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New Resistance Sources to Russian Wheat Aphid (*Diuraphis noxia*) in Swedish Wheat Substitution and Translocation Lines with Rye (*Secale cereale*) and *Leymus mollis*

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Abstract

Andersson S.C., Johansson E., Baum M., Rihawi F., El Bouhssini M. (2015): New resistance sources to Russian wheat aphid (*Diuraphis noxia*) in Swedish wheat substitution and translocation lines with rye (*Secale cereale*) and *Leymus mollis*. Czech J. Genet. Plant Breed., 51: 162–165.

Russian wheat aphid is an important pest in many wheat growing countries of the world. Different resistance genes to the pest have previously been identified. However, some biotypes of the pest are virulent to most of these genes. Swedish wheat-rye and wheat-*Leymus*, consisting of 235 accessions with substitutions and translocations, were investigated for resistance to the aphid. A total of 86 accessions were shown to be either resistant or moderately resistant. Resistance was found particularly in accessions having substitutions of 1R instead of 1D [1R(1D) or 1R(1D) + 6R(6D)], in translocations to 3D or 5A (3DL.3RS and 5AL.5RS) and in accessions with introgressions of *Leymus mollis.* Resistances to Russian wheat aphid obtained from the hereby reported chromosomes and combinations have not previously been reported. These rye and *Leymus* genes can thus be useful for widening the pool of resistance genes for future breeding of cultivars resistant to Russian wheat aphid.

Keywords: alien introgressions; aphid resistance; *Dnr* genes; *Triticum aestivum*; 1R

The Russian wheat aphid (RWA), *Diuraphis noxia* (Homoptera: Aphididae), is a pest of wheat (*Triticum* spp.) and barley (*Hordeum vulgare* L.) spread to many parts of the world. Resistance to RWA has previously been reported in wheat through the presence of certain genes (*Dn1-Dn9*, *Dnx*, *Dny* and *Dnr1-Dnr4*). The *Dnr1-Dnr4* and *Dn7* (*Dnr*) genes have been found to be located on the rye chromosomes 1RL, 3RS, 4R, 7R, and 1RS, respectively, and are transferred through introgressions to wheat (Marais *et al.* 1994; Lukaszewski *et al.* 2001; Smith *et al.* 2004). The 1BL.1RS (*Dn7*) is one of the most frequently used resistance sources (Haley *et al.* 2004; Porter *et al.* 2005). There is a need to identify new resistance sources due to new biotypes of the aphid evolving and due to the poor baking quality associated with the 1BL.1RS (Graybosch *et al.* 1990; Baum & Appels 1991).

The aim of the present investigation was to screen a large number of wheat-rye and wheat-*Leymus* introgressions to identify new sources of resistance to the Russian wheat aphid.

The plant material consisted of spring and winter wheat substitutions and translocations of rye and *Leymus* spp. The spring wheat-rye and wheat-*Leymus* consisted of a total of 57 accessions crossed with advanced breeding lines of hexaploid spring triticale, VT828039, VT828041, VT83591, and VT83615, three varieties of hexaploid spring triticale, Drira, Beagle, and CIMMYT 1974, and one advanced breeding line of hexaploid spring hybrid of *Leymus racemosus*. The introgressions within the spring wheat-rye material in the present study consisted of 41 accessions with a substitution of the corresponding wheat chromosome to one of 1R, 2R, 3R, 5R, and 6R, one accession with double substitution of 1R(1D) and 6R(6D), twelve translocations with 1DL.1RS or 3DL.3RS and three accessions with substitutions of *L. racemosus*. The winter wheat-rye material consisted of a total of 185 accessions from crosses of wheat with advanced breeding lines of hexaploid triticale Sv876012, Sv876032, Sv856003, and the triticale varieties Uno, Otello, Malysh 8x-6x, a double wheat-rye substitution with rye chromosomes 1R and 2R, and wheat-*L. mollis* hybrids called AD99. The wheat cultivars used in crosses were Holme, Kraka, and Goerzen, which were used as wheat parents in the crosses of triticale × wheat and AD99 × wheat, and in the backcrosses. The introgressions within the winter material included 107 accessions with substitutions of one or several R chromosomes including 1R, 2R, 4R, 6R, and 7R of which some had inverted 1R, 51 translocations of the long or short arm of 1R, 2R and 5R. Furthermore, two wheats from parental crosses, four triticale advanced lines from parental crosses, mostly with the wheat D-genome and partially with the A and B genome, and 21 hybrids with *L. mollis* were included in the accessions of the winter material. The controls were susceptible check AYT-98-RF-9346 and resistant check IG-107166, both from ICARDA, Syria.

The screenings were conducted in greenhouses at ICARDA, Tel Hadya, Syria in 2011 and 2012. The RWA used were collected yearly from Tel Hadya and reared on wheat with different degree of susceptibility to the pest. The experiments were carried out in a greenhouse at 19–20°C, with light/dark photoperiod 16/8h and relative humidity of about 60%. The accessions were planted in a randomized (alpha design) order together with susceptible and resistant controls in each planting tray, in a mixture of soil, sand, and peat (2:1:1). Evaluation was done when symptoms were clearly seen on susceptible checks, using the ICARDA *D. noxia* damage scale with 1–3 scale for leaf rolling (LR) and 1–6 scale for leaf chlorosis (LC) (El Bouhssini *et al.* 2011). In the initial screening, 5 seeds per plot were planted in 30 × 21 × 5 cm metal flats with 5 × 4 plots. The plants were infested at one-leaf stage with a mixture of RWA nymphs and adults with 5–10 aphids per plant, with a total of 25–50 per accession. Evaluation was done 26–29 days after infestation. In the second advanced screening, selected accessions from the first screening results were repeated at four separate times.

In total, 235 of the 242 accessions investigated germinated and 86 of the germinated accessions (36.6%) showed resistance (n = 23) or moderate resistance (n = 63) against RWA. None of the accessions showed a highly resistant response. The accessions showing resistance in the advanced screenings were those having different introgressions from 1R, 3RS, 1R & 6R, 5R, and unidentified material from *L. mollis* (Table 1). The main part of the resistance found was in accessions where chromosome 1D had been substituted for 1R. Thus, this is probably the first finding of resistance to RWA in a 1R(1D) material. It is unclear whether the resistance is conferred by the genes Dnr1 and/or Dn7 or whether it is a novel source. Many known resistant genes in wheat are located on chromosomes 1 or 7 in the D-genome (e.g. McIntosch *et al.* 2008) meaning that a substitution of chromosome 1D might also influence other resistance genes than those towards RWA. Also, genes encoding important proteins associated with bread-making quality are located on chromosome 1D (Johansson *et al.* 2013). The resistant control line with 1BL.1RS translocation showed a similar level of resistance as was noted in the 1R(1D) materials. Accessions with substitutions of 6R to 6D [6R(6D)] were always combined with a substitution of 1R and the resistances in those accessions are therefore most likely the result from 1R.

Resistance was also found in accessions with 3DL.3RS. As to our knowledge, no previous studies have shown resistance to RWA in wheat material with translocation of 3RS into the wheat D-genome. Resistance has never previously been reported in wheat material with introgressions from 5R or *Leymus*. Of the 23 accessions of winter wheat materials containing 5AL.5RS from different parental crosses, three showed resistance and eleven moderate resistance in the initial screening.

To conclude, the screened wheat substitutions and translocations contained resistance genes against RWA not previously reported as well as in constitutions not previously described. A part of the examined material has also previously been investigated for different diseases (Forsström 2002; Hysing *et al.* 2006, 2007), as well as for root characteristics and competition abilities (Bertholdsson *et al.* 2012). Thus, the present material is of relevance also for studies of various diseases/pests and performance in other important characters

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Table 1. Resistant accessions in an advanced screening for resistance to Russian wheat aphid in wheat-rye and wheat-*Leymus mollis* translocations and substitutions

Accession/No.	Rye donor/cross	Translocation/substitution	LR	LC
			(mv)	
SW1	VT828041	1R(1D)	2	2
SW2	VT828041	1R(1D)	2	2
SW3	Drira	1R(1D)	2	2
SW4	VT83591	1R(1D)	2	2
SW5	Beagle	1R(1D), 6R(6D)	2	2
SW6	Beagle	3DL.3RS	2	2
SW7	Beagle	3DL.3RS	2	2
Res. Check IG-107166	Dn7	1BL.1RS	1.1	2
Sus. Check AYT-98-RF-9346			3	4.1
WW1	(Sv876032 × H) × K	1R(1D)	2	2
WW2	(Sv876032 × H) × K	1R(1D), 6R(6D)	2	2
WW3	(Sv876032 × H) × K	1R(1D), 6R(6D)	2	2
WW4	(Sv876032 × H) × K	1R(1D), 6R(6D)	2	2
WW5	(Sv876032 × H) × K	1R(1D), 6R(6D)	2	2
WW6	(Sv876032 × H) × K	1R(1D), 6R(6D)	2	2
WW7	Sv856003 × H	?(5D)?	2	2
WW8	(AD99 × K) × K	?	2	2
WW9	(AD99 × K) × K	?	2	2
Res. Check IG-107166	Dn7	1BL.1RS	2	2
Sus. Check AYT-98-RF-9346			3	4.9

Each of selected accession was repeated four times; each control SW n = 12; control WW sus. n = 16; control WW res. n = 20; LR – leaf rolling, LC – leaf chlorosis; scale (LR–LC): 1–1 and 1–2 = highly resistant, 2–2 = resistant, 2–3 = moderately resistant, 3–3 moderately susceptible, 3–4, 3–5, 3–6 = susceptible; SW – spring wheat; WW – winter wheat; mv – mean value

to obtain wheat lines usable in breeding for resistance to a large range of diseases and pests.

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