

A NEW GENE SOURCE FOR HIGH POSITIVE DEVIATIONS OF GRAIN PROTEIN CONCENTRATION FROM THE REGRESSION ON YIELD IN WINTER WHEAT

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ABSTRACT

High protein concentration is one of the main requirements for baking quality in wheat, and is of economic importance for farmers since a premium is often paid for this attribute. Improving both grain yield and protein content has been a difficult task, because the two traits are negatively correlated. We collected data on grain yield and grain protein concentration from yield trials with 25 entries, designed as square lattice in 3 replications in two years, 5 locations and different management variants, totalling 25 conditions. Eleven Romanian winter wheat cultivars and the Russian cultivar Bezostaya 1 were common in all conditions and were included in the calculation of Grain Protein Deviations (GPD) from the regressions on grain yield. The winter wheat line Profund, bred at NARDI Fundulea, showed high and relatively stable positive GPD in all yield trials, in very different conditions in which yields varied between 2046 and 9838 kg ha⁻¹, and protein concentration between 8.6 and 15% on average over all tested cultivars.

The GPD of this line was on average +1.24% and was positive in all trials. This unusual performance might be due to the presence of genes introgressed from *Aegilops tauschii*, possibly complemented with favourable genes present in the Romanian cultivar Pitar.

The line Profund could be recommended as a potential parent in breeding for improved GPD.

Key words: grain protein deviations (GPD), yield (GY), grain protein concentration (GPC), *Aegilops tauschii*, regression GPC/GY.

INTRODUCTION

Wheat provides about 20% of the calories and is an important protein source for a large portion of the world's population (FAOSTAT). Therefore, global wheat production needs to increase in the upcoming decades to cover the rising demand for this grain (Hernández-Espinosa et al., 2018).

Elevated protein concentration is one of the main requirements for high baking quality in wheat, so it is of economic importance to food manufacturers, and is also of economic importance for farmers since a premium is often paid for this attribute (Aguirrezábal et al., 2014).

There are many studies related to the negative relationship between grain yield (GY) and grain protein concentration (GPC) (Simmonds, 1995; Feil, 1997; Triboi et al., 2006; Oury et al., 2007; Bogard et al., 2008; Marinciu and Săulescu, 2008, 2009) and this presents a major obstacle to the simultaneous improvement of these two traits in breeding programmes. Unfortunately, the global rise in GY has been associated with a concomitant decrease in GPC (Oury et al., 2003). This negative relationship was related to genetic incompatibility (linkage, pleiotropy), partitioning efficiency, and competition for photosynthetic energy between Nitrogen and Carbon (Feil, 1997; Triboi et al., 2006).

The classical agronomic strategy for achieving high GY coupled with a good level of GPC is to grow varieties having high GY potential and then to boost their GPC through a protocol in which the final fertilizer application is delayed to just before heading (Taulemesse et al., 2016). On the other hand, there is a trend to reduce fertilization due to the large economic and ecologic cost of excessive mineral fertilizer usage (Rothstein, 2007).

Monaghan et al. (2001) suggested that „the use of Grain Protein Deviations (residuals from regression of grain protein concentration on grain yield) provides a selection criteria in wheat breeding programs to screen for increased grain protein concentration without a concurrent grain yield reduction”; „a higher grain protein concentration than predicted from grain yield is under genetic control and thus may be improved through breeding”. This study is an attempt to identify a possible source of genes

for high Grain Protein Deviations, based on multi-environment trials in two years, in contrasting conditions.

MATERIAL AND METHODS

Data on grain yield and grain protein concentration were collected from yield trials with 25 entries, designed as square lattice in 3 replications in two years and 5 locations. Twelve entries were common in all conditions and were included in this study, namely the Romanian winter wheat cultivars: Glosa, Litera, FDL Miranda, Izvor, Otilia, Pitar, Pajura, Semnal, Ursita, Unitar, Profund, plus the Russian cultivar Bezostaya 1, used as long term check. Their genealogy is presented in Table 1. All Romanian cultivars are semidwarf and early maturing, their amplitude in heading date being smaller than 2-3 days. Only Bezostaya 1 is a normal height cultivar, heading about 4 days later.

Table 1. Genealogy of the 12 cultivars included in this study

Cultivar	Origin	Genealogy
Glosa	NARDI Fundulea, Romania	F135U2-1/F508U1-1//F135U3-1
Litera	NARDI Fundulea, Romania	ERYT26221/F96869G1-1//Glosa
FDL Miranda	NARDI Fundulea, Romania	ERYT26221/F96869G1-1//Glosa
Izvor	NARDI Fundulea, Romania	Karl/F201R2-111//F508U1-1
Otilia	NARDI Fundulea, Romania	F96052G16-2/Faur
Pitar	NARDI Fundulea, Romania	Litera/F00099GP2
Pajura	NARDI Fundulea, Romania	Izvor/F96012G2-2//Glosa
Semnal	NARDI Fundulea, Romania	F05511GP4/Litera
Ursita	NARDI Fundulea, Romania	F00628G34-2/2*Glosa
Unitar	NARDI Fundulea, Romania	M1-Izvor/M1-00628g34
Profund	NARDI Fundulea, Romania	Murga/F03124G//Pitar
Bezostaya 1	KNIISH Krasnodar, Russia	Lutescens 17/Skorospelka 2

The yield trials covered a large amplitude of environmental and management conditions. In four of the five locations, yield trials were organised on two levels of Nitrogen fertilization in spring (recommended and no nitrogen in the spring), and in Fundulea additional management variants included late sowing

(two weeks later than the optimal date), two fields differentiated by the level of Nitrogen fertilization (medium and high), both in 2016 and 2017, and foliar treatment with fungicides to control foliar diseases in 2017. As a result, the cultivars were tested in 25 different environmental conditions (Years*Management) (Table 2).

Table 2. Short description of the environmental conditions at the five testing locations

Region	Location Soil type	Year	Field	Sowing date	Nitrogen fertilization (kg N ha ⁻¹)		Preceding crop	Rainfall (October - July) mm	
					Autumn	Spring			
Southern	Fundulea Chernozem pH:6.3-6.8 humus: 3%	2016	Field 1	a	Optimal	0	137	Peas	435.1
				b	Optimal	0	0		
			Field 2	c	Optimal	0	90		
				d	Late	0	90		
		2017	Field 1	e	Optimal + foliar treatment	0	137	Peas	
				f	Optimal	0	137		
				g	Optimal	0	0		
			Field 2	h	Optimal	0	90	Peas	
	i	Late	0	90					
	Șimnic Luvisoil, pH: 5.7-5.9 Humus: 1.8%	2016	Field 1	a	Optimal	40	90	Peas	730.9
				b	Optimal	40	0		
		2017	Field 1	c	Optimal	40	90		
				d	Optimal	40	0		
	Albota Brown luvisoil pH:5.02-5.03 Humus: 2.7%	2017	Field 1	a	Optimal	24	110	Sunflower	568.4
b				Optimal	24	0			
Centre	Brașov Cambic chernozemoid pH: 7.2 Humus: 5.2%	2016	Field 1	a	Optimal	0	70	Rape	622
				b	Optimal	0	0		
		2017	Field 1	c	Optimal	0	100	Potato	
				d	Optimal	0	0		
	Turda Chernozem pH: 7 Humus: 3.5%	2016	Field 1	a	Optimal	50	50	Peas	753.4
				b	Optimal	50	0		
		2017	Field 1	c	Optimal	50	50	Mustard	
				d	Optimal	50	0		
	Târgu-Mureș Brown pH: 5.7 Humus: 1.9%	2016	Field 1	a	Optimal	90	0	Clover	573.9
		2017	Field 1	b	Optimal	80	0	Soybean	477.5

Based on simulations made to determine the minimum experimental design, Oury and Godin (2007) showed that „at least five sites per year for two consecutive years were necessary to have a good assessment of the GY – GPC relationship and hence reliable estimates of GPD”. Therefore, our set of data could be considered sufficient.

The variation of experimental conditions was reflected by the grain yield and protein concentration averaged over all cultivars tested in a trial, as well as by the variation of the correlation coefficients between grain yield and grain protein concentration (Table 3). Average grain yield of the trials varied between 2046 and 9838 kg ha⁻¹, and protein

concentration between 8.6 and 15%. Correlation between grain yield and grain protein concentration varied from 0 and -0.79, being significant in 17 out of 25 trials.

RESULTS

We calculated deviations from the regression grain yield and grain protein concentration for all 25 available trials, performed in two years with various management variants, regardless if the correlation between the two traits was or not significant. At the limit, when correlation is 0, the calculated deviation is equivalent to the difference from the average of all cultivars.

Table 3. The correlation coefficient between grain yield and grain protein concentration in all 25 trials

Location	Condition	Average yield of the trial (GY) kg ha ⁻¹	Average protein concentration (GPC) of the trial (%)	Coefficient of correlation GY-GPC
Fundulea	a	4496	14.8	-0.61
	b	4674	12.6	-0.55
	c	5144	12.8	-0.51
	d	5200	12.6	-0.36
	e	7276	14.0	-0.64
	f	6656	14.0	-0.57
	g	6143	13.0	-0.09
	h	6142	13.0	-0.26
	i	5823	14.0	-0.29
Simnic	a	3784	10.2	-0.66
	b	3752	9.8	-0.46
	c	6860	9.9	-0.57
	d	5043	9.8	-0.33
Albota	a	3023	15.0	-0.53
	b	2046	15.0	-0.46
Brasov	a	6883	13.1	0
	b	5770	11.6	-0.25
	c	9838	13.8	-0.40
	d	9215	13.4	-0.62
Turda	a	7731	12.3	-0.72
	b	7228	10.6	-0.75
	c	6262	12.2	-0.76
	d	5754	8.6	-0.79
Târgu-Mureş	a	7461	13.8	-0.36
	b	9681	13.1	-0.61

Coefficients in **bold** are significant at $p < 5\%$.

In 2016, in the trials performed in Southern region, the average deviations from the regression GY-GPC varied from -0.71 in the cultivar Semnal, with negative deviations

in all trials, to +1.39 in the line Profund, which had positive deviations in all trials from this region, at both Nitrogen fertilization rates (Table 4).

Table 4. Deviations from the regression grain yield – grain protein concentration in trials from the Southern region in 2016

Cultivar	Regular N fertilization				Low N		Average
	Fundulea a	Fundulea c	Fundulea d	Simnic a	Fundulea b	Simnic b	
Profund	1.48	1.85	0.96	1.65	1.01	1.39	1.39
Bezostayal	0.76	0.78	0.71	0.52	1.41	0.52	0.78
Glosa	0.78	1.09	0.19	0.61	1.03	0.33	0.67
Litera	-0.24	0.96	0.98	-0.08	0.87	0.00	0.42
Faur	-0.60	0.79	0.99	-0.33	1.22	0.08	0.36
11368g	0.26	0.38	0.60	0.00	0.36	-0.15	0.24
Pitar	-0.37	0.36	0.34	0.04	0.31	0.33	0.17
Lv6125	0.72	-0.41	-0.12	-0.34	0.42	0.58	0.14
Lv6113	1.49	-0.49	-0.48	0.36	-0.21	-0.11	0.09
Lv6111	1.26	-0.21	-0.73	0.32	-0.71	0.16	0.02
Boema	-0.08	-0.81	0.14	0.05	0.43	0.35	0.01
Lv6110	0.98	-0.05	-0.25	-0.10	-0.58	-0.53	-0.09
S119	0.44	-0.28	-0.15	-0.18	-0.08	-0.31	-0.09
Alex	0.92	0.20	-0.72	-0.53	-0.11	-0.59	-0.14
Otilia	-0.73	0.12	-0.20	-0.28	-0.19	0.16	-0.19
Adelina	-0.78	0.22	-0.03	-0.60	-0.12	-0.01	-0.22

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S1120	0.08	-0.75	-0.67	-0.21	0.54	-0.32	-0.22
Pajura	-1.07	-0.13	-0.13	0.25	-0.98	0.11	-0.32
Miranda	-0.71	0.16	-0.17	-0.19	-0.48	-0.66	-0.34
A38-04	0.64	-1.27	-0.99	0.33	-1.04	-0.14	-0.41
Ursita	-0.74	-0.49	0.18	-0.31	-0.9	-0.26	-0.42
Izvor	-1.70	-0.89	-0.44	0.10	-0.93	0.05	-0.63
Unitar	-1.26	-0.86	0.24	-0.68	-1.11	-0.57	-0.71
Semnal	-1.48	-0.63	-0.25	-0.16	-1.33	-0.39	-0.71

In 2016, in the Centre region, the average deviations from the regression grain yield and grain protein concentration varied from -0.53 in the cultivar Dumbrava, which had

only negative deviations, to +0.74 in the line Profund, for which deviation were all positive (Table 5).

Table 5. Deviations from the regression grain yield – grain protein concentration in trials from the Centre region, in 2016

Cultivar	Regular N fertilization			Low N		Average
	Turda a	Braşov a	Târgu-Mureş a	Turda b	Braşov b	
Profund	0.36	0.69	0.98	0.61	1.06	0.74
Bezostayal	0.61	0.95	1.59	0.12	0.12	0.68
T124-11	0.79	-0.76	0.3	0.57	1.23	0.43
Otilia	0.25	0.27	0.64	0.08	0.82	0.41
Glosa	0.48	1.16	-0.36	0.19	0.5	0.39
Semnal	0.53	0.86	-0.06	0.14	0.17	0.33
T42-05	0.26	-0.17	1.11	0.31	-0.05	0.29
Ursita	0.14	0.39	-0.13	0.67	0.18	0.25
Litera	-0.19	0.66	0.57	0.12	-0.03	0.23
Pitar	0.46	0.03	0.22	0.25	0	0.19
T123-11	0.25	-0.29	0.54	0.13	-0.16	0.1
Pajura	0.5	0.53	-0.7	0.12	-0.2	0.05
Izvor	-0.04	0.56	-1.17	0.16	0.67	0.04
Unitar	0.43	-0.04	-0.31	0.07	-0.12	0.01
Codru	-0.11	-0.39	0.25	0.05	-0.46	-0.13
Boema 1	0.25	0.4	-1.18	-0.23	-0.51	-0.25
T150-11	-1.07	-0.18	0.37	-0.71	0.23	-0.27
T55-01	-0.45	-1.09	0.49	-0.7	0.34	-0.28
T62-01	-0.88	-0.32	0.73	-0.11	-0.9	-0.29
Miranda	-0.24	0.01	-1.43	-0.25	0.31	-0.32
11838G8	-0.04	-1.13	0.16	0.3	-1.58	-0.46
T19-10	0.16	-1.39	-1.25	0.3	-0.28	-0.49
Dumbrava	-0.89	-0.1	-0.27	-1.13	-0.28	-0.53

In 2017, in the Southern area, the average deviations from the regression GY-GPC varied from -0.84 in the cultivar Miranda, to

+1.59 in the line Profund, for which deviations were positive in all trials (Table 6).

Table 6. Deviations from the regression grain yield – grain protein concentration in trials from the Southern region, in 2017

Cultivar	Regular N fertilization						Low N			Average
	Fundulea e	Fundulea f	Fundulea h	Fundulea i	Simnic c	Albota a	Fundulea g	Şimnic d	Albota b	
Profund	0.64	1.36	1.07	1.89	0.75	3.04	2.13	1.37	2.07	1.59
Voievod2	1.25	1.25	0.85	0.90	0.26	1.20	1.43	0.77	0.80	0.97
Bezostayal	1.63	1.10	1.03	1.12	-0.08	0.71	1.14	1.01	0.00	0.85
Voinic	0.73	0.82	0.57	0.86	0.89	-0.23	0.48	1.72	0.65	0.72

Lv6110	1.08	1.31	-0.22	0.25	0.39	0.36	-0.49	-0.41	1.98	0.47
Voievod1	0.23	0.64	0.60	0.21	0.07	0.37	0.86	0.93	0.04	0.44
Litera	0.44	0.03	1.18	0.52	-0.10	0.56	-0.44	-0.21	0.93	0.32
Pitar	0.25	-0.02	0.53	0.79	0.27	0.48	-0.11	0.01	-0.08	0.23
Ursita	0.37	0.29	0.16	0.26	-0.46	0.33	0.00	-0.37	0.50	0.12
Simnic60	0.50	0.23	0.08	-0.40	-0.53	-0.62	1.41	-0.42	0.58	0.09
Otilia	-0.14	-0.47	0.03	0.06	0.67	-0.12	-0.57	-0.40	0.76	-0.02
Adelina	0.35	-0.27	-0.51	-0.43	0.02	-0.85	0.29	-0.35	0.85	-0.10
Vestitor	-0.42	0.20	-0.47	-0.06	0.15	-0.05	0.87	1.12	-2.25	-0.10
Lv6111	0.29	0.02	0.00	-0.41	0.17	-1.05	-0.32	-0.50	0.69	-0.12
Glosa	0.17	-0.34	-0.25	0.14	-0.22	0.71	-0.96	-1.22	0.13	-0.20
Lv6125	0.13	0.12	-0.26	-0.47	-0.01	-0.44	-0.46	0.80	-1.71	-0.25
Lv6113	-0.01	-0.36	0.02	-0.32	0.23	-1.37	-0.63	0.90	-0.89	-0.27
Pajura	-1.16	-0.49	-0.52	-0.16	-0.28	-0.80	-0.15	0.23	-0.04	-0.37
Boema1	-0.97	-0.97	0.03	-0.19	-0.16	-0.09	-0.35	-0.75	-0.24	-0.41
Semnal	-1.03	-0.81	-0.12	-0.56	-0.42	-0.22	-0.44	-1.18	0.07	-0.52
Alex	-0.74	0.21	-1.06	-0.46	-0.11	-0.14	-0.35	-0.55	-1.51	-0.52
Izvor	-0.43	-1.24	-0.72	-0.28	-0.71	0.73	-0.63	-0.42	-1.22	-0.55
Unitar	-1.19	-0.80	-1.18	-0.78	-0.43	-0.71	-0.73	-0.29	-0.44	-0.73
A 4-10	-1.13	-0.40	-0.12	-0.81	-0.02	-1.30	-0.39	-0.94	-2.04	-0.79
Miranda	-0.84	-1.42	-0.72	-1.67	-0.32	-0.51	-1.59	-0.86	0.37	-0.84

In 2017, in the Centre region, the average deviations from the regression GY-GPC varied from -0.63 in the cultivar Miranda, to

+1.05 in the line Profund (Table 7). Again, for this line deviations were positive in all trials performed in the region.

Table 7. Deviations from the regression grain yield – grain protein concentration in trials from the Centre region in 2017

Cultivar	Regular N fertilization			Low N		Average
	Turda c	Braşov c	Târgu-Mureş b	Turda d	Braşov d	
Profund	0.92	1.65	0.34	0.18	2.15	1.05
Voinic	1.48	0.35	0.65	0.11	0.30	0.58
Ursita	0.77	0.20	0.66	0.16	1.03	0.56
Bezostaya1	-0.19	1.56	1.10	0.26	-0.10	0.53
T95-12	0.35	0.24	1.79	0.21	-0.15	0.49
Pitar	0.28	0.67	-0.05	0.36	1.11	0.47
T118-11	0.24	0.75	-0.28	-0.07	0.96	0.32
Litera	0.15	0.26	0.38	-0.09	0.08	0.16
Codru	-0.57	0.18	0.03	-0.18	0.21	-0.07
Voievod1	-0.94	0.43	0.33	-0.21	0.65	0.05
Izvor	0.38	-1.01	-0.12	-0.36	-0.37	-0.3
Semnal	-0.24	-0.16	0.03	-0.12	0.38	-0.02
Andrada	0.00	0.75	-0.52	0.06	-0.22	0.01
T19-10	0.47	-1.09	0.25	0.82	-0.51	-0.01
Dumbrava	-0.52	0.98	-1.31	-0.11	0.19	-0.15
Unitar	0.18	-0.49	-0.62	0.10	-0.02	-0.17
Pajura	-0.25	-0.79	-0.30	0.44	-0.01	-0.18
Glosa	-0.08	-0.70	-0.56	0.31	-0.22	-0.25
T109-12	-0.11	-0.14	-0.35	-0.46	-0.57	-0.33
T123-11	-0.06	-0.38	0.19	-0.19	-0.74	-0.24
Otilia	-1.07	-0.33	-0.54	0.12	-0.31	-0.43
T124-11	0.18	-0.67	0.08	-0.46	-0.89	-0.35
T143-11	-0.60	-0.45	-0.26	-0.37	-0.68	-0.47
Vestitor	-0.87	-0.69	-0.51	-0.18	-0.94	-0.64
Miranda	0.09	-1.11	-0.44	-0.35	-1.32	-0.63

Oury and Godin (2007) found that the correlations between grain yield and grain protein concentration, calculated environment by environment, appeared highly variable due to high “genotype \times environment” interactions for grain yield and grain protein concentration. “The use of mean values, calculated on the 21 series of GEVES trials, enabled a better assessment of the relationship between the two characters, and

an algorithm was proposed to avoid bias due to potential outliers”. Although in our study the deviations from the regression grain yield – grain protein concentration calculated environment by environment for the line Profund were noticeably consonant, we also used the mean values calculated for all the 25 yield trials, without eliminating any outliers (Table 8 and Figure 1).

Table 8. Grain yield – grain protein concentration averaged over 25 yield trials performed in 2016 and 2017

Cultivar	Deviations from the regression GY-GPC	Grain yield		Grain protein concentration	
		kg ha ⁻¹	CV	%	CV
Profund	1.24	6012	27.7	13.92	15.3
Ursita	0.37	6803	33.5	12.31	16.0
Bezostaya 1	0.27	4954	37.9	13.95	15.7
Litera	0.21	6053	30.3	12.85	15.7
Pitar	0.18	5948	33.9	12.92	15.1
Glosa	-0.01	5869	31.8	12.80	15.1
Otilia	-0.07	6153	31.1	12.48	14.7
Unitar	-0.29	6689	34.8	11.75	15.4
Semnal	-0.30	6217	35.7	12.19	15.7
Pajura	-0.37	5781	33.7	12.53	14.3
Izvor	-0.50	5815	32.2	12.36	12.6
Miranda	-0.74	5906	34.4	12.04	15.5

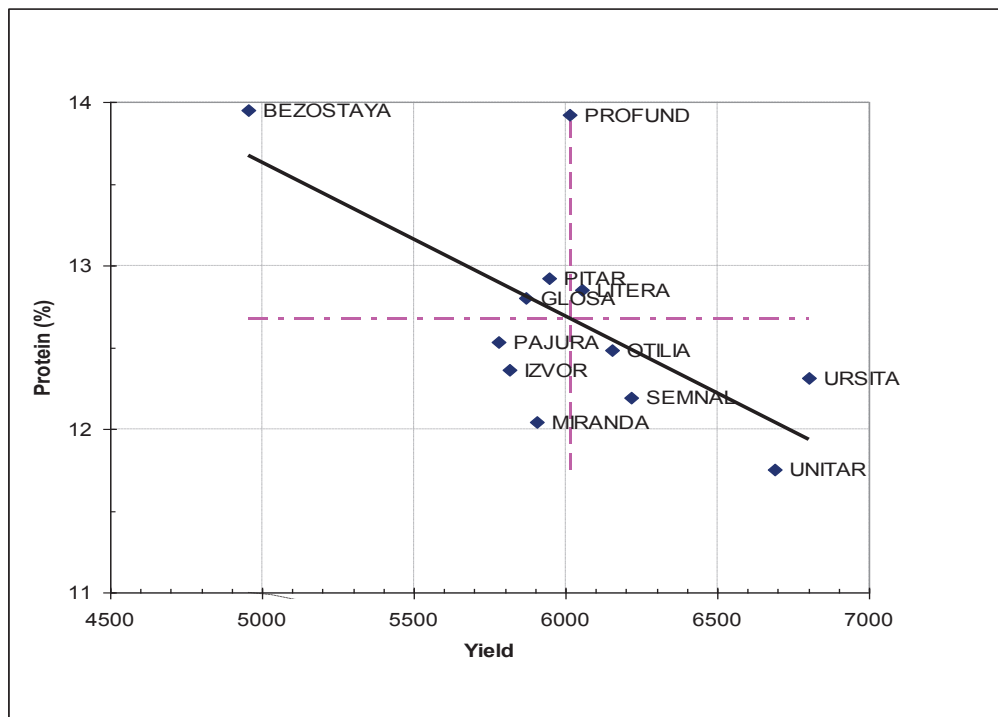


Figure 1. Relationship between average grain yield and grain protein concentration in all 25 yield trials performed in 2016 and 2017 ($r = -0.62^*$)

The line Profund, was ranked on 2nd place for protein content (after Bezostaya 1 that had the lowest yield) and on 6th place for yield, on average for all trials. It was outstanding for its high deviation from the regression grain yield – grain protein concentration, recording an average protein concentration higher by 1.24% than expected based on its grain yield. This deviation was higher than the one recorded for the medium height cultivar Bezostaya 1 (0.27%) and considerably higher than the one found in the cultivar Pitar, earlier described as having the best deviation among the cultivars along which was tested (Marinciu et al., 2015).

DISCUSSION

High grain protein contents were reported in common and durum wheat carrying gene(s) introgressed from *Triticum turgidum* L. var. *dicoccoides* (Joppa et al., 1997; Chee et al., 2001; Mesfin et al., 2000), mostly explained by faster senescence causing higher N translocation to grains (Uauy et al., 2015). However, the effects of these genes are very dependent on the interaction with the environment and the genetic background, making them often associated with lower yields (Brevis and Dubcovsky, 2010; Facundo et al., 2013). This explains the interest in looking for high protein deviations from the regression on yield, instead of just protein concentration.

Monaghan et al. (2001) stated that “High grain protein deviation may be achieved through increased N accumulation after anthesis, combined with efficient re-translocation of vegetative N reserves”. More recently Bogard et al. (2010) observed that “Under most environments, GPD was significantly related to post-anthesis N uptake, independently of anthesis date and total N at anthesis”. This leads to the hypothesis that genetic variability for GPD could be associated with variations in satiety for N. Such internal regulations of N uptake could represent a potential node of genetic variability that might explain the increased ability of some genotypes to capture N after flowering in a way that was independent of

the level of N uptake realised before flowering (Taulemesse et al., 2016).

In our research the line Profund was noticed by having positive deviations from the regression grain yield – grain protein concentration in all 25 trials performed in widely different environments, the average protein content being 1.24 % higher than the one expected from the regression on yield. Preliminary observations (data not shown) indicated that Profund accumulated more Nitrogen after anthesis, and also showed slower leaf senescence, than other analysed cultivars.

The line Profund was selected from the hybrid combination Murga/03124G//Pitar. Murga was selected as parent in crosses mainly based on its “stay green” trait and foliar disease resistance. According to Genetic Resources Information System for Wheat and Triticale (GRIS), the pedigree of the CIMMYT line Murga (sin. CMSS-93-B-00686-S) is MUNIA/ALTAR-84//AMSEL. However, CIMMYT breeders suspect this pedigree might be wrong because Murga has many traits similar with *Aegilops tauschii* derivatives and therefore this line is probably a synthetic wheat derivative (Ravi Singh, *personal communication*). On the other hand, Pitar, the last parent in the genealogy of Profund, is a recently released cultivar described as high quality and relatively high protein wheat (Marinciu et al., 2015). In this study, Pitar had on average a positive grain protein concentration of 0.18%.

We suggest that the outstanding performance of Profund regarding grain protein concentration might be due to genes inherited from *Aegilops tauschii* via Murga, possibly complemented with favourable genes present in Pitar. The contribution of genes transferred from *Aegilops* to an improved grain protein concentration could be another example of using interspecific hybridization as a source of variation for wheat grain quality improvement (Alvarez and Guzmán, 2017).

Many studies concluded that the deviation from this relationship (grain protein deviation or grain protein concentration) has strong genetic basis (Monaghan et al., 2001; Oury and Godin, 2007). Preliminary data

suggest that many progenies of crosses with Profund inherited high grain protein concentration, but further studies are necessary to determine how well GPD was transmitted in crosses.

CONCLUSIONS

The winter wheat line Profund, bred at NARDI Fundulea, showed high and relatively stable positive grain protein concentration in 25 yield trials performed in two consecutive years, in very different conditions in which yields varied between 2046 and 9838 kg ha⁻¹, and protein concentration between 8.6 and 15% on average over all tested cultivars.

The grain protein concentration of this line was on average +1.24% and was positive in all trials. This unusual performance might be due to the presence of genes introgressed from *Aegilops tauschii*, possibly complemented with favourable genes present in the Romanian cultivar Pitar.

The line Profund could be recommended as a potential parent in breeding for improved grain protein concentration.

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