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ОВЕС (*AVENA L.*).

**РАСПРОСТРАНЕНИЕ, СИСТЕМАТИКА, ЭВОЛЮЦИЯ И
СЕЛЕКЦИОННАЯ ЦЕННОСТЬ.**

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**OAT (*AVENA L.*).
DISTRIBUTION, TAXONOMY, EVOLUTION
AND BREEDING VALUE.**

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В книге сделан обзор отечественной и зарубежной литературы, а так же приведены собственные результаты исследований культурных и дикорастущих видов овса. Представлены данные по распространению, морфологическим и кариологическим особенностям, молекулярно-биологическому изучению, систематики, эволюции и селекционно-генетической ценности видов овса.

Монография предназначена для научных работников генетико-селекционных учреждений и преподавателей высших учебных заведений биологического и сельскохозяйственного профиля.

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Изучение конкретных видов в системе рода с использованием всех современных методов исследования, позволяет точно установить градации соподчинения и уточнить границы между отдельными группами видов. Планомерное изучение отдельных видов рода в целом дает информацию о локализации центров их формообразования. Род *Avena* L. представлен культурными видами, имеющими большое практическое значение, и дикорастущими видами, интересными как объекты таксономических исследований и источники селекционно ценных признаков для использования в селекции. Система рода *Avena* L. насчитывает 26 видов, которые имеют три уровня пloidности и представлены ди-, тетра- и гексапloidными группами видов, большинство из которых являются дикорастущими. В каждой группе имеются культурные виды овса, довольно хорошо изученные в селекционном плане: *A. strigosa* Schreb. ($2n=14$), *A. abyssinica* Hochst. ($2n=28$) и *A. byzantina* С.К. и *A. sativa* L. ($2n=42$).

Виды рода *Avena* L. отличаются большим морфологическим и эколого-географическим разнообразием. В мировой литературе накоплено значительное количество данных о многочисленных формах и видах всего рода, центрах их наибольшего разнообразия и происхождения. Однако описания видов и результаты их изучения чаще всего фрагментарны или касаются случайного набора образцов, комплексный подход к изучению ботанического разнообразия и селекционных признаков отсутствует. До сих пор многие проблемы остаются до конца нерешенными: нет единого мнения о происхождении видов овса, их систематическом положении, существует некоторая путаница по голозерным формам диплоидного и гексапloidного культурного овса.

Овес посевной (*Avena sativa* L.) – одна из наиболее важных зерновых сельскохозяйственных культур на земном шаре, занимающая около 20 млн. га пахотных земель. Селекционная проработка современных сортов овса довольно высока. Вовлечение разнообразного, географически отдаленного, местного и дикорастущего материала в селекционный процесс, при использовании наряду с традиционными методами селекции достижений современной молекулярной генетики, отвечает требованиям улучшения данной культуры и сокращения генетической эрозии. Обширный ареал дикорастущих и, особенно, сорно-полевых видов охватывает весь зерновой пояс земного шара, распространившись от пустынь до полярных районов земледелия, что способствует формированию широкого внутривидового разнообразия признаков, полипloidного ряда этих видов. Сравнительное изучение дикорастущих видов овса в таксономическом и селекционном отношении вызвано широким интересом селекционеров к их практическому использованию, чему немало спо-

способствовало развитие цитологических, иммунологических, биохимических и других исследований. Широкий диапазон адаптации дикорастущих видов к неблагоприятным факторам внешней среды, их приспособленности к разнообразным почвенно-климатическим условиям, устойчивости к патогенным организмам, некоторых признаков, связанных с элементами повышенной продуктивности и качества - представляет уникальный источник исходного материала для селекции.

Данная публикация представляет интерес для ботаников, селекционеров, научных работников и студентов биологических и сельскохозяйственных вузов.

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ЗАКЛЮЧЕНИЕ

Овес - одна из наиболее распространенных и важных зерновых культур, которая в мировом производстве зерновых занимает 5-е место. Посевы этой культуры в 2004 г. в мире составили свыше 11,7 млн. га с валовым сбором 26,9 млн. т., при средней урожайности 2,3 т/га. Однако размещение его в различных природно-экономических зонах мира неодинаково.

В России овес высевают от северных границ возможного земледелия до южных регионов. К сожалению, в последние годы в силу субъективных причин наблюдается устойчивая тенденция значительного сокращения площадей под овсом (с 12 млн. га до 3 млн. га). Однако для устойчивого земледелия России, особенно в экстремальных условиях большинства северных регионов, интерес к возделыванию овса может быть востребован. К тому же в этом направлении существует зарубежный и российский опыт возделывания этой культуры.

Складывающаяся неблагоприятная ситуация с сокращением площадей под посевами овса, может привести к тому, что из ведущего производителя овса в мире Россия может стать ведущим мировым импортером овса, что повлечет за собой большие финансовые издержки. Все это может еще уменьшить продовольственную безопасность России. Кроме этого, не будут востребованы современные и вновь создаваемые сорта овса, которые успешно создаются селекционерами России. В свою очередь, это может привести к сворачиванию исследовательской работы с овсом, поисков новых направлений селекции по качественным признакам зерна и, в конечном счете, прекращению селекционной работы в ряде регионов России, что приведет к использованию сортов зарубежной селекции, которые чаще всего не приспособлены к экстремальным российским условиям выращивания. Такая ситуация может еще больше повлиять на сокращение посевных площадей и ухудшение качество зерновой продукции.

С другой стороны Россия имеет все необходимые объективные условия для получения максимального и высококачественного урожая зерна овса. Она обладает даже в настоящее время относительно других стран большими площадями под овсом, которые могут быть реально увеличены. Необходимо существенно увеличить процент зерна используемого для переработки на продукты питания, что может сделать эту часть растениеводства более экономически выгодной и привести к более здоровому изменению режима питания россиян. Для всего этого Россия располагает большим сортиментом районированных сортов овса разнообразных по хозяйственно важным признакам хорошо адаптированных ко всем регионам страны. Ряд сортов обладает повышенными показателями качества зерна, и могут уже в настоящее время использоваться для пищевых целей. У России

есть богатейшая мировая коллекция образцов овса, которая является исходным материалом для создания новых высокопродуктивных и высококачественных сортов овса с использованием традиционных методов селекции и до переноса отдельных аллелей генов в селекционный материал. Путем улучшения процесса семеноводства и качества производственных посевов овса Россия могла бы стать экспортером овса, так как ни в одной стране мира нет более благоприятных почвенно-климатических условий для выращивания этой хозяйственно важной культуры. И в связи с этим, Россия могла бы занять достойное место лидера не только по производству овса, но и как ведущего мирового экспортера этой культуры.

В то же время, к сожалению, в России столь важная зерновая культура при наличии большого разнообразного материала от староместных сортов-популяций до районированных сортов овса не достаточно изучается по целому ряду аспектов. С генетической точки зрения, у овса, по сравнению с другими зерновыми культурами, не достаточно идентифицировано генов, контролирующих важнейшие селекционные и морфологические признаки. Изучение биохимических показателей отражает только кормовые достоинства овса. Мало изучено разнообразие овса для использования на пищевые и лекарственные цели, хотя известно с древних времен, что это диетическая и, в некоторых случаях, лечебная культура, которая широко используется в народной медицине. Использование дикорастущих видов овса в селекции затруднено в связи с трудностью переноса генетической информации в культурные виды. В то же время, зарубежные селекционеры довольно широко используют данный генетический материал для разнообразных целей селекции. В России в селекции овса, в силу разных причин, огромный потенциал дикорастущих видов практически не используется.

Таким образом, проведенный анализ мировой литературы и данных нашего комплексного многолетнего исследования позволил уточнить филогенетические связи, таксономические характеристики и пути эволюции видов овса. На основе всестороннего анализа эколого-географических особенностей в распространении ареалов видов овса проведено географическое изучение распределения морфологических и селекционно ценных признаков, расширяющее представление о потенциальных возможностях отдельных видов и всего рода в целом, что позволяет вести целенаправленный подбор исходного материала для селекции. Многочисленные исследования в этом направлении и практические результаты селекции овса, особенно за рубежом, говорят о том, что использование дикорастущих видов, наряду с сортовым разнообразием культурных видов, является наиболее перспективным направлением селекции овса для расширения его генетической основы и уменьшения генной эрозии этой культуры.

Summary

This book presents a review of publications and analyses the results of evaluation performed on a representative set of oat accessions of all *Avena* L. species. The global VIR oat collection is represented by comprehensive specific and intra-specific diversity of both cultivated (10,000 accessions) and wild (2,000 accessions) species of *Avena*. Full botanic and ecological diversity of cultivated species is incorporated in the landraces varieties-populations collected in 1910s – 1920s. A majority of these forms came from the centres of origin and diversity of this crop, providing a universal overview on the total geographic diversity of oat. With this in view, oat species became the subject of complex investigation in order to specify the system of the *Avena* genus, direction of its evolution and phylogenetic links between the species. At the same time, further search for taxonomy and utilization of new oat breeding sources for breeding purposes is one of the objectives pursued by Vavilov Institute of Plant Industry (VIR) in studying its global germplasm collections.

It is the availability of total botanical and eco-geographic diversity and its complex study that may provide an opportunity to identify centres of origin and variability of this or that genus or species.

Complex analysis of broad literary review and utilization of the karyotype structure data confirmed by the results of RAPD and avenin spectrum analysis confirmed identification of two basic genomes which had most likely participated in the formation of species in *Avena*, namely the A and C genomes. As for the B and D genomes, they seem to be derivatives of the A genome. In addition to the data obtained during the study of the species containing these genomes, clear-cut differences have been discovered in the areas of their distribution.

Numerous researches have proven that the C genome goes through all ploidy levels unchanged, with small variation, thus being considered one of the basic genomes in oat. Our investigations of the karyotype *A. macrostachya* Balan. have shown that this species is an autotetraploid with the AA genome [Loskutov & Abramova, 1999]. On the other hand, the analysis of chromosome structure indicates that *A. macrostachya* is related to the C-genome species [Rodionov et al., 2005]. At the same time, this species is characterized by a symmetrical karyotype and a set of morphological characters attesting to its true primitivity. All this is confirmed by the most primitive perennial type of development and by cross-pollination, which is typical for a group of species of oat-like grasses within the subgenus *Avenastrum* C. Koch [Loskutov, 2003]. Meanwhile, according to A. V. Rodionov *et al.* [2005], the division of the phylogenetic oat lines carrying A and C genomes was accompanied by accumulation of differences in dispersed repetitions and accumulation of transitions and transversions specific for each branch. Later the C-genome line segregated phylogenetic branches of *A. macrostachya* from the progenitor of the other species with the C genome, and after that the progenitors of *A. macrostachya* doubled their chromosome number and generated large blocks of C-heterochromatin which caused an unusual C-banding pattern of chromosomes in C genomes of diploid and polyploid species.

Afterwards the A genome developed independently from the C genome, which brought about lots of A-genome variants (Al, Ap, Ad, Ac, As), and finally produced a cultivated diploid species (*A. strigosa* Schreb.) with the As genome. RAPD analysis and studying avenin protein markers made it possible to conclude that in spite of all differences between species with the A genome they have indirect evolutionary affinity [Loskutov et al., 1999; Loskutov & Perchuk, 2000]. Genesis of tetraploid species became possible either after the doubling of the chromosome number in one of the diploid species (AA) or with spontaneous hybridization of two closely related (AB = AA') diploid species. This resulted in raising ploidy to a higher level and bringing into existence a group of tetraploid species with either AB or AA' genomes, which provided an opportunity for the development of a cultivated tetraploid species (*A. abyssinica*) containing the AB genome. Later, diploid species with A and C genomes united into one genotype (*A. canariensis*, Ac and *A. ventricosa*, Cv), where the A genome in one of intermediate forms transformed by structural divergence into a D genome or, as it is now assumed, into an A'' genome.

The species with A and AB (AA') genomes and a biaristulate lemma tip (sectio *Aristulatae* (Malz.)) had in most cases a disarticulated floret. Some of them have cultivated analogues with the same ploidy level (*A. wiestii* Steud., *A. hirtula* Lagas. – *A. strigosa* Schreb.; *A. vaviloviana* (Malz.) Mordv.– *A. abyssinica* Hochst.) and wider areas of distribution (*A. wiestii*, *A. hirtula* and *A. barbata*), being rather active weeds (*A. clauda* Dur., *A. pilosa* M.B., *A. damascene* Rajh. et Baum, *A. longiglumis* Dur. and *A. barbata*). Obviously, this group seems apparently had no part in the development of hexaploid oats [Loskutov, 2003].

This publication presents historical review of botanical systems of genus *Avena*. Modern taxonomy is presented on the basis of complex evaluation of *Avena* species. It has been shown that the species with the C and AC genomes, whose characteristic feature, i.e. the presence of a bidentate lemma tip (section *Avenae*), is typical for hexaploid species, are transitional ancestral forms (looks like *A. ventricosa*, *A. canariensis* or *A. magna*) in the evolution of hexaploid oats. This group includes diploid species *A. ventricosa* Balan., *A. bruhnsiana* Grun., *A. canariensis* Baum and *A. agadiriana* Baum et Fed. as well as tetraploid species *A. magna* Murph. et Terr., *A. murphyi* Ladiz. and *A. insularis* Ladiz., that bear only disarticulated spikelets and do not have direct cultivated analogues.

Significant differences between tetraploid species with AB and AC genomes have been confirmed by the data of RAPD analysis and avenine protein markers [Loskutov et al., 1999; Loskutov & Perchuk, 2000]. Further on, the species with three genomes A, C and D underwent hybridization and produced an allohexaploid species, the progenitor of *A. sterilis*, which generated a large group of species, including hexaploid *A. byzantina* and *A. sativa* with the ACD (ACA'') genome. Divergence of A and C, two major genomes of the genus *Avena*, may be traced by the karyotype structure, avenine protein marker spectra and RAPD data [Loskutov & Abramova, 1999; Loskutov et al., 1999; Loskutov & Perchuk, 2000]. Besides, distinctive differences were found in the areas of distribution of the species containing these genomes [Loskutov, 2003].

Acting as such transitional progenitors for cultivated hexaploid species of *Avena*, in our opinion, may be wild diploid and tetraploid forms possessing a characteristic feature typical for hexaploids, that is the presence of two denticles on the tip of the lemma (section *Avenae* Losk.).

Presumably in the western part of the Mediterranean region, where the richest specific diversity of *Avena* is concentrated, spontaneous hybridization of diploid and tetraploid species from the group of transitional forms with genomes A, C and D initiated development of all allohexaploid species. The occurrence of the largest diversity of polyploids in the eastern part of Anterior Asia, where soil and climate conditions are harder than in the western Mediterranean areas, was confirmed by N. I. Vavilov's [1926] statement about greater hardiness of this group of species, as compared with diploid ones, because allopolyploid species promote development of extremely differentiated ecotypes, which played an important role in the evolution. Proceeding from the centre of origin toward the South-Western Asiatic centre, smaller-seeded and more adaptive hexaploid forms of wild species began to occur.

The whole diversity of cultivated oats was proven by N. I. Vavilov [1926] to have a weedy field origin. As its species moved northwards, oat replaced basic crops by weeding them and became an independent crop for itself. This process may be clearly traced in Spain on the cultivated diploid species *A. strigosa* Schreb., in Ethiopia on *A. abyssinica* Hochst., in Turkey and Iran on *A. byzantina* C. Koch and weedy forms of *A. sativa* subsp. *sativa* convar. *asiatica* Vav. and *A. sativa* subsp. *sativa* convar. *volgensis* Vav. At present, all these cultivated forms (non-shattering by themselves) became weeds [Loskutov, 2004].

Analysis of the global diversity of local varieties available in the VIR oat collection, much of which was collected by N. I. Vavilov himself during his Mediterranean exploration (1926-1927) [Loskutov, 1999], has shown that the greatest intraspecific variability of diploid cultivated species *A. strigosa* Schreb. is concentrated in Great Britain, Germany, Spain and especially Portugal. This species, according to the classification of N. A. Rodionova et al. [1994], is divided into three subspecies: *A. strigosa* subsp. *strigosa* Thell., *A. strigosa* subsp. *brevis* Husn.

and *A. strigosa* subsp. *nudibrevis* (Vav.) Kobyl. et Rod., with distinct geographic differentiation. A majority of diverse forms representing *A. strigosa* subsp. *strigosa* Thell were widespread in Spain, Portugal, Germany and Great Britain; besides, some of the forms had their origin in several other European countries. Local forms of *A. strigosa* subsp. *brevis* Husn. most typically originated from Portugal, Great Britain and, to a lesser extent, Spain. As for the naked forms of *A. strigosa* subsp. *nudibrevis* (Vav.) Kobyl. et Rod., the only possible centre of their origin is Great Britain; elsewhere these plants could only be exogenous.

Naked forms have most likely originated as a result of further metamorphosis of the caryopses disarticulation mechanism. If we get a closer view on the cycles of wild, cultivated and naked oat plant forms, the nature of disarticulation of the florets (caryopsis) would vary from complete disarticulation of the caryopsis at maturity (florets or spikelets) with a distinctly expressed callus (wild type) through solid attachment (cultivated covered type) up to unhindered detachment of the caryopsis from the lemma (cultivated naked type).

Distribution of *A. strigosa* Schreb. northwards into Great Britain was accompanied by changes in the environments, thus expanding the habitats of the forms of *A. strigosa* subsp. *brevilis* Husn., and later producing recessive mutations of the type characteristic of naked forms of *A. strigosa* subsp. *nudibrevis* (Vav.) Kobyl. et Rod., which had been described by Linneus as *A. nuda* L.

A. abyssinica Hochst. has a lot in common with *A. vaviloviana* (Malz.) Mordv. and is considered its cultivated analogue. Scanty intraspecific diversity of *A. abyssinica* Hochst., represented by six plant forms in the rank of botanical varieties, as described in *Cultivated Flora* [Rodionova *et al.*, 1994], is limited to the territory of the contemporary Ethiopia. As regards a majority of its morphological characters, this species is very uniform. Its wild relative *A. vaviloviana* (Malz.) Mordv., widespread only within the same territory, is not rich in morphological forms as well, as witnessed by our investigations and confirmed by avenin protein marker studies [Loskutov, 2003]. Obviously, both *A. vaviloviana* (Malz.) Mordv. and *A. abyssinica* Hochst., having found in Ethiopia the most favourable climate and soil conditions for distribution into the south of the Mediterranean centre, were unable to move further on because of more severe arid climate in the countries adjacent to Ethiopia. It should be mentioned that diploid and hexaploid cultivated species incorporate naked forms, while tetraploids do not contain them. The most probable reason, in our opinion, is that the species of this group were unable to disperse far from their centre of origin, had no recessive mutations and consequently produced no naked forms.

The progenitor of the whole group of hexaploid species was the large-seeded *A. sterilis* L., with disarticulated separate spikelets. This species underwent mutations in the manner of caryopses dispersal, which led to the development, on the one hand, of the cultivated species *A. byzantina* C. Koch, and on the other, of the wild species *A. occidentalis* Dur. shattering by separate caryopses and occurring presently only on the Canary Isles (Spain). It is highly probable that, owing to the changes in the disarticulation type, *A. occidentalis* Dur. had previously occupied vast areas; besides, its dominating type of development is winter or semi-winter, and we consider it primary, compared to the spring type. In the process of eastward distribution *A. sterilis* L. became differentiated into more adaptive small-seed forms of *A. ludoviciana* Dur., which underwent mutations in the Anterior Asiatic centre that changed their caryopses disarticulation type. It led, in its turn, to the appearance of weedy field forms of *A. sativa* L. As for *A. occidentalis* Dur., moving eastwards it acquired earlier ripening, typically spring forms which combined into a separate species, *A. fatua* L. This species, with disarticulated single florets, became a harmful weed and infested vast areas in the north and east of Europe and Asia. Weak sensitivity to vernalization and strong reaction to the length of day was reported to indicate true spring nature of *A. fatua* L., which enabled it to occupy by weeding the most extensive agricultural territories on the Earth. True spring nature of this species proves that it was secondary in origin as compared with *A. sterilis* L. and *A. ludoviciana* Dur. [Loskutov, 2001a].

Analysis of numerous landraces collected by N. I. Vavilov (1926-27), P. M. Zhukovsky (1925-27) and V. V. Markovich (1926-28) during their explorations and collecting missions

[Loskutov, 1999] has shown that the greatest intraspecific diversity of *A. byzantina* C. Koch may be found in the Mediterranean region. The primary centre of morphogenesis for *A. byzantina* C. Koch is within the territories of Algeria and Morocco, where its richest endemic botanical diversity is available. The presence of multiple intermediate plant forms in Turkey suggests that this region was a secondary centre of diversity for this species. Another direction of distribution for hexaploid forms was the northward course. New climate conditions provoked mutations of a *sativa* type, which, as it was initially with *A. byzantina* C. Koch, contaminated wheat and barley fields. RAPD analysis [Loskutov & Perchuk, 2000] helped to ascertain that plants representing cultivated species *A. sativa* L. and *A. byzantina* C. Koch formed comparatively small groups, remote from each other, which may serve as a proof of their geographic isolation during domestication: *A. byzantina* C. Koch entering cultivation from the western part of the Mediterranean and *A. sativa* L. from the South-Western Asiatic centres of origin of cultivated plants.

Studying intraspecific diversity of covered accessions of *A. sativa* subsp. *sativa* L. (Rodionova et al., 1994) has shown that weedy field forms of this subspecies (*A. sativa* subsp. *sativa* convar. *asiatica* Vav. and *A. sativa* subsp. *sativa* convar. *volgensis* Vav.) are localized in the territories of Iran, Georgia and Russia (Daghestan, Tatarstan, Bashkortostan and Chuvashia). The groups of intraspecific variability of *A. sativa* subsp. *sativa* convar. *asiatica* Vav. and *A. sativa* subsp. *sativa* convar. *volgensis* Vav., characterized by primitive or transitional traits and weeding crop fields, demonstrated distinct attachment to certain areas. Analysis of the VIR collection data on attribution of local accessions collected in 1920-30's to different species has shown that forms of *A. sativa* subsp. *sativa* convar. *asiatica* Vav. have their richest diversity only in Iran and Georgia, where all three botanical varieties of this group were identified, while in Daghestan only one of these varieties was found. Another group, *A. sativa* subsp. *sativa* convar. *volgensis* Vav., has four botanical varieties, and Tatarstan harbours the greatest diversity of them (all 4 botanical varieties). Three varieties were identified in Bashkortostan, Chuvashia and Ulyanovsk Province, two were found in Udmurtia, and only one of them in Kirov Province, Saratov Province and Mordovia. In other regions of covered oat distribution these forms are absent. It is very likely that covered forms of *A. sativa* subsp. *sativa* L., weedy from the beginning, started to be introduced into cultivation and spread in all directions from the South-Western Asiatic centre across Iran farther into Georgia, Daghestan and Middle Volga Region (Saratov and Ulyanovsk Provinces, Tatarstan, Chuvashia and Bashkortostan).

One more subspecies, *A. sativa* subsp. *nudisativa* (Husnot.) Rod. et Sold., or naked hexaploid oat, according to N. I. Vavilov [1926], originated from specific mountain region of north-west part of China. It is reported in publications that hull-less oat was known in China as early as in the 5th century A. D. [Zhukovsky, 1964]. Getting farther eastwards from its main centre of diversity (South-Western Asiatic centre of crop origin), with a change of growing conditions, *A. sativa* L. produced naked-seeded mutations, which finally settled in new habitats.

While analyzing data on intraspecific diversity of naked landraces of *A. sativa* L., it came out that among the Mongolian germplasm samples collected by V. E. Pisarev's mission (1922-1923) [Loskutov, 1999], where all four botanical varieties of the subspecies were identified. Three botanical varieties had their origin in China, four in Mongolia (two of them are strictly endemic for these regions), two in one of the adjacent Russian provinces, and another two in the other. The remaining forms of naked oat, representing two most widespread variants, originated from the European part of Russia or other European countries. It leads to the conclusion that the The part dedicated to the breeding value of oat species contains the analysis of literary sources and results of studying a set of oat species according to several commercial traits. Highly variable response to photoperiod and vernalization illustrated the level of polymorphism for these characters within the cultivated and wild gene pools of the genus *Avena*. The results of this study have demonstrated that for the majority of wild species under evaluation cold requirements have more influence on the date of heading and the duration of the vegetative period than daylength. It has also been shown that the response of wild *Avena* species to vernalization is to some extent linked with the geographic distribution of the accession and the response to daylength is species-dependent. No

strict correlation between species, their geographical origins and response to photoperiod was observed, although several daylength-insensitive forms of various species originated from latitudes south of 40⁰N.

As a result of the study when crown rust (caused by *Puccinia coronata* Cda. f. sp. *avenae* Faser et Led.) resistance had been assessed on the level of species, it was observed that most diploid wild species missed this character. Among the tetraploid species, resistance was observed in most species. Hexaploid species *A. sterilis* was the most resistant and promising for character-targeted breeding. *A. ludoviciana* and *A. occidentalis* may also be regarded as promising. 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 Africa, such as Tunisia, Algeria and Morocco.

While assessing stem rust (caused by *Puccinia graminis* Pers. f. sp. *avenae* Eriks.) resistance, variation of responses in the species studied was wider than in cultivated oats. At the same time, among few diploid species only medium resistance to this disease was identified. Tetraploid wild species were characterized as strongly susceptible to this pathogen. 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 (caused by *Hordeum virus nanescens* Rademacer et Schwarz.) was observed in the diploid species with A-genome variants. An overwhelming majority of tetraploid species with different genomes had medium tolerance to this virus, except highly susceptible *A. agadiriana* and *A. murphyi*. All hexaploid species basically demonstrated medium tolerance to BYDV, with *A. occidentalis* having the highest percentage of resistant accessions. The strongest and medium tolerance was 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*.

Resistance to powdery mildew (caused by *Erysiphe graminis* D. C. f. sp. *avenae* Em. March.), oat leaf blotch (caused by *Helminthosporium avenae* Eidam.), oat leaf blight (caused by *Septoria avenae* Frank.) and oat necrotic mottle (caused by *Mirothecium verrucaria* Ditmar. ex Fr.) was demonstrated by the accessions with different ploidy levels collected in various regions.

The results of our field researches and literary review reported great diversity in the structure and separate elements of panicle. Variation of these descriptors was insignificant throughout the years of study. Analyzing the panicle structure on the species level certified that such parameters as panicle length, number of spikelets and panicle density varied greater in the diploid wild species than in other groups of species.

Besides, field evaluation of wild oat species cast light on the rich diversity in kernel characters. Analyzing the percentage of husk and size of kernels on the species level helped to determine that diploid wild species had greater variation of these descriptors than the other groups of species. On the whole, it was ascertained that diploid species had the highest values of huskness percentage and the lowest of kernel size. Two tetraploid species *A. magna* and *A. murphyi* were also distinguished for large size of their kernels, since their 1000 grains weight reliably exceeded maximal average values of all species studied. Hexaploid species demonstrated even less variation in the structure of kernel than tetraploid ones. *A. fatua* was reported to be among the species with the lowest percentage of huskness, while *A. sterilis* had the highest values among this group of species. Variation of kernel size was insignificant among these species, being comparable with *A. sativa*.

The data of biochemical research on wild and weedy field oat species showed the highest groat protein content in the accessions of 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*. High nutritive value of protein was notable in tetraploid *A. barbata*. Hexaploid species appeared to have the percentage content of lysine and other essential amino acids in protein comparable with the level of *A. sativa*. Noteworthy for high groat oil content were accessions of diploid *A. pilosa* and *A. canariensis*, tetraploid *A. murphyi* and *A. magna*, hexaploid *A. fatua*, *A. ludoviciana* и *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 was reported in the forms of diploid *A. hirtula*, *A. longiglumis* and *A. wiestii*, tetraploid *A. barbata*, *A. vaviloviana* and *A. magna*, hexaploid *A. fatua* and *A. ludoviciana*. At the same time, biological activity of such oil is determined by the correlation between linoleic and oleic acids, which should be equal to one. This correlation was observed in the accessions of diploid *A. ventricosa*, *A. clauda*, *A. pilosa* and tetraploid *A. vaviloviana*. The research resulted in mapping the geographic distribution of intraspecific diversity with regard to all oat species and forms. It appeared 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.

These studies and literary review confirmed that spp. *A. sterilis* and *A. ludoviciana* are the most promising and important both in terms of grain quality and in terms of transferring this trait onto cultivated oat. The research resulted in finding intra-specific variation in biochemical parameters under study, which opens a possibility to search for forms with a set of commercially valuable properties and high grain quality.

Increasing abiotic resistance of the released cultivars, to a great extent, provides for conservation of the biodiversity of major agricultural crops. In view of this, specific priority should be attributed to the research aimed at seeking new sources of edaphic resistance among wild relatives of cereal crops, since cultivated species in the process of evolution have in most cases lost the characters that initially belonged to their wild ancestors.

The results of evaluation of aluminium tolerance have shown that the wild species (diploid and tetraploid ones) carrying a C genome had low level of resistance to the excessive content of aluminum and hydrogen ions in the nutrient media, while the carriers of A and B genomes were more frequently characterized as having high alum resistance. The analysis has made it clear that some accessions that we have identified as resistant originated in the environments with excessive moisture or in mountainous areas. It seems very likely that the long-term life of plant forms under soil and climate environmental stress has led to the development of efficient protective mechanisms against unfavourable edaphic factors in these genotypes. All the forms of cultivated oats identified in the process of this study may be recommended for utilization in breeding practice.

The analysis of wide literary review and results of studying such an representative set of accessions of genus *Avena* with different ploidy levels made it possible to display intra-specific diversity on all the characters involved. A part of tetraploid species and especially hexaploid ones identified as sources of the assessed descriptors may be directly included in the breeding process for resistance to biotic and abiotic factors, agronomic traits, and grain quality for feed and food. Numerous researches in this direction and practical results of oat breeding have evidenced that utilization of wild species alongside with the varietal diversity of cultivated forms is the most promising trend of oat breeding, capable of broadening genetic base and reducing genetic erosion of this crop.