

INFLUENCE OF POPULATION SIZE ON ESTIMATES OF GENETIC VARIANCES, HERITABILITY AND PREDICTED GAINS IN TWO TROPICAL MAIZE POPULATIONS

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Abstract

The cost of evaluating large sample size is a limitation in population improvement programme. A study was conducted in Ibadan and Ikeneto to assess the influence of population size on estimates of genetic variability and predicted gains in two maize populations. Four population sizes tagged P-250, P-200, P-150 and P-100 were generated from each of the two maize populations using NCII mating scheme. The experiment was laid out in a randomized incomplete block design in two replications. Data were collected on agronomic and yield traits. Genetic parameters and narrow-sense heritability were estimated from combined analysis of variance. The type of gene action controlling each trait is consistent in all the population sizes although values were higher in other population size compared to P-250 for most of the traits studied. Means, heritability estimates and predicted gains were higher in P-200 and P-150 compared to P-250 especially for yield and yield traits. Estimates of heritability and gains were also high in P-100 but this was not consistent especially for yield traits. Considering the cost of evaluating large number of samples in population improvement programme, sample size of only 150 could be used without compromising variability and genetic progress.

Keywords: Heritability; Maize (*Zea mays*); Population size; Predicted gains; Recurrent selection

Running title: Genetic gains as influenced by population size in maize.

Introduction

Recurrent selection has been widely used in population improvement of maize. It contributes greatly to the genetic improvement of maize hybrids in the U.S. Recurrent selection programs in the BSSS maize population led to the development of widely used maize inbred lines such as B73 and B84 (Hallauer *et al.*, 1983). As a cyclical breeding procedure, recurrent selection improves population performance and maintains genetic variability through increase in the frequency of favorable alleles in the population. The number of individuals intermated is the most critical aspect of the intermating phase of recurrent selection programs (Hallauer, 1992).

Gains from selection can be increased by increasing selection intensity (Sprague and Eberhart, 1977) which is proportional to the number of lines selected for intermating and the number of lines evaluated. For a given selection intensity, an increase in the number of individuals selected requires an increase in the number of lines evaluated. The number of individuals intermated approximates the effective population size, N_e , in recurrent selection programs (Vencovsky, 1978; Labate *et al.*, 1997).

Theoretical studies have shown that genetic variance decreases with small population size or after a 'population bottleneck' due to genetic drift. The concept of effective population size was introduced by Wright (1931) to address the phenomenon of random genetic drift. Genetic drift is the random fluctuation of gene frequencies in small populations. When a small number of individuals are selected for recombination due to small size of individuals evaluated, there is fluctuation in the frequency of desirable alleles in the population.

However, there are a lot of limitations in evaluating large number of individuals in term of management and cost of resources such that there is a trade-off between selection intensity and number of individuals intermated in maintaining genetic variability. There is need to know the minimum acceptable number of individuals to be evaluated and hence selected, specifically in maize where effective population size is crucial in recurrent selection programs, without jeopardizing the genetic variability and genetic gains in advanced cycle of selection. However, this information is very scanty in the literatures. Smith (1979) hinted that effective population size needs to be increased in selection

procedures to reduce the rate of accumulation of inbreeding due to random genetic drift. Guzman (1998) reported that there was little to no advantage of using larger effective population sizes to maintain genetic variability for short-term recurrent selection. Brim and Burton (1979) conducted a recurrent selection study for increased protein in two soybean populations using different effective population sizes. They concluded that reduced effective population size and number of lines tested per cycle had little effect on progress.

This study aims at determining the influence of four population sizes but with common selection intensity, on genetic variances, heritability and predicted gains in two maize populations.

Material and Methods

Progeny Development

Two maize populations DMR ESR-W and DMR ESR-Y were used for this study. Full-sib and half-sib progenies were generated in each population using NCII mating scheme. Four different sample sizes were developed for evaluation in each maize population namely P-100, P-150, P-200 and P-250. For P-100, 40 S₁ lines were grouped into four sets, each set having 10 lines. Out of the 10, five were designated as males and five as females to generate 25 full-sib progenies per set. This gave 100 individuals in all for evaluation. For P-150, 60 S₁ lines were grouped into six sets each containing 10 lines. Each set produced 25 progenies giving rise to 150 individuals for evaluation. For P-200 and P-250, 80 and 100 S₁ lines were used to generate 200 and 250 individuals respectively for evaluation.

Agronomic Practices

Evaluations were carried out at Ibadan (Lat. 7° 22'N, Long 03° 58'E) in the derived savanna and Ikenne (Lat. 6° 54'N, Long. 03° 42'E) in the humid forest of Nigeria in two seasons. A Randomized Incomplete Block Design with two replications was used. Each plot was a single row of 3m length. Two seeds were planted per hole but thinned to one plant per hill at three weeks after planting (WAP). A maximum of 13 plants per plot was obtained resulting in plant density of 53,333 plants/ha.

Weeds were controlled using pre-emergence herbicide. One hand weeding was done at 4WAP and another herbicide spray at 8WAP. N.P.K. 15:15:15 was applied at 10 days after planting (DAP) at the rate of 60kgN/ha, while urea was applied at 6 weeks after planting (WAP) at the same rate.

Data Collection

Days to 50% pollen shed and 50% silking were determined as the number of days from planting to the day when half of the plants in a plot shed pollen and had silk extrusion, respectively. Plant aspect was rated per plot after anthesis on a scale of 1-9, 1 representing vigorous and appealing plants without lodging, leaf defoliation, nor disease symptoms and carrying their first ear at the middle of the plant, while 9 represents lodged, diseased and defoliated plants with their first ear closer to the soil surface or to the tassel. Data on plant height was collected on five competitive plants per plot from the soil surface to the base of the tassel and the average determined. Ear aspect was rated per plot based on the neatness and filling of grains on the cobs on a scale of 1-9, 1 representing clean and well-filled ears, and 9 for ears with scanty and rotten or damaged grains. Ear length and diameter were taken on five representative cobs per plot using ruler and the average calculated. Ear length was taken from tip of the cob to the base, while the diameter was taken at the middle of the cob. Some quantities of maize were shelled from the harvested cobs per plot to determine grain moisture content which was done using Dickey-John moisture meter. Number of ears per plant was calculated by dividing the total number of ears at harvest by number of plants harvested per plot. Grain yield (t/ha) was adjusted to 14% moisture.

Data Analyses

Statistical analyses were conducted separately for the two maize populations. After analysing data for each, data were pooled over environments. Analysis of variance for North Carolina Design II was performed using PROC GLM of SAS (Version 9.2). Random model was assumed for the analysis (entries, locations and seasons were assumed random). Additive genetic variance (σ_a^2), dominance variance (σ_d^2) and environmental variance were estimated from the mean squares for ANOVA according to Hallauer and Miranda, (1988) as follows:

$$\begin{aligned}\sigma_m^2 &= (MS_M - MS_{MF} - MS_{ME} + MS_{EMF})/ref, \\ \sigma_a^2 &= 4\sigma_m^2 = 4\sigma_f^2 \\ \sigma_{mf}^2 &= (MS_{MF} - MS_{EMF})/re = 1/4\sigma_d^2, \\ \sigma_d^2 &= 4\sigma_{mf}^2 \\ \sigma_e^2 &= MS_e/er\end{aligned}$$

The standard errors of variance estimates and the narrow-sense heritability estimates were also calculated as described by Hallauer and Miranda, (1988). Narrow-sense heritability (h^2) was estimated as:

$$h^2 = 4\sigma_m^2 / [\sigma^2_{er} + 4\sigma_{me}^2/e + 4\sigma_{mfe}^2/e + 4\sigma_{mf}^2 + 4\sigma_m^2]$$

Influence of Population Size on Estimates of Genetic Variances, Heritability and Predicted Gains

Genetic gain was determined using the formula:

$$\Delta G = i \cdot c \cdot \sigma_{ph} \cdot h^2$$

(Hallauer and Miranda, 1988)

where i = standardized selection differential often referred to as K , c = parental control, σ_{ph} = phenotypic standard deviation (square root of phenotypic variance), h^2 = narrow-sense heritability estimate for the trait under consideration. 10% selection intensity was used for irrespective of population size.

Result

Genetic parameters and predicted gains for agronomic traits for DMR ESR-W maize population

Additive variance was significantly higher than dominance variance for days to 50% pollen shed and silking with low environmental variance (Table 1).

However, additive variance and environmental variance reduced from P-250 to P-100. Narrow-sense heritability was moderate to high for all the agronomic traits ranging from 12% for plant aspect in P-150 to 52% for days to 50% silking in P-100. Heritability estimate slightly increased from P-250 to P-100 for days to 50% pollen shed and silking, but reduced slightly for plant height and plant aspect. It was highest in P-100 for both traits (Table 1). Heritability was however highest in P-200 for plant height and ear aspect. Means of traits reduced from P-250 to P-100 for days to 50% pollen shed and silking, but increases for plant height and plant aspect. Gains per cycle would reduce slightly from P-250 to P-100 for days to 50% pollen shed and silking, but lowest in P-150 for both traits. Gains per cycle would be smallest in P-100 for plant height (3.38) and in P-150 for plant aspect (5.03) (Table 1).

Table 1. Estimates of genetic variances, heritability and genetic gains for agronomic traits in DMRESR W for the four population size

Traits	N	$\sigma^2_a \pm S.E$	$\sigma^2_d \pm S.E$	σ^2_e	σ^2_{ph}	$h^2 (\%) \pm S.E$	Mean	Genetic gains	Gain/cycle
Days to 50% anthesis	250	2.22±0.51	1.91±0.44	0.04	5.81	38.17±0.09	50.22	1.62	3.22
	200	2.21±0.50	1.65±0.45	0.03	5.64	39.29±0.09	50.18	1.64	3.27
	150	1.40±0.35	1.20±0.45	0.00	4.40	31.88±0.08	49.89	1.18	2.36
	100	1.54±0.33	0.39±0.44	0.00	3.74	41.08±0.09	49.72	1.40	2.81
Days to 50% silking	250	2.82±0.59	1.50±0.42	0.03	6.17	45.71±0.10	51.24	2.00	3.90
	200	2.92±0.59	1.05±0.40	0.02	5.90	49.44±0.10	51.18	2.11	4.13
	150	2.14±0.45	0.63±0.37	0.00	4.61	46.47±0.10	50.74	1.76	3.46
	100	1.95±0.39	-0.02±0.37	0.00	3.75	52.05±0.10	50.56	1.77	3.51
Plant height (cm)	250	73.79±22.12	141.98±33.28	0.00	343.87	21.45±0.06	162.53	7.00	4.31
	200	76.60±22.24	135.26±35.31	0.00	343.53	22.30±0.06	162.13	7.27	4.49
	150	58.85±18.52	122.40±33.88	0.00	285.59	20.61±0.06	162.95	6.13	3.76
	100	54.71±19.47	143.54±43.87	0.00	299.17	18.29±0.07	164.81	5.57	3.38
Plant aspect (1-9)	250	0.09±0.04	0.24±0.06	0.04	0.44	21.40±0.08	3.05	0.25	8.18
	200	0.09±0.04	0.26±0.06	0.04	0.48	19.53±0.08	3.06	0.24	7.76
	150	0.06±0.03	0.20±0.07	0.00	0.53	12.11±0.06	3.08	0.15	5.03
	100	0.07±0.04	0.24±0.09	0.00	0.57	12.65±0.07	3.11	0.17	5.41
Ear aspect (1-9)	250	0.04±0.04	0.27±0.05	0.00	0.54	7.10±0.07	3.68	0.09	2.49
	200	0.06±0.04	0.15±0.06	0.04	0.41	15.12±0.09	3.68	0.17	4.61
	150	0.05±0.03	0.10±0.06	0.00	0.46	10.38±0.06	3.56	0.12	3.48
	100	0.06±0.03	0.15±0.08	0.00	0.52	11.34±0.07	3.58	0.14	4.02

* N: Population size; σ^2_a : additive variance; σ^2_d : dominance variance; σ^2_e : environmental variance; σ^2_{ph} : phenotypic variance; h^2 : narrow-sense heritability; S.E: standard error

Genetic parameters and predicted gains for yield and yield traits for DMR ESR-W maize population

Additive variance was generally lower than dominance variance for all the yield traits including yield, although dominance variance had equal value with additive variance in some population sizes for instance P-200 and P-100 for ear diameter (Table 2).

Additive variance was however larger than dominance variance in P-250 for number of ears per plant although not significant. Dominance variance estimate was larger in P-150 for all the yield traits except for yield itself. Environmental variance was lower than dominance variance in all population sizes for grain yield. Heritability ranged from low to moderate for yield and yield and yield traits but highest in P-200 for ear diameter (17.49%). It

increased for grain yield from P-250 to P-150 where it was highest (14.94%) (Table 2). Means increased slightly for grain yield from P-250 (4.56 tons/ha) to P-150 (4.86tons/ha). It however reduces from P-250 to P-100 for ear length and ear diameter. Gains per cycle would increase for grain yield from 4.12% in P-250 to 6.64% in P-150 where it would be highest. There would be reduction in number of ears per plant from 3.27% in P-200 to 2.17% in P-100. Gains would be highest in P-150 for grain yield (6.64%), in P-200 for number of ears per plant (3.27%) and in P-100 for ear diameter (1.47%).

Genetic parameters and predicted gains for agronomic traits for DMR ESR-Y maize population

Dominance variance was larger than additive variance for days to 50% anthesis and silking, plant and ear aspect for all the population sizes (Table 3). Additive

variance was larger than dominance variance for plant height. Values of genetic variances were highest for P-250 and P-100 for almost all the agronomic traits. Environmental variance was generally lower than genetic variance for all the traits irrespective of population size. Heritability was moderate for all the traits ranging from 19.61% for days to 50% silking in P-250 and P-100 to 33.95% for plant height in P-200. Heritability was highest in P-200 for almost all the traits studied except for plant height where it was highest in P-150. Heritability in P-150 and P-100 were almost the same as in P-250 for almost all the agronomic traits studied. Means increased slightly from P-250 to P-150 for days to 50% anthesis and silking, and plant height. Gains per cycle in P-100 would be similar to what would be obtained in P-250 for almost all the

Table 2. Estimates of genetic variances, heritability and genetic gains for yield traits in DMRESR W for the four population size

Traits	N	$\sigma^2_a \pm S.E$	$\sigma^2_d \pm S.E$	σ^2_e	σ^2_{ph}	$h^2 (\%) \pm S.E$	Mean	Genetic gains	Gain/cycle
Grain yield (tons/ha)	250	0.14±0.10	1.04±0.21	0.08	1.64	8.33±0.06	4.56	0.19	4.12
	200	0.16±0.10	1.05±0.22	0.08	1.67	9.51±0.06	4.59	0.22	4.71
	150	0.23±0.08	0.59±0.20	0.00	1.51	14.94±0.06	4.86	0.32	6.64
	100	0.20±0.09	0.69±0.26	0.00	1.56	12.54±0.06	4.83	0.28	5.71
Ears per plant	250	0.00±0.01	-0.00±0.01	0.02	0.02	13.26±0.27	0.98	0.03	3.04
	200	0.00±0.00	0.00±0.00	0.00	0.01	17.00±0.11	0.98	0.03	3.27
	150	0.00±0.00	0.00±0.00	0.00	0.01	12.32±0.10	0.98	0.02	2.17
	100	0.00±0.00	0.00±0.00	0.00	0.01	10.85±0.08	0.98	0.02	2.17
Ear length (cm)	250	0.06±0.10	0.38±0.20	0.24	0.94	6.38±0.10	12.94	0.11	0.84
	200	-0.08±0.09	0.61±0.23	0.22	0.99	-8.33±0.09	12.95	-0.15	-1.13
	150	-0.04±0.06	0.93±0.20	0.40	0.15	-26.56±0.42	9.80	-0.18	-1.87
	100	0.03±0.06	0.45±0.18	0.86	-1.57	-2.04±-0.04	9.92	-	-
Ear diameter (cm)	250	-0.01±0.02	0.02±0.03	0.06	0.06	-13.67±0.25	4.38	-0.06	-1.38
	200	0.01±0.01	0.01±0.01	0.02	0.04	17.49±0.15	4.27	0.06	1.38
	150	0.01±0.01	0.04±0.02	0.00	0.15	2.98±0.04	3.34	0.02	0.61
	100	0.01±0.01	0.01±0.03	0.00	0.13	7.84±0.05	3.35	0.05	1.47

* N: Population size; σ^2_a : additive variance; σ^2_d : dominance variance; σ^2_e : environmental variance; σ^2_{ph} : phenotypic variance; h^2 : narrow-sense heritability; S.E: standard error; Variances and heritability with negative values were taken as zero

Table 3. Estimates of genetic variances, heritability and genetic gains for agronomic traits in DMRESR Y for the four population size

Traits	N	$\sigma^2_a \pm S.E$	$\sigma^2_d \pm S.E$	σ^2_e	σ^2_{ph}	$h^2 (\%) \pm S.E$	Mean	Genetic gains	Gain/cycle
Days to 50% anthesis	250	1.53±0.46	3.25±0.81	0.00	6.23	24.50±0.07	49.66	1.08	2.17
	200	1.08±0.31	1.98±0.38	0.03	4.11	26.33±0.08	49.65	0.94	1.89
	150	1.12±0.34	2.48±0.53	0.00	4.84	23.10±0.07	49.77	0.89	1.80
	100	1.00±0.46	3.25±0.81	0.00	6.23	24.50±0.07	49.66	1.08	2.17
Days to 50% silking	250	1.02±0.36	2.55±0.72	0.00	5.20	19.61±0.07	50.75	0.79	1.55
	200	0.86±0.27	1.67±0.36	0.05	3.66	23.51±0.07	50.86	0.79	1.55
	150	0.84±0.29	2.04±0.49	0.00	4.29	19.64±0.07	50.95	0.72	1.41
	100	1.02±0.36	2.55±0.72	0.00	5.20	19.61±0.07	50.75	0.79	1.55
Plant height (cm)	250	90.44±23.63	53.41±31.59	0.00	267.46	33.81±0.09	188.91	9.73	5.15
	200	76.49±19.80	43.19±21.36	0.00	239.39	31.95±0.08	189.69	8.70	4.59
	150	80.14±20.26	38.24±23.68	0.00	236.49	33.89±0.09	191.25	9.17	4.80
	100	90.44±23.63	53.41±31.59	0.00	267.46	33.81±0.09	188.91	9.73	5.15
Plant aspect (1-9)	250	0.07±0.03	0.07±0.06	0.02	0.32	23.44±0.09	3.07	0.23	7.60
	200	0.06±0.02	0.10±0.04	0.04	0.23	28.11±0.11	3.04	0.23	7.71
	150	0.06±0.03	0.11±0.05	0.03	0.27	21.41±0.10	3.05	0.20	6.41
	100	0.07±0.03	0.07±0.06	0.02	0.32	23.44±0.09	3.07	0.23	7.60
Ear aspect (1-9)	250	-0.04±0.05	0.34±0.14	0.00	0.75	-4.81±0.06	3.80	-0.07	-1.93
	200	0.05±0.04	0.28±0.09	0.00	0.74	6.45±0.06	3.82	0.10	2.56
	150	0.02±0.04	0.29±0.10	0.00	0.73	2.48±0.06	3.78	0.04	0.98
	100	-0.04±0.05	0.34±0.14	0.00	0.75	-4.81±0.06	3.80	-0.07	-1.93

* N: Population size; σ^2_a : additive variance; σ^2_d : dominance variance; σ^2_e : environmental variance; σ^2_{ph} : phenotypic variance; h^2 : narrow-sense heritability; S.E: standard error; Variances and heritability with negative values were taken as zero agronomic traits. Gains per cycle for all the agronomic traits would be lower in P-150 which is more desirable (Table 3).

Genetic parameters and predicted gains for yield and yield traits for DMR ESR-Y maize population

Dominance variance was larger than additive variance for all the traits irrespective of population size (Table 4). Environmental variance was much lower than dominance variance. Estimate of dominance variance in P-250 was similar to what was obtained in P-100 for almost all the agronomic traits. Narrow-sense heritability ranged from low to high with the lowest in P-250 for grain yield (3.98%), and highest in P-150 for ear diameter (97.89%). Heritability in P-200, P-150 and P-100 were much larger than in P-250 for all the yield traits except number of ears per plant (Table 4). Gains per cycle would be smaller in P-250 compared with other population sizes except for number of ears per plant. However, gains per cycle for number of ears per plant in P-250 would be similar to what would be obtained in P-100. Highest gains would be obtained in P-150 for grain yield and ear diameter in this maize population (Table 4).

Discussion

The type of gene action controlling a trait guides plant breeders in selection method to use. In this study, additive variance was larger than dominance variance

for days to 50% anthesis and silking in DMR ESR-W population, while dominance variance was larger for other traits irrespective of the population size. However, dominance variance was larger than additive variance for these two traits in DMR ESR-Y population irrespective of the population size indicating that additive gene action controls the traits in DMR ESR-W while dominance gene action controls them in DMR ESR-Y. This further revealed that estimates of genetic variances differ with maize populations. The consistency in the population sizes as regards gene action controlling different traits suggested that the population sizes used in this study would have little or no effect on extent of variability in the maize populations. Márquez-Sánchez & Hallauer (1970a & b) using full-sib derived from NCI design reported that a sample size of approximately 200 plants would be sufficient to estimate genetic parameters in maize. Souza *et al.* (2018) using half-sib generated in three maize populations with sample

Table 4. Estimates of genetic variances, heritability and genetic gains for yield traits in DMRESR Y for the four population size

Traits	N	$\sigma^2_a \pm S.E$	$\sigma^2_d \pm S.E$	σ^2_e	σ^2_{ph}	$h^2 (\%) \pm S.E$	Mean	Genetic gains	Gain/cycle
Grain yield (tons/ha)	250	0.09±0.13	1.34±0.41	0.00	2.38	3.98±0.05	4.83	0.11	2.23
	200	0.09±0.08	0.72±0.20	0.15	1.16	7.57±0.07	4.83	0.14	2.97
	150	0.09±0.10	1.01±0.28	0.25	1.23	7.57±0.08	4.89	0.15	3.02
	100	0.09±0.13	1.34±0.41	0.28	1.54	6.15±0.08	4.83	0.13	2.78
Ears per plant	250	0.00±0.00	0.00±0.00	0.00	0.01	27.85±0.16	0.94	0.04	4.72
	200	0.00±0.00	0.00±0.00	0.00	0.01	11.90±0.12	0.94	0.02	2.08
	150	0.00±0.00	0.01±0.00	0.00	0.01	10.30±0.11	0.94	0.02	1.98
	100	0.00±0.00	0.00±0.00	0.00	0.01	27.85±0.16	0.94	0.04	4.72
Ear length (cm)	250	0.08±0.06	0.56±0.19	0.00	1.12	6.84±0.05	10.29	0.13	1.24
	200	0.08±0.05	0.38±0.10	0.10	0.62	13.56±0.09	10.89	0.19	1.81
	150	0.09±0.06	0.45±0.13	0.10	0.72	12.15±0.08	10.39	0.18	1.75
	100	0.08±0.06	0.56±0.19	0.12	0.77	10.00±0.08	10.29	0.15	1.50
Ear diameter (cm)	250	0.01±0.05	0.03±0.01	0.00	0.07	13.27±0.06	3.48	0.02	1.80
	200	0.01±0.00	0.02±0.01	0.01	0.02	31.40±0.14	3.50	0.09	2.49
	150	0.00±0.00	0.01±0.01	0.01	0.01	97.89±0.47	3.49	0.12	3.43
	100	0.01±0.01	0.04±0.01	0.01	0.03	27.38±0.13	3.48	0.09	2.58

* N: Population size; σ^2_a : additive variance; σ^2_d : dominance variance; σ^2_e : environmental variance; σ^2_{ph} : phenotypic variance; h^2 : narrow-sense heritability; S.E: standard error

sizes of 90, 140 and 80, respectively, also reported existence of wide variability at the population level. Dominance variance controlled all yield and yield traits in both maize populations and this is consistency with all the population sizes. Higher narrow-sense heritability was observed in P-150 and P-200 for different yield traits except for number of ears per plant in DMR ESR-Y. Oliveira *et al.* (2015) working on three maize populations with sample sizes of 200,180 and 180, respectively in three replications however reported higher estimates of additive genetic variance for grain yield(316.1, 266.4 and 258.4g/plant respectively).The result of this study simply suggested that progress may be slow for improvement of grain yield in the maize populations.

Heritability estimate was higher in other population sizes compared to P-250 for almost all the traits in the two maize populations. Heritability for days to 50% anthesis and silking was highest in P-100 and the predicted gains were similar to those that would be obtained in P-150 in DMR ESR-W. Heritability was however highest in P-200 for most agronomic traits in DMR ESR-Y although gains in these traits would still be high which is not desirable. Heritability for grain yield though generally low, was highest in P-150 with high predicted gains for both maize populations. The low heritability for grain yield in the present study suggested that progress may be slow for improvement of grain yield in both maize populations.It however indicated possibility of using a population size of 150 without much loss of efficiency. Guzman (1998) reported that the use of smaller sample size of as low

as 100 would not compromise genetic progress in a short-term maize breeding program.

Result of predicted gains revealed that yield and yield parameters would increase better in P-150 and P-200 than in other population sizes except for number of ears per plant in DMR ESR-Y. For instance, in DMR ESR-W, a yield increase of 0.22ton/ha and 0.32ton/ha would be obtained in P-200 and P-150 respectively compared to 0.19tons/ha in P-250. Similarly, in DMR ESR-Y, higher gains of 0.14ton/ha and 0.15ton/ha would also be realized in P-200 and P-150 respectively compared with 0.11tons/ha in P-250. Although there would be increase in all the agronomic traits studied with selection in both maize populations which is not so desirable, the increase would be lowest in P-150. This result indicated that with population size of 150 and 10% selection intensity, genetic variability would still be maintained and genetic progress would not be compromised.Lorenz (2013) on selection response and predicted accuracy reported a higher accuracy when 150 individuals were phenotyped than when 250 were phenotypedusing similar selection intensity.On the contrary, Viana (2007) reported that effective size of 160 does not provide improved populations with minimum genotypic variability. They however stated that in the populations with lower effective sample size (160 and 400), the loss of favorable genes is restrictedto recessive genes with reduced frequencies.

Conclusion

Considering the cost and time of evaluating larger population sizes of as high as 250-300, and hence selection of large number for recombination, it can be concluded that population size of only 150 individuals could be used without compromising genetic progress. Although population size of 100 still gave some reasonable result, the results were not consistent most importantly for yield and yield traits in this study for it to be considered. Genetic drift may not necessarily result in an immediate and drastic decrease in genetic variance. Hence, there is little to no advantage of using larger effective population size to maintain genetic variability for short-term recurrent selection.

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