

PROTEIN CONTENT, THOUSAND KERNEL WEIGHT (TKW) AND VOLUMETRIC MASS (VM) VARIABILITY IN A SET OF WHEAT MUTATED AND MUTATED/RECOMBINANT DH LINES

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Abstract

The genetic progress towards quality and productivity improvement was and still remains a major concern in wheat breeding as generally these traits are negatively correlated. Consequently, any additional useful variability identification could contribute to attain this goal. Besides natural variability, exploitation by classical hybridization method, artificial mutagenesis can also be used to generate a different and new genetic variability. The special advantages of induced mutation are that variants with desired traits can often be produced in high frequencies, in a short time, in a chosen genetic background without disrupting the original genetic constitution of the crop. By using DH technology it become possible to perform a rapid and easier selection for desired plant type and, particularly for traits controlled through recessive alleles that constitute the greatest majority of genetic variability produced by irradiation with gamma rays. Many studies have demonstrated the role of thousand kernel weight traits in expression of productivity parameters and the protein content in expression of quality parameters in the wheat gene pool. In this paper is briefly described a study regarding protein content, thousand kernel weight (TKW) and volumetric mass (VM) variability generated by using a specific mutagenic protocol consisting in recurrent irradiation, hybridization and DH-technology.

Key words: *mutated/recombinant lines, variability, protein content, TKW, volumetric mass.*

INTRODUCTION

Wheat is an important crop plant, as it provides the necessary food for 35-40% of the world population. Since the main destination of wheat is the use in bakery, the quality improvement was one of the objectives pursued by breeders and according to them, the phenotypic expression of wheat quality is given by the interaction between genotype, environmental conditions and crop technology and the bakery quality is determined by the wheat quality and bakery technology (Săulescu, 1984; Kadar et al., 2002).

Although there is a genetic determinism regarding protein contents, this is often disturbed by growing conditions, such as wheat may have protein content between 6.9% and 22.00% (Vogel et al., 1973).

At this time, however, the pressure of climatic change, losses caused by the emergence of new breeds of disease, population increasing emphasized the need for higher wheat

productions and superior protein content. For accomplish these endeavors is necessary to identify and use new and different genetic variability sources. Besides the classical intra and inter specific hybridization method, the mutagenesis has become in our days a valuable approach in providing new and different genetic variability; more 3000 mutants were released as new cultivars in around 170 cultivated species (Lagoda, 2009).

In wheat mutations with favorable effects in multiple directions, such as increasing resistance to diseases (Campbell et al., 2012), improved nutrition quality by decreasing the phytic acid level (Guttieri et al., 2004), and even shortening the growing season were obtained (Chen and Dubcovsky, 2012).

Molecular markers and TILLING method (Targeting Induced Local Lesions in Genomes) are modern genetic tools that allow the mutation identification and localization.

At NARDI Fundulea by using a specific mutagenic protocol including two genotypes,

two irradiation cycles, hybridization and technology (*Zea* system), were obtained over 524 mutant and mutant/recombinant DH lines, among which exists phenotypic variability for many traits (Giura, 2011). The aim of this work was to identify the variability regarding high protein content, TKW and VM in the analyzed material that may be induced by mutagenesis.

MATERIALS AND METHODS

A set of 524 mutated and mutant/recombinant DH lines obtained at NARDI Fundulea by A. Giura, was analyzed for protein content, thousand kernel weight (TKW) and volumetric mass (VM). The lines were hand planted in field trial in 2014-2015 seasons in pair of rows, 1 m long, 25 cm between rows and spaced apart 50 cm between pairs.

TKW measurements were established using the Contador machine and volumetric mass was determined using a 100-ml graduated cylinder and an analytical balance for weighing. Protein content was performed using Infratec™ 1241 Grain Analyser that use a non-destructive spectroscopic technique based on naturally occurring electromagnetic spectrum. For protein determinations were necessary to weigh about 60 grams wheat samples.

The results obtained were compared with those registered for parental genotypes, the cultivar Izvor and the advanced breeding line F00628G-34.

RESULTS AND DISCUSSIONS

Protein content. The dispersion for protein content is presented in Figure 1. The majority of DH lines were grouped in ranges of 13.5%-15% protein, interval in falling and the Izvor parent, 13.7%. The other parent, F00628G-34 line, has lower protein content, 12.2%. The lower protein content of 11% was recorded in only one line and the highest of 19.5% in two lines.

Thousand kernel weight and volumetric mass. Variation of these two analyzed traits is presented in Figure 2 and Figure 3. As expected, majority of lines were grouped in the interval classes that include both parental genotypes, the parent Izvor being however

quoted as having superior values compared to the parent F00628G-34.

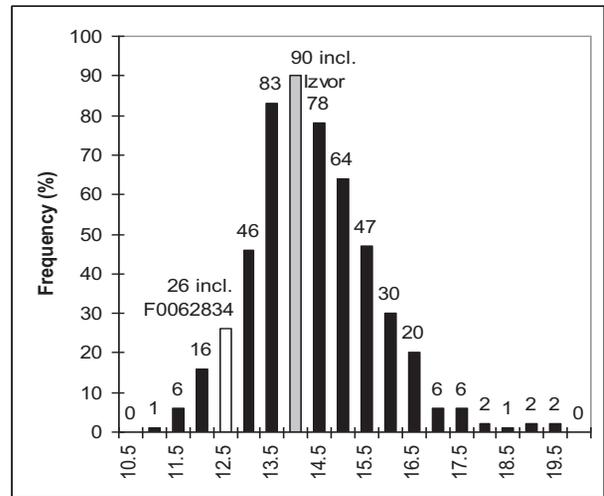


Figure 1. Protein content variation in different wheat lines

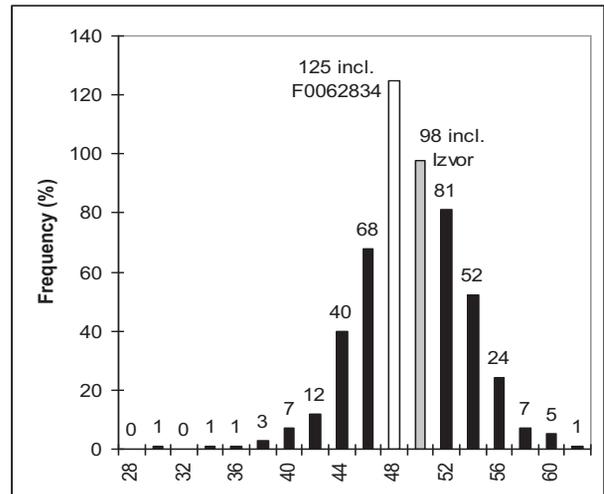


Figure 2. Distribution of lines in intervals for thousand kernel weight

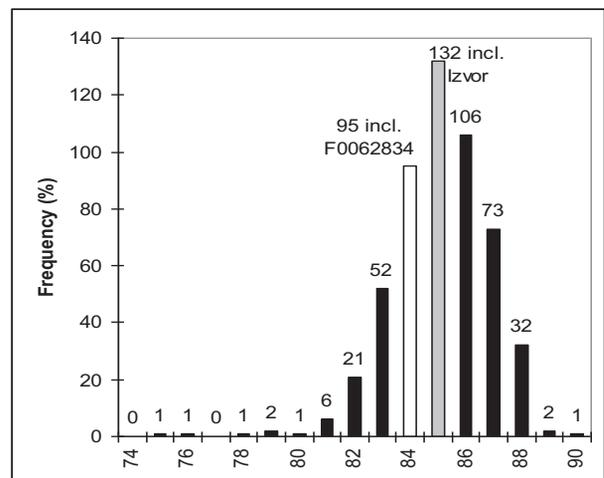


Figure 3. Distribution of lines in intervals for volumetric mass

Although the correlation coefficient between protein content and TKW are generally negative, it is small and non significant; and several mutant lines obviously deviated from the regression lines (Figure 4).

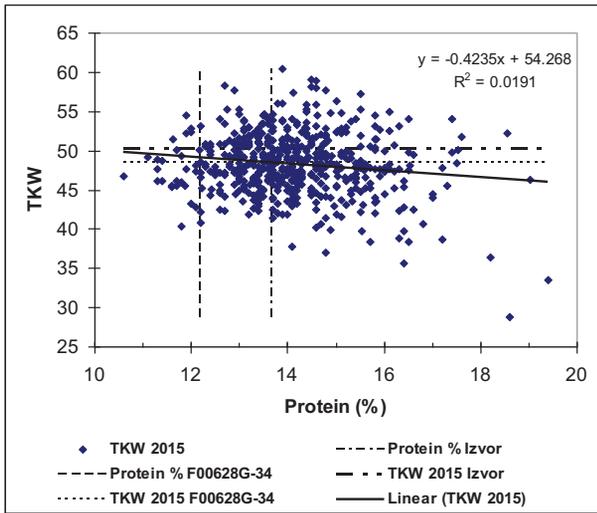


Figure 4. Distribution of lines depending on TKW and protein content

As regard the correlation between protein content and volumetric mass it was found a similarly negative correlation. However, some lines presented high values for both parameters, like AiII 202 and BiII 106 (Figure 5).

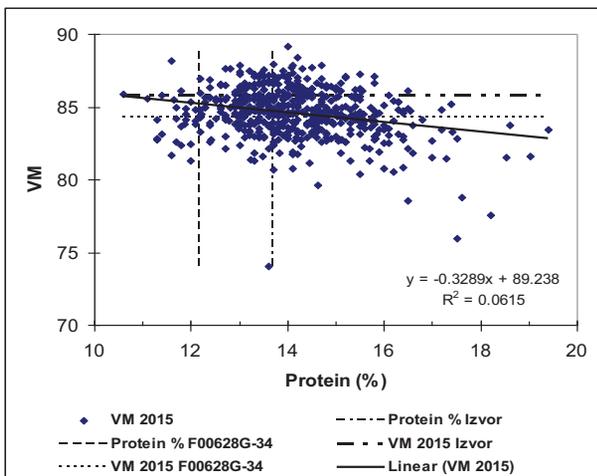


Figure 5. Distribution of lines depending on VM and protein content

A total of 125 lines which expressed high protein content (> 15%), higher values than the parents Izvor (13.7%) and F00628G-34 (12.2 %) in terms of 2015 conditions were selected for further experiments and analysis.

Although no significant correlation between protein content and TKW were detected, a total of 32 lines combined higher TKW values and protein content than their parents (Figure 6).

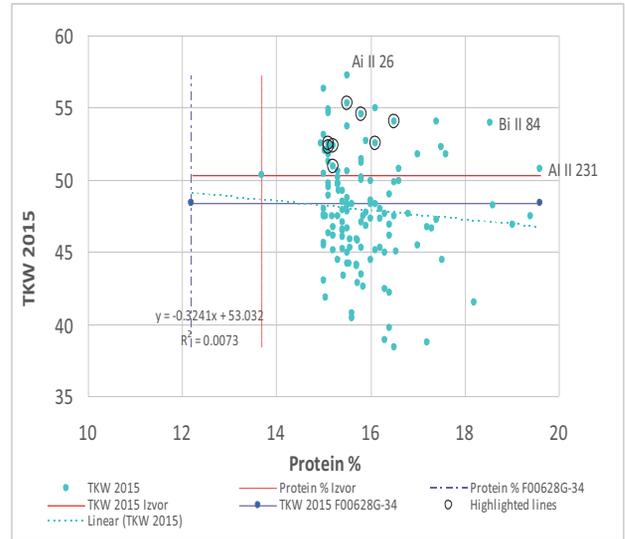


Figure 6. Distribution of lines with protein content >15% in correlation with TKW values

The line distribution depending on protein content and volumetric mass indicates that the negative relationship is maintained but there are lines that deviate from this regression, expressing both high protein content and high volumetric mass (Figure 7).

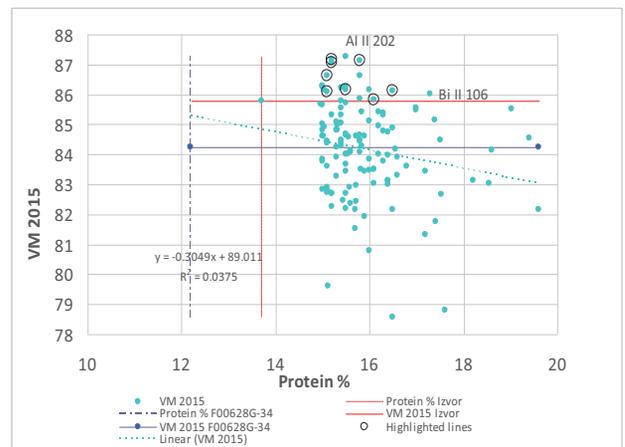


Figure 7. Distribution of lines with protein content >15% in correlation with VM values

By analyzing the distributions of 125 lines for protein content and TKW, on the one hand, and the protein content and VM on the other hand, have been noticed 8 lines that shows superior values than parents, for all these 3 parameters,

which can be considered valuable lines for use in breeding (Table 1).

Table 1. Lines with high protein content and superior values for volumetric mass and TKW

Genotype	Protein %	TKW 2015	VM 2015
Ai II 50	15.1	52.51	86.61
Ai II 72	16.1	52.5	85.81
Ai II 109	15.2	52.33	87.06
Ai II 175	16.5	54.04	86.13
Ai II 20	15.5	55.3	86.17
Ai II 83	15.1	52.23	86.08
Ai II 97	15.8	54.5	87.12
Bi II 104	15.2	50.87	87.17
Izvor (Control)	13.7	50.31	85.80
F00628G-34 (Control)	12.2	48.63	84.24

CONCLUSIONS

This study highlights the variability obtained on three parameters, namely the protein content, TKW and VM and the importance of the interaction between them on the wheat DH mutated and mutated/recombinant lines produced at NARDI Fundulea.

The results obtained in this investigation confirm the expectation that artificial mutagenesis combined with DH - technology generated simultaneously a large amount of variability regarding TKW, protein content, volumetric mass and fixed in homozygous condition.

During the experiments were selected 8 lines, Ai II 20, Ai II 50, Ai II 72, Ai II 83, Ai II 97, Ai II 109, Ai II 175 and Bi II 104, with higher

values for analyze parameters which could represent a valuable gene source for use in wheat breeding and genetic studies.

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