

Grain quality of drought tolerant accessions within the MRI Zemun Polje maize germplasm collection

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Abstract

Maize Research Institute Zemun Polje (MRI) gene bank created an elite drought tolerant core collection of 40 accessions, based on field trials and general combining ability with inbred lines from the main heterotic groups (Lancaster, Iowa Stiff Stalk Synthetic – BSSS and Iodent). A total of seven genetic groups were identified. Seven accessions showed good combining abilities with three testers from chosen heterotic groups, thus forming a distinctive genetic group (Unknown). In the present research, accessions with drought tolerance were also analyzed for grain quality, as these two traits are becoming highly important due to global warming and population growth. Kernel macronutrients contents (oil, protein and starch) were determined using Near Infrared Spectroscopy (NIR). Oil, protein and starch contents were significantly higher in introduced populations than in landraces for 0.43%, 0.12% and 0.85%, respectively ($p < 0.01$). The greatest progress from the selection based on the expected genetic gain (ΔG) for 5% selection intensity would be obtained for oil (14.74%) followed by protein (10.14%). Landraces showed the least potential for the grain quality improvement due to the lowest expected ΔG for the three macronutrients. The differences between macronutrient content among genetic groups defined them as potentially favourable sources for a specific trait. According to ΔG values, the greatest progress in breeding would be accomplished for increased oil content with accessions from the Unknown group. Identification of the accessions with several favorable traits is valuable for simultaneous breeding for drought tolerance and grain quality.

Additional key words: gene bank; genetic gain; macronutrients; pre-breeding.

Introduction

Maize is among the three most widely grown crops in the world, with expectation to be with the greatest global production by 2025 (Rosegrant *et al.*, 2008). However, only a small part of existing maize germplasm is commercially used – in USA less than 5% (Taba *et al.*, 2004). It is considered that among 300 existing races of maize only two are utilized in temperate regions —Corn Belt Dent in USA and European flints in Europe and six in tropics— various Tuxpeños, Cuban Flint, Suwan 1, ETO, Tusón and Costeño (Goodman, 2005). Breeders are usually concentrated to already adapt improved materials, due to the fact that identification of superior genotypes among gene

bank accessions for the most important traits is very expensive and time consuming.

A link between genetic resources and plant breeding is defined as a pre-breeding concept. It refers to all the activities aimed to identify favourable traits/alleles from unadapted materials or adapted ones that did not pass any kind of modern selection. The germplasm that underwent pre-breeding is more useful and attractive to the breeders (Nass & Paterniani, 2000).

Due to the predicted global warming and human population growth, drought tolerance and grain quality are becoming increasingly important traits for pre-breeding and breeding programs. Drought is one of the most important factors limiting maize production. Even in the areas where average rainfall is adequate

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Abbreviations used: BSSS (Iowa Stiff Stalk Synthetic); ΔG (expected genetic gain); CGV (coefficient of genetic variability); HLM (hectoliter mass); 100KW (100 kernel weight); MRI (Maize Research Institute); NIR (near infrared spectroscopy); SI (selection intensity).

for maize its distribution is often insufficient and therefore causes yield losses. That is why both private and public breeders are more and more interested in incorporation of maize genetic resources in breeding programs for higher and more stable yields under drought (Blum, 1996; Edmeades *et al.*, 2003; Tuberosa & Salvi, 2006).

The biggest proportion (80%) of maize in the world is produced for animal feed but it is often used as staple food in developing and under-developed countries. Nutritional quality of maize is determined by macronutrients (starch, lipids, and proteins) and micronutrients (carotenoids, tocopherols, minerals, phytic acid, anthocyanins, and other phenols) of the grain, which depend on both genetic and environmental factors. Many studies showed an existence of great variability for grain quality in maize genetic resources (Berardo *et al.*, 2009; Flint-Garcia *et al.*, 2009; Mladenovic Drinic *et al.*, 2011), but the breeding for high-yielding hybrids using narrow genetic base leads to a great uniformity in kernel type and nutritive value. Most of the germplasm stored in gene banks has undergone selection for particular human needs and probably favourable sources of quality traits exist within these materials. The significance of grain quality is shown through achievements of the Germplasm Enhancement of Maize (GEM) project (Pollak, 2003). The project resulted in 65 GEM varieties released until 2009 with improved amino acid profiles, an oil content greater than 4.5%, a protein content greater than 13%, and specific starch thermal properties.

Maize germplasm collections comprise landraces, improved populations, inbred lines, reference hybrids, and genetic stocks. Although approximately 50,000 maize accessions exist in germplasm banks worldwide, most of them have never been evaluated for useful traits. The reasons for low utilization are the lack of evaluation data, documentation, and information, as well as poor linkages between gene banks and breeders.

Gene bank at Maize Research Institute Zemun Polje (MRI, Belgrade, Serbia) is among the ten largest in the world, maintaining over 6,000 accessions (FAOSTAT, 2010). It contains landraces from the former Yugoslav territories as well as introduced inbred lines, synthetics, composites, and landraces from about 50 foreign countries. After the initial testing of the whole collection under managed stress environment (MSE) in Egypt, a subset of 10% accessions was tested in temperate climate regions (Macedonia and Serbia). Based on the field trials' results and general combining ability, an elite drought core collection of 41 accessions was estab-

lished (Babic *et al.*, 2011; Anđelković & Ignjatović-Mičić, 2012).

The objectives of the presented research were: 1) to identify accessions from the MRI drought tolerant core that have favourable macronutrient contents and 2) to predict genetic potential for the grain quality improvement. In this way, an integration of the identified accessions for drought tolerance and grain quality in conventional maize breeding programs for temperate region would be enabled.

Material and methods

Plant material

Grain macronutrient content was determined for 40 accessions, which make the MRI gene bank drought core collection. The core consists of 15 introduced inbred lines (IL), 12 introduced populations (IP-six open pollinated varieties and six synthetics), and 13 landraces (L) from former Yugoslav territories that belong to different genetic groups and have different combining abilities (Table 1).

The 40 accessions from the elite drought tolerant core were multiplied in two replications according to completely randomized block design (RCBD) in 2011, inbred lines were selfed and populations multiplied via pair crossing by hand (*i.e.* full-sibbing). At least 80 ears were collected per multiplied population. Each multiplied population was dried and shelled and samples of kernels from the centre of the ear were prepared for grain quality analysis.

Macronutrient measurements

Near Infrared Spectroscopy (NIR) analysis (Infratec 1241 Grain Analyser, Foss, Denmark) was used for starch, oil, and protein content analysis. Samples of non-destructed seed (300 g per sample) from each replicate of multiplied seed were scanned twice. Spectra were collected between 800 nm and 1,100 nm. The same representative sample from each accession was used for determining physical quality through hectolitre mass (HLM) and 100 kernel weight (100KW).

Statistical analysis

All chemical analyses, HLM and 100KW, were performed in two replicates and the results were statisti-

Table 1. Origin, kernel type and combining ability of maize accessions in elite drought tolerant core collection

Type	Country of origin	Kernel type	Genetic group	Combining ability
<i>Introduced inbred lines</i>				
IL1	Former Soviet Union	Flint	Lancaster	BSSS-Iodent
IL2	Former Czechoslovakia	Semi-flint	Lancaster	BSSS-Iodent
IL3	Poland	Flint	Lancaster	BSSS-Iodent
IL4	Former Czechoslovakia	Semi-flint	Lancaster	BSSS-Iodent
IL5	USA	Dent	Lancaster-BSSS	Iodent
IL6	USA	Semi-dent	Lancaster-BSSS	Iodent
IL7	Former Soviet Union	Semi-flint	Lancaster-BSSS	Iodent
IL8	Former Soviet Union	Dent	Lancaster-BSSS	Iodent
IL9	Former Czechoslovakia	Semi-dent	Iodent	BSSS-Lancaster
IL10	Former Czechoslovakia	Dent	Iodent	BSSS-Lancaster
IL11	Former Soviet Union	Dent	Iodent	BSSS-Lancaster
IL12	Former Czechoslovakia	Flint	Iodent	BSSS-Lancaster
IL13	Former East Germany	Flint	Iodent-BSSS	Lancaster
IL14	Greece	Semi-flint	Iodent-Lancaster	BSSS
IL15	Georgia	Dent	Iodent-Lancaster	BSSS
<i>Introduced populations</i>				
IP1	Brazil	Semi-flint	Lancaster	BSSS-Iodent
IP2	Pakistan	Semi-flint	Lancaster	BSSS-Iodent
IP3	USA	Semi-flint	Lancaster	BSSS-Iodent
IP4	France	Dent	Lancaster-BSSS	Iodent
IP5	USA	Dent	Lancaster-BSSS	Iodent
IP6	Iran	Semi-flint	Unknown	BSSS-Lancaster-Iodent
IP7	Iran	Dent	Unknown	BSSS-Lancaster-Iodent
IP8	Argentina	Semi-flint	Unknown	BSSS-Lancaster-Iodent
IP9	USA	Semi-dent	Unknown	BSSS-Lancaster-Iodent
IP10	USA	Dent	Unknown	BSSS-Lancaster-Iodent
IP11	Former Soviet Union	Semi-flint	Iodent-Lancaster	BSSS
IP12	USA	Semi-flint	Iodent-Lancaster	BSSS
<i>Landraces</i>				
L1	Bosnia and Herzegovina	Flint	BSSS	Lancaster-Iodent
L2	Bosnia and Herzegovina	Semi-flint	Lancaster	BSSS-Iodent
L3	Serbia	Semi-flint	Lancaster	BSSS-Iodent
L4	Bosnia and Herzegovina	Semi-flint	Lancaster	BSSS-Iodent
L5	Serbia	Dent	Lancaster-BSSS	Iodent
L6	Serbia	Semi-dent	Unknown	BSSS-Lancaster-Iodent
L7	Macedonia	Dent	Unknown	BSSS-Lancaster-Iodent
L8	Slovenia	Semi-dent	Iodent	B,L
L9	Bosnia and Herzegovina	Flint	Iodent	B,L
L10	Serbia	Semi-flint	Iodent-Lancaster	BSSS
L11	Bosnia and Herzegovina	Dent	Iodent-Lancaster	BSSS
L12	Bosnia and Herzegovina	Semi-flint	Iodent-Lancaster	BSSS
L13	Croatia	Flint	Iodent-Lancaster	BSSS

BSSS (Iowa Stiff Stalk Synthetic).

cally analyzed. One factorial analysis of variance (ANOVA) for trials set up according to the RCBD was conducted. All statistical analyses were done in MSTAT-C software. Pearson's phenotypic correlation

coefficient was used for determining correlations between protein, starch, and oil.

Students' *t*-tests between average values of inbred lines, landraces, and introduced populations were

performed to determine statistical differences in chemical composition of the three groups of accessions.

The components of variance, broad sense heritability, and genetic gain were estimated according to Sing & Chaudhary (1985). The heritability in broad sense was calculated as:

$$h^2(\%) = (\sigma^2g/\sigma^2p) \cdot 100,$$

where σ^2g and σ^2p are the genotypic and phenotypic variance, respectively.

Expected genetic gain (ΔG) was estimated as:

$$\Delta G = K \cdot \sigma p \cdot h^2,$$

where K is the standardized selection differential, σp is the phenotypic standard deviation and h^2 is the broad sense heritability.

Results

Oil content varied from 2.8 to 5.5% among all analyzed accessions, *i.e.* it ranged from 2.8 to 5.5% within IL, 3.8 to 5.5% within IP, and 3.6 to 5.4% within L. Protein content ranged from 9.6 to 15.2% for all accessions, 10.6 to 15.2% within IL, 9.9 to 13.8% within IP, and 9.6 to 13.9% within L. Finally, total extent of variation in starch content was from 66.6 to 71.6%, ranging from 66.6 to 70.2% within IL, 67.9 to 71.6% within IP, and 67.4 to 70.6% within L.

Students' *t*-test was performed on the mean values of the macronutrients (Table 2). The highest average contents of oil and starch was found in IP, while the highest average content of protein was found in IL. The *t*-test results showed that IP had significantly higher oil content than both IL and L ($p < 0.05$ and $p < 0.01$, respectively) and also significantly higher starch content ($p < 0.001$ and $p < 0.01$, respectively). Protein content was significantly higher in IL compared to the other two types of accessions ($p < 0.01$).

HLM and 100KW results are presented in Table 3. Landraces had the highest average (32.39 g) and IP the lowest (20.48 g) 100KW. Regarding HLM, IL had the highest (12.97 kg hL⁻¹) and L the lowest (11.84 kg hL⁻¹) value. The *t*-test results showed that L had significantly higher 100KW than both IL and IP ($p < 0.001$ and $p < 0.01$, respectively) and also significantly different HLM compared to the other two types of accessions ($p < 0.05$ and $p < 0.001$, respectively).

Expected genetic gain (ΔG) for macronutrients contents was estimated for all three groups of accessions under different selection intensities (Table 4). The highest $\Delta G_{\%}$ for 5% of selection intensity (SI) was found for oil (14.74%) followed by proteins (10.14%). ΔG for starch was low (2.50% for SI of 5% and 1.70% for SI of 20%) and no further improvement of this trait can be expected.

Genetic parameters for macronutrients in grain for the five maize genetic groups (Lancaster, Lancaster-

Table 2. Mean values and significance of *t*-tests of macronutrients content among the three groups (IL, introduced inbred lines; IP, introduced populations; and L, landraces) of maize accessions in elite drought tolerant core collection

	Mean (%)	IL	IP	Df	L	Df
<i>Oil</i>						
IL	4.25	—	*	25	ns	26
IP	4.70		—		**	23
L	4.27				—	
<i>Protein</i>						
IL	12.97	—	**	25	**	26
IP	11.96		—		ns	23
L	11.84				—	
<i>Starch</i>						
IL	68.30	—	***	25	ns	26
IP	69.52		—		**	23
L	68.67				—	

Df: degrees of freedom. ***,** Significant at $p < 0.05$, $p < 0.01$ and $p < 0.001$, respectively. ns: not significant.

Table 3. Mean values and significance of *t*-tests of 100 kernel weight (100KW) and hectoliter mass (HLM) between the three groups (IL, introduced inbred lines; IP, introduced populations; and L, landraces) of maize accessions in elite drought tolerant core collection

	Mean	IL	IP	Df	L	Df
<i>100KW (g)</i>						
IL	20.83	—	***	25	***	26
IP	20.48	—	—		**	23
L	32.39	—	—		—	
<i>HLM (kg hL⁻¹)</i>						
IL	12.97	—	ns	25	*	26
IP	11.96	—	—		***	23
L	11.84	—	—		—	

Df: degrees of freedom. *.,*** Significant at $p < 0.05$, $p < 0.01$ and $p < 0.001$, respectively. ns: not significant.

BSSS, Unknown, Iodent and Iodent-Lancaster) are shown in Table 5. The BSSS and Iodent-BSSS groups had only one representative each and genetic parameters could not be estimated for them.

Physical characteristics, 100KW and HLM, were also measured for the five genetic groups. The Iodent group had the lowest average 100KW (27.63 g) and the highest was found for the Lancaster group (30.57 g). The Unknown group had the lowest (74.96 kg hL⁻¹), while the Lancaster-BSSS group had the highest (76.43 kg hL⁻¹) average HLM (data not presented).

Phenotypic correlations between the analyzed traits for the five genetic groups are shown in Table 6. In the Lancaster group, the two most pronounced correla-

tions, both negative, were found between 100 KW and oil, *i.e.* protein content. In the Lancaster-BSSS group, two highly negative correlations were found between protein and HLM, *i.e.* starch. An unexpected strong positive correlation between oil and 100 KW was found in the Unknown group. Since the breeding would not be practiced for this group as a whole, new correlations will be calculated after dividing this group into opposite genetic pools. A strong negative correlation between protein and 100 KW was determined in the Iodent group and between starch and oil content in the Iodent-Lancaster group. A strong positive correlation between oil and HLM was determined in the Iodent-Lancaster group.

Table 4. Expected genetic gain (ΔG) of maize accessions (IL-introduced inbred lines, IP-introduced populations and L-landraces) in elite drought tolerant core for selection intensities (SI) of 5, 10 and 20%

Group of accessions	SI	ΔG_{abs}			$\Delta G_{\%}$		
		Oil	Protein	Starch	Oil	Protein	Starch
IL	5%	2.31	1.91	1.27			
IP		1.06	1.73	1.55			
L		1.25	1.80	0.95			
All genotypes		1.78	2.08	1.40	14.74	10.14	2.50
IL	10%	1.97	1.62	1.08			
IP		0.90	1.47	1.32			
L		1.06	1.53	0.81			
All genotypes		1.52	1.77	1.19	12.59	8.63	2.12
IL	20%	1.57	1.30	0.86			
IP		0.72	1.17	1.05			
L		0.85	1.23	0.65			
All genotypes		1.21	1.41	0.95	10.02	6.88	1.70

ΔG_{abs} : expected genetic gain (in %). $\Delta G_{\%}$ expected genetic gain (in % of a mean).

Table 5. Range, mean values, broad sense heritability (h^2), genotypic coefficient of variation (CGV) and expected genetic gain (ΔG) from selection for macronutrients in maize grain in five genetic groups in the elite maize drought tolerant core (in %)

Genetic group	Range	Mean	h^2	CGV	SI 5		SI 10		SI 20	
					ΔG_{abs}	$\Delta G_{\%}$	ΔG_{abs}	$\Delta G_{\%}$	ΔG_{abs}	$\Delta G_{\%}$
<i>Lancaster</i>										
Oil	3.6-5.4	4.39	94.02	8.99	2.17	49.43	1.84	41.91	1.47	33.49
Protein	9.6-13.8	11.73	95.08	7.42	2.98	25.42	2.53	21.58	2.03	17.31
Starch	66.9-70.8	68.87	90.77	1.67	1.84	2.67	1.56	2.27	1.25	1.82
<i>Lancaster-BSSS</i>										
Oil	3.2-5.3	4.23	89.63	10.11	2.34	55.33	1.98	46.82	1.59	37.6
Protein	9.9-15.0	12.25	98.72	11.05	4.62	37.71	3.93	32.08	3.14	25.63
Starch	67-71.3	69.57	93.11	2.46	2.76	3.97	2.35	3.38	1.88	2.7
<i>Unknown</i>										
Oil	2.8-5.0	2.8-5.0	97.20	16.35	3.93	92.47	3.34	78.59	2.67	62.82
Protein	10.6-13.9	10.6-13.9	91.80	6.94	2.83	22.61	2.41	19.25	1.93	15.42
Starch	67.9-69.5	67.9-69.5	98.13	1.16	1.32	1.92	1.12	1.63	0.90	1.31
<i>Iodent</i>										
Oil	3.6-5.2	3.6-5.2	97.73	8.62	2.11	48.51	1.72	41.15	1.43	32.87
Protein	11.4-13.6	11.4-13.6	97.76	4.27	1.81	14.36	1.53	12.14	1.23	9.76
Starch	67.1-69.4	67.1-69.4	89.63	4.27	1.22	1.78	1.03	1.50	0.83	1.21
<i>Iodent-Lancaster</i>										
Oil	3.7-5.5	3.7-5.5	91.91	9.39	2.33	48.88	1.98	41.54	1.58	33.14
Protein	10.8-14.0	10.8-14.0	75.29	5.29	1.94	15.78	1.65	13.42	1.32	10.74
Starch	66.6-70.5	66.6-70.5	95.63	1.78	2.00	2.93	1.70	2.49	1.36	1.99

SI: selection intensity (%). ΔG_{abs} : genetic gain (in %). $\Delta G_{\%}$: genetic gain (in % of a mean).

Discussion

The core collection is a limited set of accessions representing, with a minimum of repetitiveness, the genetic diversity of a crop species (Frankel, 1984). Maize core collections were established in the different regions: Taba *et al.* (1998) created a core of Caribbean maize accessions from CIMMYT genebank; Malosetti & Abadie (2001) created a core for Uruguayan maize landraces and Li *et al.* (2004) created a core for Chinese landraces. Representative maize core collections in Europe were formed through the GENRES project (Gouesnard *et al.*, 2005). An identification of the best sources for the trait(s) of interest within core collections can be followed through their transfer into elite genotypes (Gouesnard *et al.*, 2005).

Combining ability of the accessions is of major importance for application in maize breeding. Gene bank collections are usually divided into races mostly formed on pedigree data and morpho-biological traits. However, their efficient use in pre-breeding/breeding programs substantially depends on their combining ability that is not correlated with race classification. The distribution of accessions according to their com-

binning abilities was done in our research forming seven distinct genetic groups, which implies that the formation of a core collection in maize needs a thorough previous study of heterotic patterns. The genetic group Unknown is of particular interest because it showed good combining abilities with testers from all the three major heterotic groups.

An elite drought tolerant core collection was created through a selection of the accessions of MRI gene bank under managed drought stress environment in subtropical region and subsequent field trials in temperate climate regions. Due to the global warming and human population growth, breeding strategies have to enhance grain quality without compromising grain yield and tolerance to abiotic (or biotic) stresses. A set of accessions from the elite drought tolerant core with useful chemical composition was identified. Compared to 1,245 accessions from different parts of the world in Berardo *et al.* (2009), maximum values for oil content in our accessions were in the range of their lower values and our best performing accessions considering crude proteins had the same values as their selected genotypes.

A large study on chemical compounds and physical properties of maize grain on 71 accessions represent-

Table 6. Phenotypic correlations among kernel traits for five genetic groups in the elite maize drought tolerant core

Group	HLM	Oil	Protein	Starch
<i>Lancaster</i>				
100KW	-0.165 ^{ns}	-0.458***	-0.473***	0.430*
HLM		0.084 ^{ns}	0.437**	0.162 ^{ns}
Oil			0.463**	-0.280 ^{ns}
Protein				-0.264 ^{ns}
<i>Lancaster-BSSS</i>				
100KW	-0.082 ^{ns}	0.174 ^{ns}	-0.358 ^{ns}	0.198 ^{ns}
HLM		0.293 ^{ns}	-0.750****	0.617**
Oil			-0.583**	0.449 ^{ns}
Protein				-0.879****
<i>Unknown</i>				
100KW	0.492 ^{ns}	0.861****	-0.340 ^{ns}	0.237 ^{ns}
HLM		0.260 ^{ns}	-0.067 ^{ns}	0.269 ^{ns}
Oil			-0.630**	0.101 ^{ns}
Protein				-0.379 ^{ns}
<i>Iodent</i>				
100KW	-0.082 ^{ns}	-0.210 ^{ns}	-0.879****	0.472 ^{ns}
HLM		0.503 ^{ns}	0.196 ^{ns}	0.150 ^{ns}
Oil			0.452 ^{ns}	-0.581**
Protein				-0.611**
<i>Iodent-Lancaster</i>				
100KW	-0.041 ^{ns}	0.061 ^{ns}	-0.445 ^{ns}	0.182 ^{ns}
HLM		0.635****	0.496**	-0.455*
Oil			0.421 ^{ns}	-0.675****
Protein				-0.620****

****,***,**,*,* Significant at $p < 0.1$, $p < 0.05$, $p < 0.01$, and $p < 0.001$, respectively. ns: not significant.

ing landraces from Latin America was conducted by Narváez-González *et al.* (2006). The values for protein content were higher and lower for oil content compared to our experiment. Chander *et al.* (2008) evaluated 87 inbred lines from China. Protein, starch, and oil were measured among other traits. Compared to our results protein contents were similar, while starch and oil had higher values in our experiment.

The dissimilarities of protein and oil contents found in experiments are probably due to the differences in environments and genetic background of the material (Dudley *et al.*, 2007). A variation in chemical composition of the maize kernel among accessions can also be the consequence of adaptation to specific environments (Camussi *et al.*, 1980). To minimize this variation, all kernels from different genotypes should be multiplied in the same year, as it was done in our experiment.

However, considering that we obtained data only from a single location, the results should be taken with some precaution because presence of environmental influence and genotype \times environment interactions could not have been determined.

Genetic correlations between chemical components of maize kernel are given in Dudley *et al.* (2007). A high negative correlation was found between protein and starch content (-0.915). On the other hand, the genetic correlation between protein and oil was not significant, while it was negative and intermediate between starch and oil. In our research, negative significant correlations between starch and oil, *i.e.* starch and protein, were determined in two genetic groups (Iodent and Iodent-Lancaster). In the Lancaster-BSSS group, the correlation between starch and protein (negative) was significant, while in genetic groups Lancaster and Unknown those correlations were non-significant. A low correlation between kernel weight and grain quality components was found in Dudley *et al.* (2007). In our experiment, kernel weight was significantly negatively correlated with oil and protein content in the Lancaster group and with oil in the Unknown group. Correlations between kernel weight and starch content were mostly non-significant.

The correlations between grain chemical composition and classification into agro-ecological groups (races) were not found for drought tolerant core accessions. Similar results were obtained in other experiments. In Campbell *et al.* (2010) model, a core collection for grain quality was established on NITS (near-infrared transmittance) analyses of 306 accessions from nine agro-ecological sites of Chile representing 17 races of maize. NITS results were only partially correlated with classification into races and the region of origin. Moreover, Berardo *et al.* (2009) have found that analysis of chemical compounds in maize kernel was not in clear correlation with the geographical origin in *European Union Maize Landrace Core Collection* (EUMLCC). Variability in the grain chemical composition in these experiments could be the consequence of adaptation to special climatic conditions. This could also be stated for the drought tolerant core accessions analyzed for grain quality. Among the compounds of maize grain, starch has the greatest positive influence on grain yield-high correlation (0.91) between starch content and 100KW was found in the study of Hegyi *et al.* (2007). As the selection in our experiment was done for increased grain yield during drought stress, it is possible that the chosen genotypes have reached the

plateau for starch content. A correlation between starch and kernel weight was not significant, probably indicating a greater quality (higher proportion of oil and protein) of the selected genotypes. Only in the Iodent-Lancaster genetic group, which has high protein content, the low starch level is in accordance with commonly obtained negative correlation between starch and protein in the maize kernel.

Heritability in broad sense (h^2) was much higher for macronutrients in our research than in Chander *et al.* (2008). Indeed, h^2 values in our elite core ranged from 75.29 (Iodent-Lancaster group) to 98.72% (Lancaster-BSSS group) for protein, from 89.63 (Iodent-Lancaster group) to 97.73% (Unknown group) for oil, and 89.63 (Iodent group) to 98.13% (Unknown group) for starch. Values presented in the study of Chander *et al.* (2008) indicate a greater genetic variability of macronutrients in our material. These findings represent substantial opportunity for breeders to include these materials into future pre-breeding/breeding programs. Coefficients of genetic variation (CGV) in our experiment were greater for oil than they were for protein (except in group Lancaster-BSSS) and they were very low for starch content. The same trends were obtained by Chander *et al.* (2008), e.g. significant differences were estimated between the CGVs for macronutrient content.

The information about variability is not sufficient for improvement of any trait. Thus, the ΔG from selection estimated from coefficients of variability and heritability is of great importance. For example, the Iodent-Lancaster group could be a good source of high oil content, while the Lancaster-BSSS group could be considered as a good source of increased starch content. According to ΔG values, the greatest progress in breeding would be accomplished for increased oil content with accessions from the Unknown group. Regarding the protein content, the greatest progress could be expected from accessions within the Lancaster-BSSS group. However, ΔG values for starch were low for each of the genetic groups.

The differences between macronutrient content among genetic groups defined them as potentially favourable sources for a specific trait. The greatest progress for grain quality improvement of the drought tolerant core is expected from the higher selection intensity (5%, in comparison to 10% and 20%). However, in this way, the genetic variability could be exhausted in a short time. It could be assumed that the selection intensity of 20% should be applied in these gene pools primarily because the grain quality is secondary while

drought tolerance is the main trait for selection. For instance, considering that maximum kernel oil content was 5.5%, new genotypes with at least 8.5% oil content could be created based on the ΔG with 20% selection intensity.

Generally, according to the results of the ΔG for grain quality, the greatest progress from selection would be obtained for oil followed by protein content. A multiple trait selection would be desirable for the simultaneous improvement of drought tolerance and grain quality in breeding programs with this material.

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