

# Genetic and monosomic analysis of spike speltoidy introgressed into bread wheat from *Aegilops speltoides* Tausch

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## INTRODUCTION

The spelta type of spike found in some hexaploid wheats (AABBDD,  $2n=42$ ) is a complex of morphological traits characterized by glumes keeledness, rachis toughness, low spike density and poor threshing. This genetic complex is clearly expressed in the species *Triticum spelta* L. and now considered to be controlled by locus *Q* situated in 5A chromosome (Mac Gene, 2003)<sup>1</sup>. The early genetic investigations of speltoidy were carried out in the first 20 years of the 20<sup>th</sup> century. At that time the Russian geneticist Yu. Philipchenko studied the trait in detail in crosses of *T. spelta* with different bread wheat genotypes<sup>2</sup>. He was the first who worked with this trait as a quantitative one. He proved the gene of *T. spelta* to be dominant to the free-threshing type of bread wheat with the main effect on spike length. Also he showed that this gene manifests early in plant development, 37-40 days after sowing.

Discovery of the orthologous series of genes in cereal genomes suggested the existence of homoeoallelic genes in the genomes of wild relatives of the hexaploid species. The aim of this work is to investigate the possibility of the existence of a homoeologous gene for speltoid spike in a bread wheat line after introgression from *Aegilops speltoides* Tausch.

## MATERIALS AND METHODS

The "Arsenal" collection of bread wheat which includes the lines with different introgressions from the winter accession of *Aegilops speltoides* Tausch was developed on the base of spring awnless cultivar 'Rodina'<sup>3</sup>. The line 84/98w from this collection was kindly provided by Dr. Inna Lapochkina (Institute of Agriculture of Non-Chernozem Regions of Russia, Nemchinovka, Moscow Region). It is characterized with the winter type of development and has awned and speltoid spike (Fig.1). Presence of these traits indicates a possible introgression from the *Ae. speltoides* genome into chromosome 5A of wheat. Monosomic lines of cv. Saratovskaya 29 (S29) on chromosomes of 5th homoeologous group, as well as the spring awnless sample of *T. spelta* (k-24724, VIR, S-Petersburg), were used for monosomic and genetic analysis. Investigations involving F<sub>1</sub>, F<sub>2</sub> and F<sub>3</sub> families were carried out in a green-house during two seasons. Conventional statistical procedures were used for evaluation of quantitative data.

## RESULTS AND DISCUSSION

The spikes of the maternal cultivar, Rodina, and paternal sample of *Ae. speltoides* and introgression line 84/98<sup>w</sup> are presented on Fig.1. It may be supposed that such morphological traits as speltoidy, awnedness as well as the winter habit of the line are the result of introgression into the long arm of chromosome 5A. It is known that it carries the marker genes *Q*, *B1* and *Vrn-A1*, responsible for these traits<sup>1</sup>.



Fig.1. Spikes of cv. Rodina, *Ae. speltoides*, (k-389) and introgression line 84/98<sup>w</sup>, correspondingly

For checking this supposition, F<sub>1</sub> monosomic analysis was carried out for the line 84/98<sup>w</sup>. It was crossed with the lines mono 5A, mono 5B and mono 5D of spring early cultivar S29. As could be seen from Table 1, only monosomic F<sub>1</sub> hybrids involving chromosome 5A delayed the flowering date compared to the other hybrids, monosomic lines and S29. It is known that cv. S29 carries two genes for spring habit, *Vrn-A1* and *Vrn-B1* (O. I. Maystrenko, unpublished results). F<sub>1</sub> hybrid mono5A S29 × 84/98<sup>w</sup> retains only the gene *Vrn-B1*, situated on chromosome 5B. This gene is weaker in its manifestation than the gene *Vrn-A1* on chromosome 5A and delays the flowering. Therefore, the line 84/98<sup>w</sup> carries the introgression in chromosome 5A.

At the same time it can be seen from Table 1 that the line 84/98<sup>w</sup> has a longer spike than the maternal cultivar. F<sub>1</sub> hybrids had significantly longer spikes and more

spikelets than S29 and the monosomic lines. Therefore, the introgressed fragment also contains the gene influencing the form of spike. It causes spike elongation and an increased number of spikelets in both hemi- and heterozygous states. Its effect is similar to the one found by Yu. Filipchenko for the gene from *T. spelta*.

In order to investigate the interaction of this factor with the known gene *Q*, situated on chromosome 5A a cross with the accession of *T. spelta* was made. Measurement data of quantitative characteristics in F<sub>1</sub> were processed using two-way ANOVA. It was found that the spikes of F<sub>1</sub> hybrids significantly exceeded the parental forms for such spike parameters as spike length and number of spikelets (Table 2). Length of rachis segment and density index (number of spikelets on 10 cm of spike) did not differ significantly from the parental forms. All of them were late ripening and poor threshing. The latter characteristic was inherited from *T. spelta*. Such plants were named superspeltoids. In F<sub>2</sub>, positive and negative transgressions for all spike traits were observed, which may be explained by the influence of several genes and their alleles in controlling the traits. At the same time, the plants with the superspeltoid type of spike segregated again (Fig.2, spike 3). They were also late ripening and had poorly threshed spikes. Study of F<sub>3</sub> and F<sub>4</sub> families grown from such plants again showed segregation of speltoid and superspeltoid genotypes. Therefore, the regular segregation for two phenotypes in the pedigree of such genotypes was observed which

might suggest a constant heterozygosis of the *Q* locus and the gene introgressed from *Ae. speltooides* on chromosome 5A of hybrids. The two genes manifest as homoeoallelic and interact additively<sup>4</sup>. We suggest to give the symbol *Q<sup>s</sup>* to the new gene introgressed from *Ae. speltooides*. The main peculiarity in manifestation of this new gene consists in free-threshing character of the line 84/98<sup>w</sup> – the trait which differs it from *T. spelta*.

## REFERENCES

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Table 1. Spike parameters and flowering date of S29 monosomic lines and their hybrids F<sub>1</sub> with introgression line 84/98w<sup>†</sup>

Genotypes	Spike length	Number of spikelets	Days till flowering
cv. Rodina	7,4±0,4	17,1±1,4	40-43
S29	6,0±0,3	10,5±1,0	50-52
84/98w	10,8 ± 0,9	16,1 ± 2,6	Needs vernalization
Mono 5A C29	7,4 ± 0,4	10,3 ± 0,4	55-60
F1 mono 5A C29 X 84/98w	9,7 ± 1,3 *	15,3 ± 1,9 **	90-92
Mono 5B C29	7,1 ± 0,4	11,7 ± 0,7	47-51
F1 mono 5B C29 X 84/98w	10,6 ± 1,0 ***	15,2 ± 0,7 ***	45-53
Mono 5D C29	6,5 ± 0,4	12,1 ± 0,6	47-52
F1 mono 5D C29 X 84/98w	9,8 ± 0,7 ***	16,9 ± 2,1 ***	47-52

<sup>†</sup>Hybrid were compared to the appropriate monosomic line

Table 2. Spike parameters of speltoid forms and their hybrids F<sub>1</sub> and F<sub>2</sub> (data of 2003 and 2004 years)

Genotypes	Spike characteristics			
	Length, cm	Number of spikelets	Length of rachis segment, mm	Index of compactness
<i>T. spelta</i> (k-24724)	11,5	15,1	6,65	13,2
Line 84/98w	10,7	14,9	6,40	14,0
F1 84/98w × <i>T. spelta</i> L.	16,4**	22,4**	6,40	13,7
F <sub>crit</sub>	5,02			
F	163,9	130,1	0,93	3,0
LSD <sub>0,01</sub>	1,5	2,4	0,95	1,4
F <sub>2</sub> (range)	7,0-20,0	13-30	3-7	11,6-27,8

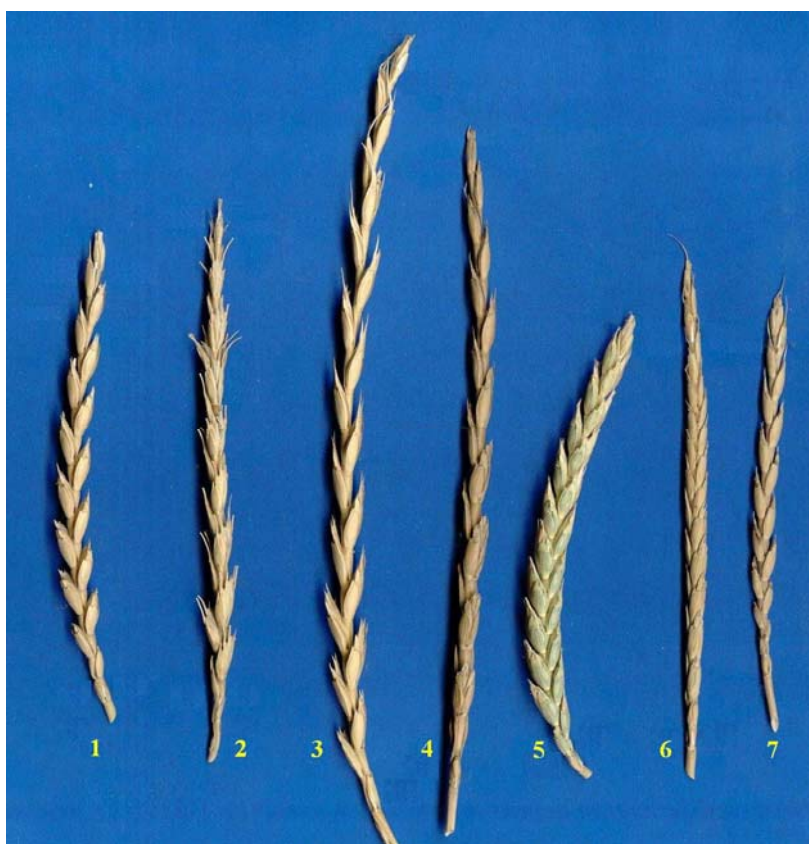


Fig.2. Spikes of *T. spelta* (1), line 84/98<sup>w</sup> (2, awns cut) and F<sub>2</sub> plants (3-7) obtained from the cross between them