Genetic analysis of glume colour in common wheat cultivars from the former USSR

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Summary

Genotypes for the glume colour character have been studied in 27 cultivars of common wheat (Triticum aestivum L.) originated from old landraces, and 1 specimen of T. petrovavlovskii Udcz. et Migusch. by means of analysis of the F2 populations.

The following tester lines have been used: white-glumed ‘Novosibirskaya 67’, ‘Diamant’ I, and ‘Federation’, carrying the Rg1 gene alone; lines RL5405 and near-isogenic ‘Saratovskaya 29’ × 5 (T. turgidum ssp. Zhuk./T. tauschii (Coss.) Schmal.), carrying Rg2; line (1A ‘CS’ × ‘Strela’) with Rg3.

The red glume colour in 21 cultivars of tritium aestivum and in the accession of T. petrovavlovskii has been shown to be determined by the single gene Rg1, located on chromosome 1B. Five cultivars carrying the gene Rg3 for red glumes on chromosome 1A have been revealed. The cultivars ‘Zhniia’ and ‘Iskra’ carry the gene Rg3 alone. The red glume colour in the cultivars ‘Milturum 321’, ‘Milturum 2078’, ‘Sredneural’skaya’ is controlled by two genes, Rg1 and Rg3. In two common wheat cultivars, ‘Sarrubra’ and ‘Krasnoyarskaya 1103’ the red glume colour is determined by Rg1, inherited from local populations (‘Turka’ and ‘Kubanka’ respectively) of tetraploid wheat T. durum Desf. var. hordeiforme Host. Wide occurrence of the Rg1 gene in common wheat has been confirmed. On the contrary, none of the investigated varieties carries the gene Rg2.

Introduction

Information on the genetic diversity of parental forms and manifestation of their commercial and morphological features is of paramount importance for breeders. Glume colour is one of such characters in wheat. It may be white, red, or black. The red colour of glumes varies in intensity from pale pink to reddish-brown (Vavilov, 1962).

In most common wheat cultivars the red colour of glumes is controlled by a single dominant gene (Unr. 1950; Fletcher & McIntosh, 1972; Aliev & Musayev, 1981; Zeven, 1988). It has been reported by several authors that the red glume colour in hexaploid wheats is controlled by two genes (Vavilov, 1962, Filipchenko, 1979). The digenic mode of inheritance of the character in some Swedish cultivars of common wheat has also been noticed by Nilsson-Ehle (1909, cited in Zeven, 1983).

The gene Rg1, determining the red glume colour, is located on chromosome 1B (Unr., 1950). Another gene for glume colour, Rg2, has been found in T. tauschii (Coss.) Schmal., the donor of D genome of common wheat (Rowland & Kerber, 1971). By means of ditelosomic analysis the genes Rg1 and Rg2 have been demonstrated to be located on the short arm of chromosome 1B and the long arm of chromosome 1D respectively (Fletcher & McIntosh, 1972; Payne et al., 1986; Rowland & Kerber, 1974). Jones et al. (1990) has attributed Rg2 to the short arm of chromosome 1D. Yelokhina (1989) has investigated F2 hybrids from crosses of a ‘Milturum 553’ monosomic series with white-glumed ‘Irtyshanka 10’ and demonstrated that the red glume colour of the cultivar ‘Milturum 553’ is
controlled by two genes located on chromosomes 1B and 1A. Chromosome 1AS has been shown to carry the gene Bg, controlling the black colour of glumes and tightly linked with the gene Hg (hairy glume) (Vavilov, 1962; Sears, unpublished data cited in McIntosh, 1988; Law & Chapman, 1974; Panin & Netsvetaev, 1986). Presence of two genes for red glumes on chromosomes 1B and 1A has been confirmed by monosomic analysis of an F2 population of the cultivar ‘Strela’ done by O.I. Maystrenko (unpublished data). The novel gene, located on 1A, has been designated as Rg3. Ditosomic analysis has confirmed Rg3 to the short arm of chromosome 1A. So the red colour of glumes is controlled by three dominant genes, Rgl, Rg2, and Rg3, located on the short arms of chromosomes 1B, 1D, and 1A, respectively.

Presence of genes inhibiting the red colour of glumes on chromosomes 3A and 7B has been demonstrated by Bhowal & Jha (1969), Goud & Sadananda (1978).

*Triticum petropavlovskyi* Udacz. et Migusch., a new wheat species, discovered in China in the 50s, has red glumes. It is closely related to species with ABD genomes. The collection of the Vavilov All-Russian Plant Breeding Institute (St. Petersburg) contains several accessions of *T. petropavlovskyi*, which have not yet come under the scrutiny of genetics (Dorofeev et al., 1987). Maystrenko et al. (1997) have performed a genetic study and comparison between the hexaploid species *T. petropavlovskyi* and the hexaploid species *T. aestivum*. They have shown that *T. petropavlovskyi* bears at least 13 dominant genes controlling morphological and physiological traits and determining regular bivalent chromosome conjugation. These dominant genes are allelic, have identical functions in both species, and occur on the same chromosomes in each of the three genomes: A, B and D. The gene for elongated glumes, E22, specific for *T. petropavlovskyi*, seems to have come into being as a gene mutation. E2 is not allelic to Egl (P) of *Triticum polonicum* L. and does not occur on chromosome 7AL. On the ground of their own data, the authors consider *T. petropavlovskyi* as a novel group of hexaploid wheats rather than a species in its own right. They attribute E2 to mass morphological genes, like Q, C and S1 (Morris & Sears, 1967).

The objective of the present study was to investigate inheritance and occurrence of Rg genes in modern and old local cultivars of *T. aestivum* and in *T. petropavlovskyi*.

### Materials and methods

#### Cultivars


#### Tester lines

The following lines were used as testers:

2. ‘Diamant’ I (‘D’). Carries Rgl on chromosome 1B. Genotype Rg1Rg1rg2rg2rg3rg3 (Aliev & Musayev, 1981).
3. ‘Federation’ I (‘F’). Carries Rgl on chromosome 1B. Genotype Rg1Rg1rg2rg2rg3rg3 (Ukrain, 1950).
4. RL5405. A synthetic hexaploid (2n = 42 = AABB-DD), obtained by combining *Triticum timopheevii* (T. tauschii) (i:s29 Rg2). The near-isogenic line i:s29 Rg2 had been developed by Maystrenko et al. (1996) by back-crossing of ‘Saratovskaya 29’ with the