

Using of wild species genetic diversity in plant breeding.

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Abstract

This research presents the field results of studying of wild oat species with different ploidy level. The evaluation was targeted at agronomic traits and resistance to the most widespread diseases: crown and stem rusts and barley yellow dwarf virus (BYDV). Besides, representative collection of all species has been analyzed for groat protein content – amino acid and groat oil content – fatty acid composition. The study representative set of accessions of genus *Avena* L. species helped to determine intraspecific diversity in all researched characters. All identified sources may be involved in the conventional and other breeding process for disease resistance, agronomic traits and grain quality in oats.

Media summary

This research presents the field results of studying wild oat species with different ploidy level. The evaluation was targeted at agronomic traits and resistance to the most widespread diseases.

Key words

Avena species, taxonomy, agronomic characters, disease resistance, protein, oil, response to photoperiod and vernalization

Introduction

The practical importance of interspecies hybridization lies in combining properties of different species that drifted apart in the process of evolution. The vast area of distribution of wild relatives of crop species allows for the formation of extensive intra-specific diversity of characteristics. The cultivated species in most cases have lost numerous traits initially inherent in their wild ancestors. Resistance to unfavorable environmental factors, wide range of adaptation to different edaphic and climate conditions, resistance to pathogens, a number of characters framing increased productivity and quality – all of these present unique sources of variation for crop improvement. Comparative analysis of the whole specific diversity of crops was incited by an interest to use these forms in breeding practice, re-enforced lately by new developments in genetics, such as molecular biology and genomics. Fusion of high yield and different valuable parameters in one cultivar has been the goal of breeding in the past years. According to many researchers the utilization of intra- and inter-specific hybridization in conventional breeding, together with various modern breeding techniques, may increase plant adaptation and the percentage of qualitative kernel components in the crop to a very high level.

As to the practical significance of inter-specific crosses, they allow transfer of agriculturally important traits from wild and weed species to cultivated ones. Crosses between species of equal or different ploidy levels have long attracted the attention of researchers. The genus *Avena* L., which includes many species, has three ploidy levels and is represented by di-, tetra-, and hexaploids. All *Avena* L. species are subdivided into two groups according to their crossability: all weed hexaploid species readily crossable with cultivated oat; diploid and tetraploid species are either not directly crossable, produce sterile hybrids in subsequent generations, or requiring tissue culture methods for hybridization. Cross incompatibility presents the greatest difficulty in transferring genes from diploids and tetraploids to hexaploids. The use of various techniques such as backcrosses, mutants, genetic intermediates and methods of biotechnology or GMO techniques can usually overcome this problem. These breeding methods allow many agriculturally important traits to be transferred into cultivated oat for extending its gene pool as well as the gene pool of the entire genus.

Materials and Methods

For this reason, investigating the gene pool of wild species to extend the genetic potential of cultivated oat species was initiated. At present, VIR possesses a rich collection of *Avena* L. species, which contains about 2000 accessions of twenty-two wild species. The wild accessions represent numerous morphological variants reflecting their wide geographic distribution in the Mediterranean countries. A representative collection was made in Transcaucasia, where wild oat species are the most diverse in the CIS countries.

The search for, and utilization of, new sources of genetic variation for breeding purposes is one of the objectives pursued by Vavilov Institute of Plant Industry (VIR) in studying its global germplasm collections.

A decade of studying the representative set of 2000 accessions of genus *Avena* L. with different ploidy levels has made it possible to disclose intra-specific diversity of all characters involved in the research. The research was based on the International Descriptors of *Avena* L. (1984) and Oat Descriptors List (1985). This will contribute to a targeted search for the best breeding sources and broadening the genetic base of future released oat cultivars.

Results and discussion

Some field agronomical characters were evaluated for breeding purposes in oat species. This evaluation of wild oat species cast light on the rich diversity in kernel characters. On the whole, it was established that diploid species had the highest values of husk percent and the smallest size of kernel. The lowest percentage of husk (43-46% on the average) was observed in *A. damascena*, *A. wiestii* and *A. hirtula*. Kernel size was notable in forms of *A. longiglumis* with 1000 grain weight over 14 g. Two tetraploid species, *A. magna* and *A. murphyi*, were also distinguished for a large size of their kernels, since their 1000 grains weight (23.5-23.8 g) reliably exceeded maximal average values of all species studied.

When crown rust resistance was assessed at the level of species in a field study it was observed that most diploid wild species had no resistance. Among the tetraploid species resistance was observed in most species (*A. barbata*, *A. magna*, *A. murphyi*, *A. insularis*, *A. macrostachya*). Resistance was most expressed in the hexaploid accessions from Spain, Italy, Turkey, Israel and Iran. Resistant forms for all groups of species came mostly from North African countries such as Tunisia, Algeria and Morocco (Loskutov, 2003).

When assessing stem rust resistance the variation of responses in the species studied was wider than in cultivated oats. At the same time, among a few diploid species (*A. pilosa*, *A. longiglumis*, *A. hirtula*) only medium resistance to this disease was identified. Tetraploid wild species were characterized as strongly susceptible to this pathogen, with the exception of some forms of *A. barbata*, *A. magna*, *A. insularis* and *A. macrostachya*. All hexaploid wild species, on the average, demonstrated medium resistance to the agent of stem rust. Resistant forms were identified among the accessions from Italy, Iran, Iraq, Israel, Tunisia, Algeria, Morocco and Ethiopia. Group resistance to major obligate fungal diseases (crown and stem rust) was observed in the forms belonging to species *A. longiglumis*, *A. canariensis*, *A. hirtula*, *A. barbata*, *A. agadiriana*, *A. magna*, *A. insularis*, *A. macrostachya*, *A. occidentalis* and *A. sterilis*.

Medium tolerance to BYDV was observed in the diploid species with A genome variants. A majority of tetraploid species (*A. barbata*, *A. vaviloviana*, *A. magna*, *A. macrostachya*) with different genomes had medium tolerance to this virus. All hexaploid species basically demonstrated medium tolerance to BYDV, with *A. occidentalis* having the highest percentage of resistant accessions. The highest and medium levels of tolerance were typical of the oat forms from Greece, Turkey, Syria, Israel, Morocco, Algeria and Tunisia. Comparing the data of BYDV resistance and strong aphid colonization ascertained identification of BYDV resistant accessions belonging to diploid species *A. clauda*, *A. pilosa*, *A. damascena*, *A. canariensis* and *A. hirtula*.

The data of biochemical research on wild and weedy field oat species showed the highest groat protein content (over 20.0%) in accessions across all ploidy levels - diploid (*A. longiglumis* and *A. atlantica*), tetraploid (*A. magna* and *A. barbata*), and hexaploid (*A. sterilis*). Potential sources of high protein content would be *A. murphyi* and *A. occidentalis* (over 19.0%). High nutritive value of protein was notable in the tetraploid *A. barbata* (5.6% of lysine in protein). Hexaploid species appeared to have a higher percentage content of lysine and other essential amino acids in protein compared with the level in cultivated *A. sativa*. Noteworthy for high groat oil content (7-10%) were accessions of the diploid species *A. pilosa* and *A. canariensis*, the tetraploid species *A. murphyi* and *A. magna*, and hexaploid species *A. fatua*, *A. ludoviciana* and *A. sterilis*. The quality of oil in oat may be determined by the content of monounsaturated fatty acids, such as oleic acid capable of prolonging oil preservation time during storage. The highest content of oleic acid (over 46% of the sum of fatty acids) was detected in the diploid species *A. hirtula*, *A. longiglumis* and *A. wiestii*, the tetraploid species *A. barbata*, *A. vaviloviana* and *A. magna*, and hexaploid species *A. fatua* and *A. ludoviciana*. At the same time, biological activity of such oil is determined by the correlation between linoleic and oleic acids that should be equal to one. This correlation was observed in the accessions of diploid forms *A. ventricosa*, *A. clauda*, *A. pilosa*, and the tetraploid *A. vaviloviana*. This research resulted in mapping the geographic distribution of intra-specific diversity with regard to all oat species and forms. It emerged that accessions with high groat protein content had originated mainly from Israel, Morocco and Azerbaijan, while those with high groat oil content from the Ukraine, Azerbaijan, Georgia and Morocco (Loskutov, 2004).

The wide diversity in response to photoperiod and vernalization illustrated the level of polymorphism for these characters within all wild genepools of the genus *Avena* L. In addition, forms differing in the sensitivity to photoperiod and vernalization were found. The results of evaluation of aluminium tolerance have shown that wild species (diploid and tetraploid) carrying the C genome had low levels of resistance to edaphic factors, while the carriers of A and B genomes were more frequently characterized as having high aluminium resistance.

The comprehensive study of the entire range of species with different ploidy level in the genus *Avena* L. made it possible to illustrate intra-specific diversity on all characters observed. The diploid, tetraploid and especially the hexaploid species identified as sources of the assessed characters may be included in conventional and other breeding process for disease resistance, agronomic traits, and grain quality for feed and food. Use of the diverse wild oat species with regard to their morphological traits, geographic occurrence and ecological preference is the most promising method for reducing genetic erosion of cultivated varieties.

References

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