

## Analysis of the Distribution of *Triticum timopheevii* Zhuk. Genetic Material in Common Wheat Varieties (*Triticum aestivum* L.)

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**Abstract**—The database of the world gene pool of wheat was scanned by pedigree and the participation of genetic material from *T. timopheevii* in the creation of 3088 varieties of common wheat was established. The spatial and temporal dynamics of the propagation of these varieties was studied. Using the analysis of pedigrees, a diversity of *T. timopheevii* donors was studied. The specificity of donors of the genetic material *T. timopheevii* for the regions of wheat breeding was established. The main source of resistance genes for most varieties is accession D-357-1 from the Georgian variety-population of Zanduri. This significantly reduces the diversity of the genetic material of *T. timopheevii* used in wheat breeding. In 369 varieties and 184 lines, the genes for resistance to pathogens from *T. timopheevii* were identified. The genes of *T. timopheevii* are distributed mainly in winter varieties, as well as spring varieties sown in autumn. The value of donors as sources of *T. timopheevii* genes is ambiguous, despite the fact that most of them come from the same D-357-1 accession. The *Sr36* gene is most commonly found in the United States, Western Europe, and Australia; it was transferred from the Wisconsin-245 line through Arthur or TP-114-1965a. The *Pm6* gene is distributed in Western Europe; it was transferred from the pre-breeding line Wisconsin 245/5\*Cappelle-Desprez//Hybrid-46/Cappelle Desprez. The gene *Lr18* is more common in the United States; it was transmitted by the Blueboy or Vogel 5 varieties from the Coker-55-9 line. The extremely limited set of genes for resistance to pathogens from *T. timopheevii* used in commercial varieties and the specificity of their geographical distribution are possibly associated with the uniqueness of the G subgenome and plasmon in this species, its low potential for plasticity, and tolerance to drought. In addition, the imperfection of the methods of pre-breeding and recombination breeding prevents the elimination in translocation of close linkage of target genes with undesirable ones.

**Keywords:** wheat, variety genealogical profiles, donors, *T. timopheevii*, geographical distributions, temporal dynamics

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### INTRODUCTION

The modern wheat breeding sharply needs new genes responsible for the resistance to different diseases. In the last 70 years the genetic material of *T. timopheevii*, which contains resistance genes to rust, powdery mildew, and some other diseases, was transferred into wheat in order to protect it against pathogenic fungi.

*Triticum timopheevii* Zhuk. ( $2n = 4x = 28$ , GGA<sup>t</sup>A<sup>t</sup>) was identified by P.M. Zhukovsky in the spring landrace Zanduri in Georgia. Nowadays, this variety is not cultivated anymore [1]. The Zanduri wheat was formed in the humid and moderately cool climate zone 400–800 above sea level in Western Georgia [2]. It is believed that in this zone the selection for the high resistance to three types of rust (leaf, stem, and yellow rust), powdery mildew, and some other pathogens

took place. This seems promising for use in practical wheat breeding [1, 3].

Apart from the *Triticum timopheevii* (Zuk.) Zhuk., the *Timopheevii* A. Filat. et Dorof. section involves *T. araraticum* Jakubz. ( $2n = 4x = 28$ , GGAA), *T. militinae* Zhuk. et Migush ( $2n = 4x = 28$ , A<sup>b</sup>A<sup>b</sup>GG), and *T. zhukovskyi* Menabde et Eriezjan. ( $2n = 6x$ , genome GGA<sup>t</sup>A<sup>t</sup>AmAm). First of all, all these species differ from other representatives of the *Triticum* genus in the GG subgenome and a unique plasmon (genome definition according to [4]).

Wheats of the *Timopheevii* group were used several times in crosses with other species in order to transfer the immunity genes. Presently, in the wheat genome of the *Timopheevii* group, the genes controlling resistance to stem rust are registered, *Sr36* (2BS), *Sr37* (4BL), and *Sr40* (2BS); to leaf rust, *Lr18* (5BL), *Lr50* (2BL), *LrTt1* (2A), and *LrTt2* (5BL); to powdery mil-

dew, *Pm6* (2B), *Pm27* (6B), *Pm37* (7AL), and *MIAG12* (7AL); and to winter wheat leaf blotch, *SnbTM* (3AL) [5].

In the present study, we used terms “sources” and “donors” [6]. The “sources” were the accession of *T. timopheevii* which carried resistance genes against diseases; “donors” were the pre-breeding lines into which the genetic material of *T. timopheevii* was introgressed, as well as the lines and varieties obtained from them in which a compromise between the alien gene presence and an acceptable level of agriculturally valuable traits was achieved.

One of the first genes transferred into the common wheat from *T. timopheevii* ssp. *timopheevii* was the *Lr18* gene. It is presently not in use because of its low efficacy against the majority of brown rust races. Moreover, it was found out that this gene is sensitive to high temperatures, and at the temperature above 25°C, it becomes ineffective [7]. Another brown rust resistance gene, *Lr50*, originates from the wild species *T. timopheevii* ssp. *araraticum* [5]. This gene still remains effective in several regions of the United States.

The first successful attempt to use *T. timopheevii* as a gene source for the resistance against pathogens was the obtainment of spontaneous translocation which contained the *Sr36/Pm6* in the chromosome 2B [8]. Presently, the *Sr36* gene is assigned to the group of genes providing effective tolerance to the most aggressive race of stem rust, Ug99. The same group unites the genes *Sr37* [9] and *Sr40*, which was transferred into the hexaploid wheat from the accession of *T. araraticum* [10]. The *Sr40* gene provides effective tolerance to Ug99 in both young seedlings and adult plants [11].

The *Pm6* gene has been widely used to obtain wheat varieties resistant to the powdery mildew and remains one of the effective genes in different regions throughout the world, including Europe, China, and North America [12, 13]. The *Pm27*, *Pm37*, and *MIAG12* genes are not used for wheat breeding.

Such a limited set of wheat pathogen resistance genes of the *Timopheevii* group transferred into the commercial varieties is, probably, due to the uniqueness of their G subgenome and the plasmon, low plasticity potential, and resistance to drought, heat, and other abiotic stresses, as well as to imperfection of pre-breeding and recombinant breeding approaches aimed at overcoming the tight linkage between the targeted genomes and undesirable ones.

Long-term studies carried out at the Vavilov Institute of Plant Genetic Resources [14, 15] and at the Institute of Cytology and Genetics of the Siberian Branch of the Russian Academy of Sciences [16, 17] showed that introgression of the desired genes/traits from species of the *T. timopheevii* group into common wheat is connected with several obstacles, because the direct hybridization is followed by infertility of the F<sub>1</sub>

hybrids and long period of the hybrid karyotype stabilization.

In the 1950s, it was shown that *T. timopheevii* cytoplasm controls the cytoplasmic male sterility (CMS), while nuclear genes (*Rf* genes) recovered fertility. It was proposed to use these features to obtain hybrid common wheat [18]. However, the technology of heterotic hybrids did not become widespread [19].

The goal of this work was to study the diversity of donors of the *T. timopheevii*, which have been used in a variety of regions throughout the world, and to study the spatial and temporal dynamics of the *T. timopheevii* genetic material distribution in common wheat varieties.

## MATERIALS AND METHODS

The object of this study was a set of common wheat varieties the pedigrees of which contained *T. timopheevii*. The GRIS4.0 application [20] and the world wheat gene pool database [21] were used to analyze pedigrees and to compose genealogical profiles.

Genealogical search through the database resulted in selection of 3088 varieties, which were obtained in different countries throughout the whole period of use of *T. timopheevii* in common wheat breeding. Genealogical profiles of these varieties contained *T. timopheevii*. Analyzing the genes, we selected 369 varieties and 184 lines which carried resistance genes to rust and/or powdery mildew obtained from *T. timopheevii* and were identified by different authors by phytopathological tests and/or molecular markers. There is no data on the presence of these genes in other varieties. It is noteworthy, that the presence of *T. timopheevii* in the cultivar profile does not necessarily indicate the presence of introgression from this species, as multiple crossings and selections may have led to elimination of genetic material of *T. timopheevii*.

The computer tracing of pedigrees allowed us to group the varieties by the *T. timopheevii* donors and by the lines of primary pre-breeding.

## RESULTS AND DISCUSSION

### *Geographical Distribution of Varieties with T. timopheevii in Their Pedigrees*

The wide distribution of genetic material of *T. timopheevii* began from the obtainment of the introgression lines Wisconsin 245 (CI-12633) and Wisconsin 249 (CI-12632) in 1948. Both lines were selected by R. Allard at the University of Wisconsin in the combination PD-2666-A-2-2-2-15-6-3\*3/(D-357-1) *T. timopheevii* [8].

In the 1950s, on the basis of this material, the obtainment of the varieties began in the United States, United Kingdom, Germany, Australia, and India. In the 1960s, this process spread to France, Italy, China, Kenya, and South Africa. In the 1970s, the wheat varieties which carried the Wisconsin 245 and/or Wisconsin