Study of common wheat lines with genetic material *Aegilops speltoides* for leaf rust resistance

Davoyan E.R., Davoyan R.O., Zubanova Y.S., Mikov D.S., Boldakov D.M.

National Center of Grain named after P.P. Lukyanenko, Krasnodar, Russia

E-mail davayan@rambler.ru

Key message. The results of evaluating introgressive lines by resistance to leaf rust and the presence of molecular markers in them linked to the known resistance genes *Lr28*, *Lr35*, *Lr51*, *Lr10*, *Lr26*, *Lr34* are presented.

Keywords: *Ae. speltoides*; Leaf rust; *Lr*-genes; introgressive lines; molecular markers

The gene pool of the species *Ae. speltoides* Tausch ($2n = 2x = 14$) genome (SS) has a significant reserve for disease resistance, in particular for leaf rust (*Puccinia triticiniae* Erikss.), which is one of the most widespread and harmful wheat diseases. Currently, it is known about the transfer of leaf rust resistance genes *Lr28*, *Lr35*, *Lr36*, *Lr51*, *Lr47*, *Lr66* from this species to common wheat. Based on the application of chromosome engineering methods, the authors created a number of cytologically stable common wheat lines with introgressions from *Ae. speltoides*, which are characterized by high disease resistance, high protein content and other valuable traits (Davoyan et al., 2009). These lines are thought to carry the leaf rust genes transmitted by *Ae. speltoides* transferred from Avrodes, as well as genes *Lr10*, *Lr26*, *Lr34* transmitted from recipient varieties Krasnodar 99, Kavkaz, Aurora, respectively.

The object of the study was 26 lines of common wheat obtained with the participation of the synthetic form Avrodes (ABS). Infection and assessment of resistance to leaf rust was carried out in the adult stage in the field. Identification of *Lr* genes was carried out using PCR with primers marking the genes *Lr28*, *Lr35*, *Lr51*, *Lr47*, *Lr66*.

The synthetic form Avrodes exhibits high level of resistance to leaf rust (reaction type 1-). Disease resistance in the studied lines varied from high with a reaction type of 1 – (in lines 151, 247, 391, 397, 594, 597, 608, 610, 680, 787, 1189, 1261) and 1 (in lines 157, 235, 248, 363, 393, 636) to moderate - reaction type 2 (lines 153, 253, 609, 865) and susceptible reaction type 3,4 (211, 351, 357, 604). Previously, in our studies, it was found that Avrodes does not carry *Lr47* and *Lr66* genes in its genome (Davoyan et al., 2012), and therefore the studied material was not screened for the presence of molecular markers linked to them. Marker BCD260F1/35R2 linked to the *Lr35* gene was not detected. Marker CSS421570 linked to the *Lr28* gene was identified in the synthetic form of Avrodes and line 608. Line 597 revealed a marker linked to the *Lr51* gene. Lines 151, 153, and 609 carry a marker linked to the 1RS.1BL translocation, which contains the *Lr26* gene. Molecular markers linked to the *Lr10* and *Lr34* genes are identified in lines 247, 351, 604 and 157, 211, 253, respectively. The desired markers were not detected in lines 248, 363, 594, 680, 787, 357, and 865. Lines carrying both single resistance genes and their combinations were selected. The combination of the *Lr26*+*Lr51* genes was identified in lines 1189, 1261 with the high level of resistance to disease. A combination of the *Lr10* and *Lr34* genes was found in lines 391, 393, 397, 610, 636. In line 608, the *Lr34* gene was combined with the *Lr28* gene. A line 235 with a combination of genes (*Lr10*+*Lr26*+*Lr34*) was selected. The presence of the *Lr28*, *Lr51* genes in the studied lines suggests the presence of genetic material from *Ae. speltoides* in them. Resistance to leaf rust in line 597 can be controlled by the single presence of the *Lr51* gene, in lines 1189, 1261 as a result of its combination with the *Lr26* gene. In line 608, resistance is due to the presence of the *Lr28* gene in combination with *Lr26*, and in line 235 due to a combination of 3 genes. Resistance to leaf rust in lines 391, 393, 397, 610, 636 may be due to the presence of a combination of two genes *Lr10* and *Lr34* at the bottom, and in the case of line 235, pyramids of three genes. Resistance to leaf rust in lines 248, 363, 594, 680, 787, 865, created with the participation of Avrodes, in which markers linked to the *Lr28*, *Lr35*, *Lr51*, *Lr10*, *Lr26*, and *Lr34* genes were not detected can be controlled by another gene(s) other than those.

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