

## **Analysis of *Per Se* and Genetic Diversity of Maize Synthetic Populations for Grain Quality: Implications for Breeding**

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**Abstract.** The objective of this research was to determine whether phenotypic and genetic diversity could be identified for maize grain quality traits (percentage of starch, protein, oil, fiber and ash) and agronomic traits. 59 maize synthetic populations which differed in earliness and for geographic origins were evaluated in the field at the Agricultural Research Station Turda - Romania, for their *per se* value. Each synthetic population was tested only one year and was characterized for their ear characteristics and grain quality attributes. The grain oil and ash content showed high variability among genotypes.

The experiment was conducted over 2 years (2006-2007) and 2 locations (Turda and Targu-Mures). Analysis of variance showed significant differences among the genotypes for all traits studied. General combining ability (GCA) effects were more important for grain content than specific combining ability (SCA). The occurrence of low interactions between synthetic populations and testers for all characters suggested the occurrence of high statistical additive effects expressed whatever the system of population evaluation. These results support breeding effort towards the genetic improvement of grain quality traits in "Turda" maize germplasm.

**Key words:** variability among synthetic populations, maize, grain quality.

### **INTRODUCTION**

Maize crop is an integral part of our agriculture and has a potential to compete with its multi-products. In order to have access to global market, there is need to improve the quality of crop with judicious use of inputs. International demand for quality parameters such as oil, starch, carbohydrates and protein is increasing. To meet such requirements within and out side country, it is desired to tailor varieties with a favorable comprise of yield and quality components. To this end, it is necessary to explore germplasm to explore genetic variability for such quality traits and their association with grain yield and other yield attributes (Lavergne *et al.*, 1991; Mohammadi and Prasanna, 2003; Has *et al.*, 2004; Goodman, 2005; Smith *et al.*, 2005; Has *et al.*, 2009).

Maize breeding for grain quality traits can both diversify and add economic value of end-use products. Conservation and utilization of useful genetic diversity is the basis for long-term genetic gain on economically desirable traits, and can aid in preventing losses due to biotic and abiotic stress (Pollak and Scott, 2005; Osorno and Carena, 2008).

Since most grain quality traits are inheritance quantitatively, similar breeding methods used for grain yield improvement could be used to improve for grain quality. The biochemical composition of maize kernel has been modified by use of recurrent selection methods and mutant alleles (Dudley and Lambert, 2004; Pollak and Scott, 2005). Extensive testing of new

genotypes (synthetic populations) using mating design has permitted the estimation of general (GCA) and specific combining ability (SCA), allowing the assignment of genotypes into heterotic groups that can be used for breeding purposes (Hallauer and Miranda, 1988). For grain quality traits also can be used as genetic diversity indicators in the same way that agronomic traits have been used (e.g., numerical taxonomy), providing valuable information about the genetic relationships among genotypes (Robutti *et al.*, 2000; Osorno and Carena, 2008). These studies can classify and characterize the germplasm contained in breeding programs and germplasm banks to make more accurate decisions about parental selection for breeding purposes.

The objectives of this research were: 1) to explore the variability existing for some chemical components of the grain in a large range of maize synthetic populations and 2) to identify genotypes that could be interesting in terms of nutritional value and estimate the extent of genetic variability, heritability and correlation for various ear characteristics and grain quality components to formulate a selection criterion.

## MATERIALS AND METHODS

### *Material and cross designs.*

1) Maize samples used in this study consisted of 59 synthetics/composites of which 30 synthetics have been created at the Agricultural Research and Development Station Turda – Romania (ARDS Turda) and 29 synthetics acquired from different countries (Spain, Italy, Germany, USA - University of Minnesota, University of Pennsylvania). All synthetic populations are currently used in the framework of breeding and genetic program at ARDS Turda. The studied genotypes differed by germplasm source, grain type, maturity classification (very early, early, intermediate and late) and grain appearance and color.

2) Seven early maturing maize synthetic populations derived from three different breeding programs: 1) *per se* selection (Tu Syn 3 (*per se*) (1)), 2) recurrent selection (Tu Syn Mara, Tu Syn 1, Tu Syn 8), 3) recurrent reciprocal selection (Tu SRR 2I(5D) (1), Tu SRR 5D (2I) (1), Tu SRR 5DR (6I) (4)) were used in this study (Tab. 1) They are genetically broad-based populations improved for agronomic traits. These synthetic populations are under continuous genetic improvement for agronomic traits: grain yield capacity, early maturity, resistance to root and stalk lodging. These synthetic populations have not been improved for grain quality.

Tab. 1

*Per se* values of for quality grain content in parental forms,  
synthetic populations and inbred lines used as testers

No. crt.	Parental forms	Quality grain content:				
		Starch	Oil	Protein	Fiber	Ash
		%				
Synthetic populations = fathers						
1.	Tu Syn Mara	62.3	6.7	13.1	5.9	5.5
2.	Tu Syn 1	63.0	6.0	13.0	4.9	4.7
3.	Tu Syn 8	62.4	6.4	12.8	5.5	5.2
4.	Tu SRR 2I(5D) (1)	63.1	6.3	12.9	5.6	4.9
5.	Tu SRR 5D (2I) (1)	68.4	4.6	13.0	5.5	1.6
6.	Tu Syn 3 (per se) (1)	65.8	5.6	12.5	5.2	4.0
7.	Tu SRR 5DR (6I) (4)	66.8	5.2	12.8	5.5	2.6
Mean		64.5	5.8	12.9	5.4	4.1
Inbred lines - testers = mothers						
1.	TC 184 cms C	68.5	3.4	12.4	3.9	0.7

2.	TC 209	69.5	3.7	13.2	4.5	0.2
3.	CO 255	66.8	4.2	13.8	4.9	0.1
4.	TD 233	68.0	3.3	13.3	3.5	1.7
Mean		68.2	3.7	13.2	4.2	0.7
Check hybrids						
1.	Turda Mold 188	68.8	8.2	11.5	5.4	2.8
2.	Turda 165	67.8	5.0	12.3	5.4	2.8
3.	Turda SU 181	66.8	5.0	12.8	5.3	2.5
4.	Turda 201	68.6	4.9	12.3	5.4	2.6
Mean		68.0	5.0	12.2	5.4	2.7

### *Experimental designs.*

1) Each genotype (synthetic populations) was grown in separate but adjacent trials. Experimental plots were 2-rows, 5 m - long, with 0.7 m spacing between two rows without replications. Plant densities averaged 60,000 plants/hectare in each trial.

2) Seed from the crosses was produced in a factorial mating design . were crossed with four testers (inbred lines): two flint inbred lines (TD 233 and CO 255) and two dent inbred lines (TC 184 and TC 209). The test crosses and their parental forms were evaluated in two years 2006 and 2007, in two locations Turda and Targu-Mures respectively, for both *per se* and test cross performances. Complete block designs were used with 3 replications for *per se* and testcross trials respectively. Plant densities averaged 60000 pl/ha in each experiment. Plots were 2-rows, 5m-long, with 0.7 m spacing between two rows.

Four checks were also sown in *per se* trials.

The following ear traits were measured: ear length (cm), number of grains/ear (no.), type and color of grains (notes), cob color (notes). A sample of 500 g of kernels was collected from every plot in all environments. At least six plants in each experimental plot were sib-pollinated by pollen from the same plot to avoid xenia effects. Approximately five hand-pollinated ears per row were harvested, after physiological maturity, and bulked for chemical analysis. In addition, 50 grains from the middle of each plot were removed and used for measuring moisture concentration. For each plot, a representative 50 g sample of the grain was ground, and the concentration of starch, protein, oil, fiber and ash in the ground (flour) sample was determined with a Dickey-John Instalab 600 near-infrared reflectance analyzer, after curve calibration.

### *Analysis of variance.*

1) All grain physical quality tests were performed in duplicate, and the mean value was analyzed statistically. Analyses of variance (ANOVA) using a one-factor model without replications were done for each trait and for each group of genotypes (Ceapoiu, 1968).

2) Analysis of variance in testcross was performed for all traits within and among environments. Analysis of Gardner and Eberhart (1966) was used to partition genetic and environmental effects. Genotypes were considered as fixed effects while environments and replication (locations) within each environment were considered as random effects. GCA and SCA values were calculated following the procedure describes by Griffing (1956) Model II, for factorial analysis:

$$\hat{g}_m \text{ or } \hat{g}_n = \frac{\sum_m X_{m.}}{m} \cdot \frac{\sum_n X_{.n}}{n} \quad (\text{Cabulea, 1975})$$

$$\hat{g}_m \text{ or } \hat{g}_n = \text{GCA effects of "m" and "n" parent}$$

m = parental inbred lines used as father

n = inbred lines-tester used as mother

$X_m$  = „m” parent sum

$X_{..}$  = general sum

$$\hat{s}_{mn} = X_{mn} - X_{..} - (\hat{g}_m + \hat{g}_n)$$

$\hat{s}_{mn}$  = SCA effect of the cross among „m” x „n”

Heterosis values (H%) were calculated for grain quality traits after formula elaborated by Hallauer and Miranda (1988),  $H\% = 100 \times (F_1 \text{ mean} - \text{parents mean}) / \text{parents mean}$

## RESULTS AND DISCUSSIONS

### 1. Statistical analysis of grain content and ear traits in some maize synthetic populations.

In present study, we used a maize germplasm collection, representing *per se* and genetic diversity of synthetic populations, to predict the food quality of grain and some ear traits. For each trait, the number of samples analyzed (N), the mean of values, the range of variation, the SD, the coefficient of variation among genotypes (CV), and standard error of laboratory (SEL) are shown in Tab. 2. Each genotype was analyzed separately by ANOVA, using a one-factor model with three replications.

Phenotypic variability (CV) of ear traits (Tab. 2) presented values above 5%, ranging from 11.9% for no. grain rows/ear to 84.8% for cob color.

In general, the starch content varied between 57.2 and 71.8%, the protein content varied between 12.0 and 14.9%, while the oil content ranged between 3.9 and 7.4%. This is in agreement with the data available in the literature for proximate analysis (Berardo *et al.*, 2009).

The coefficients of phenotypic variation (CV) were over 5% for most grain components (Tab. 2); they were higher for percentage of oil (16.9%) and a lower level for starch content (4.6%). Although, there is little variation in the percentage of starch in the germplasm studied here, there appears to be differences in the percentage of recoverable starch in these materials. Only Tu Comp. A (RRS) (1) synthetic was identified with high level of starch content (71.8%) (Tab. 3).

The data about synthetics showed a range among the genotypes for oil concentration from 3.5% to 7.3%. A similar range of variation (5.26 and 7.17%) was observed by Berardo *et al.* (2009) in a collection of 93 landraces. High oil concentrations were found in the following synthetics: Tu Syn 1 (7.4%), Tu Syn (3) (*per se*) (1) (7.3%), Tu Syn 2 (7.3%) and Syn. 57 Marano-Italy (7.2%).

All these genotypes characterized by high oil grain content can be used as high oil maize source material in a breeding program. These high oil synthetic populations have a large reduction in the starchy endosperm (Tab. 2 and 3) and most of them are characterized by flint or semi-flint grain type. For this germplasm Smith (1990) supported that pedigree selection has been used to develop some elite high oil lines.

Starch grain content was negatively and significantly correlated with protein, oil, fiber and ash. The results showed that an increase in starch content may decrease protein, oil, fiber and ash content ultimately, so breeding for high starch genotypes require a moderate balance among these quality grain traits. The results are in accord with Saleem *et al.* (2008).

The data presented in Tab. 4 indicated that grain oil contents were positively and significantly correlated with fiber and ash content and with some ear traits: ear length, grain color. Negative and significant correlation was found between oil and starch contents in synthetic populations analyzed.

## 2. The analysis of genetic relationships among 7 synthetic populations, using ear and quality trait data.

Analysis of variance showed significant differences among the genotypes for all traits studied (Tab. 5). General combining ability (GCA) effects were more important for grain content than specific combining ability (SCA). The occurrence of low interactions between synthetic populations and testers for all characters suggested the occurrence of high statistical additive effects expressed whatever the system of population evaluation. Most synthetic populations in this study have had one or two cycles of recurrent selection for agronomic traits and, therefore, they should be considered to be highly selected genotypes.

*Grain starch content.* Significant differences were detected among genotypes and parents (table 4). The GCA effects were larger for starch content than SCA effects, indicating that additive effects were more important for the trait.

Similar to other quality traits, heterosis was not significant, suggesting that SCA effects were significant only for some crosses but not different enough from parental values to produce a heterotic response (Tab.6).

Two of the seven best crosses, based on starch content, were the only parents with a positive GCA value different from zero: Tu SRR 5DR (6I) (4) and Tu SRR 5D(2I)(1). These synthetics would be a good source of alleles to increase grain starch content (Tab. 6, 9).

*Grain oil content.* Significant differences were detected among genotypes and parents (Tab. 5). The GCA effects were larger for oil content than SCA effects, indicating that additive effects were more important for the trait. Only one synthetic population Tu SRR 2I(5D) (1) had positive GCA value that were different from zero (Tab. 7). Eleven of 28 crosses showed SCA values significantly different from zero at  $P \leq 0.05$ . These results are also supported by the presence of heterosis for this trait at the crosses with the synthetics Tu SRR 5D(2I)(1) and Tu SRR 2I(5D) (1), as constant parents.

*Grain protein content.* Analysis of variance showed significant differences among all genotypes (Tab. 5), but, when genotypes were sorted in descending order by their grain protein percentage, no significant differences were detected among the top of 28 genotypes. No significant differences were detected among the seven synthetic populations *per se* (Tab. 1), but, there were significant differences among crosses (Tab. 8).

GCA effects are higher than SCA for grain quality traits (Rodrigues and Chaves, 2002; Reif *et al.*, 2005). Two synthetic populations Tu SRR 2I (5D) (1) and Tu Syn 8 had positive GCA value different of zero.

Only three crosses CO 255xTu Syn 8, TD 233 x Tu Syn 8 and TD 233 x Tu SRR 5DR (6I)(4) showed positive heterosis values that were statistically different from zero (Tab. 8).

Some synthetic populations were noted by their breeding value to transmit more positive grain quality components (Tab.9):

- Tu SRR 2I(5D) (1) was remarked by its additive inheritance of grain content in: oil, protein, fiber and ash;
- Tu Syn 8 has a good general combining ability for protein and ash;
- Tu SRR 5D (2I) (1), Tu Syn 3 (*per se*) (1), Tu SRR 5DR (6I) (4) may be considered as valuable source in improving grain content in starch.

Tab. 2

Mean, Range of Variation, CV and LSD for grain quality content and some ear traits

Traits	Starch	Oil	Protein	Fiber	Ash	Ear length	No. rows/ear	No. grains/ear	Grain* type	Grain** color	Cob *** color
Unit	% / 100 grams dry matter					cm	no.	no.	notes		
Count	59	59	59	59	59	59	59	59	59	59	59
Mean	65.9	5.4	13.6	5.4	2.1	18.58	14.6	484	2.98	3.95	3.49
Range	14.6	3.5	2.9	2.9	5.68	30	7.2	426	4.00	6.00	6.00
Minimum	57.2	3.9	12.0	3.7	0.17	13	12	322	1.00	2.00	1.00
Maximum	71.8	7.4	14.9	6.6	5.85	43	19.2	749	5.00	8.00	7.00
Standard Deviation	3.02	0.91	0.71	0.62	1.53	5.15	1.74	99.4	1.78	1.22	2.96
Sample Variance	9.13	0.83	0.51	0.38	2.36	26.49	3.04	9872	3.15	1.50	8.74
Standard Error	0.39	0.12	0.09	0.08	0.20	0.67	0.23	12.9	0.23	0.16	0.38
Confidence Level (95.0%)	0.79	0.24	0.19	0.16	0.40	1.34	0.45	25.9	0.46	0.32	0.77
CV %	4.6	16.9	5.2	11.5	72.9	27.7	11.9	20.5	59.7	30.9	84.8

\*note for grain type: 1 = flint; 5 = dent; \*\*note for grain color: 1 = white; 3 = yellow; 9 = red; \*\*\*note for cob color: 1 = white; 9 = dark red

Tab. 3

Synthetic populations with increased *per se* values of grain quality content

Grain content in:	Starch		Oil		Protein		Fiber		Ash	
Genotype	Mean %	Dif. +/- $\bar{X}$	Mean %	Dif. +/- $\bar{X}$	Mean %	Dif. +/- $\bar{X}$	Mean %	Dif. +/- $\bar{X}$	Mean %	Dif. +/- $\bar{X}$
Tu Syn 1 - Ro	60.3	-5.5**	<b>7.4</b>	2.1***	13.0	-0.6	5.2	-0.2	4.89	2.78***
Tu Syn 2 - Ro	59.8	-6.0**	<b>7.3</b>	2.0***	13.7	0.1	5.7	0.3	5.04	2.93***
Tu Syn (3) (per se) (1) - Ro	60.7	-5.1*	<b>7.4</b>	2.1***	13.6	0.0	6.3	0.9	4.88	2.77***
Tu Syn 8 (per se) (1) - Ro	61.2	-4.6*	<b>6.7</b>	1.4**	13.7	0.1	5.2	-0.2	3.97	1.86***
Tu SRR Comp. A (Comp. B)(1) Ro	<b>71.8</b>	<b>6.0**</b>	3.9	-1.4*	12.0	-1.6	4.3	-1.1	0.35	-1.76***
Minnesota Syn AS-A	66.8	1.0	5.2	-0.1	<b>14.7</b>	1.1***	<b>6.6</b>	1.2*	1.17	-0.94*
Minnesota Syn AS-B	68.0	2.2	4.6	-0.7	<b>14.4</b>	0.8***	6.0	0.6	0.38	-1.73***
Syn 54 Marano – Italy	62.7	-3.1	<b>6.6</b>	1.3*	13.4	-0.2	5.4	0.0	4.33	2.22***
Syn 55 Marano – Italy	61.1	-4.7*	<b>6.6</b>	1.3*	13.5	-0.1	4.6	-0.8	3.79	1.68***
Syn 57 Marano - Italy	61.1	-4.7*	<b>7.2</b>	1.9***	13.8	0.2	6.3	0.9	5.85	3.74***
Cisa Early – Spain	62.4	-3.4	6.3	1.0	<b>14.4</b>	0.8***	6.1	0.7	4.28	2.17***
Exotic Early – Spain	65.1	-0.7	5.4	0.1	<b>14.3</b>	0.7**	5.8	0.4	2.03	-0.08

Coruna Early – Spain	62.2	-3.6	<b>6.6</b>	1.3*	14.0	0.4*	6.2	0.8	4.57	2.46***
Coruna Prolific Syn-Spain	61.9	-3.9	<b>6.5</b>	1.2*	14.2	0.6**	5.9	0.5	3.58	1.47***
Syn H4 – Trnava - Slovakia	64.8	-1.0	5.5	0.2	<b>14.9</b>	1.3***	6.3	0.9	2.11	0.00
Argentinian Flint x Pirat ♂	63.3	-2.5	5.6	0.3	<b>14.3</b>	0.7**	5.2	-0.2	2.71	0.60
CHN-43 / Comp. Nord	67.4	1.6	4.1	-1.2*	14.5	0.9***	4.9	-0.5	0.28	-1.83
<b>Media (X̄)</b>	<b>65.8</b>	0	<b>5.3</b>	0	<b>13.6</b>	0.0	<b>5.4</b>	0.0	<b>2.11</b>	0.00
LTD 0.05		4.2		1.1		0.4		1.0		0.71
0.01		5.5		1.4		0.5		1.3		0.94
0.001		7.1		1.8		0.7		1.7		1.21

Tab. 4

Phenotypic correlations among some ear traits and grain quality content in 59 synthetic populations

Traits	Ear length	No. row of grain/ear.	No. grain /ear	Grain type	Grain color	Cob color	Starch	Protein	Oil	Fiber
Ear length	1.00									
No. row of grain/ear.	0.19	1.00								
No. grain /ear	<b>0.36</b>	<b>0.75</b>	1.00							
Grain type	-0.19	0.11	0.18	1.00						
Grain color	0.20	0.00	-0.01	-0.36	1.00					
Cob color	-0.20	0.02	0.13	0.64	-0.22	1.00				
Starch	-0.17	-0.04	-0.02	<b>0.48</b>	-0.47	0.37	1.00			
Protein	0.03	-0.10	-0.10	-0.02	0.02	-0.10	-0.25	1.00		
Oil	0.43	0.07	0.15	<b>-0.54</b>	<b>0.41</b>	-0.39	<b>-0.79</b>	0.03	1.00	
Fiber	0.01	-0.11	-0.02	0.14	-0.11	0.06	-0.31	0.29	0.43	1.00
Ash	0.38	-0.02	0.04	-0.67	0.46	-0.44	<b>-0.74</b>	0.14	0.88	0.22
P 5%	0.25									
	0.33									

Tab. 5

Genetic variances ( $s^2$ ) involved in the expression of grain yield and grain content (2 years: 2006-2007; 2 localities: Turda, Tg. Mureș)

Source of variation	GL	Grain yield	Grain quality content:				
			Starch	Oil	Protein	Fiber	Ash
TOTAL	111						
Years (Y)	1	1297.44	97.32	4.56	83.49	7.82	18.30
Replications (Locations) (L)	1	18120.40	5.94	0.003	8.64	16.97	25.83
Error (a)	1	233.17	47.58	3.79	20.49	3.43	20.51
GENOTYPES (G)	27	154.41 **	6.04 **	0.36 **	0.94 **	0.47 **	1.44 **
- Additive actions (Am) (GCA) (fathers)	(6)	163.17 **	12.80 **	0.88 **	0.42	0.77 **	4.92 **
- Additive actions (An) (GCA) (mothers)	(3)	894.16 **	15.31 **	0.17	5.81 **	0.92 **	0.29
- Non-additive interactions (NA) (SCA)	(18)	28.20	2.24	0.21	0.31	0.30	0.47
GENOTYPES x YEARS (GxA)	27	14.40	1.34	0.12	0.24	0.20	0.43
- Am x A	(6)	25.19	1.74	0.16	0.23	0.22	0.90 *
- An x A	(3)	9.12	0.28	0.06	0.09	0.41	0.23
- NA x A	(18)	11.69	1.45	0.12	0.27	0.16	0.31
Error (b)	54	24.31	1.38	0.12	0.35	0.17	0.30

\* and \*\* significant at  $P \leq 0.05$  and  $P \leq 0.01$ , respectively based on F-tests.

Tab. 6

Mean percentage of grain **starch** for crosses (m x n) (7 synthetic populations x 4 testers), GCA effects and heterosis values

Synthetic populations	Mean percentage of grain starch for crosses (m x n)					GCA effects $\hat{g}_n$	Heterosis values (%)			
	TC 184 cmsC	TC 209	CO 255	TD 233	Mean		TC 184 cmsC	TC 209	CO 255	TD 233
Tu Syn Mara	67,4*	67,3	65,5	66,2	66,6	-0,1	2.6	<b>2.9</b>	2.1	1.8
Tu Syn 1	66,3	65,2	66,5	68,2***	66,5	-0,2	1.9	0.7	1.8	<b>3.2</b>
Tu Syn 8	69,1***	65,3	66,1	65,1	66,4	-0,3	<b>3.6</b>	- 0.1	1.5	0.3
Tu SRR 2I(5D) (1)	67,2	64,7	65,4	64,1	65,3	-1,4	2.0	- 0.5	0.4	- 0.4
Tu SRR 5D(2I) (1)	67,5*	67,4*	67,8**	66,5	67,3	<b>0,5</b>	- 0.8	- 1.4	0.1	- 1.6
Tu Syn 3 (per se) (1)	67,2	67,9***	65,8	66,4	66,8	0,1	- 0.1	0.7	- 0.8	- 0.1
Tu SRR 5DR (6I) (4)	69,2***	69,2***	66,8	68,0***	68,3***	<b>1,5</b>	<b>2.9</b>	<b>3.2</b>	- 0.6	0.9
Mean	67,7**	66,7	66,2	66,3	<b>66,7</b>					
GCA effects $\hat{g}_m$	<b>1,0</b>	0,0	-0,5	-0,4						

\*, \*\* and \*\*\* significant at  $P \leq 0.05$ ,  $P \leq 0.01$  and  $P \leq 0.001$



Tab. 7

Mean percentage of grain **oil** for crosses (m x n) (7 synthetic populations x 4 testers), GCA effects and heterosis values

Synthetic populations	Mean percentage of grain oil for crosses (m x n)					GCA effects	Heterosis values (%)			
	TC 184 cmsC	TC 209	CO 255	TD 233	Mean	$\hat{g}_n$	TC 184 cmsC	TC 209	CO 255	TD 233
Tu Syn Mara	4,8	5,1	5,5**	5,2	5,2	0,0	- 0.1	- 3.8	- 2.8	6.0
Tu Syn 1	5,4*	5,6***	5,3	4,8	5,2	0,1	10.6	9.3	3.9	8.5
Tu Syn 8	4,3	5,5**	5,1	5,8***	5,2	0,0	- 6.1	6.9	- 1.9	11.3
Tu SRR 2I(5D) (1)	5,4*	6,0***	5,5**	5,7***	<b>5,6***</b>	<b>0,5</b>	11.3	14.0	2.9	16.7
Tu SRR 5D(2I) (1)	5,3	5,3	4,9	5,2	5,2	0,0	27.5	22.9	11.4	29.1
Tu Syn 3 (per se) (1)	5,3	4,7	5,3	5,1	5,1	-0,1	17.8	5.4	8.2	12.4
Tu SRR 5DR (6I) (4)	4,5	4,5	5,3	4,4	4,7	-0,5	4.7	3.4	10.6	8.2
Mean	5,0	5,2	5,2	5,2	<b>5,1</b>					
GCA effects $\hat{g}_m$	-0,2	0,1	0,1	0,0						

\*, \*\* and \*\*\* significant at  $P \leq 0.05$ ,  $P \leq 0.01$  and  $P \leq 0.001$

Tab. 8

Mean percentage of grain **protein** for crosses (m x n) (7 synthetic populations x 4 testers), GCA effects and heterosis values

Synthetic populations	Mean percentage of grain protein for crosses (m x n)					GCA effects	Heterosis values (%)			
	TC 184 cmsC	TC 209	CO 255	TD 233	Mean	$\hat{g}_n$	TC 184 cmsC	TC 209	CO 255	TD 233
Tu Syn Mara	12,3	12,0	13,4***	12,9	12,6	-0,2	- 3.5	- 8.7	- 4.1	- 3.0
Tu Syn 1	12,7	13,4***	13,4***	12,4	13,0	0,1	- 3.9	- 3.8	- 0.7	- 6.5
Tu Syn 8	12,1	13,1*	13,6***	13,5***	<b>13,1*</b>	<b>0,2</b>	- 3.2	- 1.5	<b>1.5</b>	<b>0.4</b>
Tu SRR 2I(5D) (1)	12,5	13,2**	13,3***	13,8***	<b>13,2**</b>	<b>0,3</b>	- 3.6	- 5.0	- 1.1	- 1.5
Tu SRR 5D(2I) (1)	12,0	12,7	12,8	13,1*	12,7	-0,2	- 5.5	- 6.1	- 4.5	- 1.9
Tu Syn 3 (per se) (1)	12,5	13,2**	13,4***	12,5	12,9	0,0	- 2.0	- 3.5	- 0.4	- 3.1
Tu SRR 5DR (6I) (4)	12,0	12,0	12,9	13,6	12,6	-0,2	- 5.6	- 11.5	- 2.3	<b>0.4</b>
Mean	12,3	12,8	<b>13,2**</b>	<b>13,1**</b>	<b>12,8</b>					
GCA effects $\hat{g}_m$	-0,6	-0,1	<b>0,4</b>	<b>0,2</b>						

\*, \*\* and \*\*\* significant at  $P \leq 0.05$ ,  $P \leq 0.01$  and  $P \leq 0.001$

Tab. 9

GCA effects of parental synthetic populations for quality grain content

No. crt.	Parental forms	Quality grain content:				
		Starch	Oil	Protein	Fiber	Ash
		%				
Synthetic populations = fathers						
1.	Tu Syn Mara	- 0.1	0.0	- 0.2	- 0,2	<b>0,3</b>
2.	Tu Syn 1	- 0.2	0.1	0.1	0,1	0,1
3.	Tu Syn 8	- 0.3	0.0	<b>0.2</b>	- 0,3	<b>0,3</b>
4.	Tu SRR 2I(5D) (1)	- 1.4	<b>0.5</b>	<b>0.3</b>	<b>0,4</b>	<b>0,6</b>
5.	Tu SRR 5D (2I) (1)	<b>0.5</b>	0.0	- 0.2	<b>0,2</b>	- 0,5
6.	Tu Syn 3 (per se) (1)	<b>0.1</b>	- 0.1	0.0	- 0,1	- 0,1
7.	Tu SRR 5DR (6I) (4)	<b>1.5</b>	- 0.5	- 0.2	- 0,2	- 0,7

## CONCLUSIONS

The screening of the Turda and foreign synthetic populations in our collection revealed the presence of a wide genetic variability for some grain components.

Some genotypes were identified as interesting sources in breeding programs for enriching grain content in:

- **oil** (> 6.5%): Tu Syn 1 (7.4%), Tu Syn 3 (*per se*) (1) (7.4%), Tu Syn 2 (7.3%), Syn 57 Marano – Italy (7.2%), Tu Syn 8 (*per se*) (1) (6.7%), Syn 54 Marano – Italy (6.6%), Syn 55 Marano – Italy (6.6%), Coruna Early – Spain (6.6%);

- **protein** (> 14.0%): Syn H4 Trnava – Slovakia (14.9%), Myn. Syn AS-A (14.7%), Myn. Syn AS-B (14.4%), Cisa Early – Spain, Syn Argentinean flint (14.3%);

- **starch** (> 70.0%): Tu SRR Composit A (Composit B) (1).

Starch grain content was negatively and significantly correlated with protein, oil, fiber and ash, therefore an increase in starch content may decrease protein, oil, fiber and ash content ultimately, so breeding for high starch genotypes require a moderate balance among these quality grain traits.

Negative and significant correlation was found between grain oil content with grain type (dent); grain starch content were positively and significantly correlated with grain type (dent).

General combining ability (GCA) effects were more important for grain content than specific combining ability (SCA).

Heterosis for grain starch content was not significant, suggesting that SCA effects were significant only for some crosses but not different enough from parental values to produce a heterotic response.

Some synthetic populations were noted by their breeding value to transmit more positive grain quality components Tu SRR 2I (5D) (1) was remarked by its additive inheritance of grain content in: oil, protein, fiber and ash; Tu Syn 8 has a good general combining ability for protein and ash; Tu SRR 5D (2I) (1), Tu Syn 3 (*per se*) (1), Tu SRR 5DR (6I) (4) may be considered as valuable source in improving grain content in starch.

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