КРАТКОЕ СООБЩЕНИЕ • BRIEF REPORT

Greenbug resistance in barley landraces from Uzbekistan

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Background. The greenbug (*Schizaphis graminum* Rondani) can significantly reduce the yield of barley and other cereals in the southern regions of Russia. Cultivation of resistant varieties can significantly limit the pathogen's harmfulness. At the same time, specific interaction with the genotypes of the host plant, characteristic of *S. graminum*, requires a continuous search for new resistance donors to broaden the genetic diversity of barley cultivars.

Materials and methods. The resistance of 178 accessions of barley landraces from Uzbekistan to the Krasnodar greenbug population was tested in laboratory experiments. Juvenile plants were infested with aphids of different ages, and when the susceptible control died (cv. 'Belogorsky'), resistance was assessed on a 0 to 10 (plant death) rating scale. Plants with a damage rate of 1–4 points (up to 30% of the leaf surface being damaged) belonged to the resistant class; damage rate of 5–8 points indicated moderate resistance of plants, and that of 9–10 meant susceptibility. In addition, we assessed the aphid damage of the winter barley cultivar 'Post', protected by the previously identified resistance gene *Rsg1*.

Results and conclusions. We identified 52 barley accessions as heterogeneous for the studied trait. In six accessions, plants with high (points 3 to 4) and moderate (5 to 8) resistance were identified; 6 accessions were differentiated into 3 phenotypic classes: resistant, moderately resistant, and susceptible; and in 40 accessions the manifestation of the resistance component varied within 5 to 7 points (from 31 to 60% of the leaf surface being damaged). The distinctly expressed resistance of 12 accessions is controlled by alleles of resistance genes that differ from *Rsg1*. After selection for resistance, the identified accessions can be used in breeding.

Key words: *Hordeum vulgare* L., *Schizaphis graminum* Rondani, genes for resistance, plant breeding.

Устойчивость к обыкновенной злаковой тле образцов местного ячменя из Узбекистана

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Актуальность. Обыкновенная злаковая тля *Schizaphis graminum* Rondani способна существенно снизить урожайность ячменя и других злаковых культур в южных регионах России. Вредоносность фитофага может лимитировать возделывание устойчивых сортов. В то же время характерное для *S. graminum* специфическое взаимодействие с генотипами растения-хозяина определяет необходимость постоянного поиска новых доноров устойчивости для расширения генетического разнообразия сортов ячменя.

Материалы и методы. В лабораторных экспериментах изучили устойчивость 178 образцов местного ячменя из Узбекистана к краснодарской популяции насекомого. Ювенильные растения заселяли разновозрастными тлями и при гибели восприимчивого контроля (сорт 'Белогорский') оценивали устойчивость по шкале от 0 до 10 (гибель растений). К классу устойчивых относили растения с баллами 1–4 (повреждено до 30% листовой поверхности), поврежденность 5–8 баллов свидетельствовала об умеренной устойчивости растений, 9–10 – о восприимчивости. Кроме того, оценили поврежденность тлей сорта озимого ячменя 'Post', который защищен идентифицированным ранее геном устойчивости *Rsg1*.

Результаты и выводы. Выделили 52 гетерогенных по изученному признаку образцов ячменя. У шести образцов выявлены растения с высокой (3–4 балла) и умеренной (5–8 баллов) устойчивостью, 6 образцов дифференцированы на 3 фенотипических класса: устойчивый, умеренно устойчивый, восприимчивый, а у 40 образцов проявление устойчивого компонента варьировало в пределах 5–7 баллов (повреждено от 31 до 60% листовой поверхности). Отчетливо выраженная устойчивость 12 образцов контролируется аллелями генов устойчивости, отличающимися от *Rsg1*. После отбора по устойчивости выделившиеся образцы могут быть использованы в селекции.

Ключевые слова: *Hordeum vulgare* L., *Schizaphis graminum* Rondani, гены устойчивости, селекция растений.

Introduction

Cereal crops in Southern Russia are significantly damaged by greenbug (*Schizaphis graminum* Rondani). Breeding and cultivation of resistant varieties is the radical, cheapest and most environmentally friendly way to reduce the harm. The insect is characterized by differential interaction with host plants, which determines the need for a constant search for new resistance donors for breeding.

There are two known genes controlling the resistance of barley (*Hordeum vulgare* L.) to *S. graminum*, effective against certain greenbug biotypes in the United States. Korean winter barley varieties, Omugi and Dobaku, were used to develop commercial cultivars protected by the dominant *Rsg1* gene, which controls resistance to greenbug biotypes B–G, I–K, CWR, and WWG, but not to H (Atkins, Dahms, 1945; Puterka et al., 1988; Anstead et al., 2003). The second dominant gene, *Rsg2*, which determines resistance to the same greenbug biotypes as *Rsg1* but, unlike *Rsg1*, is effective against the TX1 biotype, was identified in PI 426756 from Pakistan (Merkle et al., 1987; Anstead et al., 2003; Porter et al., 2007).

According to the results of our experiments, barley landraces are a valuable enrichment source for the bank of genes effective against *S. graminum*. For example, a study of 1358 barley accessions from the countries of East and South Asia resulted in finding heterogeneous forms with different expression levels of their resistance to the Krasnodar greenbug population. High resistance in 98 accessions is controlled by alleles nonidentical to the alleles of the previously identified *Rsg1* gene (Radchenko et al., 2014).

Studying 48 barley accessions from Uzbekistan for resistance to the Krasnodar population of *S. graminum* disclosed a rather high (18.4%) frequency of forms differing in the level of resistance expression. High resistance of at least three accessions is controlled by alleles different from *Rsg1* (Radchenko et al., 2017). It should be mentioned that the tested set is only a small part of the accessions that arrived to the VIR collection from Uzbekistan. The purpose of this study was to complete the research into the hereditary diversity of barleys from Uzbekistan in the context of their resistance to greenbug.

Materials and methods

Laboratory experiments were conducted to assess 178 accessions of local barleys from Uzbekistan for their resistance to the Krasnodar population of *S. graminum* collected at the Kuban Experiment Station of VIR, Gulkevichy District. Besides, the winter barley cv. 'Post' (k-31204, USA) with the earlier identified resistance gene *Rsg1* was also included in the tests.

The tests were carried out in a controlled light room, where the air temperature was maintained at 20–25°C. Aphids were cultivated on wheat seedlings of cv. 'Leningradskaya 98'. Plant tissues necrotize in the places of greenbug feeding, making it possible to assess the damage. To assess resistance, seeds were sown in rows into plastic trays filled with nonsterile potting soil. Each tray contained two rows of the nonresistant control cv. 'Belogorsky' (k-22089), 10 rows of the tested accessions, and cv. 'Post'.

Mixed-age aphids were dropped on juvenile plants (4–5 insects per plant), and when the control died (usually 10–14 days after colonization), resistance was assessed using the scale from 0 (no damage) to 10. Plants with points 1 to 4 (up to 30% of the leaf surface was damaged) were classified as resistant, and 9 to 10 as susceptible (Radchenko, 2008). The accessions identified as resistant were retested.

Results and discussion

The screening resulted in identifying 52 heterogeneous accessions. Six accessions yielded plants with high (points 3 to 4) and moderate (5 to 8) resistance, 6 accessions were differentiated into 3 phenotypic classes: resistant, moderately resistant, and susceptible (Table), and in 40 accessions the manifestation of resistance varied from 5 to 7 (31 to 60% of the leaf surface was damaged).

Table. Greenbug resistance scores in barley accessions

Таблица. Образцы ячменя, выделившиеся по устойчивости к обыкновенной злаковой тле

VIR catalogue No. / № по каталогу ВИР	Accession / Образец	Variety / Разновидность	Resistance scores / Устойчивость, балл
2995	Local	*pallidum*	3, 7, 9
5104	«	*nigrum, pallidum*	3, 4, 7
6104	«	*pallidum*	3, 5
6105	«	*pallidum, pyramidatum*	3, 7, 8
6110	«	*pallidum, nutans*	3, 4, 7
26086	«	*pallidum*	3, 7, 9
26090	«	*pallidum*	3, 5, 8
26119	«	*pallidum*	3, 7, 9
26128	«	*pallidum*	3, 7, 9
26133	«	*pallidum*	3, 5, 9
26160	«	*pallidum*	3, 5, 9
27894	Nutans 54	*nutans*	3, 4, 8
31204	Post (control)	*pyramidatum*	7, 8, 9
22089	Belogorsky (control)	*pallidum*	9, 10

Significant variability of the studied trait may be induced by the expression of genes with low expressivity and/or (more likely) the presence of clones differing in virulence to the tested barleys in the Krasnodar greenbug population.

The earlier (Radchenko et al., 2017) assessment of 48 accessions from Uzbekistan succeeded in identifying one resistant barley form and two heterogeneous ones, with the damage score in their resistance components from 3 to 8, or 6.25% of the total number of accessions tested. In these experiments with 178 barley accessions, 12 heterogeneous forms were identified for distinct manifestations of the trait (points 3 to 4) in plants of the resistance component, or 6.74%.

The damage on cv. 'Post' plants with the *Rsg1* resistance gene varied from 7 to 9 points, i.e., clones virulent to this cultivar prevailed in the Krasnodar greenbug population. Obviously, the accessions whose damage in their resistance components scored 3 points (Table) were protected by alleles of resistance genes that differ from the previously identified *Rsg1* gene.

Conclusions

As a result of testing 178 local barley accessions from Uzbekistan, a fairly significant (6.74%) percentage of plant forms with distinct manifestations of greenbug resistance was observed. Heterogeneous forms were identified, differing in the expression level of resistance to the Krasnodar population of *Schizaphis graminum*. The distinctly expressed resistance in 12 accessions is controlled by alleles of resistance genes that differ from the previously identified *Rsg1*. The identified accessions are of interest for immunity-targeted barley breeding.

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