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MORPHO-ANATOMICAL ANALYSIS OF SPIKE OF WHEAT GENOTYPES

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Abstract

The goal of the paper is to find, by means of an analysis of morpho-anatomical characteristics of the spike of tetraploid and hexaploid wheat genotypes, characteristics which most strongly influence the differences in yield. The hexaploid genotypes have a significantly longer spike, with a greater number and mass of grain/spike. For both groups, a normal distribution of the number and mass of grain/spikelet of a main shoot spike is notified. An analysis shows that the hexaploid genotypes have a greater cross section rachis area, and a greater number of the smaller vascular bundles, in comparison to the tetraploid ones.

Key words:
wheat, spike, morpho-anatomical analysis

1. INTRODUCTION

In different wheat cultivars, the total contribution of nonleaf green organs, including spikes and peduncles, accounts for about 40–50% of grain mass per spike, which is higher than the total contribution of the flag leaves and penultimate leaf blades [23, 1, 24]. In wheat, all parts of the spike, such as the awn, glume, lemma, palea, pericarp, and even peduncle, are capable of photosynthetic CO_2 fixation, and a considerable portion of grain mass derives from the photosynthesis of these organs [6, 18, 24]. Results of [13] suggested that awns play a dominant role in contributing to large grains and a high grain yield in awned wheat cultivars, particularly during the grain-filling stages.

To what extent will the spike realize its genetic potential depends on genetic factors and a number of physiological and biochemical processes both in the spike itself and in the whole plant. Besides by these factors, the yield is strongly influenced by environmental factors [20, 21]. The number of formed flowers per spike is higher than the number of formed grain [7]. One possible way how to affect assimilate distribution is to increase grain weight through increasing grain number [19, 8,]. Besides all other factors, flower formation is affected by the presence of adequate vascular tissue [12]. Analysing the twenty-six winter wheat varieties of different earliness and stem height [16] concluded that under conditions favourable for both a high rate of assimilate production and high sink capacity, the number and size of vascular bundles, and especially the phloem cross-sectional area, limit wheat productivity.

The goal of the paper is to find, by means of an analysis of morpho-anatomical characteristics of the spike of two tetraploid and two hexaploid wheat genotypes, those characteristics which most strongly influence the differences in final yield.

2. MATERIAL AND METHODS

The morpho-anatomical analysis of the main shoot was done in two tetraploid (NSD 3/93 and Novinka) and two hexaploid (NS032 and NSP11) wheat genotypes. The experiment was conducted in field conditions, applying random block system with three replications, with planting density of 650-700 seedlings/m^2. The main shoot spikes were sampled during physiological maturity for the morphological analysis of the spike. For the anatomical analysis of the rachis, the sampling was done 10 days before full physiological maturity. For both analyses the sample was 30 spikes per genotype. Cross sections of the rachis, 20 μm thick, were made with Leica CM 1850 cryostat. Sections were observed and measurements made using Image Analyzing System Motic 2000 and included cross sections made at the 2nd, 8th and 13th internodes. The following characteristics were analysed: spike length, mass and number of grains per spike, mass and number of grains per spikelet, area of the cross section of the rachis, as well as number, height and width of central vascular bundles. The data were statistically processed using STATISTICA for WINDOWS version 8.0. The significance of differences in mean values of measured parameters was determined using Duncan's test, between the genotypes of the same ploidity level (means marked with the same letter do not differ) and t-test, between the genotypes that differ in ploidity level (* – significant for 0.05% and ** – significant for 0.01%).

3. RESULTS AND DISCUSSION

Yield is influenced by adequate production of photosynthetic assimilates and by the adequate capacity of the acceptor organ to accept products of photosynthesis. As the source and the acceptor of assimilates are affected by the effects of feedback, it is often difficult to determine whether it is the source or the acceptor that limits the yield in a particular case [25]. In our research, a significantly longer spike, with greater number and mass of grain/spike was found in the hexaploid genotypes (Table 1). Larger biomass, number of spikes and larger grain yield per plant in hexaploid wheat in comparison with tetraploids were found by [9].

Our results show that with the hexaploids the number of grains per spike is a more variable characteristic than grain mass or spike length, whereas with the tetraploids it is grain mass/spike which is a more variable characteristic (Table 1). The number of grains per unit area and the mass of individual grains are considered to be two main factors of yield [22]. Research has proved that the number of grains is a characteristic which has a stronger effect on the variation in grain yield, whereas the mass of grain is a more stable characteristic [10, 21]. During the period after flowering, the grain yield of wheat is either limited by the acceptor or co-limited by both the source and the acceptor, but is never limited by the source of assimilates [22].

Table 1. The spike morphological characteristics of wheat genotypes *

Genotype		Spike length (cm)		Grain number/spike		Grain mass/spike (g)	
		$\bar{X}$ ±Se (CV%)		$\bar{X}$ ±Se (CV%)		$\bar{X}$ ±Se (CV%)	
T	NSD3/93	6.5 ± 0.1 (2.3)	a	29.1± 0.2 (1.4)	a	1.2 ± 0.1 (12.2)	a
	Novinka	6.1 ± 0.0 (0.5)	b	30.3 ± 0.6 (3.9)	a	1.3 ± 0.0 (4.6)	a
$\bar{X}$		6.3 ± 0.2		29.7 ± 1.6		1.25 ± 0.3	
H	NS 032	8.6 ± 0.1 (0.3)	a	41.6 ±1.1 (2.4)	a	1.5 ± 0.0 (0.1)	a
	NSP 11	8.1 ± 0.1 (0.2)	b	39.3 ± 0.7 (1.4)	b	1.8 ± 0.0 (0.1)	b
$\bar{X}$		8.3 ± 0.2		40.4 ± 1.6		1.6 ± 0.1	
t- test		*		*		*	

* T-(tetraploid), H-(hexaploid), $\bar{X}$ (means), Se (standard errors) and CV (coefficients of variation %)

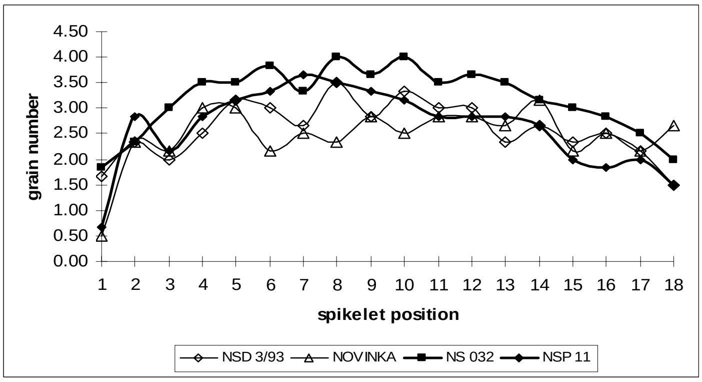

Figure 1. Distribution of grain number/spikelet for tetraploid and hexaploid genotypes

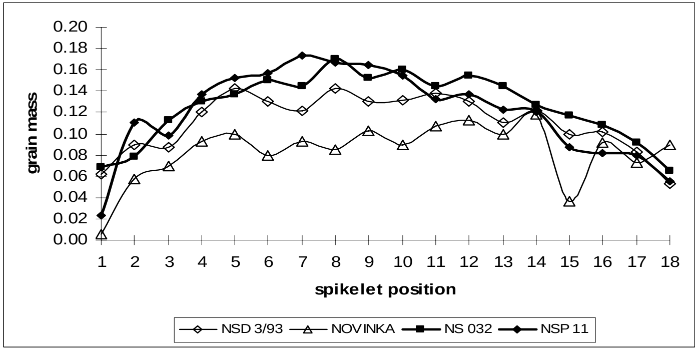

Figure 2. Distribution of grain mass/spikelet for tetraploid and hexaploid genotypes

The analysis of the number and mass of grain/spike of the main shoot in different positions in the spike shows greater variability and dispersion of these parameters in the tetraploid genotypes than in the hexaploid genotypes. In both groups these values rise from the basal spikelet (1st) to the more central ones, so they are highest from the 8th spikelet, and then they fall as we progress towards the 18th spikelet (Fig. 1, 2).

Miralles and Slafer [14] indicate that the mass of basal grains (grain next to the rachis) in central spikelets of the spike is larger than the mass of grains found in the same position in apical or basal spikelets. Similar findings are reported by [3], grains from the lower and middle section of the spike and the proximal floret positions were heavier than those from the upper spike section and the distal floret positions. The values for the number of grain/spike range from 0.5 (1st spikelet – Novinka) to 4.0 (8th spikelet – NS 0.32) grains, and for the grain mass from 0.005g (1st spikelet – Novinka) to 0.173g (7th spikelet – NSP 11). Hexaploid genotypes have a greater number and mass of grains in almost all examined positions of the spikelet (Fig. 1, 2). Variability of grain mass in wheat is a result of the interaction between the potential to gather nutrients and the realization of this potential [11]. To a large extent, grain mass also depends on the speed and duration of the grain-filling period, as well as on the combination of these factors [2, 17, 4, 22, 15].

Significant differences between tetraploid and hexaploid genotypes were found in cross section rachis area for 2nd, 8th and 13th internodes level (Table 2, 3 and 4). Higher values were obtained in hexaploids. The values for number, height and width of vascular bundles of tetraploid genotypes were similar to the values of hexaploid genotypes for all internode levels.

Table 2. The anatomical 2nd internode rachis characteristics of wheat genotypes

		2nd internode							
	genotype	cross section rachis area ($\mu m^{2}*10^{4}$)		number of vascular bundles		height of vascular bundles (μm)		width of vascular bundles (μm)	
		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)	
T	NSD 3/93	213±18.0 (30.5)	a	17.1±1.2 (12.2)	b	176.4±2.9 (2.9)	a	151.9±2.2 (2.5)	a
	Novinka	190±6.1 (9.6)	a	23.3±0.5 (3.8)	a	172.2±5.7 (5.7)	a	150.5±5.9 (6.7)	a
	$\overline{X}$	201.5 ± 14.0		20.2 ± 0.9		174.3 ± 4.1		151.2 ± 5.2	
H	NS 032	315±31.2 (38.3)	a	21.8±0.3 (2.3)	a	174.7±6.1 (6.1)	a	160.9±8.7 (9.3)	a
	NSP 11	337±22.4 (25.7)	a	22.5±0.6 (4.9)	a	176.4±1.0 (1.0)	a	162.0±2.5 (2.6)	a
	$\overline{X}$	326.0 ± 15.6		22.1 ± 0.5		175.5± 2.1		161.4 ± 3.5	
t- test		*		ns		ns		ns	

Table 3. The anatomical 8th internode rachis characteristics of wheat genotypes

		8th internode							
	genotype	cross section rachis area ($\mu m^{2}*10^{4}$)		number of vascular bundles		height of vascular bundles (μm)		width of vascular bundles (μm)	
		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)	
T	NSD 3/93	105±5.7 (21.1)	a	12.6±0.7 (10.3)	b	166.4±4.5 (4.6)	a	150.0±2.0 (2.3)	a
	Novinka	112±6.3 (17.2)	a	17.1±0.9 (9.3)	a	159.8±7.9 (8.5)	a	134.4±7.9 (10.2)	b
	$\overline{X}$	108.5 ± 12.9		14.8 ± 0.7		163.1± 3.4		142.2 ± 3.6	
H	NS 032	199±21.0 (29.1)	b	15.0±0.3 (4.0)	a	163.9±7.6 (7.9)	a	135.4±3.7 (4.6)	b
	NSP 11	247±7.1 (17.3)	a	15.0±0.8 (8.6)	a	169.5±6.9 (7.0)	a	150.9±5.1 (5.8)	a
	$\overline{X}$	223 ± 8.4		15.0 ± 0.5		166.7 ± 3.4		143.1 ± 3.2	
t- test		**		ns		ns		ns	

The mass and volume of mature grain are highly correlated with the diameter of vascular bundles in the terminal internode [17]. The increase in the participation of assimilates which are transported to the spike is related to the adequate increase of phloem area, through which the assimilates are transported [6]. The variation in the development of the vascular system of the terminal internode affects the variation in the development of the seed. Pande et al. [17] think that these two factors are genetically related and that this is why wide variation of the vascular system of the terminal internode would be used to further increase the grain mass.

Table 4. The anatomical 13th internode rachis characteristics of wheat genotypes

		13th internode							
	genotype	cross section rachis area ($\mu m^{2}*10^{4}$)		number of vascular bundles		height of vascular bundles (μm)		width of vascular bundles (μm)	
		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)		$\overline{X}$ ±Se (CV%)	
T	NSD 3/93	84.0±6.4 (29.1)	a	7.4±0.6 (13.5)	b	162.5±2.7 (2.8)	a	144.5±4.4 (5.3)	a
	Novinka	62.0±1.5 (7.3)	b	10.7±0.2 (3.7)	a	148.6±6.8 (7.9)	b	130.2±7.8 (10.4)	a
	$\overline{X}$	73.0 ± 11.9		9.0 ± 0.5		155.5 ± 6.6		137.3 ± 3.4	
H	NS 032	113±7.5 (18.9)	b	8.9±0.2 (3.4)	a	158.3±3.0 (3.3)	a	135.5±6.8 (8.7)	a
	NSP 11	159±7.1 (31.1)	a	8.6±0.5 (9.3)	a	154.1±3.1 (4.1)	a	138.1±1.7 (2.2)	a
	$\overline{X}$	136 ± 27.2		8.7 ± 0.3		156.2 ± 1.8		136.8 ± 2.2	
t- test		**		ns		ns		ns	

The results of this paper confirm the findings from the literature about the longer spike, larger number and mass of grain/spike of hexaploid genotypes. Higher variability and dispersion of the number and mass of grain/spikelet of the main shoot in different positions in the spike were found in the tetraploid genotypes. The largest number and mass of grain per spikelet are detected in central spikelets in both groups. The analysis of the cross section of the rachis of tetraploid and hexaploid genotypes shows that significant differences exist only in the area of cross section of the 2nd, 8th and 13th internodes. The number and dimensions of central bundles of tetraploid and hexaploid wheat genotypes do not differ significantly. An analysis of the number and area of all vascular bundles, as well as the share of hlorenchyma in the peripheral parts of the rachis at individual levels of the rachis, will give more complete data in the anatomical analysis of the rachis.

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