Inheritability of number of fertile tillers per plant in spring barley hybrids

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Abstract

The aim of this study was to clarify the genetic nature of the source material and to determine the type of inheritability of the trait productive tillers per plant for spring barley hybrids. In each of the three years were conducted 30 diallel crosses. As parents were used six accessions of spring barley. The results from the study provided broad information about the genetic control of the trait number of fertile tillers per plant. The trait has been found to be controlled by a genetic system where the dominant action of genes outperforms the additive and is of greater importance for inheriting the trait.

Keywords: spring barley; inheritability; genetic components; number of fertile tillers per plan

INTRODUCTION

The knowledge about genetic structure and way of trait inheritability helps to choose the right strategy for selection of desirable source parental forms for creating hybrids with desired breeding traits (Eshghi & Akhundova, 2009; Ilker et al., 2010; Zhang et al., 2015).

Of particular importance for achieving greater productivity is to study the interconnections between the yield components and yield and to obtain information about their inheritability in the hybrid generations. Oftentimes, the varieties with good phenotypical manifestation of the traits when used as parents show unsatisfactory results for a given trait (Valcheva, 2000; Mersinkov, 2000). In most cases, the most important yield elements are inherited additively to the full dominance or overdominance of the better parent. Some research scientists determine productive tillering as one of the significant traits affecting barley yield (Dimova et al., 2007; Mihova, 2013; Popova, 2018). In their research, Zahour et al. (1987), Chowdhry et al. (1992), Kashif et al. (2003), Eshghi & Akhundova (2009), Vasileva & Marcheva (2016) established that the inheritability of productive tillering is greatly affected by overdominance. Other authors point out that productive tillering is inherited additively (Saini et al., 2013; Adel & Ali, 2013) or dominantly (Usikova, 1975) from the parent with higher value of the trait. Productive tillering is a trait, which vary to a great extent depending on the year conditions (Tapsell & Thomas, 1983; Thomas & Tapsell, 1985; Dimova, 2015; Bonchev, 2017). It is inherited additively (Islam & Darrah, 2005; Eshghi & Akhundova, 2010; Potla et al, 2013; Yadav et al., 2015) or dominantly (Sharma et al., 2002; Rohman et al., 2006; Vasileva, 2014) and overdominantly in direction of the parent having the higher value (Usikova, 1975; Yadav & Sahi, 1985; Puhalskiy et al., 1989; Mersinkov, 2000; Popova, 2018).

The aim of this study was to clarify the genetic nature of the source material and to determine the type of inheritability of the trait productive tillers per plant for spring barley hybrids.

MATERIAL AND METHODS

The study was conducted in the period of 2009-2011 at the Institute of Agriculture in Karnobat, Bulgaria. In a hybridization nursery were carried out 30 diallel crosses. In the diallel crosses were used 6 parent varieties of spring barley - Scarlett, Fink, Barke, Zernogradskij 73, Bitrana and 3717C-60. The parents and hybrids were sown by hand in three replications of 6 rows each, nine seeds per row. At the beginning and at the end of each row were sown four seeds of wheat and two rows of wheat as border rows between the plots. Biometric measurements were taken annually from the parents to determine the trait values.

In accordance with Ognyanova's directions, two parameters were determined in the diallel combination, showing the effect of genetic difference on phenotype (Genchev et al., 1975). The additive dominant relations of the trait were analyzed through the correlation of the two parameters (d/a). In the statistical processing of data were applied analyses of variance and calculus of variations and used software program JMP version 5.0 1a, 2002. The graphic analysis of the trait spike length was built and interpreted according to Mather (1949) and Jinks (1954).

The period of testing covers three years and can be defined as extreme for barley development, where 2009 was characterized with continuous soil drought in April, May and June, 2010 – with more rainfall, especially in May, June and July. The most meteorologically favorable year was the third one in the studied period. (Figures 1 and Figure 2).

RESULTS AND DISCUSSION

The parental components used in the specific diallel combination were contrasting by the studied

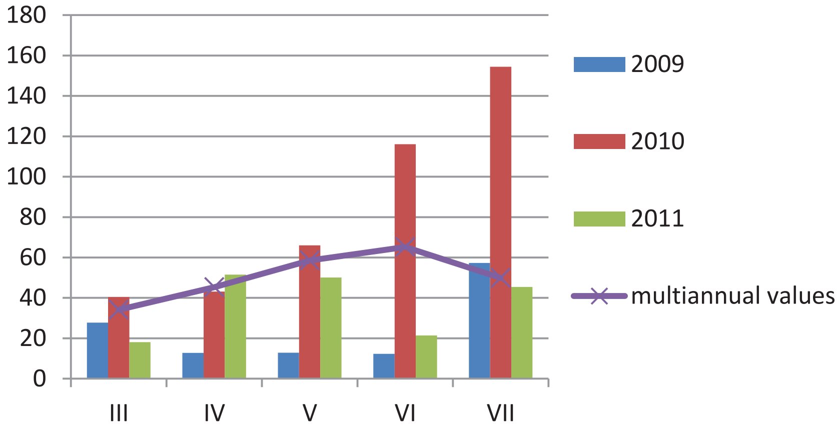


Figure 1. Average amount rainfall during the period

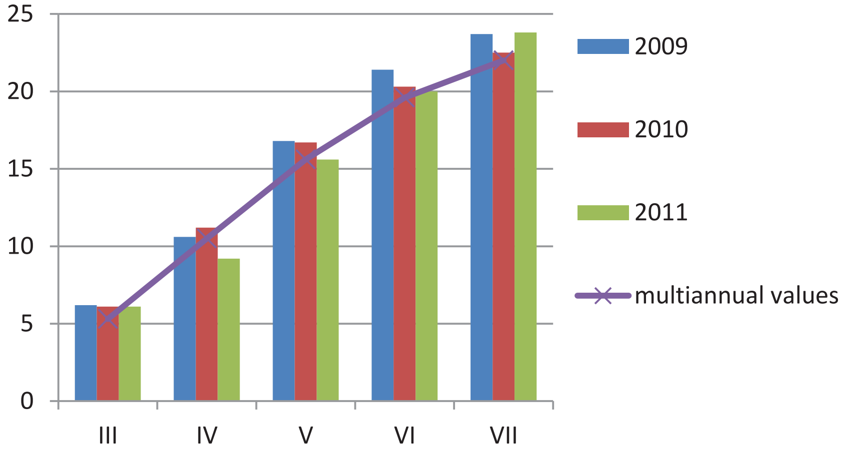


Figure 2. Average monthly temperatures for the period

trait. The parents can be divided into three groups. The first group included varieties Scarlett and Fink. Scarlett maintained a higher number of fertile tillers over the three-year period, whereas the trait in Fink had more significant variation by years. The other varieties used in the diallel combination changed their values of the trait over the years. Varieties Zernogradskij 73, Barke and 3717C-60 had medium manifestation of the trait and belonged in the second group, whereas Bitrana had weak tillering (Table 1).

Table 1. Number of fertile tillers per plant of parents and F1 hybrids

Parents and hybrids	Number of fertile tillers per plant							
	2009 year		2010 year		2011 year		Average of the period	
	number	d/a	number	d/a	number	d/a	number	d/a
Scarlett	5.08		5.05		5.12		5.08	
Fink	4.60		4.04		5.17		4.60	
Barke	4.21		3.52		4.98		4.24	
Zernofradskij 73	4.50		4.30		4.53		4.44	
Bitrana	3.48		3.93		4.50		3.97	
3717C-60	3.60		4.03		4.92		4.18	
Average	**4.25**		**4.15**		**4.87**		**4.42**	
P_1 x P_2	4.69	-0.63	4.49	-0.12	5.15	0.20	4.78	-0.25
P_1 x P_3	4.52	-0.30	4.50	0.32	4.95	-1.43	4.66	0.00
P_1 x P_4	4.77	-0.07	4.50	0.47	4.82	-0.02	4.70	-0.19
P_1 x P_5	4.20	-0.10	4.30	0.34	4.94	0.42	4.48	-0.08
P_1 x P_6	4.53	0.25	4.53	-0.02	4.93	-0.90	4.66	0.07
P_2 x P_3	4.36	-0.24	4.00	0.87	5.08	0.05	4.48	0.33
P_2 x P_4	4.58	0.60	4.33	1.21	4.97	0.37	4.63	1.37
P_2 x P_5	4.40	0.64	3.99	0.04	4.71	-0.37	4.37	0.27
P_2 x P_6	4.12	0.04	3.95	-17.00	5.09	0.36	4.39	0.00
P_3 x P_4	4.37	0.10	4.12	0.59	4.59	-0.73	4.36	0.20
P_3 x P_5	3.74	-0.29	3.61	-0.27	4.76	0.08	4.04	-0.48
P_3 x P_6	3.97	0.21	3.91	0.61	4.96	0.33	4.28	2.33
P_4 x P_5	4.43	0.86	4.16	0.24	4.54	1.67	4.38	0.74
P_4 x P_6	4.53	1.06	4.29	0.93	4.89	0.85	4.57	2.00
P_5 x P_6	3.43	-1.83	3.94	-0.50	4.63	-0.38	4.00	-0.71
Average	**4.31**		**4.17**		**4.87**		**4.45**	
LSD	0.18		0.06		0.11			
Variability of parents and hybrids								
P min	3.48		3.52		4.50		3.97	
P max	5.08		5.05		5.17		5.08	
F_1min	3.43		3.61		4.54		4.00	
F_1 max	4.77		4.53		5.15		4.78	

P_3 x P_6 and P_4 x P_6, where inheritability average for the period showed positive overdominance. Their parents had medium manifestation of the trait, but in the created hybrids, the number of fertile tillers per plant had a value far exceeding the source forms.

Over the studied period, the number of fertile tillers per plant, average for the parental varieties, ranged from 4.15 tillers in 2010 to 4.87 tillers in 2011. The hybrids showed similar results in this trait by years. The lowest tillering average for F_1 was reported in 2010 – 4.17 tillers, and the highest values were in 2011– 4.87 tillers. The variance of number of fertile tillers per plant average for the studied period was greater in the parental varieties (from 3.97 tillers to 5.08 tillers) and lower in the crosses – from 4.00 to 4.78 tillers. Ten of the crosses inherited the trait additively, and three of them (P_1 x P_4, P_1 x P_5 and P_3 x P_5) retained the degree and direction of inheritance in the three years of the study. The hybrids with additive inheritability average for the period changed the type of inheritability by years from additive to partially dominant. With hybrids P_4 x P_5 and P_5 x P_6 the inheritability of trait was incompletely dominant.

Overdominant inheritance was observed in crosses P_2 x P_6, P_4 x P_5 and P_5 x P_6 in each year of the study. There should be a very tentative approach in the breeding selection for hybrid combinations P_2 x P_6 and P_5 x P_6, where parents of weak and medium fertile tillering are used. There the inheritability is overdominant in the direction of low values of the trait.

In cross P_4 x P_5, the inheritability showed positive overdominance in 2011, when the conditions of the year were most favorable. It showed that selection of elite plants can be carried out in the hybrid for higher fertile tillering. Breeding selection finds interest in crosses

The conditions in the studied years led to change in the type of inheritance in the two crosses from incomplete dominance to additive and full dominance. However, it was still possible to select elite plants for greater tillering.

More detailed information about the number of fertile tillers per plant was obtained from the analysis of diallel schedules (Figures 3, 4, 5).

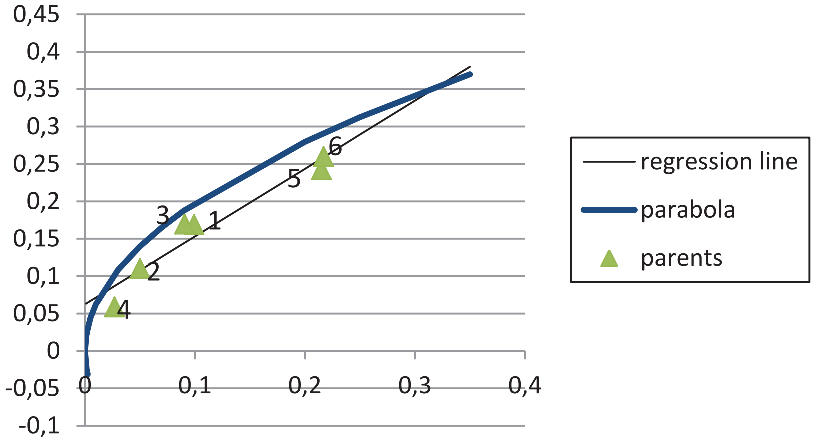
The regression line in the three of the years of the study crossed the Y-axis above the beginning of the coordinate system, which means incomplete dominance in inheriting the trait of number of fertile tillers per plant. In 2009, the parents Fink and Zernogradskij 73 were located at the beginning of the regression line. They had low values of Wr+Vr (Table 2) and high negative correlation (r=-0.76) with the phenotype expressions of the trait. It shows that they had the most dominant genes which determine the number of fertile tillers per plant.

Varieties Scarlett and Barke occupied a medium position on the regression line, which means approximately equal distribution of dominant and recessive genes. On the top end of the regression line are Bitrana and 3717C-60. There the trait was mainly under the control of recessive genes.

In 2010, parents Zernogradskij 73, Fink and Scarlett preserved their position. Varieties Zernogradskij 73 and Fink were at the beginning of the regression line and there the trait was determined by the dominant genes. Variety Scarlett in this year was also in the middle of the line and demonstrated balance between dominant and recessive genes. On the upper end of the regression line was variety Barke and its position showed the presence of recessive genes. The change in the variety position speaks about strong influence of the environmental conditions and there also took part various genetic systems which controlled fertile tillering. Other similar cases in barley were also described by the research scientists Mersinkov (2000), Madic et al. (2006) and Dimova (2015).

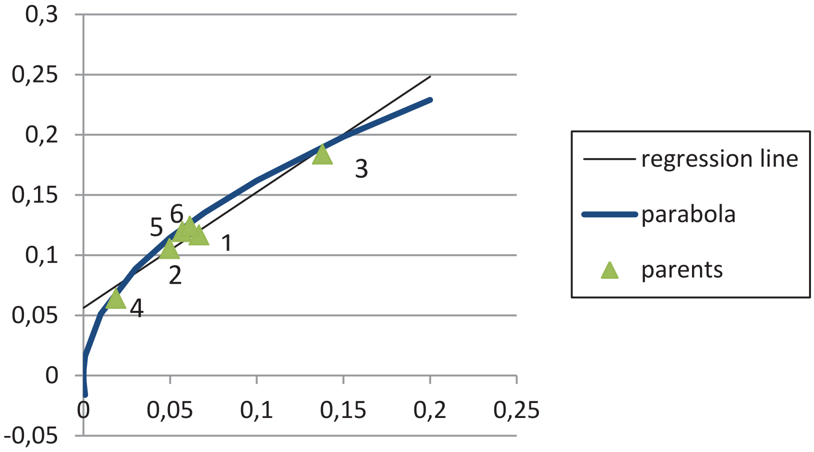
Similar behavior was observed with Bitrana and 3717C-60, which during the first year of the study were located on the upper side of the line, whereas in 2010 they were in the middle. The values of sum Wr+Vr in this year followed the position of the varieties from the diallel schedule (Table 2). A mean negative, unproven correlation between Wr+Vr and the phenotype expressions of the trait was established.

The third year of the study was meteorologically favorable for barley growing. The parental varieties had high values of number of fertile tillers per plant and there was no good differentiation between them. The values of sum Wr+Vr, which also served to rank the presence of dominant genes, were also close. This explained the position of all the varieties at the beginning of the regression line and showed that they had more dominant genes responsible for the manifestation of the trait. The results corresponded to the ones obtained by Madic & Djurovic (1996) and Madic et al., (2006). The lack of correlation in 2011 showed the presence of dominant genes with effect in different directions. Scarlett and Zernogradskij 73 were the parents with highest values of the trait in these years and with lowest sum of Wr+Vr, which



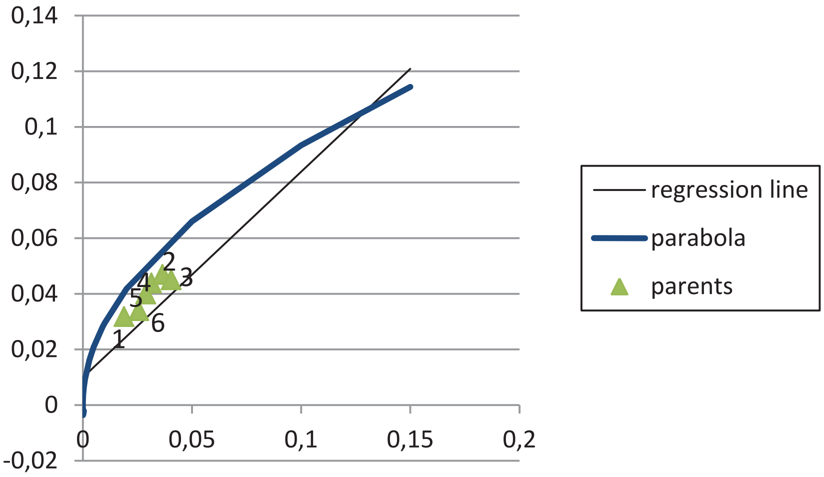
Wr=Vr. 0.908+0.062
1-Scarlett
2-Fink
3-Barke
4-Zernogradskii 73
5-Bitrana
6-3717C-60

Figure 3. Diallel diagram for number of fertile tillers per plant in 2009 year



Wr=Vr. 0.961+0.056
1-Scarlett
2-Fink
3-Barke
4-Zernogradskii 73
5-Bitrana
6-3717C-60

Figure 4. Diallel diagram for number of fertile tillers per plant in 2010 year



Wr=Vr. 0.738+0.0099
1-Scarlett
2-Fink
3-Barke
4-Zernogradskii 73
5-Bitrana
6-3717C-60

Figure 5. Diallel diagram for number of fertile tillers per plant in 2011 year

proved the presence of a high number of dominant genes.

Most parental forms changed their position in the different years of the study. It was reported in literature that under various environmental conditions the trait was determined by the different set of genes (Saulescu, 1970). Bitrana and 3717C-60 were recessive by the trait of fertile tillers per

Table 2. Number of fertile tillers per plant and domminat genes ranking of the parents

№	Varieties	Number of fertile tillers per plant		Domminat genes		
		g	rang	$W_r + V_r$	rang	±r
F_1 – 2009 year						
1.	Scarlett	5.08	1	0.2679	4	
2.	Fink	4.60	2	0.1601	2	
3.	Barke	4.21	4	0.2600	3	
4.	Zernogradskij 73	4.50	3	0.0856	1	
5.	Bitrana	3.48	6	0.4572	5	-0.76
6.	3717C-60	3.60	5	0.4768	6	
	Average for 2009 year	**4.25**		**0.2846**		
F_1 – 2010 year						
1.	Scarlett	5.05	1	0.1834	4	
2.	Fink	4.04	3	0.1550	2	
3.	Barke	3.52	6	0.3218	6	
4.	Zernogradskij 73	4.30	2	0.0827	1	
5.	Bitrana	3.93	5	0.1765	3	-0.49
6.	3717C-60	4.03	4	0.1854	5	
	Average for 2010 year	**4.15**		**0.1841**		
F_1 – 2011 year						
1.	Scarlett	5.12	2	0.0507	1	
2.	Fink	5.17	1	0.0753	4	
3.	Barke	4.98	3	0.0834	5	
4.	Zernogradskij 73	4.53	5	0.0855	6	
5.	Bitrana	4.50	6	0.0688	3	-0.36
6.	3717C-60	4.92	4	0.0596	2	
	Average for 2011 year	**4.87**		**0.0706**		
F_1 – 2009-2011 years						
1.	Scarlett	5.08	1	0.1673	3	
2.	Fink	4.60	2	0.1301	2	
3.	Barke	4.24	4	0.2217	4	
4.	Zernogradskij 73	4.44	3	0.0846	1	
5.	Bitrana	3.97	6	0.2342	5	-0.53
6.	3717C-60	4.18	5	0.2406	6	
	Average for 2009-2011 years	**4.42**		**0.1798**		

Table 3. Genetic components of number of fertile tillers per plant

Genetic components	F_1 2009 year	2010 year	2011 year	Average for the during
Parameters				
D	0.3766±0.0550	0.2593±0.0068	0.0742±0.0250	0.2367±0.0289
F	0.0901±0.0773	0.0450±0.0246	-0.0038±0.0022	0.0438±0.0347
H_1	0.6512±0.0481	0.3964±0.0107	0.1336±0.0028	0.3937±0.0205
H_2	0.2412±0.0463	0.0930±0.0074	0.0906±0.0055	0.1416±0.0197
h^2	0.0081±0.0166	0.00186±0.0010	-0.0072±0.0001	0.00092±0.0059
Traits				
H_1/D	1.729	1.529	1.800	1.686
$\sqrt{}\ H_1/D$	1.315	1.236	1.342	1.298
F_1-P	0.063	0.030	-0.003	0.030
$H_2/4H_1$	0.093	0.059	0.170	0.107
k	0.024	0.038	0.0003	0.021
h^2/H_2	0.034	0.020	-0.079	-0.009
K_d/K_r	1.200	1.151	0.962	1.104
H_1-H_2	0.410	0.303	0.043	0.252
$F^2/\sqrt{}4D(H_1-H_2)$	0.0103	0.0036	0.0001	0.0047
Inheritability H^2	97.27	98.95	86.48	94.23
Inheritability h^2	82.43	90.80	62.92	78.72

plant average for the period of testing. They had the highest values of Wr+Vr and low manifestation of the trait.

In parents Scarlett and Barke was observed approximately the same correlation of dominant and recessive genes. The low values of $r_{(wr+vr)}$ average for the period, even though not statistically proven, gave reasons to accept that in the hybrids of the diallel combination took part genes of opposite effect.

The calculated genetic components of the trait fertile tillers per plant are presented in Table 3. The additive parameter D, which assesses the additive genetic effect in the populations of the diallel combination, had lower values compared to the dominant parameter H_1. It shows that the additive effect of the genes has lesser importance for the variance of the trait. The dominant genetic effect surpassed the additive in the three years of the study and reflected the greater significance of the dominant variance in inheritability. The findings confirmed the results of Madic et al. (2006). The positive sign of parameter F average for the period and in 2009 and 2010 expressed the prevalence of the dominant alleles in the genetic system. At the same time, it had very low values and tended to zero, which speaks of equal proportions of the dominant and recessive alleles. In 2011, F had a negative value and expressed prevalence of the recessive genes.

The average degree of dominance in the whole cross expressed by the correlation H_1/D was 1.686, which shows that in the inheritability of this trait the decisive role was played by the overdominance effects.

The index $\sqrt{}H_1/D$ equals 1.298 and expresses full dominance in each locus. The average degree and direction of dominance expressed by the difference between the mean values of the crosses minus the mean values of the parents (F_1-P) indicates that the dominance was in the direction of decreasing the trait values. The nature of the distribution of dominant and recessive alleles in the parental forms, expressed by the ratio between the dominant parameters $H_2/4H_1$, average for the period was 0.11. Its value was lower than 0.25, which shows uneven distribution of the dominant and recessive alleles in the parents. This was also confirmed by the ratio K_d/K_r, whose value was 1.104 and demonstrated the prevalence of the dominant over recessive alleles.

The analysis of indexes $H_2/4H_1$, H_1-H_2 proved the disproportionate distribution of the dominant and recessive genes in the parents participating in the diallel combination. The values of k и h^2/H_2 did not express the exact number of the genes as there was genetic effect in opposite directions at hand. Ognyanova & Moynova (1971), Mersinkov (2000), Dimova (2015) also established an unrealistically small value of the effective factors and pointed that the reason for that was the fact that dominance was not in one direction.

The index $F^2/\sqrt{4D(H_1-H_2)}$ average for the period and by years had a value of zero, which showed dominance strongly varying by locus. Inheritability in the broad sense H^2 ranged from 86.48 % to 98.95 %, and in the narrow sense h^2 – from 62.92 % to 90.80 %. The obtained high values of the inheritability coefficients in the broad sense pointed to a possibility to conducting an effective selection of genotype by phenotype. Similar results were also obtained by other research scientists for barley and other cereal crops (Yadav et al., 2002; Sandeep et al., 2002; Soylu, 2002; Ismail et al., 2003; Eshghi & Akundova, 2009, Basciftci et al., 2013; Darabad et al., 2021). The established high coefficients of inheritability in the narrow sense are a precondition for high efficiency of selective breeding by this trait in the early segregating generations F_2-F_3 (Erkul et al., 2010; Raikwar, 2015).

CONCLUSIONS

The trait number of fertile tillers per plant is controlled by a genetic system in which the additive-dominant action of genes prevails. Dominant gene action outperforms additive in all three years of study and indicates a predominance of dominant alleles in the genetic system. The appearance of the symptom is determined by one gene or one group of genes, and their dominance is not in one direction. It is possible to effectively select genotype by phenotype by the trait number of fertile tillers in the early segregating generations.

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