



Genetic variability for grain yield components in maize populations

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Abstract

The genetic variability of five promising tropical and tropical-temperate maize populations introduced or developed in Benin was studied for grain yield components (number of grains per ear and grain weight). The populations are: EV8443SR, an elite tropical population and four tropical-temperate populations (F1 and BC1 of two crosses between EV8443SR and the temperate populations FS14 and DEA): EV8443SR × FS14 (EF), EV8443SR × (EV8443SR × FS14) (EFE), EV8443SR × DEA (ED), and EV8443SR × (EV8443SR × DEA) (EDE). Random sets of S1 families of the populations were evaluated in two tropical locations (savanna and forest zones) in Benin using 12 × 12 triple lattices. No significant difference among population genetic variances was observed in any of the two crosses studied. For number of grains per ear, the highest expected genetic progress was obtained in the population EF in cross EV8443SR × FS14 and in the population EDE in cross EV8443SR × DEA. For grain weight, the highest expected genetic progress was obtained in the 50% tropical 50% temperate population (EF or ED) in savanna zone and in the tropical parent EV8443SR in forest zone. EV8443SR appeared better than, or practically equal to, the tropical-temperate populations, as a foundation population to increase number of grains per ear and grain weight.

Keywords: Benin, breeding, genetic variability, grain yield components, maize.

Introduction

Maize is the most cultivated cereal crop in the world after wheat (FAO, 2013). It is utilized as human food, animal feed, and industrial raw material. In Benin, maize is the most cultivated food crop; but, its mean yield is low (less than 1.5 t/ha) (FAO, 2013) due to several constraints including the deficiencies of the varieties (Abadassi, 2014). A lot of improved varieties have been introduced from the International Institute of Tropical Agriculture (IITA) and the International Maize and Wheat Improvement Center (CIMMYT). But, they don't satisfy the producers and consumers' needs and must be improved for key agronomic traits. Promising populations were derived from some of those varieties; but they need to be improved for few agronomic traits notably grain yield. According to Agbaje et al. (2000), grain yield is positively correlated with number of grains per ear in maize. Similarly, Bocanski et al. (2009), Nastasic et al. (2010) and Yusuf (2010) reported that maize grain

weight is positively correlated with grain yield. Selection for high number of grains per ear or grain weight may, therefore, increase grain yield in maize populations. Genetic variability studies are essential in plant breeding. They determine the choice of the most efficient selection strategy. Several authors including Albrecht and Dudley (1987), Crossa and Gardner (1987), Iglesias and Hallauer (1989), Eagles and Hardacre (1990), Hoffbeck et al. (1995), Abadassi and Hervé (2000), Yusuf (2010), Shanthi et al. (2011), Rajesh et al. (2013), Hussain and Hassan (2014) and Kumar et al. (2014) conducted genetic variability studies in maize. But the results vary with trait and population. This work was, therefore, initiated to study the genetic variability of five promising maize populations introduced or developed in Benin for grain yield components.

Materials and Methods**Statistical analysis****Populations and evaluation**

The populations studied are:

- EV8443SR, an elite tropical maize population bred by IITA and CIMMYT from Population 43 of CIMMYT and cultivated in Benin and other African countries
- EV8443SR × FS14 (EF), a tropical-temperate population resulting from the cross between EV8443SR and FS14, a temperate synthetic bred by the French National Institute of Agricultural Research
- EV8443SR × (EV8443SR × FS14) (EFE), a tropical-temperate population obtained in backcrossing EV8443SR × FS14 to EV8443SR
- EV8443SR × DEA (ED), a tropical-temperate population derived from the cross between EV8443SR and DEA, a single hybrid widely cultivated in France
- EV8443SR × (EV8443SR × DEA) (EDE), a tropical-temperate population obtained in backcrossing EV8443SR × DEA to EV8443SR.

Random sets of 40 S1 families of EV8443SR and 50 families of each of the other populations were grown for evaluation in Benin, at Bembéréké (North-Benin, savanna zone, latitude: 9°58'N; longitude: 2°44'E; altitude: 358 m) and Allada (South-Benin, degraded forest zone; latitude: 6°42'N; longitude: 2°7'E; altitude: 105 m) in 12 × 12 triple lattices (one lattice per cross). Each entry was planted in two 2 m rows. The spacing was 0.80 m between rows and 0.50 m between consecutive hills on each row. The plots were overplanted and thinned to 2 plants per hill (50000 plants.ha⁻¹). Fertilization and weeding were optimal. Rainfall was sufficient and well distributed.

Two grain yield components were studied: number of grains per ear and grain weight. One thousand grain weight was recorded per plot at 15% moisture. Number of grains per ear (nge) was computed as follows:

$$\text{nge} = (\text{gwe}/\text{tgw}) \times 1000$$

gwe = grain weight per ear
tgw = 1000 grain weight.

Analysis of variance was performed for each trait. Genetic variance components and their standard errors were estimated using the restricted maximum likelihood method of Varcomp Procedure on SAS system (SAS Institute, 1982). Separate analyses of variance were realized for each population in randomized complete block designs according to the model of Hallauer and Miranda (1981). The two locations were pooled when residual variances were homogeneous at the 5% level. All the effects, except repetition effect, were considered as random.

Broad sense heritability (h^2) was estimated per trait and population as follows:

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2/r} \text{ for 1 location}$$

$$h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2/r + \sigma_{gl}^2/l} \text{ for pooling analysis}$$

σ_g^2 = genetic variance; σ_e^2 = error variance; σ_{gl}^2 = genotype × location interaction variance; r = number of repetitions per location; l = number of locations.

Expected genetic progress in one cycle of selection (G) was computed using the formula:

$$G = ih^2 p \quad (\text{Gallais, 1990})$$

i = standardized selection differential; h^2 = narrow sense heritability; p = square root of phenotypic variance.

A selection pressure of 10% corresponding to $i = 1.755$ was used. Narrow sense heritability was not estimable in the design used and was replaced by broad sense heritability. Therefore, the genetic progress was probably overestimated. But population comparisons should be valid since the same bias applied to all populations.

Predicted means after one cycle of selection (mean before selection + G) were calculated and compared to identify the best foundation population.

Results and Discussion**Genetic variability**

Significant differences ($P < 0.05$) among entries appeared in all trials for all traits. Table 1 to 5 give estimates of genetic variances and their standard errors per trait and population.

No significant difference was observed among estimates of genetic variance in any cross. Introgression of the temperate material FS14 or DEA did not, then, have a significant effect on the genetic variance of the tropical population EV8443SR for number of grains per ear and grain weight. EFE and EDE are 75% tropical 25% temperate populations whereas EF and ED are 50% tropical 50% temperate populations. Similarity of tropical parent and tropical-temperate population genetic variances may be due to:

- linkage disequilibrium present in the tropical-temperate populations which could have hindered the release of some useful genetic variation
- a high variability of the tropical parent EV8443SR
- a low genetic divergence between tropical and temperate parents.

Abadassi and Hervé (2000) noted also similarity of tropical parent, 75% tropical 25% temperate population and 50% tropical 50% temperate population genetic variances for grain yield in the two crosses. The same authors found, however, that, for plant height, 50% tropical 50% temperate population genetic variance was significantly lower than 75% tropical 25% temperate population genetic variance in cross EV8443SR × FS14 and significantly higher than tropical parent genetic variance in cross EV8443SR × DEA. Increases in genetic variance through introgression were also reported by Albrecht and Dudley (1987), Crossa and Gardner (1987), Iglesias and Hallauer (1989), Eagles and Hardacre (1990) and Hoffbeck et al. (1995). The dissimilarities may be due to the genetic constitution of the parents of the crosses.

Table 1. Estimates of genetic variances and their standard errors in cross EV8443SR × FS14 (pooled analysis)

Trait	Population		
	EV8443SR	EFE	EF
1000 grain weight (g)	1861 ± 659a	965 ± 316a	1409 ± 425a

Variances followed by the same letter have overlapping 95% confidence intervals.
 EF = EV8443SR × FS14; EFE = EV8443SR × (EV8443SR × FS14).

Table 2. Estimates of genetic variances and their standard errors in cross EV8443SR × FS14 at Bembéréké

Trait	Population		
	EV8443SR	EFE	EF
Number of grains per ear	1802 ± 806a	1740 ± 937a	1845 ± 682a

Variances followed by the same letter have overlapping 95% confidence intervals.
 EF = EV8443SR × FS14; EFE = EV8443SR × (EV8443SR × FS14).

Table 3. Estimates of genetic variances and their standard errors in cross EV8443SR × FS14 at Allada

Trait	Population		
	EV8443SR	EFE	EF
Number of grains per ear	1419 ± 649a	1172 ± 491a	2072 ± 665a

Variances followed by the same letter have overlapping 95% confidence intervals.
 EF = EV8443SR × FS14; EFE = EV8443SR × (EV8443SR × FS14).

Table 4. Estimates of genetic variances and their standard errors in cross EV8443SR × DEA at Bembéréké

Trait	Population		
	EV8443SR	EDE	ED
Number of grains per ear	1648 ± 908a	2439 ± 921a	1610 ± 919a
1000 grain weight (g)	1351 ± 475a	1011 ± 328a	1488 ± 451a

For each trait, variances followed by the same letter have overlapping 95% confidence intervals.
 ED = EV8443SR × DEA; EDE = EV8443SR × (EV8443SR × DEA).

Expected genetic progress and best foundation population

Mean, estimates of broad sense heritability (h^2), expected genetic progress (G) and predicted mean after one cycle of selection (PM) per trait and population are shown in tables 6 to 9. G was

probably overestimated since it was computed using broad sense heritability. However, population comparisons should be valid because the same bias applied to all populations. For number of grains per ear, the highest G was obtained in the population EF in cross EV8443SR × FS14 and in the population EDE in cross EV8443SR × DEA

Table 5. Estimates of genetic variances and their standard errors in cross EV8443SR × DEA at Allada

Trait	Population		
	EV8443SR	EDE	ED
Number of grains per ear	835 ± 526a	1291 ± 858a	457 ± 270a
1000 grain weight (g)	1406 ± 439a	768 ± 227a	1159 ± 313a

For each trait, variances followed by the same letter have overlapping 95% confidence intervals. ED = EV8443SR × DEA; EDE = EV8443SR × (EV8443SR × DEA).

Table 6. Mean (M), broad sense heritability (h^2), expected genetic progress (G) and predicted mean after one cycle of selection (PM) (selection pressure = 10%) per population and trait in cross EV8443SR × FS14 at Bembéréké

Trait	Population											
	EV8443SR				EFE				EF			
	M	h^2	G	PM	M	h^2	G	PM	M	h^2	G	PM
Nge	309	0.42	48	357	318	0.40	46	364	274	0.57	56	330
Tgw (g)	221	0.73	55	376	277	0.72	46	323	256	0.78	58	314

Nge = number of grains per ear; Tgw = 1000 grain weight; EF = EV8443SR × FS14; EFE = EV8443SR × (EV8443SR × FS14).

Table 7. Mean (M), broad sense heritability (h^2), expected genetic progress (G) and predicted mean after one cycle of selection (PM) (selection pressure = 10%) per population and trait in cross EV8443SR × FS14 at Allada

Trait	Population											
	EV8443SR				EFE				EF			
	M	h^2	G	PM	M	h^2	G	PM	M	h^2	G	PM
Nge	244	0.52	48	292	246	0.51	43	289	226	0.65	65	291
Tgw (g)	289	0.73	64	353	257	0.72	46	303	258	0.78	58	316

Nge = number of grains per ear; Tgw = 1000 grain weight; EF = EV8443SR × FS14; EFE = EV8443SR × (EV8443SR × FS14).

Table 8. Mean (M), broad sense heritability (h^2), expected genetic progress (G) and predicted mean after one cycle of selection (PM) (selection pressure = 10%) per population and trait in cross EV8443SR × DEA at Bembéréké

Trait	Population											
	EV8443SR				EDE				ED			
	M	h^2	G	PM	M	h^2	G	PM	M	h^2	G	PM
Nge	301	0.40	44	345	276	0.30	48	324	227	0.38	44	271
Tgw (g)	311	0.66	52	363	280	0.64	45	325	243	0.68	55	298

Nge = number of grains per ear; Tgw = 1000 grain weight; ED = EV8443SR × DEA; EDE = EV8443SR × (EV8443SR × DEA).

Table 9. Mean (M), broad sense heritability (h^2), expected genetic progress (G) and predicted mean after one cycle of selection (PM) (selection pressure = 10%) per population and trait in cross EV8443SR × DEA at Allada

Trait	Population											
	EV8443SR				EDE				ED			
	M	h^2	G	PM	M	h^2	G	PM	M	h^2	G	PM
Nge	219	0.39	31	250	203	0.33	36	239	160	0.37	23	183
Tgw (g)	240	0.74	57	297	227	0.70	41	268	223	0.75	52	275

Nge = number of grains per ear; Tgw = 1000 grain weight; ED = EV8443SR × DEA; EDE = EV8443SR × (EV8443SR × DEA).

For grain weight, the highest G was obtained in the 50% tropical 50% temperate population at Bembéréké and in the tropical parent at Allada.

The tropical parent EV8443SR had a PM higher than those of the tropical-temperate populations for number of grains per ear and grain weight in cross EV8443SR × DEA. EV8443SR appeared, therefore, as the best foundation population to increase number of grains per ear and grain weight in that cross. In cross EV8443SR × FS14, EV8443SR had a PM superior to those of the tropical-temperate populations for grain weight and can, hence, be considered as the best foundation population to increase grain weight in that cross. In the same cross, for number of grains per ear, the highest PM was obtained in the population EFE at Bembéréké and in the population EV8443SR at Allada. But the PM of the two populations were very close in the two locations. EV8443SR and EFE appeared, therefore, practically equal, as a foundation population to increase number of grains per ear in cross EV8443SR × FS14.

Conclusion

No significant difference among population genetic variances was observed in any of the two crosses studied. Introgression of the temperate material FS14 or DEA did not, then, have a significant effect on the genetic variance of the tropical population EV8443SR for number of grains per ear and grain weight. For number of grains per ear, the highest expected genetic progress was obtained in the population EF in cross EV8443SR × FS14 and in the population EDE in cross EV8443SR × DEA. For grain weight, the highest expected genetic progress was obtained in the 50% tropical 50% temperate population at Bembéréké and in the tropical parent at Allada. The tropical parent EV8443SR appeared better than, or practically equal to, the tropical-temperate populations, as a foundation population to increase number of grains per ear and grain weight.

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