

Combining ability for the grain wet gluten content in durum wheat

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Abstract

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To determine the gene action and nominate good combiners for the wet gluten content of grain in durum wheat, a diallel cross was performed. Five modern durum wheat varieties were included in the half diallel combination – Victoria (BG), Deni (BG), Superdur (AT), Progress (BG) and Predel (BG). The experiments were conducted in the experimental field of the Field Crops Institute in Chirpan by block method in three replications in the period 2014–2016. The necessary technological analyses were performed in laboratory conditions according to the relevant standard for measuring the wet gluten content. Statistical data processing shows that the dominance and over dominance effects have a very important role in inheritance. Both the additive (GCA) and the non-additive (SCA) gene effects have reliable significance in inheritance of the trait, with the preponderance of the non-additive ones (SCA). Significant combiners that increase the value of the trait and ones that reduce it have been nominated. Two crosses with significant SCA effects: Superdur × Progress and Progress × Predel were identified.

Keywords: durum wheat; wet gluten content; diallel cross; combining ability

Introduction

Wet gluten content in durum wheat grain is a very important technological indicator related to the quality of pasta products. Wet gluten content in grain is directly dependent on genotype, environment, and technology of growing. The correlation with the protein content is always high and positive and indicates interconnections between them. The use of diallel crossing for combining various parent lines provides important information about the gene action in inheritance of quantitative traits. Obtaining systematized information about the gene action of quantitative traits and the combining ability of genotypes is a major means of improving breeding programs related to grain quality. Sprague and Tatum (1942) initially defined combining ability as the relative ability of the genotype to convey the desired change in the progeny. They determine that general combining ability (GCA) is mainly due to additive and additive × additive gene effects, while specific combining ability (SCA) is due to the non-

additive gene effects, i.e. dominance and epistasis. Griffing (1956) shows in his work a successful method of obtaining information about GCA and SCA in the first generations. It is considered that inheritance of the traits in wheat from diallel crosses is of an additive and non-additive type. Akram et al. (2011) and Pansuriya et al. (2014) reveal that both the additive and the non-additive gene effects (dominance and epistasis) have a reliable significance in inheritance of the wet gluten content. The prevalence of non-additive gene effects in inheritance of this trait is reported by some authors (Khodadadi et al., 2012; Pansuriya et al., 2014; Ahmad et al., 2017). While other authors (Akram et al., 2011; Sadeghi et al., 2012) have found that the additive gene effects have greater influence in the manifestation of wet gluten content. Tang et al. (2011) reported that wet gluten content may be used in direct breeding of wheat quality.

The discrepancies in these results are most likely to be due to the differences in the used parents and the environmental conditions, which requires conducting of genetic

analyses for specific parent and growing conditions. The objective of the study is to obtain information about the genetic nature in the manifestation of wet gluten content in durum wheat and to determine the breeding value of the genotypes included in the study.

Materials and Methods

Modern varieties of durum wheat grown in production: Victoria (BG), Deni (BG), Superdur(AT), Progress (BG) and Predel (BG) are crossed in a half diallel design. Parents, F_1 and F_2 hybrids were harvested for 3 years (2014 - 2016), thus providing three generations of F_1 and two of F_2 . The experiments were carried out in the experimental field of the Field Crops Institute in Chirpan, by block method in three replications. Meteorological conditions during the three years of the study are characterized by higher than the multi-annual norm. The first two harvest years of 2014 and 2015 are favorable in terms of soil moisture and rainfall higher than the average perennial. The third harvest year is characterized as the hottest and at the same time with 20% less precipitation. Parents and F_1 were sown in two rows and F_2 in 5 rows. The sowing was conducted in 2 m long rows with 20 cm row spacing and 5 cm between plants. The precursor was peas for green mass and the accepted technology for growing durum wheat was applied. From each replication 20 plants were randomly selected from parents and F_1 and 30 from F_2 . Half of the seeds were used to sow the relevant F_2 generations,

and the other half for technological analysis. The wet gluten content was determined in percentage according to BDS EN ISO 21415-2:2008. The data obtained were statistically processed for combining ability following method 2 model I by Griffing (1956) with Burow & Coors (1993) program for each individual year. From the same data, the degree of dominance was determined by Ognyanova (1975).

Results and Discussion

In Table 1 are presented the mean values of wet gluten content in grain for all tested cases. The variation over the years is in wide range from 27.01 to 38.5. Among the parental with the highest amount of wet gluten in the grain are Superdur variety for 2014, Progress variety for 2015 and Deni variety for 2016. Among the hybrids combinations the highest values have the crosses Superdur \times Progress and Superdur \times Predel. The most favorable for high wet gluten content are the years 2014 and 2016 with higher mean values in the diallel scheme. Reliable genetic diversity has been established in parents and the hybrids combinations. Table 1 contains the relevant indices determining the degree of dominance and the direction (increase or decrease). In F_1 -2014 in hybrid combinations predominates over dominance towards the better parent. In F_1 -2015 all kinds of dominance occurred in the inheritance, in most cases the direction noticed was towards the weaker parent. In F_1 -2016, was found dominance and overdominance towards the negative direction. For the

Table 1. Mean values and indexes of inheritance for wet gluten content in grain (%)

Parents	Code	2014 y.	2015 y.	2016 y.		
Victoria	11	28.3	29.15	31.4		
Deni	22	30.1	29.89	36.2		
Superdur	33	34.36	28.14	33.53		
Progress	44	31.00	32.1	31.03		
Predel	55	34.20	31.67	30.23		
Hybrid combinations		F_1 -2014 y.	F_1 -2015 y.	F_1 -2016 y.	F_2 -2015 y.	F_2 -2016 y.
Victoria x Deni	12	33.83od+	29.11cd+	29.86od-	27.73od-	32.96pd-
Victoria x Superdur	13	31.7i	27.17od-	38.2od+	27.01od-	33.8cd+
Victoria x Progress	14	31.6cd+	30.57i	30.9cd-	28.94cd-	34.7od+
Victoria x Predel	15	33.2pd+	28.76cd-	31.86cd+	27.44od-	29.8cd-
Deni x Superdur	23	33.1i	26.95od-	29.26od-	29.06i	29.86od-
Deni x Progress	24	33.03od+	31.78cd+	29.63od-	30.47i	28.53od-
Deni x Predel	25	35.8od+	30.85i	30.30od-	32.84od+	30.33cd-
Superdur x Progress	34	37.06od+	32.52cd+	31.4od-	31.00pd+	31.13cd-
Superdur x Predel	35	38.5od+	28.95pd-	30.1od-	27.46od-	32.06i
Progress x Predel	45	36.4od+	29.69od-	32.16od+	29.41od-	33.3od+
M \pm m		33.47 \pm 0.71	29.82 \pm 0.44	31.73 \pm 0.64	29.48 \pm 0.46	31.92 \pm 0.54

i – intermediate, cd – complete dominance, pd – partial dominance, od – over dominance, minus – decrease, plus – increase

F₂ generation over the two years indices show that inheritance in the direction towards the weaker parent also prevails. Matuz & Beke (1996) reported negative over dominance in inheritance of this trait. From the results presented, it is evident that basically in inheritance of the wet gluten content in grain predominate complete and over dominance in both directions and there is manifestations of intermediate inheritance. Ahmad et al. (2016) and Patel (2018) also reported for over dominance in both directions in expression of this trait.

The data from the conducted ANOVA are presented in Table 2. The results reveal significant differences between genotypes for all years of study, significant GCA effects and significant SCA effects. Therefore, it was observed significant participation of both the additive gene effects (GCA) and the non-additive gene effects (SCA) in the trait inheritance. This coincides with the results obtained by other authors Akram et al. (2011) and Pansuriya et al. (2014). In Table

Table 2. ANOVA by years for General combining ability (GCA), Specific combining ability (SCA) and relation to variance of GCA and SCA (σ_g^2/σ_s^2) for wet gluten content in grain

Year	Source of variance	Sum of squares	Mean squares	Significant (*, **, ***)
F ₁ -2014	Genotype	314.8	22.486	***
	GCA	178.8	44.705	***
	SCA	135.9	13.599	***
	Error	12.243	0.437	
	σ_g^2/σ_s^2	0.33		
F ₁ -2015	Genotype	126.87	9.06	***
	GCA	76.72	19.18	***
	SCA	50.15	5.01	*
	Error	84.80	3.02	
	σ_g^2/σ_s^2	1.015		
F ₁ -2016	Genotype	262.17	18.76	***
	GCA	39.21	9.80	***
	SCA	223.5	22.35	***
	Error	44.59	1.59	
	σ_g^2/σ_s^2	-0.085		
F ₂ -2015	Genotype	138.81	9.91	***
	GCA	70.99	17.74	***
	SCA	67.82	6.78	**
	Error	69.57	2.48	
	σ_g^2/σ_s^2	0.36		
F ₂ -2016	Genotype	187.26	13.376	***
	GCA	22.71	5.67	*
	SCA	164.55	16.45	***
	Error	93.03	3.32	
	σ_g^2/σ_s^2	-0.11		

* – P ≤ 0.05 ; ** – P ≤ 0.01 ; *** – P ≤ 0.001 ; n.s. – no significant

2 is given the ratio between variance of GCA and SCA – (σ_g^2/σ_s^2). When this ratio is greater than one, a major influence of additive gene effects is assumed, while it is less than one -non-additive gene effects have a greater influence. Our results indicates preponderance of non-additive gene effects over the additive one ($\sigma_g^2/\sigma_s^2 < 1$) in most of the cases (different years and generations). Other authors also report the prevalence of non-additive gene effects (Khodadadi et al., 2012; Pansuriya et al., 2014; Ahmad et al., 2017). Only for the F₁-2015 case this value is above one, which denotes the opposite phenomenon - preponderance of additive gene effects. A similar results were reported by Akram et al. (2011) and Sadeghi et al. (2012). Understanding of the genetic control of the traits is fundamental demand for purposeful management of available genetic variability. The choice of the most suitable breeding method depends mainly on the combining ability behaviour like nature of gene action involved in the control of the trait. The greater influence of non-additive gene effects in the expression of the trait implies effective selection to be made in later segregated generations when these effects are greatly reduced. Sadeghi et al. (2012) also report that an effective selection by this trait has to begin in later segregation generations.

Genetic information regarding wet gluten content contribute significantly in the selection of desirable parents and resulting progenies to develop and execute effective breeding programme to create high quality varieties. Table 3 contains the parental GCA values and the SCA of the crosses. As a good combiner for increasing wet gluten content in grain, with two positive significant GCA values (F1-2015 and F2-2015), is Progress variety. In the other years its values are negative, but only one of them is significant. Superdur and Predel varieties have two significant positive and two significant negative values. Their fifth value is positive, but not significant. In previously investigations was found that Superdur and Predel are good combiners for some agronomic traits. Both varieties increase number of grain per spike and reduce plant height in their hybrids (Dragov & Dechev, 2015; Dragov, 2017). Victoria has three significant negative GCA values. In the other two cases it has two positive values, one of which is significant. Deni variety has only one significant negative value for GCA, which suggests that its role is insignificant in the manifestation of the trait. The use of above mentioned varieties with significant GCA effects in durum wheat breeding can accelerate the creation of materials with high quality that meet the requirements of users. It can be seen that varieties notably change their values for that trait depending on the environmental conditions. On the other hand, this is largely related to the interaction of the genotype with the environment. Thus, it is suggested that breeding for

Table 3. Values for General combining ability (GCA) of parents and Specific combining ability (SCA) of crosses for wet gluten content in grain

Code and genotype	2014y.	2015 y.	2016 y.	2015 y.	2016 y.
Parents / Error of parents	±0.20	±0.53	±0.38	±0.48	±0.56
11 Victoria	-1.99*	-0.71*	0.45*	-1.07*	0.35n.s.
22 Deni	-0.70*	-0.06n.s.	0.14n.s.	0.42 n.s.	0.36n.s.
33 Superdur	1.17*	-1*	0.79*	-0.87*	0.33n.s.
44 Progress	-0.11n.s.	1.4*	-0.61*	1.01*	-0.26n.s.
55 Predel	1.63*	0.38n.s.	-0.79*	0.5*	-0.79*
Hybrid combinations	F ₁ -2014 y.	F ₁ -2015 y.	F ₁ -2016 y.	F ₂ -2015 y.	F ₂ -2016 y.
Crosses /Error of crosses	±0.45	±1.2	±0.87	±1.08	±1.25
12 Victoria x Deni	3.04*	0.07n.s.	-2.47*	-1.1*	0.31n.s.
13 Victoria x Superdur	-0.96*	-0.92n.s.	5.2*	-0.53n.s.	1.17n.s.
14 Victoria x Progress	0.22n.s.	0.05n.s.	-0.68n.s.	-0.49n.s.	2.67*
15 Victoria x Predel	0.08n.s.	-0.72n.s.	0.46n.s.	-1.48*	-1.68*
23 Deni x Superdur	-0.85*	-1.79*	-3.41*	0.02n.s.	-2.79*
24 Deni x Progress	0.36n.s.	0.61n.s.	-1.64*	-0.45n.s.	-3.49*
25 Deni x Predel	1.39*	0.70n.s.	-0.79n.s.	2.42*	-1.15n.s.
34 Superdur x Progress	2.52*	2.3*	-0.5n.s.	1.37*	-0.87n.s.
35 Superdur x Predel	2.21*	-0.24n.s.	-1.64*	-1.66*	0.6n.s.
45 Progress x Predel	1.4*	-1.91*	1.82*	-1.60*	2.43*

* - $P \leq 0.05$; n.s. – (no significant)

this trait in our target environment would be effective only when material is tested over a wide range of growing conditions (years). Estimation of combining ability of the parents is requisite to recognize good hybrid combinations that can produce segregants with superior quality trait.

Considering greater influence of non-additive gene effects in inheritance of the wet gluten content, crosses with significant SCA effects have to be identified. In the crosses (Table 3), there are several significant good combinations concerning SCA effects. Crosses with significant SCA effects are important for improving the trait. The combination Victoria × Deni has three significant values, with only one positive. Victoria × Superdur and Victoria × Predel have one positive and one negative significant value. Deni × Superdur has only negative values that are significant in most cases. We define as the most promising the combinations: Superdur × Progress, Deni × Predel and Progress × Predel, which have the greatest number of significant positive values for SCA and their negative values are no significant. Two of the promising combinations are the result of crossing parents with a high x high GCA. The remaining crosses have no significant SCA effects and are not of interest for the breeding for this trait. The announced crosses with significant SCA effects can be used in the breeding program to improve durum wheat quality. Easier obtaining of transgression forms by the trait wet gluten content in grain is expected from them.

Conclusion

It is evident from the combining ability analysis that the non-additive gene effects (dominance and epistasis) have a major role in inheritance of the wet gluten content in grain. They are accompanied by significant involvement in inheritance of both additive (GCA) and non-additive (SCA) gene effects. It is recommended that the effective selection can begin in the later segregated generations. Good combiners with high GCA effects for enhancing the trait wet gluten content in grain have been nominated. These varieties may be used as donors to improve the grain quality in durum wheat breeding program. Two promising combinations with significant SCA effects by means of which transgressive forms are easy to obtain have been identified.

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