropical America, also considered the primary centers of yam diversity and domestication (Asiedu *et al*., 1997).

Yam is an elite tuber and choice crop in West Africa, playing a remarkable role in the socio-cultural lives of the community, especially during traditional ceremonies and festivities (Obidiegwu and Akpabio, 2017; Mignouna *et al*., 2023). Commercial farmers, specifically the women, can obtain a good income from its production, further processing, and marketing. The fresh and processed products of white yam possess tremendous potential as a source of income for over 300 million people in Africa (Alabi *et al*., 2019). The fresh tuber product serves as raw materials for various industrial applications. Fresh healthy tubers can maintain a longer shelf life than other root and tuber crops, ensuring food security, even at times of general scarcity.

The yam crop is highly essential in the diet and economic life of the people in West Africa, the Caribbean islands, parts of Asia, and Oceania (Maziya-Dixon *et al*., 2017). West Africa is the leading producer of yam, growing over 90% of the worldwide production estimated at 73,000,000 tons, with West Africa accounting for over 93% (Aighewi *et al*., 2020). In Sierra Leone, yam is an indispensable food crop traditionally grown for household consumption. The crop ranks as the third most notable root and tuber crop cultivated in the country (Norman, 2010).

Despite the enormous importance of *D. rotundata* as a food crop, its potential has not been fully realized due to genetic and environmental factors, high production costs, limited availability of improved genotypes, and limited funding for its research and development. Botanical seed germination has been notably a critical criterion in determining plant population size and distribution in the different communities (Chen *et al*., 2012; Norman *et al*., 2020a). Populations developed through diverse hybridization methods exhibited dissimilar degrees of pollination success, fruit setting, and seed development in yams (Norman *et al*., 2018). Botanical seeds generated from natural and controlled cross combinations revealed considerable genetic viability, seedling growth, and progress (Norman *et al*., 2020a). These growth and improvement traits and other related attributes determine the adaptability and selection of crops in the target environments (Orkwor *et al*., 1998).

Identifying and selecting superior recombinant progeny lines possessing desired traits is one of the key activities in current plant breeding programs. Within a breeding population, the effective selection depends on the detailed knowledge of the heritable variations, genetic correlation among traits of economic importance, and the expected occurrence of the desired progenies within the breeding population (Norman, 2019). Assessment of genetic parameters has extensively progressed in crop breeding activities for optimization of various breeding schemes and selection of an efficient breeding technique used for genetic improvement (Falconer and Mackay, 1996). However, limited data about genetic parameter estimates of botanical seed germination, seedling growth, and growth indices in early generation families of white yam exist.

Moreover, a dearth of knowledge exists on seed-tuber yield potential in early generation families of white yam. Therefore, the acquisition of such knowledge is imperative for the efficient development and utilization of the seedling management techniques to enhance the seed germination, higher seedling vigor index, and seed tuber yield potential in white yam (Norman *et al*., 2020a). The presented research provides vital information based on the estimates of genetic parameters, variability in growth and fresh tuber yield traits. These will contribute to the assessment of early generation families that would enhance the probability of identifying superior clones needed for the adaptability and selection of crops in test environments.

The research questions that prompted this study included the following: a) Does the significant variation exist among early generation families of white yam (*D. rotundata*) for growth, fresh tuber weight, and related yield traits? and b) Does the genetic effects contribute more than the non-genetic effects to the total phenotypic variability in early generation white yams? Thus, the latest study aimed at determining the genetic parameter estimates of growth traits and assesses fresh tuber weight potential of the early generation botanical seed-families of white yam (*D. rotundata*) generated by using biparental cross mating system.

MATERIALS AND METHODS

Experimental location

The pre-nursery trial establishment commenced during the cropping season 2020-2021 at the Molecular Biology lab and the nursery at the shed-house facility of the yam improvement program, Njala Agricultural Research Centre (NARC), Njala, Sierra Leone.

Breeding material, design, and management

Experimental units totaling 1,000 comprised 100 botanical seeds belonging to 10 white yam families as study samples. The included 10 seed-families were TDr190068, TDr190065, TDr190055, TDr190053, TDr190051, TDr190048, TDr190046, TDr190023, TDr190016, and TDr190113. The breeding material came from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria. The parental genotypes and the obtained families of the botanical seed material are available in Table 1.

The pre-nursery experiment layout used the completely randomized design (CRD) with four replicates. The sterilized topsoil placed in perforated polyethylene seedling trays and slightly soaked comprised the media. The seeds attained soaking in clean water for 20 h before sowing in sterilized rich topsoil placed in perforated seedling trays. Botanical seeds planting totaled 25 per seedling tray. The planted seeds fell in holes created in the sterilized topsoil-growing medium on September 21, 2020. The well-labeled trays at the time of sowing obtained watering at two days interval until six weeks after sowing (WAS).

Laying out, the nursery experiment had an unbalanced randomized complete block design (RCBD). The interspatial and intraspatial block spaces were 0.5 m apart. Each polythene bag (pot) bore filling with sterilized topsoil and irrigated to field capacity before transplanting. The seedlings' transplanting proceeded in holes created in the crest of the sterilized topsoil and irrigated to field capacity every three days until six months after transplanting (MAT).

Data recorded

The data recorded comprised the various parameters, i.e., days to first emergence (DAYFE), days to 50% seed emergence (DAYSE), seedling vigor index at six, weekly germination count, fresh tuber weight, and fresh tuber number. The assessment of germination parameters was daily, counting from days of first germination to the day germination ceased. Weekly germination counts started from three to six weeks after sowing. The seedling vigor index (SVI) estimation was the product of germination percent multiplied by seedling height (Hossain *et al*., 2006).

The germination index (GI) computation used a similar description in the association of official seed analysis (AOSA, 1983) as:

$$\mathrm{GI} = \frac{(\text{No. of germinated seeds})}{(\text{Days of first count})} + \cdots + \frac{(\text{No. of germinated seeds})}{(\text{Days of last count})}$$

Table 1. Phenotypic attributes of *Dioscorea rotundata*-crossing parents used in the study.

Crossing parents	Family code	Female clone attributes	Male clone attributes
TDr3010 × TDr1500043	TDr190016	Profuse flowering with wide window	Low soil nutrient adaptability, dry matter content (DMC) =32.0-34.7%, no oxidation, yield=37.4 t ha^{-1}
TDr2826A × TDr1500135	TDr190023	Oxidation (-), DMC=32.0%, stable yellow flesh color	Low soil nutrient adaptability, oxidation (-)
TDr2826A × TDr1500096	TDr190046	Oxidation (-), DMC=32.0%, stable yellow flesh color	No oxidation, low soil adaptability, high DMC, yield=31.2 t ha^{-1}
TDr3010 × TDr1500100	TDr190048	Profuse flowering with wide window	Low soil nutrient adaptability, high DMC, oxidation (-), yield=36.0 t ha^{-1}
TDr3010 × TDr1500031	TDr190051	Profuse flowering with wide window	Low soil nutrient adaptability, yield=35 t ha^{-1}
TDr1401220 × TDr9501932	TDr190053	DMC=32.0%, oxidation (-), stable creamy white flesh color	DMC=36.0-36.7%, no oxidation, virus resistant, high flowering, cooking quality, multiple tubers, yield=29.2 t ha^{-1}
TDr1400012 × TDr1500135	TDr190055	Oxidation (-), DMC=32.0%, stable yellow flesh color	Low soil nutrient adaptability, oxidation (-)
TDr1100873 × TDr0900324	TDr190065	Oxidation (-), good DMC, stable creamy flesh color	Oxidation (-), DMC=30.0-32.0%, stable creamy flesh color
TDr9518544 × TDr1500043	TDr190068	Earliness, cooking quality, multiple tubers, oxidation (-)	Low soil nutrient adaptability, DMC=32.0-34.7%, no oxidation, yield=37.4 t ha^{-1}
TDr9700917 × TDr1500096	TDr190113	Virus tolerant, early bulk, high flower	No oxidation, low soil nutrient adaptability, high DMC, yield=31.2 t ha^{-1}

Data analysis

The growth variables data first underwent a linear mixed model using the residual maximum likelihood (REML) procedure to estimate the variance parameters (Patterson and Thompson, 1971). The GenStat Statistical package ver. 12, VSN International, Hemel Hempstead application further analyzed the data. From the variance component analysis, determining different genetic parameters, such as, heritability broad sense (H^2), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), and expected genetic advance (GA) continued. The GCV and PCV results followed a standard formula (Burton and Devane, 1953).

$$\frac{\sqrt{\sigma^2 v}}{\bar{x}} \times 100$$

Where:

$\sigma^2 v$ is the respective variance for genetic and phenotypic component for the trait from the final model in the REML analysis, and $\bar{x}$ is the trait mean value.

Categorizing the genotypic coefficient of variation and phenotypic coefficient of variation values employed the proposed technique as follows (Deshmukh *et al.,* 1986): Values >20% = high, values ranged between 10%–20% = medium, and values <10% = low.

Heritability (broad sense) determination used a standard formula (Robinson *et al*., 1949):

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where: $\sigma^2 g$ and $\sigma^2 p$ are the total genetic and phenotypic variances, respectively. The H^2 values ranked as low for values that range from 0%–30%, moderate for values ranging between 30%–60%, and high for those >60%.

The genetic advance estimation considered the standard equation (Shukla *et al*., 2006):

$$\text{Genetic advance (GA)} = K \times H^2 \times \sigma p$$

Where, K is the selection differential (which was 2.06 at 5% intensity), H^2 is heritability (broad-sense) due to total genetic effect, and σp is the phenotypic standard deviation.

The genetic advance values had classification as low for values <10%, moderate for values ranging from 10%–20%, and high for values >20% (Shukla *et al*., 2006).

Data based on the number of tubers per plant and tubers weight per plant reached evaluation using the analysis of variance procedure of GenStat version 16 statistical package. The least significance difference ($LSD_{0.05}$) helped compare the treatment means differences. The residuals of data for the various parameters incurred checking first for normality and homogeneity using the Shapiro–Wilk test and Bartlett's test to ensure the data's normal distribution.

RESULTS AND DISCUSSION

Seed emergence related growth attributes

The early generation yam families were significantly ($P < 0.001$) varied for average days to first emergence (DAYFE), days to 50% emergence (DAYSE), germination index (GI), and seedling vigor index (SVI) (Table 2, Figures 1 and 2). Family TDr190016 germinated earliest (14.5 days), reaching 50% germination at 20 days after sowing. Families TDr190053 and TDr190113 took the longest period (20 days after sowing) to germinate, by reaching 50% germination at 32 and 49 days after sowing, respectively. Family TDr190048 exhibited the highest germination index (2.73) and seedling vigor index (1240.9), whereas family TDr190113 had the lowest germination index value (0.94) and was among the families with low vigor index, ranging from 262.3 to 475.8.

Table 2. Breeding values of germination and seedling vigor index traits of early generation families of white yam.

Family	Days to first emergence (days)	Days to 50% emergence (days)	Germination index	Seedling vigor index
TDr190016	14.5	20.3	2.55	854.4
TDr190023	17.8	25.0	1.86	1072.7
TDr190046	16.0	26.5	1.86	1091.7
TDr190048	16.5	20.8	2.73	1240.9
TDr190051	18.8	26.0	1.93	823.1
TDr190053	21.3	32.3	1.18	429.8
TDr190055	19.3	32.8	1.17	262.3
TDr190065	17.8	29.0	1.49	420.7
TDr190068	19.0	31.8	1.15	737.3
TDr190113	20.0	49.0	0.94	475.8
Mean	18.1	29.3	1.69	740.9
S.E.D.	1.2	1.8	0.18	48.0

S.E.D. = Standard error of difference.

White Guinea yam seed families showed significantly ($P < 0.001$) increased mean percent seed emergence (PSE) (Table 3). The mean percent seed emergence at 42 days after sowing ranged from the highest (95.0) in family TDr190048 to the lowest (44.0) in the family TDr190113. Families with the highest and lowest percent seed emergence values at 42 DAS were also among families with the highest and lowest percent germination at 21 to 42 DAS.

In yam families, the genetic and environmental effects considerably contributed to the variation in traits performance with different degrees (Table 4). The genetic effects contributed highly to the total phenotypic variation than the environmental effects for most traits (days to 50% emergence, germination index, seedling vigor index, and seeds percent emerged at 21, 28, 35, and 42 days after sowing). However, the environmental effects contributed higher to the phenotypic variance of the days to first emergence. The phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) values for all traits (Table 4). Traits with high phenotypic coefficient of variation were days to 50% emergence, germination index, seedling vigor index, percent of seeds emerged at 21 and 28 days after sowing, and pooled percent of seeds emerged. Traits with higher genotypic

Figure 1. Photos showing botanical seedlings of families TDr190068 (A), TDr190065 (B), TDr190055 (C), TDr190053 (D), and TDr190051 (E) sampled at six weeks after sowing.

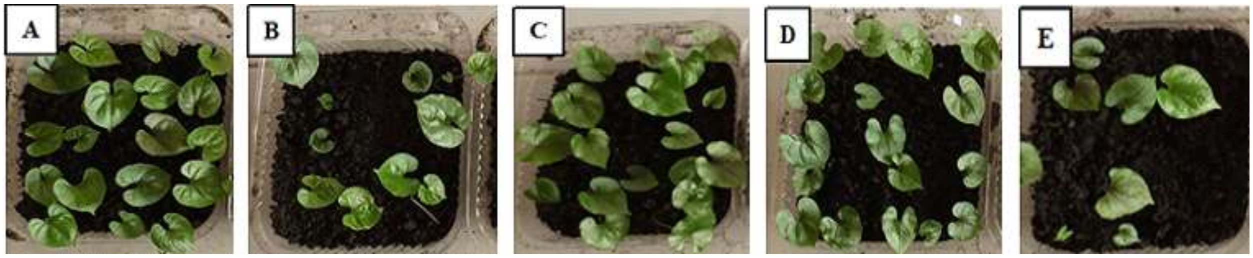

Figure 2. Photos showing botanical seedlings of families TDr190048 (A), TDr190046 (B), TDr190023 (C), TDr190016 (D), and TDr190113 (E) sampled at six weeks after sowing.

Table 3. Breeding values of percent of seeds emerged (PSE) of early generation families of white yam.

Family	Sampling time in days after sowing (DAS)				Pooled PSE
	21 DAS	28 DAS	35 DAS	42 DAS	
TDr190016	64.0	80.0	82.0	82.0	77.0
TDr190023	20.0	69.0	76.0	78.0	60.8
TDr190046	31.0	61.0	72.0	73.0	59.3
TDr190048	58.0	90.0	94.0	95.0	84.3
TDr190051	20.0	67.0	81.0	86.0	63.5
TDr190053	6.0	32.0	60.0	66.0	41.0
TDr190055	8.0	34.0	57.0	61.0	40.0
TDr190065	12.0	50.0	67.0	71.0	50.0
TDr190068	8.0	37.0	55.0	56.0	39.0
TDr190113	9.0	31.0	41.0	44.0	31.3
Mean	23.6	55.1	68.5	71.2	54.6
S.E.D.	5.1	8.1	7.0	6.7	7.9

S.E.D. = Standard error of difference, DAS = Days after sowing.

Table 4. Genetic parameter estimates of the growth traits measured in 10 families of white yam.

Trait	VG	VE	VP	PCV (%)	GCV (%)	H_B (%)	GA
Days to first emergence (days)	1.6	3.0	4.6	11.9	7.1	35.5	8.7
Days to fifty percent emergence (days)	32.9	6.6	39.5	21.4	19.6	83.2	36.7
Germination index	0.2	0.1	0.2	29.1	25.1	74.6	44.7
Seedling vigor index	55053.0	4716.0	59769.0	33.0	31.7	92.1	62.6
Percent of seeds emerged (21 days)	217.6	54.6	272.2	69.9	62.5	80.0	115.1
Percent of seeds emerged (28 days)	213.1	126.5	339.6	33.4	26.5	62.8	43.2
Percent of seeds emerged (35 days)	110.8	92.1	203.0	20.8	15.4	54.6	23.4
Percent of seeds emerged (42 days)	103.3	86.3	189.6	19.3	14.3	54.5	21.7

VG = Genotypic variance, VE = Environmental variance, VP = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, H_B = Heritability (broad sense), GA = Genetic advance.

coefficient of variation values were the germination index, seedling vigor index, percent of seeds emerged at 21 and 28 days after sowing, and pooled percent of seeds emerged. However, days to first emergence had a low genotypic coefficient of variation.

The broad sense heritability estimates ranged between 21.5% (pooled percent of seeds emerged) and 92.1% (seedling vigor index). Traits with high broad sense heritability were the day to 50% emergence (83.2%), germination index (74.6%), seedling vigor index (92.1%), and percent seeds emerged at 21 days (80.0%) and 28 days (62.8%). Findings agreed with Adewale and Kehinde (2016), who obtained high broad sense heritability for days to seedling emergence in African yam bean. Genetic advance ranged between 8.7 (days to first emergence) and 115.1 (percent seeds emerged at 21 days after sowing). High genetic advance values appeared for all the studied traits, except days to first emergence having a low genetic advance value (8.7) (Table 4). Outcomes supported the view of yam productivity increasing with improvement in genetic traits and their heritability from one generation to another (Akoroda, 1983).

Fresh tuber weight and related attributes

For the number of tubers per plant and tubers weight per plant, the early generation yam families revealed nonsignificant ($P > 0.851$) and significant ($P > 0.015$) differences, respectively (Tables 5 and 6). Family TDr190046 exhibited the highest average tuber weight per plant (30.38 g), whereas family TDr190048 (7.03 g) had the lowest tuber weight per plant. Moreover, family TDr190053 showed significantly the widest variability (2.0–160.5 g) and the maximum mean value (40.7 g) for fresh tuber weight per plant. Family TDr190048 had an average tuber weight of 7.03 g and standard deviation (11.04), producing the smallest tubers.

The average distance between the phenotypic values for the tuber weight per plant and the mean (standard deviation) was highest (55.78) for the family TDr190053, whereas family TDr190046 exhibited the lowest phenotypic value of deviation from the mean (5.47). For tuber number per plant, family TDr190023 provided the utmost standard deviation (0.65), but the families TDr190065 and TDr190068 had 0.00. Results indicated the widest variations within and among the families for tuber number per plant and tuber weight per plant. The presented results align with past findings reporting yam families with higher average distance between the genetic values and the mean implies their data points spread widely over a large range of values, whereas the data points of those with low standard deviation values are close to the mean (Norman *et al*., 2020b).

The presented research has contributed to unravel the nature and magnitude of variation in the botanical seed germination and related growth traits investigated. Existence of useful variability was evident in the progeny-families for the studied

Table 5. Variation in fresh tuber number and tuber weight of white Guinea yam seed families (crosses) generated using bi-parental mating design.

Family	Tuber number per plant		Tuber weight per plant (g)	
	Means	S.D.	Means	S.D.
TDr1900113	1.3	0.33	10.56	10.72
TDr190016	1.1	0.28	9.24	20.27
TDr190023	1.1	0.65	13.64	39.90
TDr190046	1.1	0.55	30.38	5.47
TDr190048	1.2	0.27	7.03	11.04
TDr190051	1.0	0.19	11.28	18.06
TDr190053	1.2	0.56	40.72	55.78
TDr190055	1.0	0.50	16.10	18.35
TDr190065	1.0	0.00	16.75	26.79
TDr190068	1.0	0.00	22.07	22.73
$LSD_{0.05}$	0.36		23.38	
CV (%)	37.09		144.29	

CV = Coefficient of variation, S.D. = Standard deviation, LSD = Least significance difference.

Table 6. Analysis of variance of tuber number per plant and tuber weight per plant of first-generation yam from 10 botanical seed families of white yam.

Change	d.f.	Sum of Squares	Mean Squares	Variance ratio	F (p.)
Tuber number per plant					
Replications	2	0.2239	0.112	0.66	0.518
Family	9	0.8088	0.0899	0.53	0.851
Residual	142	24.0906	0.1697		
Total	153	25.1234	0.1642		
Tuber weight per plant (g)					
Replications	2	449.4	224.7	0.31	0.737
Family	9	15818.1	1757.6	2.39	0.015
Residual	142	104456.9	735.6		
Total	153	120724.4	789.0		

traits, for further exploration through direct selection and an efficient population improvement technique. The phenotypic variance attributable to genetic and environmental factors is crucial for determining the most probable means of developing the heritable variation of traits in a breeding population through selective breeding. These findings were greatly analogous to findings, which exhibited that high heritability and genetic gain indicate their effective improvement through selective breeding (Norman *et al*., 2022, 2023).

Direct selection in the short term would typically employ the pre-existing genetic variation in the yam progeny families. These results were also consistent with the studies of Norman *et al*. (2022) and Barrie *et al*. (2022), stating in breeding populations, existing useful variability depends on the nature and magnitude of genetic and environmental factors contributing to the expression of traits. The slightly higher phenotypic coefficient of variation values compared with the genotypic coefficient of variation generally implies some traits were less sensitive to environmental effects. Traits with high phenotypic coefficient of variation and genotypic coefficient of variation authenticate the possibility of selecting clones possessing desirable values for the trait in the next clonal generation.

Traits demonstrating a high heritability and high genetic advance of the mean indicate their effective improvement through selective breeding. The traits with high heritability and high genetic advance also imply these traits were under the control of additive genes. Meanwhile, those with high heritability and low genetic advance were under non-additive genes' control, which hinder their genetic improvement through direct selection in the outcrossing crop, however, not in the clonal propagating crops like yam. These findings were in greater analogy with the proposition that traits with high, broad, and narrow sense heritability estimates imply their potential usefulness for genetic improvement (Piaskowski *et al*., 2018; Barrie *et al*., 2022). Johnson *et al*. (1955) also reported the relevance of heritability along with genetic gain for efficient predictability of response to selection.

Botanical seed germination is a crucial and vulnerable phase of crop cycle and breeding processes (Norman *et al*., 2020a; Travlos *et al*., 2020). Duration of emergence, days to 50% emergence, and percent emergence may also affect the crop yield by limiting plant population density, effective crop growth duration, and spatial arrangement. Delayed and poor germination of the botanical yam seeds of some families were possibly attributable to dormancy caused by genetic factors (Feike *et al*., 2007; Islam *et al*., 2009; Norman *et al*., 2020a). In seed germination potential of seed families, the knowledge of existing variability permits selection for either dormancy or non-dormancy (Feike *et al*., 2007). The said information also helps in devising robust and practical strategies that overcome the dormancy. Botanical seed dormancy has also been visible in yams. Physical and chemical seed treatment methods succeeded application to overcome the dormancy in various crops resulting in early and increased germination and seedling vigor (Hossain *et al*., 2006; Burson *et al*., 2009; Islam *et al*., 2009; Norman *et al*., 2020a).

In the presented study, water soaking of the yam families' seeds before sowing may have contributed to decreasing days to emergence compared with the previous study (Norman *et al*., 2020a). These findings concur with the view that water soaking of seeds before sowing greatly enhances the germination and seedling vigor (Islam *et al*., 2009; Feike *et al*., 2007). Outcomes also imply botanical seed dormancy is a crucial issue in yam population improvement requiring the management of appropriate physical and chemical treatments. This will enhance the early and increased germination and germination attributes, seedling vigor index, and fresh tuber yield potential. Delayed germination of seeds reduces the effective growth and development duration of early generation yams' families. Thus, genetic analysis of seedling traits and identification of loci controlling seed dormancy, germination, and seedling traits could be operational to combat the poor seed germination in yams (Purnomo *et al*., 2012, 2016).

The significant variations among progeny-families for the measured traits are indicative of inherent genetic differences in the yam progeny-families for germination and fresh tuber weight per plant. These results complement the findings of Norman *et al*. (2020a), who reported significant variability among the families in fresh tuber weight per plant. It refers to relevant differences in the individual progeny-family growth and growth indices estimated in populations developed through North Carolina (NC-1) and polycross mating systems.

CONCLUSIONS

The genetic parameter estimates established significant variations exist among the early generation families of white yam (*D. rotundata*) for growth and yield-related traits. The genetic effects contribute more to the total phenotypic variability for days to 50% emergence, germination index, seedling vigor index, and percent seeds emerged. Improving seed germination, growth, and tuber yield potential could also enhance the identification of superior progenies in early generation yam families.

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