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Full Length Research Paper

Selection of maize progenies for tryptophan content and grain yield

Constantino Tomás Senete[1,2], Pedro Fato[1], João Massitela[1], Otília Henrique Tamele[1]and João Cândido de Souza[2]

[1]Institute of Agricultural Research of Mozambique, PO Box 3658, Avenue of FPLM nº 2698, Maputo, Mozambique.
[2]Federal University of Lavras, Department of Biology, PO Box 3037, CEP 37200-000 Lavras, MG, Brazil.

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The incrementation of lysine, tryptophan and maize protein nutritional value in locals where maize is staple food could contribute significantly to improving the population nutritional status. The objective of this study was to estimate variance and average components related to the maize protein quality based on tryptophan and grain yield analysis, and to select from the early generations progenies which best complement with the tester for both characters. The laboratory analyses were carried out by using colorimetric reactions and the statistical analyses were based on mixed model. The experiment was set out in partially balanced square lattice with 144 treatments, two replications and 12 blocks. The estimations, associated with the assessed treatment performances made it possible to infer that both populations are promising for recurrent selection and suggested good experimental precision. The selective accuracy demonstrated the possibility of obtaining gains by selecting in both characters. For tryptophan content, the specific combining ability presented small magnitude value due the qualitative inheritance and, the additive effects might have been more important. The shrinkage effect in grain yield was more noticeable than the tryptophan content. Over 25% of the progenies contributed positively to the tryptophan content and only 3.65% to grain yield.

Key words: *Zea mays,* QPM, Mozambique, specific combining ability, shrinkage, BLUP.

INTRODUCTION

Maize (Zea mays, L.) in many African countries and particularly in Mozambique is a staple food, reaching a per capita consumption of 159 g/capita/day. An aspect of great relevance is its contribution to the consumed protein. That is, the protein consumption is 46.5 g/capita/day and, as from it, over 87% (40.5 g/capita/day) have plant origin in which maize contributes to, at least, 30% (12.3 g/capita/day) (FAOSTAT, 2014), thereby making the maize an extremely important cereal for the population.

Due to the very limited supply of protein-rich foods, the share of protein in the dietary energy supply was lower than recommended. The food diversification index was very low with an extremely limited contribution of foods of animal origin (FAO, 2011). The incrementation of nutritional value of the common foods, as maize, may contribute significantly to enhance the nutritional status of the population.

Maize grain contains 8% to 9% of protein distributed in the endosperm (around 80%) and in the embryo (around 20%). In the embryo, the fraction of non-zein proteins (60% albumins) is prevailing, constituted of high biological value structural proteins. In the endosperm, a fraction of zein-proteins (60% prolamines), storage proteins with low biological value due to imbalance of essential amino acids caused by high leucine content and

Corresponding author. Email: senetec2003@yahoo.com.br

by lysine and tryptophan deficiency (Wang *et al.,* 2014; Prasanna et al., 2001).

In quality protein maize (QPM), lysine and tryptophan contents are relatively high. This increase is explained by the decrease of zein fraction and by the increase of non-zein proteins in the endosperm proteins (Vivek*et al*., 2008).

It is considered QPM, the maize which fulfils the good qualities of vitreous and greater density grains from common maize with the protein quality of opaque maize grains, that is, good grain yield with higher biological value protein (Wang *et al.,* 2014).

The use of this maize, QPM, might contribute significantly to the per capita consumption of high biological value protein in regions where maize is staple food, having no need to increase the maize per capita consumption.

In non-QPM, all the protein fractions, except for zeins, are balanced in essential amino acid contents. However, it is known for presenting a biological value of 40% when compared to milk protein. The essential amino acids such as lysine, tryptophan and threonine are found in low quantities, being lysine the limiting amino acid followed by tryptophan. In contrast, QPM has almost double the lysine and tryptophan quantity, what makes QPM protein equivalent to around 90% of milk protein (Gupta*et al*., 2009; Sofi et al., 2009; Vivek*etal*., 2008; Bressani, 1991).

Vivek et al. (2008) suggest that analyses carried out in the whole grain which present more than 0.075% of tryptophan can be considered QPM. They can be equally considered QPM when analyses are only carried out in the endosperm and present more than 0.65% of tryptophan on the protein, since the maize presents more than eight percent of protein in the endosperm.

Tryptophan laboratorial analysis has been used as the only attribute to evaluate the maize protein nutritional quality in improvement programs for protein quality of this cereal because the lysine and tryptophan values are highly correlated, making it unnecessary the measurement of both (Mahan et al., 2014). On the other hand, there is a disadvantage in measuring lysine which is a time-consuming colorimetric reaction, and its reproducibility is affected by many factors, what makes it difficult the analysis of a larger number of samples (Nurit *et al*., 2009; Vivek *et al*., 2008).

Maize protein quality inheritance is complex and involves manipulation of three genetic systems: (1) the opaque-2 gene which must be in its recessive homozygotic form to reduce the rate of gene transcriptions that encode to zein proteins containing low quantities of lysine and tryptophan; (2) modifier genes responsible for modification in the grain texture, undesirable characteristic (soft, chalky) typical of the opaque-2 maize; and (3) non-opaque-2 genes which affect lysine and tryptophan in the grain to ensure that the concentration of these amino acids are within the upper limit of the variation observed for the maize (Nurit *et al*., 2009; Vivek *et al*., 2008).

Development and recommendation of new cultivars require a selection to be carried out among a larger number of genotypes candidates and, thus, the genotypic value estimation constitutes the core of an improvement program (Phiepo et al., 2008).

The evaluation of a larger number of genotypes might make it necessary the use of an unbalanced design (non-orthogonal) as in the case of incomplete blocks. In this case, the use of mixed models in the analysis of these data might make it possible to perform wider interferences with more accurate predictions (GonçalvesandFritshe-Neto, 2012;Bernardo, 2010; Resende, 2007; Balzariniand Milligan, 2003).

The general and specific combining abilities constitute very important and widespread examples of average genetic components. The general combining abilities (GCA) can be considered such as being the inbred lines performances due to additive genetic effects in a hybrid combination and the specific combining abilities (SCA) as the performance of specific hybrid due to non-additive genetic effects (Cruz &Carneiro, 2006; VencosvskyandBarriga, 1992; Griffing, 1956).

The combining ability can be obtained by diallel cross or by top crosses (TC). The latter one corresponds to the cross-breeding of inbred lines group with one or more testers, which can be of wide or narrow basis.

Hallauer and Carena (2009) report several simulation studies performed to select genitors and corresponding hybrids. It arises from these studies that top crosses from early generations are better hybrid predictors in their genitors advanced generations than the per se performance of the inbred lines.

Top crosses have been used to perform selection in improvement early phases to increase the process efficiency through the substantial decrease of the number of inbred lines before they reach complete homozygosis. This selection decreases the amount of resources and efforts involved in self-activities (Souza Jr., 2001; Hallauer and Miranda Filho, 1988).

In another study, Souza Jr. (2001) intend to demonstrate the efficiency increase of inbred lines selection in endogamy early generations. The inbred lines combining abilities determined in early generations remains relatively stable along the self-generations.

The use of genotypic values predictor, BLUP (better linear unbiased prediction), such as SCA maximizes the correlation between genotypic values predictions and real genetic values when the individuals are evaluated under the same environmental conditions, since it minimizes predictions error (GonçalvesandFritshe-Neto, 2012; Bernardo, 2010; Resende, 2007; Cruz andCarneiro, 2006; Balzariniand Milligan, 2003).

To date, genetic breeding studies focused on genetic components on tryptophan content in the maize grain are scarce in literature (Mahan et al., 2014), although some reports discuss a combining ability of QPM cultivars for agronomics and other traits (Wegary et al., 2014; Naidoo et al., 2012; Machida et al., 2010; Musila et al., 2010).

Development of commercial maize hybrids usually requires good knowledge of genetic components of the

breeding materials to be used. Selection of genitors based on genetic components has been used as an important approach in crops improvement. Genetic components are special in maize as it assists in identifying potential parental inbreds that can be used for producing hybrids and synthetics (Amirruzzaman et al., 2011).

A better comprehension of genetic components make it easier to plant breeders develop new cultivars of high protein quality maize. Thus, the objectives of this study were to estimate variance and average components related to maize protein quality based on tryptophan analysis and grain yield and to select progenies in early generations which best complement with the tester based on SCA estimation in mixed model as regards the protein quality and grain yield.

MATERIAL AND METHODS

Germplasm

One hundred and thirty-seven progenies S3/S4 were crossed with a tester (single cross) to synthetized top crosses. At each self-generation, these progenies were select through light box. Vivek et al. (2008) score a gradation of opacity, in light box, in a scale from 1 to 5. In which: 1: non-opaque, 2: 25% opaque, 3: 50% opaque, 4: 75% opaque, 5: 100% opaque. Grains with less opacity imply greater action of modifier genes. Thus, the 2 and 3 types were considered QPM, therefore, they were selected. The progenies development occurred in lowland tropical conditions in Mozambique (Chókwè Agricultural Research Station) from Sussuma, an open pollinated variety and Olipa, a three way cross, both commercially. From Sussuma, 26 progenies were generated and from Olipa, 111 progenies. The top crosses were synthesized at Umbeluzi Agricultural Research Station in the 2013/14 main season.

Field measurements

All parameters were considered per plot. The 137 top crosses and seven local checks were grown in partially balanced square lattice and the plot consisted of two 5-meter long rows with an inter-row spacing 0.80 m. Each plot was thinned to 42 plants. Harvesting was manually performed after the grain was mature and the plants were dried. During harvesting, grain weight and moisture were determined. Grain yield was calculated on the basis of grain weight per plot and adjusted to 12.5% moisture content and t/ha.

Laboratorial tryptophan measurements

Tryptophan analyses were performed at Mozambique Agricultural Research Institute laboratory in Maputo in 2014, according Nurit et al. (2009) methodology. A random sample of 20-30 seeds was taken in each treatment, grinded at 0.5 milimetres. Each sample (treatment) was placed into a commercial filter paper envelope 10 x 11 centimetres and left into the continuous fat extractor in 300 mililitres of hexane along four hours. After that, they were dried to ensure the hexane evaporation. For each 80 miligrammes of degreased maize meal (corresponding to each treatment), three mililitres of papain solution were added (two controls with known concentration were included: one QPM and another non-QPM), carefully mixed and submitted to 65ºC during 16 hours. Next, the tubes were left to cool down at room temperature and mixed before 3.600 revolutions per minute centrifugation during 10 minutes to ensure absence of floating particles in the supernatant. One milimeter of supernatant was taken and transferred to a glass tube where three mililitres of colorimetric reagent were added, mixed for five minutes and the tubes were incubated at 65ºC during 30 minutes to develop colour. Afterwards, the samples were left to cool down at room temperature so that, eventually, a spectrophotometer reading could be carried out with absorbance at 560 nanometres.

Experimental design and statistical analysis

The experimental for tryptophan content and grain yield was conducted in square lattice (12 x 12) partially balanced with two replications. Tryptophan analyses for the 12 treatments which form each block were performed on the same day. The data processing was performed by the use of computational system SAS (Statistical Analysis System) version 9.3 (SAS Institute, 2013), considering the replication and checks as fixed effects, the blocks and top crosses random effects. The adjusted means (BLUP means) were obtained by summing up the population average (Sussuma or Olipa progenies average) with SCA of each top cross. Gains with selection were calculated in each group of the population.

RESULTS

Variance components

Variance components estimates for tryptophan content and grain yield and their respective confidence intervals (lower limit and upper limit) associated with the estimations are in table 1. It is seen that the confidence intervals (lower limit and upper limit) were positive, that is, the variance components are different from zero. It is also noticeable that top crosses generated by Olipa progenies present a greater confidence value in relation to the interval presented by Sussuma progenies in both characters. The magnitude of variance components for tryptophan content is lower in relation to the observed

Table 1. Estimates of variance components and their confidence intervals for tryptophan content and grain yield.

	Tryptophan content			Grain yield		
Components	Estimate value ($x 10^{-4}$)	Lower limit ($x10^{-5}$)	Upper limit ($x 10^{-4}$)	Estimate value	Lower limit	Upper limit
Block	6.58	9.31	162,600	0.1520	0.0735	0.4790
Progenies of Sussuma	1.45	8.60	2.95	0.3918	0.1759	1.5029
Progenies of Olipa	1.18	8.90	1.61	0.4509	0.2987	0.7586
Residual	0.24	1.90	0.31	1.1671	1.0215	1.3464

magnitude for grain yield.

Specific combining ability

SCA positive values for tryptophan content and grain yield are desirable because high protein quality and good grain yield are extremely important attributes for maize cultivars, particularly in regions where it is the staple food. It is seen in table 2 that, with 95% of probability, 72 top crosses present SCA values for tryptophan content significantly different to zero, from which 33 are positive, whereas for grain yield, 13 top crosses with values significantly different to zero were observed and, from these ones, only 5 are positive. One can also observe that only two top crosses (TC 24 and TC 40) presented significantly positive values for SCA in both characters (tryptophan content and grain yield).**Top crosses and**

checks variability and performance

Hereinafter, mixed model analysis of variance for tryptophan content and grain yield are presented in table 3. Significant differences were not observed for the block effect in tryptophan content and checks effect for grain yield. The check effects for tryptophan content and replication for grain yield presented significant differences. That was, at least, one of the check averages was different from the others for the tryptophan content and one replication differs from another for grain yield.

Adjust means or BLUP means (population average + SCA from each top cross) for both characters seen in table 4. According to the classification suggested by Vivek et al. (2008), only nine (6.57%) from the 137 top crosses can be considered QPM (TC43, TC64, TC69, TC99, TC102, TC130, TC133, TC134 and TC135).

Still on tryptophan content in the grain, the best top cross presented over the double performance when compared to the population which generated the progeny that synthetized this hybrid (0.093 vs 0.045) (tables 4 and 5). On the other hand, when compared to the minimum phenotypic value required to be considered QPM, the best hybrid combination presented around 20% more (0.093 vs 0.075).

For the grain yield, one can notice that top crosses from Sussuma top crosses and Sussuma local check had an upper performance when compared to Olipa check and top crosses from Olipa (tables 4 and 5).

In table 5, it is seen the average performance of checks and the average of each progenies population group (top crosses average from Sussuma and top crosses average from Olipa).

Top crosses generated by Olipa progenies presented an upper performance than top crosses generated by Sussuma as well as all the checks, considering the tryptophan content. For grain yield, average performance of top crosses generated by Sussuma was higher than those generated by Olipa. However, it was lower than that from Sussuma local check and GW15WQPM.

Because there were significant differences between checks, pairwise comparisons were made with Tukey adjustment for all the 21 contrasts in order to verify which of the checks is different to the other. With 95% confidence for the estimations (table 6) it was observed that there are significant differences for the character tryptophan content in: Olipa vs. Sussuma, Olipa vs. Average of top crosses generated by Olipa progenies, Olipa A/B vs. Sussuma, Olipa A/B vs. Top crosses generated by Olipa progenies, PAN53 vs. Rutanda, PAN 53 vs. Sussuma, PAN 53 vs. Top crosses generated by Olipa progenies, PAN 53 vs. Top crosses generated by Sussuma progenies and Top crosses generated by Olipa progenies vs. Top crosses generated by Sussuma progenies.

Although the mixed model analysis of variance for grain yield have not presented significant differences (P>0,05),

Table 2. specific combining ability (SCA) for tryptophan content and grain yield.

Top cross[3]	Tryptophan content		Grain yield		Top cross[3]	Tryptophan content		Grain yield		Top Cross[3]	Tryptophan content		Grain yield		Top cross[3]	Tryptophan content		Grain yield	
	SCA	p-value	SCA	p-value		SCA	p-value	SCA	p-value		SCA	p-value	SCA	p-value		SCA	p-value	SCA	p-value
1	-0.0028	0.4949	-12.771	0.003	18	0.0068	0.0959	0.0788	0.8539	35	-0.0036	0.3000	0.2362	0.5862	52	0.0114	0.0013	-15.038	0.0006
2	-0.0197	<.0001	-0.1033	0.8092	19	-0.0003	0.9389	-0.2596	0.5437	36	-0.0055	0.1164	0.5889	0.1745	53	0.0131	0.0002	0.1801	0.6782
3	0.0071	0.0832	0.4718	0.2704	20	-0.0003	0.9377	0.2242	0.6008	37	-0.0170	<.0001	0.1584	0.7155	54	-0.0067	0.0563	-0.1925	0.6574
4	0.0009	0.8339	0.2237	0.6013	21	-0.0010	0.8135	0.6084	0.1559	38	0.0108	0.0022	0.1144	0.7919	55	0.0102	0.0039	-0.3884	0.3704
5	-0.0008	0.8371	-0.0460	0.9144	22	0.0043	0.2905	-0.4627	0.2803	39	-0.0130	0.0003	-0.1230	0.8140	56	0.0020	0.5485	0.2062	0.2062
6	-0.0128	0.0020	0.0180	0.9664	23	-0.0099	0.0162	-0.8357	0.0519	40	0.0132	0.0002	0.9319	0.0320	57	-0.0037	0.2819	-0.7148	0.0998
7	0.0180	<.0001	0.1998	0.6407	24	0.0181	<.0001	10.019	0.0199	41	0.0049	0.1595	0.1916	0.6588	58	-0.0122	0.0006	0.2789	0.5204
8	-0.0076	0.0642	0.4487	0.2950	25	0.0024	0.5553	-0.5358	0.2105	42	0.0082	0.0200	-0.3086	0.4769	59	-0.0077	0.0284	-0.2247	0.6044
9	0.0112	0.0066	0.2486	0.5620	26	-0.0131	0.0016	0.2227	0.6042	43	0.0150	<.0001	-0.2833	0.5138	60	0.0079	0.0244	-0.4592	0.2901
10	-0.0026	0.5142	0.2012	0.6382	27	-0.0101	0.0042	0.2714	0.5316	44	0.0077	0.0274	-0.0285	0.9475	61	0.0034	0.3279	-0.3949	0.3630
11	0.0148	0.0004	0.2502	0.5596	28	-0.0093	0.0083	-0.4749	0.2737	45	0.0013	0.7179	0.4413	0.3090	62	0.0037	0.2885	0.5474	0.2079
12	0.0186	<.0001	-0.5126	0.2312	29	-0.0134	0.0002	0.6091	0.1607	46	0.0132	0.0002	0.2800	0.5186	63	-0.0081	0.0216	0.1064	0.8061
13	-0.0044	0.2775	-0.2704	0.5280	30	-0.0180	<.0001	-0.3751	0.3873	47	-0.0122	0.0006	-0.5413	0.2124	64	0.0155	<.0001	0.2078	0.6318
14	-0.0055	0.1781	0.1858	0.6647	31	-0.0092	0.0091	0.3452	0.4263	48	-0.0020	0.5747	10.197	0.0190	65	-0.0247	<.0001	-0.3434	0.4291
15	-0.0174	<.0001	-0.1024	0.8110	32	0.0080	0.0223	0.1704	0.6948	49	-0.0155	<.0001	-0.1366	0.7527	66	0.0052	0.1321	0.2443	0.5737
16	-0.0197	<.0001	0.0113	0.9789	33	0.0004	0.9127	-0.2682	0.5366	50	0.0038	0.2781	0.8861	0.0415	67	-0.0168	<.0001	-0.8228	0.0583
17	0.0159	0.0001	0.0004	0.9992	34	0.0005	0.8902	0.4946	0.2549	51	0.0064	0.0671	0.4214	0.3317	68	-0.0079	0.0241	0.1478	0.7332

"Table 2. Cont..."

in this comparison significant differences were observed in the following contrasts: PAN 53 vs. Sussuma, Rutanda vs. Top crosses generated by Olipa progenies, Rutanda vs. Top crosses generated by Sussuma and Sussuma vs. Top crosses generated by Olipa progenies.

"Table 2, cont."

Top cross[3]	Tryptophan content		Grain yield		Top cross[3]	Tryptophan content		Grain yield		Top cross[3]	Tryptophan content		Grain yield		Top cross[3]	Tryptophan content		Grain yield	
	SCA	p-value	SCA	p-value		SCA	p-value	SCA	p-value		SCA	p-value	SCA	p-value		SCA	p-value	SCA	p-value
69	0.0170	<.0001	-0.3369	0.4374	87	-0.0068	0.0528	0.4860	0.2628	105	-0.0103	0.0035	-0.0185	0.9661	123	-0.0057	0.1036	-0.4405	0.3105
70	-0.0049	0.1611	0.0890	0.8376	88	-0.0045	0.1962	-0.7018	0.1065	106	0.0081	0.0214	-0.1448	0.7385	124	0.0063	0.0727	0.4485	0.3013
71	-0.0011	0.7422	0.4492	0.3010	89	0.0031	0.3714	0.0429	0.9212	107	-0.0008	0.8214	0.7502	0.0839	125	0.0021	0.5465	0.2187	0.6140
72	-0.0122	0.0006	-0.9444	0.0300	90	0.0052	0.1335	0.6961	0.1093	108	-0.0099	0.0048	-0.3287	0.4493	126	-0.0010	0.7771	0.9027	0.0379
73	-0.0153	<.0001	-0.0372	0.9317	91	0.0043	0.2156	0.4919	0.2573	109	-0.0022	0.5251	-0.1018	0.8146	127	-0.0209	<.0001	-0.6965	0.1089
74	0.0120	0.0007	-0.5326	0.2198	92	-0.0089	0.0115	-0.3090	0.4762	110	0.0126	0.0004	-0.0852	0.8441	128	-0.0008	0.8198	-0.1761	0.6844
75	-0.0077	0.0280	0.4073	0.3476	93	-0.0093	0.0080	-12.805	0.0033	111	-0.0092	0.0091	-0.3401	0.4331	129	-0.0070	0.0453	-0.2972	0.4930
76	-0.0036	0.2958	0.0345	0.9365	94	-0.0013	0.7150	0.4220	0.3306	112	-0.0049	0.1626	0.4845	0.2643	130	0.0163	<.0001	0.5431	0.2109
77	-0.0079	0.0234	0.0224	0.9588	95	-0.0161	<.0001	0.4391	0.3112	113	-0.0053	0.1273	-0.7799	0.0728	131	0.0114	0.0012	0.4451	0.3054
78	-0.0081	0.0213	0.1159	0.7892	96	-0.0054	0.1210	-0.0252	0.9537	114	-0.0195	<.0001	0.3160	0.4666	132	0.0090	0.0100	-0.8313	0.0558
79	0.0047	0.1733	-0.2941	0.4977	97	0.0026	0.4528	0.4390	0.3131	115	0.0062	0.0760	-0.3668	0.3984	133	0.0163	<.0001	0.5201	0.2306
80	-0.0031	0.3699	0.5810	0.1812	98	0.0051	0.1417	0.4334	0.3087	116	0.0122	0.0006	-0.2604	0.5485	134	0.0222	<.0001	-13.709	0.0017
81	0.0018	0.6050	-0.9428	0.0302	99	0.0311	<.0001	-0.0238	0.9562	117	-0.0065	0.0642	-0.0026	0.9952	135	0.0189	<.0001	0.4572	0.2918
82	0.0074	0.0337	-0.5408	0.2130	100	0.0099	0.0050	-0.6754	0.1200	118	0.0053	0.1248	0.1256	0.7704	136	0.0043	0.2145	-0.9931	0.0227
83	0.0036	0.3003	0.1013	0.8155	101	0.0081	0.0202	0.0216	0.9603	119	0.0041	0.2363	-0.4134	0.3403	137	-0.0036	0.3025	0.4029	0.3530
84	-0.0086	0.0144	0.0458	0.9158	102	0.0216	<.0001	0.1881	0.6647	120	-0.0062	0.0758	13.995	0.0013	.	.	.	.	.
85	0.0080	0.0226	-0.3492	0.4209	103	-0.0052	0.1340	-0.2483	0.5678	121	0.0010	0.7631	0.1614	0.7099	.	.	.	.	.
86	0.0019	0.5777	0.0654	0.8802	104	-0.0077	0.0288	0.3748	0.3877	122	-0.0020	0.5612	0.0511	0.9062	.	.	.	.	.

[3]From 1 to 26 are top cross generated by progenies of Sussuma and others by progenies of Olipa.

DISCUSSION

Variance components

The success in the selection of better progenies is intrinsically linked to an adequate experimentation because good variance components estimations are indispensable (Ramalho et al., 2012b).

One of the assumptions for the success of a plant improvement program is the existence of genetic variability in the population basis. In this study, this variability can be explained by the genetic variance component (table 1). This suggested it presents good potential to be used in the selection, as well as the possibility of providing good hybrids to their genitors.

The residual variance component for tryptophan content presented low magnitude, which highlights good precision of the experiment. The confidence interval for the block effect is also higher for tryptophan content in the grain, what indicates low variation among blocks within replication. Likewise, it is observed higher confidence interval for residual variance component, which may suggest that residual variance, is lower. This might indicate good experimental precision, which guarantees reliability for the inferences to be performed.

From the variance component estimations and prediction error variance, selective accuracy was estimated in both progenies groups (progenies from Sussuma and progenies from Olipa). One can observe that, for tryptophan content, top crosses from Sussuma and Olipa presented 94.19% and 93.48% accuracy respectively. In the matter of grain yield, top crosses from Sussuma presented 73.04% accuracy and top crosses from Olipa presented 76.37% accuracy.

Selective accuracy reflects information and procedure quality used for genetic values prediction. It is also associated with selection precision and refers to the correlation between predicted genetic values and true genetic values. Thus, the higher selective accuracy in an individual assessment, the higher confidence in the assessment and the predicted genetic value for the individual (Resende, 2007; Resende and Duarte, 2007).This selective accuracy achieved in this study, demonstrated a possibility to obtain gains from a selection in those characters.

Genetic variance component from Olipa progenies was higher than Sussuma progenies. Several studies show that high average in recurrent selection in a base population implies involving well-adapted genitors and high variance, genitors which complement each other (Ramalho et al., 2012a). In assessments performed along three years successively, it was observed that Olipa hybrid presented better performance for grain yield when compared with Sussuma (Denic et al., 2008).

Specific combining ability

Specific combinations reflect the complementarity between two genitors. Thus, hybrid combinations which show most favourable estimations for specific combining ability and which involve, at least, one of the genitors with high general combining ability are of interest (Cruz and Carneiro, 2006; Vencosvsky and Barriga, 1992). In this case, only SCAs as genetic value predictors (BLUPs) were determined.

Confidence intervals for SCA vary from negative to positive values, indicating differential in its magnitude (table 2). It is one more indicative to the existence of variability among assessed genetic material, being important attribute to a selection in an improvement program.

The significant effect of SCA observed for both characters indicates that genitor populations of these top crosses are promising in interpopulational improvement in order to obtain inbred lines that, when cross-bred, might generate hybrids with higher heterosis.

In the particular situation of positive SCA estimations, one can be assumed that the allele frequency of at least one genitor (expecting to be progeny) from the hybrid combination is positive, which contributes to increase the character value.

SCA higher value estimations for the grain yield were obtained in TC 24 (1.0019 t/ha), TC 48 (1.0197 t/ha) and TC 120 (1.3995 t/ha) combinations, what indicated that these combinations explored advantageously the dominance effects.

For tryptophan content, positive SCA estimations presented lower magnitude. One of the possible reasons could be related to the inheritance of this type of characters. Hussain et al. (2015) comments that maize grain qualitative characters inheritance (protein, lysine and tryptophan) has additive control with partial dominance. However, SCA it is expressed in function of the effects of dominance and epistasis as well as differences in genitors alleles frequency for the loci involved in the control of a given characteristic(Hallauer *et al*., 2010).

The lower magnitude SCA values in grain yield resulted in lower shrinkage which could make the estimate of the fixed effects and prediction of the random effects closer between them.

Top crosses and checks performance

On BLUP average determined for the top crosses, the populational average is the same to all genetic treatments, since in terms of estimation process; it is about the same population (Gonçalves and Frische-Neto, 2012; Resende, 2007).

In the assessments of genetic materials, the block effects, plots and environmental effects will not repeat because such effects are embedded in some proportion on the phenotypic average which proves that the average genotypes are most suitable for inference in scientific studies (Resende, 2007).

With this estimation/prediction method for genotypic values, phenotypic averages shrinkage is promoted. The averages tend to be close to each other and ensure more precise and realistic inferences. Some studs have shown that shrinkage has been used to eliminate residual effects from the environment embedded in the phenotypic data (Resende, 2007; Resende and Duarte, 2007).

Several previous studies report phenotypic values for tryptophan content and grain yield (Mahan et al., 2014; Wegary et al., 2014; Naidoo et al., 2012; Machida et al.,

Table 3. Mixed model analysis of variance for tryptophan content and grain yield.

		Tryptophan content		Grain yield	
Effect	df	f-value	p-value	f-value	p-value
Replication	1	0.65	0.4215	3.9000	0.0489
Checks	8	7.67	<0.0001	1.9100	0.0572

Table 4. Adjusted means or means BLUP (population mean + SCA of each combination) for tryptophan content and grain yield.

Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)	Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)	Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)	Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)
1	0.051	3.81	18	0.060	3.82	35	0.058	3.60	52	0.073	3.61
2	0.034	3.80	19	0.053	3.82	36	0.056	3.60	53	0.075	3.61
3	0.060	3.82	20	0.053	3.82	37	0.044	3.58	54	0.055	3.59
4	0.054	3.82	21	0.052	3.82	38	0.072	3.61	55	0.072	3.61
5	0.053	3.82	22	0.058	3.82	39	0.049	3.59	56	0.063	3.60
6	0.041	3.80	23	0.044	3.81	40	0.075	3.61	57	0.058	3.60
7	0.071	3.83	24	0.071	3.83	41	0.066	3.61	58	0.049	3.59
8	0.046	3.81	25	0.056	3.82	42	0.070	3.61	59	0.054	3.59
9	0.065	3.83	26	0.040	3.80	43	0.076	3.62	60	0.069	3.61
10	0.051	3.81	27	0.051	3.59	44	0.069	3.61	61	0.065	3.60
11	0.068	3.83	28	0.052	3.59	45	0.063	3.60	62	0.065	3.60
12	0.072	3.84	29	0.048	3.59	46	0.075	3.61	63	0.053	3.59
13	0.049	3.81	30	0.043	3.58	47	0.049	3.59	64	0.077	3.62
14	0.048	3.81	31	0.052	3.59	48	0.060	3.60	65	0.037	3.58
15	0.036	3.80	32	0.069	3.61	49	0.046	3.59	66	0.067	3.61
16	0.034	3.80	33	0.062	3.60	50	0.065	3.60	67	0.045	3.58
17	0.069	3.83	34	0.062	3.60	51	0.068	3.61	68	0.054	3.59

"...Continue..."

2010; Musila et al., 2010), therefore, it becomes difficult to compare those results with the current study.

For tryptophan content, nine top crosses presented values of more than 0.075% showing, thus, superiority in order to generate high tryptophan content hybrids and, therefore, with high protein quality. It is also important to notice that these top crosses significantly outperformed local checks.

For grain yield, highlighted values are not observed. This might be due to a minor difference among grain yield averages caused by minor variation observed in SCA for this character. It is observed, also through variance components in table 1, that confidence intervals are higher, which suggests small variation among the treatments.

When compared on average the top crosses from both groups, it is possible to observe that, for grain yield, top crosses from Sussuma presented greater performance than top crosses from Olipa and, for tryptophan content, the situation was contrary, that is, top crosses from Olipa presented greater performance for tryptophan content than top crosses from Sussuma. It might have occurred because Sussuma (for grain yield) is more adapted to the assessment region than Olipa. On the other hand, Olipa might have presented higher variability. And high variability implies in complementarity (Ramalho *et al.,* 2012a).

It became clear that progenies which generated higher performance top crosses in both characters could be selected to continue self-generations to be used in hybrids

"Table 4, cont."

Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)	Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)	Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)	Top cross[3]	Tryptophan content (%)	Grain yield (t/ha)
69	0.078	3.62	87	0.055	3.59	105	0.051	3.59	123	0.056	3.60
70	0.057	3.60	88	0.057	3.60	106	0.070	3.61	124	0.068	3.61
71	0.060	3.60	89	0.065	3.60	107	0.061	3.60	125	0.064	3.60
72	0.049	3.59	90	0.067	3.61	108	0.052	3.59	126	0.060	3.60
73	0.046	3.59	91	0.066	3.61	109	0.059	3.60	127	0.041	3.58
74	0.074	3.61	92	0.053	3.59	110	0.074	3.61	128	0.061	3.60
75	0.054	3.59	93	0.052	3.59	111	0.052	3.59	129	0.054	3.59
76	0.058	3.60	94	0.060	3.60	112	0.057	3.60	130	0.078	3.62
77	0.054	3.59	95	0.045	3.58	113	0.056	3.60	131	0.073	3.61
78	0.053	3.59	96	0.056	3.60	114	0.042	3.58	132	0.071	3.61
79	0.066	3.61	97	0.064	3.60	115	0.068	3.61	133	0.078	3.62
80	0.058	3.60	98	0.067	3.61	116	0.074	3.61	134	0.084	3.62
81	0.063	3.60	99	0.093	3.63	117	0.055	3.59	135	0.080	3.62
82	0.069	3.61	100	0.071	3.61	118	0.067	3.61	136	0.066	3.61
83	0.065	3.60	101	0.070	3.61	119	0.066	3.61	137	0.058	3.60
84	0.053	3.59	102	0.083	3.62	120	0.055	3.59	.	.	.
85	0.069	3.61	103	0.056	3.60	121	0.063	3.60	.	.	.
86	0.063	3.60	104	0.054	3.59	122	0.059	3.60	.	.	.

[3]From 1 to 26 are top cross generated by progenies of Sussuma and others by progenies of Olipa.

Table 5. Performance of the checks (adjusted means) for tryptophan content and grain yield.

	Tryptophan content (%)			Grain yield (t/ha)		
Population	Estimate value	Lower limit	Upper limit	Estimate value	Lower limit	Upper limit
GW15WQPM	0.0560	0.0491	0.0629	4.040	2.930	5.160
MACHO #5	0.0652	0.0583	0.0721	2.920	1.800	4.030
Olipa	0.0452	0.0383	0.0521	3.690	2.580	4.810
Olipa A/B	0.0480	0.0411	0.0549	3.400	2.290	4.510
PAN53	0.0421	0.0352	0.0490	2.830	1.720	3.940
Rutanda	0.0563	0.0494	0.0632	2.390	1.270	3.500
Sussuma	0.0578	0.0509	0.0647	4.840	3.730	5.960
TopOlipa[4]	0.0615	0.0593	0.0636	3.600	3.370	3.830
TopSussuma[5]	0.0534	0.0485	0.0583	3.820	3.460	4.180
Max. Top Olipa[6]	0.1030	.	.	7.238	.	.
Min. Top Olipa[7]	0.0320	.	.	0.654	.	.
Max. Top sussuma[8]	0.0800	.	.	6.629	.	.
Min. Top sussuma[9]	0.0280	.	.	0.860	.	.

[4]Top crosses generated by progenies of Olipa, [5]top crosses generated by progenies of Sussuma, [6,8]maximum values observed among the top crosses and [7,9]minimum values observed among the top crosses.

productions in advanced generations. Those top crosses will be hybrids selected from early generations. Those top crosses will be hybrids selected from early generations of inbred lines selections. This may reduce the effort in self-generation activities, maintenance a large number of progenies and also reduce the breeding process cost.

Selection gain

The expected gain estimation from a selection is a very important attribute in breeding programs. Therefore, it allows breeders to look for alternatives to improve the process efficiency. Gain from selection could be defined as the difference in the mean value of the selection criterion between the original generation and the next generation

Selection of 8% of progenies in each group among all assessed progenies based on tryptophan content was performed (Sussuma group progenies and Olipa group progenies). The Sussuma group progenies presented a 2.91% gain, and for Olipa group progenies, the gains achieved 4.0%. This result means that the expected progress with the selection depends on the heritability in generation in which the progenies where assessed. In this case, it was 15% for tryptophan content and 20% for grain yield.

Recurrent selection can contribute to increase the frequency of allele for the characteristics under study.

CONCLUSIONS

The obtained estimations, associated with the performance of assessed treatments make it possible to infer that both populations are promising for recurrent selection.

Genetic variance estimations for tryptophan content present minor magnitude, what highlights dominance of additive effects, whereas for grain productivity, genetic variance estimations present greater magnitude, which indicates dominance of non-additive effects.

Over 25% of the assessed top crosses presented SCA values for tryptophan content in the grain and 3.65% for grain yield.

For tryptophan content, one can select nine top crosses which can be used in VCU tests as soon as progenies have reached homozygosis. Four top crosses presented higher performance in both characters were selected hybrids in early generations.

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