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SIBIRSKII VESTNIK SEL'SKOKHOZYAISTVENNOI NAUKI

УЧРЕДИТЕЛИ: СИБИРСКИЙ ФЕДЕРАЛЬНЫЙ НАУЧНЫЙ ЦЕНТР АГРОБИОТЕХНОЛОГИЙ
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МИКРОБИОЛОГИЧЕСКАЯ АКТИВНОСТЬ ЧЕРНОЗЕМА В ЗАВИСИМОСТИ ОТ ХАРАКТЕРА ИСПОЛЬЗОВАНИЯ И РАЗМЕРА ПОЧВЕННЫХ АГРЕГАТОВ

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Представлены результаты исследований по изучению изменения биологической и ферментативной активности почвы в зависимости от антропогенного влияния и размера почвенных агрегатов. Работа выполнена в 2015–2021 гг. в условиях юго-востока Центрального Черноземья. Почва опытного участка – чернозем обыкновенный (сегрегационный) среднемощный среднегумусный тяжелосуглинистый. Объекты исследований – пашня с 1952 г. и залежь, используемая под сенокос с 1882 г. Показано количественное изменение отдельных групп микроорганизмов, определяемое характером воздействия на почвенный покров. Общее количество микроорганизмов как на пашне, так и в черноземах под естественной растительностью было на одном уровне – 40,0 и 39,3 млн КОЕ соответственно. Отмечены существенные различия биологической активности черноземов по отдельным группам структуры микробного ценоза. Выявлено увеличение количества бактерий аммонификаторов в пахотном аналоге в среднем на 30,7%, микромицетов – на 4,4, целлюлозолитиков – на 46,4, нитрификаторов – на 46,9, расчетного коэффициента гумуфикации – на 45,4%. По другим компонентам микробного ценоза отмечено преимущество залежных степных почв: актиномицетов на 18,5%, минерализаторов гумуса на 11,8%. Показано увеличение активности большинства групп микроорганизмов в структурных отдельностях меньшего размера – 1–5 мм. В более крупных мезоагрегатах численность КОЕ снижается. Наиболее рельефно данная закономерность прослеживается в агрогенно измененных почвах. В почвах, занятых естественной растительностью, отмечена более высокая активность биохимических процессов.

Ключевые слова: чернозем, залежь, пашня, почвенные агрегаты, микробиологическая активность, ферментативная активность

MICROBIOLOGICAL ACTIVITY OF CHERNOZEM DEPENDING ON THE USE AND SIZE OF SOIL AGGREGATES

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The results of the studies of changes in biological and enzymatic activity of soils depending on the anthropogenic influence and the size of soil aggregates are presented. The work was carried out in 2015-2021 in the conditions of the south-east of the Central Chernozem region. The soil of the experimental site is ordinary (segregational) medium–sized medium-humus heavy loamy chernozem. The objects of research are long–used arable land and the layland used for haying since 1882. The quantitative change of individual groups of microorganisms, determined by the nature of the impact on the soil cover, is shown. The total number of microorganisms in both arable land and chernozems under natural vegetation was at the same level of 40.0 and 39.3 million CFU, respectively. Significant differences in the biological activity of chernozems by individual groups of microbial cenosis structure were noted. An increase in the number of ammonification bacteria on the arable analogue was revealed by an average of 30.7%; micromycetes by 4.4%; cellulolytics by 46.4%; nitrifiers by 46.9%; calculated humification coefficient by 45.4%. According to other components of microbial cenosis, the advantage of layland steppe soils is noted: actinomycetes by 18.5%; humus mineralizers by 11.8%. An increase in the activity of most groups of microorganisms was shown in the smaller structural units of 1-5 mm. In larger mesoaggregates, CFU numbers tend to decrease. This pattern is most clearly traced in agrogenically altered soils. In the soils occupied by natural vegetation, there is a higher activity of biochemical processes.

Keywords: chernozem, layland, arable land, soil aggregates, microbiological activity, enzymatic activity

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INTRODUCTION

Chernozems, which are the predominant background soils of the Central Chernozem Zone, possess high natural fertility. Prolonged agricultural use leads to changes in their properties and quality, primarily affecting the agrochemical and agrophysical parameters of the plow layer of soil. As a result of intensive agrogenic impact, the bulk density, structural and granulometric composition, microaggregate condition, biological activity, tillable land productivity, and other indicators undergo significant transformations [1–5].

Higher crop yields are achieved under optimal soil density conditions [6]. Soil fertility regulation affects multiple aspects. The application of mineral fertilizers [7] is a radical and effective means of enhancing plant nutrition. Their use reduces the negative risks associated with drought, which is particularly relevant in the steppe regions of Russia with insufficient moisture [8].

Physical indicators, in turn, determine the direction and flow of soil processes responsible for the chemical, physicochemical, and microbiological aspects of fertility. Increased soil density can act as a restraining factor on their biological activity [9, 10]. The structural-aggregate condition is closely related to the soil's humus content [11]. Several authors have noted changes in microbial activity and fertility indicators depending on the soil's structural condition [12, 13].

The purpose of this study is to investigate the changes in the microbial cenosis structure of chernozem soil depending on the size of soil aggregates as a result of anthropogenic impact.

MATERIAL AND METHODS

The research was conducted at the Voronezh Federal Agricultural Scientific Centre named after V. V. Dokuchaev from 2015 to 2022. The study objects were a natural soil deposit formed in 1882 and a cultivated plot established in 1952. The soil deposit area has been annually used for haymaking over the course of 140 years, while the cultivated plot follows a grain-fallow crop rotation. The soil was plowed to a depth of 20-22 cm. The soil type is medium-loamy ordinary chernozem on heavy carbonate clay loams. The organic matter content is 10.2% in the deposit and 6.7% in the cultivated plot, with a pH of the soil extract ranging from 6.8 to 7.2. The exchangeable calcium content is 30-32 mmol (eq.)/100 g of soil, and magnesium content is 5-7 mmol (eq.)/100 g. Favorable moisture conditions prevailed during the years of the study, with annual precipitation exceeding 500 mm, compared to the long-term average of 430 mm.

Microbiological activity was determined using the following method[1]; ammonifying bacteria were cultivated on the meat-peptone agar (MPA), bacteria utilizing mineral forms of nitrogen and actinomycetes were cultivated on starch-ammonium agar (SAA). Soil plates were used to assess the quantity of nitrogen-fixing bacteria. The population of nitrifying bacteria was estimated through cultivation on alkaline agar, while humus mineralizers were assessed on nitrate agar.

Soil enzymatic activity was determined as follows: catalase activity was measured using the Johnson and Temple method, invertase activity was measured using the V.F. Kuprevich method, urease activity was measured using the A.Sh. Galstyan method modified by F.Kh. Khaziev on a photoelectrocolorimeter KFK-2-UHL4.2, and phosphatase activity was measured using the F.Kh. Khaziev method on KFK-2-UHL4.2[2].

The structure of the microbial cenosis was determined using fresh soil samples. In the field conditions, soil samples were dispersed into fractions of 1-2, 2-3, 3-5, 5-10, and more than 10 mm.

RESULTS AND DISCUSSION

The results of the conducted research indicate significant differences in the structure of the microbial community depending on the size of soil particles. The most noticeable differences are characteristic of arable soils. The maximum total microbial population is observed in aggregates with a minimum size of 1-2 mm - 43.1 million CFU (see Table 1). Increasing the size of soil particles to 10 mm and larger leads to a decrease in the total microbial population to 37.0 million CFU.

In chernozem soil deposits used for hayfields, the total number of microorganisms per fraction varied to a lesser extent, ranging from 38.2 to 40.8 million CFU. The exception

Табл. 1. Структура микробного ценоза (2015–2021 гг.)
Table 1. Structure of microbial cenosis (2015–2021)

Option	Soil particle size, mm	Total number	MPA	SAA	Actinomycetes	Humus mineralizers	Micromycetes	Cellulosolithics	Nitrifying agents	Humification coefficient Hl
		mln CFU					thous. CFU			
Arable land since 1952	1–2	43,1	10,3	17,9	2,69	12,1	24,8	64,7	0,47	16,4
	2–3	41,7	10,4	18,1	2,84	10,3	24,2	65,1	0,47	16,6
	3–5	36,1	8,7	15,5	2,29	9,5	24,4	61,3	0,47	13,7
	5–10	42,1	10,5	17,3	2,99	11,3	26,0	57,5	0,45	17,1
	>10	37,0	9,2	17,0	2,94	7,9	30,0	68,5	0,50	14,7
Layland since 1882	1–2	38,2	7,7	17,4	3,09	10,1	24,0	36,9	0,34	11,0
	2–3	40,8	7,0	18,1	3,48	12,3	25,5	43,2	0,33	9,7
	3–5	40,1	7,4	18,3	3,20	11,3	23,7	44,2	0,30	10,4
	5–10	37,8	7,8	15,9	2,93	11,2	23,5	45,5	0,34	11,7
	>10	39,4	7,6	15,9	3,59	12,2	27,1	46,8	0,32	11,2
$LSD_{0,95}$		0,25	0,12	0,32	0,08	0,51	0,22	0,92	0,03	

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[1] *Tepper E.Z., Shilnikova V.K., Pereverzeva G.I.* Microbiology Practicum. Moscow: Drofa, 2005. 256 p.

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was particles ranging from 5 to 10 mm, which had a population of 37.8 million CFU.

It is necessary to note a general pattern - an increase in all groups of the microbial cenosis structure in smaller soil aggregates. Microorganisms that grow on meat-peptone agar (MPA) made a significant contribution to the immobilization of organic carbon. Higher numbers of these microorganisms were observed in agrogenically transformed soils, ranging from 8.7 to 10.5 million CFU/g of soil (see Table 1). In the uncultivated section of ordinary chernozem, the number of ammonifiers varied within narrower limits, from 7.0 to 7.8 million CFU. Similar values were observed for soil aggregates regardless of their size.

Microorganisms that grow on starch-ammonium agar (SAA) actively participated in the reutilization of mineral forms of nitrogen. Higher activity of amylolytic microorganisms was observed in mesoaggregates with a size of 1-5 mm, both in the deposits and in the plowed analog. The number of microorganisms growing on SAA under natural vegetation varied within the range of 17.4-18.3 million CFU. Similar values were observed in the plowed field, ranging from 17.9 to 18.1 million CFU. It is worth noting a lower activity of this group of microorganisms in soil aggregates with an increase in their size.

Transformation coefficient of organic matter, Pm = (MPA + SAA) × (MPA/SAA), reflecting humus accumulation processes, had higher values in anthropogenically influenced chernozem soils, ranging from 13.7 to 17.1. In hayfield deposits, the values of the Pm coefficient were significantly lower, ranging from 9.7 to 11.2. Higher values of this coefficient are characteristic of agriculturally valuable fractions. Thus, plowing the soil and optimizing its physical condition with a dominance of smaller-sized fractions enhance humus accumulation processes.

Humus mineralizers had higher population numbers in the chernozem soil deposits, ranging from 10.1 to 12.3 million CFU. The plowed analogs slightly lagged behind in this regard. Higher values are characteristic of agriculturally valuable aggregate fractions, ranging from 9.5 to 12.1 million CFU. It should be emphasized that bacteria responsible for organic matter mineralization had the highest activity in arable soils within the fractions of the smallest size (1-2 mm), gradually decreasing with an increase in aggregate size. In deposit soils, on the other hand, a decrease in activity was observed with an increase in soil particle size.

Nitrogen nitrifiers play a significant role in soil fertility stabilization. In hayfield soils, their baseline activity was slightly lower compared to plowed analogs. The number of nitrifiers in hayfield deposits ranged from 0.30 to 0.34 thousand CFU. Plowing, due to the activation of microbiological processes, increased their numbers to 0.45-0.50 thousand CFU. In plowed fields, the activity of nitrifiers was similar between fractions, with the exception of the dense part of structural units with the highest quantity. In deposit analogs, the activity of nitrifiers was nearly independent of particle size, showing minimal fluctuations around the average value.

Higher content of actinomycetes was found in deposit soils, ranging from 3.09 to 3.59 million CFU. Plowing led to a noticeable decrease in this group of microorganisms, to 2.29-2.99 million CFU. In this case, there was no clear regularity in the change of actinomycete activity depending on the size of mesoaggregates. In plowed fields, the maximum content of microorganisms was observed in aggregates sized 5-10 mm and larger, ranging from 2.94 to 2.99 million CFU. In chernozem deposits, no clear regularity was identified.

Bacteria involved in cellulose decomposition play an important role as cellulolytic bacteria. Higher total baseline values were characteristic of plowed soils, ranging from 57.5 to 68.5 thousand CFU. In deposit soils, their activity was significantly lower, ranging from 36.9 to 46.8 thousand CFU. The activity of cellulolytic bacteria varied depending on the size of soil aggregates and showed peculiarities across different land types. In plowed fields, a higher population of cellulolytic bacteria was observed in aggregates sized 1-3 mm and in the dense part of soil fractions larger than 10 mm. In deposit soils, the activity of cellulolytic bacteria increased with an increase in aggregate size.

The fungal microflora belongs to the group of microorganisms responsible for the deep decomposition of organic matter. Higher levels of fungal population were observed in arable chernozem soils, ranging from 24.2 to 30.0 thousand CFU (colony-forming units) per gram of soil. In comparison, the activity of fungi in residual soils was lower, ranging from 23.7 to 27.1 thousand CFU. Similar fungal population densities were found in the agriculturally valuable fractions of both residual and arable soils, with the highest activity observed in structural aggregates.

Enzymatic activity is an important soil property. Changes in the activity of urease, phosphatase, invertase, and catalase were evaluated.

Catalase activity was higher in the long-fallow chernozem soils, ranging from 5260 to 6238 mg NH_3/100 g soil (see Table 2). Tillage practices reduced catalase activity to 4600-4812 mg NH_3. Overall, there was a general decrease in catalase activity with increasing size of soil particles.

A similar trend was observed for phosphatase activity. In layland soils, phosphatase activity was observed at levels of 122.5-160.0 mg glucose/100 g soil, while in arable chernozem soils, it ranged from 44.0 to 92.5 mg glucose/100 g soil. Higher values were found with increasing size of mesoaggregates.

Urease refers to enzymes involved in the transformation of proteins. The ammonia generated through urease activity contributes to soil fertility. Mowing layland soils exhibited higher urease activity, ranging from 268 to 354 mg phenolphthalein/100 g soil. Tillage practices results in a significant reduction in urease activity, reaching 148-174 mg phenolphthalein/100 g soil. Increased urease concentrations were observed in larger linear-size aggregates in both layland and arable soils.

Enzymes belonging to the class of oxidoreductases, such as catalase, actively participate in the transformation of humic substances. Our data showed higher catalase activity in arable chernozem soils, ranging from 20.45 to 23.75 O_2 in 3 minutes. In layland steppe soils, catalase activity was slightly lower, ranging from 18.75 to 20.30 O_2 in 3 minutes. There was a weak trend of decreasing catalase activity with increasing size of soil particles, particularly evident in the layland chernozem soils.

Physical parameters of soil structure are important indicators of soil fertility. Agrogenic influences can alter the structural-aggregate state of chernozem soils. The size of soil aggregates is a key factor determining the abundance and intensity of soil biological processes[3].

Табл. 2. Ферментативная активность почвы
Table 2. Soil enzymatic activity

Option	Soil particle size, mm	Invertase, mg NH_3/100 g of soil	Urease, mg of phenolphthalein/100 g of soil	Phosphatase, mg of glucose/100 g of soil	Catalase, O_2 in 3 min
Arable land since 1952	1–2	4812	148	44,0	22,25
	2–3	4910	152	47,5	20,75
	3–5	4600	152	66,0	20,45
	5–10	4750	174	90,0	23,75
	>10	4812	160	92,5	23,05
Layland since 1882	1–2	6238	268	122,5	20,3
	2–3	6180	332	137,5	19,85
	3–5	5710	334	145,0	19,95
	5–10	5600	354	160,0	19,3
	>10	5260	276	147,5	18,75

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Transformation of complex organic compounds occurs more intensively in small aggregates due to the higher microbial population involved in the carbon cycle.

Aggregates of small size fractions are characterized by high diversity rates[4]. Increasing linear dimensions of structural units lead to increased nitrogen oxide emissions, anaerobic conditions, and negative effects on biological processes[5]. The reason for the formation of anaerobiosis in the aggregate is the physical processes of swelling - shrinkage of the aggregates, which contribute to the almost constant maintenance of a lack of air in the aggregates[6].

CONCLUSIONS

1. Tillage and intensive agricultural use of chernozem soils lead to changes in the physical parameters of soil fertility and the direction of soil biological and biochemical processes. Biological activity is directly related to the nature of land use. The highest number of major groups of microorganisms is observed in structural units of mesoaggregates, which are considered agriculturally valuable fractions. As the size of soil particles increases, the activity of soil microflora significantly decreases. The application of agronomic practices aimed at improving the structural condition of arable soils and optimizing the composition ratio of chernozem mesoaggregates during tillage can serve as a means of improving soil fertility.
2. The number of ammonifiers increases in structural units of smaller size (1-3 mm) in agrogenically transformed soils. In this regard, the layland soil variant is more conservative with a lower population of the considered bacteria regardless of the fractions size.
3. The maximum population of soil amylolytic bacteria (SAA) is characteristic of the aggregates ranging from 1 to 5 mm. Both in arable chernozem soils and in layland soils, their sizes were approximately the same order of magnitude.
4. Significantly higher numbers of actinomycetes are observed in layland soils. The highest values are characteristic of the clumpy part of the aggregates. It can be assumed that in cultivated soils, certain processes occur more rapidly.
5. Regarding the quantity of humus mineralizers, structural fractions in the 1-3 mm range have an advantage in cultivated soils. In layland soils, no differences were found depending on the fraction size, indicating the similarity of mineralization processes in all fractions.
6. The maximum number of microfungi is found in the clumpy part of the aggregates. This is due to the high sensitivity of soil fungal microflora to aeration.
7. Phosphatase, invertase, and urease show higher activity in the soils occupied by natural vegetation. Catalase activity is higher in agricultural soil ecosystems.

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ВЛИЯНИЕ ПРИМЕНЕНИЯ БИОПРЕПАРАТОВ И ГЕРБИЦИДОВ НА ФОРМИРОВАНИЕ УРОЖАЙНОСТИ СРЕДНЕСПЕЛОГО СОРТА СОИ В УСЛОВИЯХ ПРИАМУРЬЯ

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Изучено влияние гербицидов (Бизон, Стратос Ультра) и препаратов природного происхождения (Био-Фиш, Био-Альго) на формирование урожая, посевные качества и первоначальный рост среднеспелого сорта сои Журавушка селекции Федерального научного центра «Всероссийский научно-исследовательский институт сои». Исследования проводили в 2020 и 2021 гг. на опытном поле Всероссийского научно-исследовательского института сои, расположенном в южной части Амурской области (с. Садовое Тамбовского района). Было установлено, что в среднем за два года применения препаратов природного происхождения Био-Фиш и Био-Альго для предпосевной обработки семян и вегетирующих растений увеличились сохранность растений к периоду уборки и урожайность, повысились посевные качества семян. Наибольшая сохранность к уборке наблюдалась при обработке семян перед посевом препаратом Био-Фиш, а вегетирующих растений – гербицидами (составила 93,9%, что на 6,4% больше показателей контроля и на 7,8% – варианта, где использовалась только гербицидная обработка). Анализ структуры урожая показал, что в среднем за годы исследований предпосевная обработка семян препаратом Био-Фиш и вегетирующих растений гербицидами Бизон, Стратос Ультра способствовала росту количества бобов до 5,8 шт., семян до 12,9 шт. на одно растение по сравнению с контрольным вариантом. Масса семян с одного растения увеличилась до 2,47 г относительно контроля. Применение биопрепаратов обусловило повышение биологической урожайности независимо от варианта обработки на 0,64 т/га в сравнении с контролем и на 0,66 т/га относительно гербицидной обработки.

Ключевые слова: соя, биопрепарат, гербицид, сохранность, посевные качества семян, урожайность

EFFECT OF BIOPREPARATIONS AND HERBICIDES USE ON THE YIELD FORMATION OF A MID-RIPENING SOYBEAN VARIETY UNDER CONDITIONS OF THE AMUR REGION

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The effect of herbicides (Bison, Stratos Ultra) and the preparations of natural origin (Bio-Fish, Bio-Algo) on the yield formation, sowing qualities and initial growth of the mid-ripening soybean variety Zhuravushka selected by the Federal Scientific Center "All-Russian Scientific Research Institute of Soybean" was studied. The studies were conducted in 2020 and 2021 in the experimental field of the All-Russian Scientific Research Institute of Soybean located in the southern part of the Amur Region (Sadovoye village, Tambovsky District). It was found that an average of two years of application of the preparations of natural origin Bio-Fish and Bio-Algo for pre-sowing treatment of seeds and vegetative plants increased the safety of the plants to the harvest period and crop yield, as well as improved the seed quality. The greatest preservation to harvesting was observed when the seeds were treated before sowing with Bio-Fish and the vegetative plants with herbicides (93.9%, which is 6.4% more than in the control variant and 7.8% more than in the variant where only herbicide treatment was used). Analysis of the yield structure showed that, on average over the years of research, pre-treatment of seeds with Bio-Fish and the vegetative plants with herbicides Bizon, Stratos Ultra increased the number of beans to 5.8 pieces, and the seeds to 12.9 pieces per plant compared to the control variant. Seed weight per plant increased to 2.47 g relative to the control. The use of biological preparations increased the biological yield regardless of the treatment variant by 0.64 t/ha compared to the control and by 0.66 t/ha compared to the herbicide treatment.

Keywords: soybean, biological preparation, herbicide, livability, sowing seed qualities, crop yield

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Conflict of interest

The authors declare no conflict of interest.

INTRODUCTION

Every year, soybean production volumes are increasing worldwide, including in Russia. However, soybean yield in our country still remains low. In 2020 and 2021, the area under soybean cultivation in Russia was 2.86 million and 3.07 million hectares, respectively. The majority of soybean cultivation is concentrated in the Far Eastern Federal District, particularly in the Amur region, which accounted for 67.9% (844.5 thousand hectares) in 2020 and 70.9% (882 thousand hectares) in 2021. Despite having significant cultivation areas, Russia's soybean yield is lower compared to leading countries in this field, with an average yield of 16.8 c/ha, while Canada achieves 31.2 c/ha and Brazil reaches 35.5 c/ha [1].

The profitability of soybean cultivation largely depends on the agricultural practices employed. It has been established that to ensure consistently high yields, the cultivation technology of soybeans should be improved through the use of various preparations that positively influence plant growth and development [2, 3]. In recent years, organic farming has emerged as a promising direction in agriculture, which involves, among other things, avoiding the use of chemical plant protection agents and synthetic growth stimulators. Instead, bio-preparations are used, which affect vital processes in plants [4]. The advantages of such preparations are primarily their accessibility, environmental and human safety, as well as the absence of restrictions on the time of field entry after the treatment[1] [5, 6].

For this study, biostimulants of natural origin, Bio-Fish and Bio-Algo, were chosen. Bio-Fish is a highly effective natural anti-stress adaptogen, whose main active substance is arachidonic acid (a polyunsaturated fatty acid of natural origin and a precursor to a range of physiologically active substances called eicosanoids). Plant cells cannot synthesize this acid on their own, so its additional introduction is essential. In combination with other components in the Bio-Fish preparation (chitosan, triterpene acids), arachidonic acid mobilizes the plant's defense mechanisms, making them more resistant to diseases, stimulating the full development of the root system, and ensuring the preservation of crops under extreme natural conditions. Bio-Algo is an immune stimulator made from high-quality organic concentrate of brown seaweed from northern latitudes with a high content of microelements, plant-origin hormones, amino acids, and vitamins. It acts as a biostimulant and anti-stress agent with fungicidal, bactericidal, and insecticidal properties, providing plant resistance to adverse environmental factors [7].

The purpose of the study is to investigate the influence of the natural origin preparations Bio-Fish and Bio-Algo (pre-sowing seed and vegetative plant treatment) as well as the herbicides Bizon and Stratos Ultra on the sowing qualities, initial growth, and productivity of a mid-ripening soybean variety Zhuravushka under the conditions of the Amur region.

Objectives:

1. Determine the degree of influence of the bio-preparations Bio-Fish and Bio-Algo, and the herbicides Bizon and Stratos Ultra on the initial growth and sowing qualities of the Zhuravushka soybean seeds.

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2. Investigate the effect of bio-preparations on plant preservation and yield structure of the examined variety.

3. Determine the biological seed yield of the Zhuravushka soybean variety under different treatment options.

MATERIAL AND METHODS

The experiment was conducted in 2020 and 2021 at the experimental field of the All-Russian Scientific Research Institute of Soybean located in the village of Sadovoe, Tambov District, Amur Region. The soil of the experimental plot was meadow chernozem, heavy in terms of particle size distribution, with medium permeability (density 1.02-1.10 g/cm^3, porosity 43.8%), and pH of 5.4. It contained 2.3-2.7% humus, 20-40 mg/kg ammonium nitrogen, 30-70 mg/kg nitrate nitrogen, 50-80 mg/kg available phosphorus, and 170-200 mg/kg exchangeable potassium (according to Kirsanov's method). The total area of the plot was 11.25 m^2, with a measurement area of 2.25 m^2 and a 4-fold replication. The arrangement of the plots was block-randomized.

Seed treatment with biopreparations was carried out on the day of sowing at a rate of 20 ml/ton. Treatment of vegetative plants was performed at the trifoliate leaf stage with herbicides Bizon (active substance - bentazone, concentration 1.5 l/ha) and Stratos Ultra (active substance - cycloxidim, concentration 1 l/ha) in combination with the biopreparation Bio-Algo (concentration 5 ml/l).

The following agronomic practices were applied: deep tillage without plowing in two tracks (cultivator KPE-3.8, tillage depth 10-15 cm), early spring harrowing, application of soil herbicide, and wide-row cultivation. Manual sowing (using seed drills) was carried out at optimal timing: May 24-26 in 2020 and May 26-28 in 2021. Harvesting was done manually, and the threshing of sheaves was performed on a stationary thresher. Seed quality parameters (germination energy and laboratory germination) were determined according to the applicable methods specified in GOST 12038-84, and the weight of 1,000 seeds was determined according to GOST 12042-80. Statistical analysis of the obtained data was performed using the method of variance analysis (according to B.A. Dospeshov)[2] in the Statistika 10 software.

The vegetation period of 2020 was characterized by unstable temperature regime and occasional soil overmoistening during certain stages of soybean development. The temperature regime in May was favorable for field work, with average temperatures exceeding the long-term average by 0.1-1.6 °C (see Fig. 1). The monthly precipitation sum exceeded the climatic norm by 46.2% (see Figure 2). Throughout all three ten-day periods of June, the air temperature was lower than the long-term average and deviated from the norm by 0.7-2.9 °C, resulting in delayed growth and development of soybean plants, which only managed to form the second trifoliate leaf.

In July, the average monthly air temperature exceeded the climatic norm by 2.6 °C, accelerating the accumulation of heat. The agrometeorological conditions in August (the pod formation stage) proved to be extremely challenging. The temperature during the three ten-day periods of August was below the norm by 0.25-1.28 °C, with the average monthly temperature being 1 °C lower than the norm. In the second ten-day period of August, the weather was unstable and rainy, with the amount of precipitation exceeding the long-term average almost threefold - 96 mm and 35 As a result, soybean plants were partially suppressed due to the unfavorable conditions. The significant amount of precipitation led to soil overmoistening. The rainfall in September exceeded the long-term norm by 40%, despite the air temperature being above the norm by 14.0 and 12.4 °C, respectively.

The weather conditions in 2021 were satisfactory but had deviations from the long-term average (see Fig. 1, 2). Throughout the entire vegetation period, there was an uneven temperature pattern. The total precipitation during the soybean growing season reached 509 mm, which was 68 mm higher than the long-term av-

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[2] *Dospekhov B.A.* Methodology of field experience: textbook. Moscow: Kolos, 1979. 416 p.

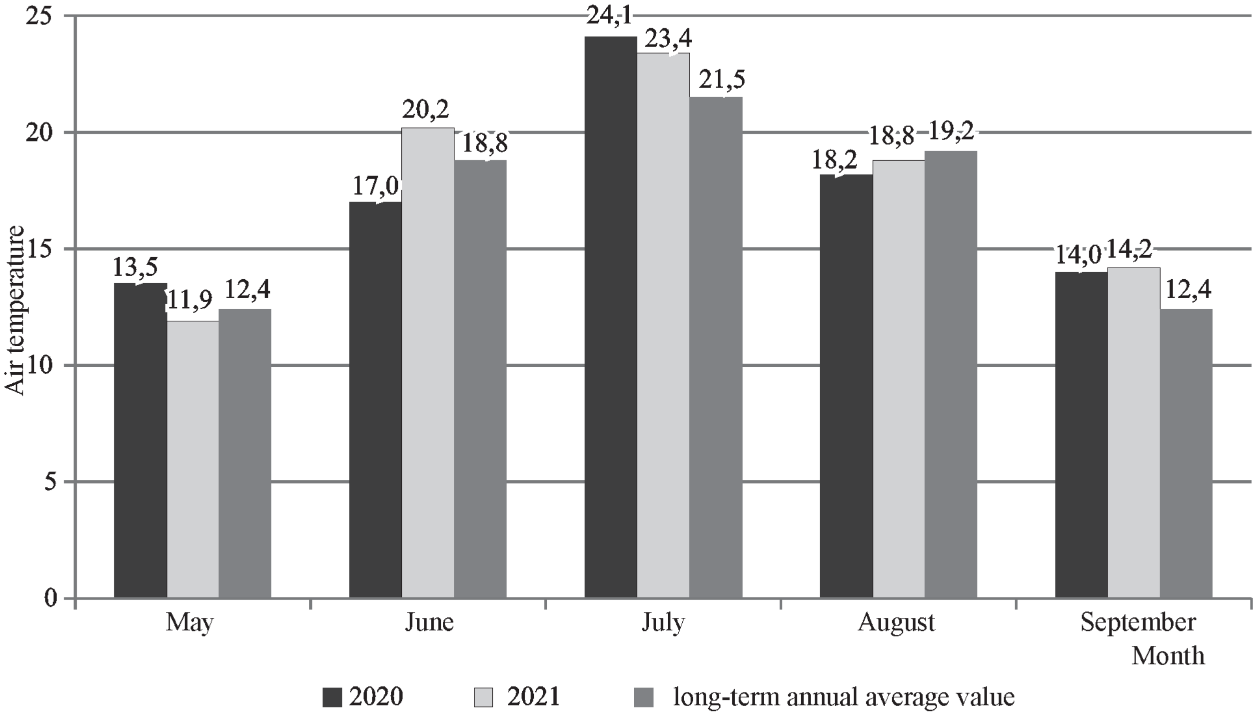

Рис. 1. Среднемесячная температура воздуха за вегетационный период (метеостанция г. Благовещенска)

Fig. 1. Average monthly air temperature for the growing season (Blagoveshchensk weather station)

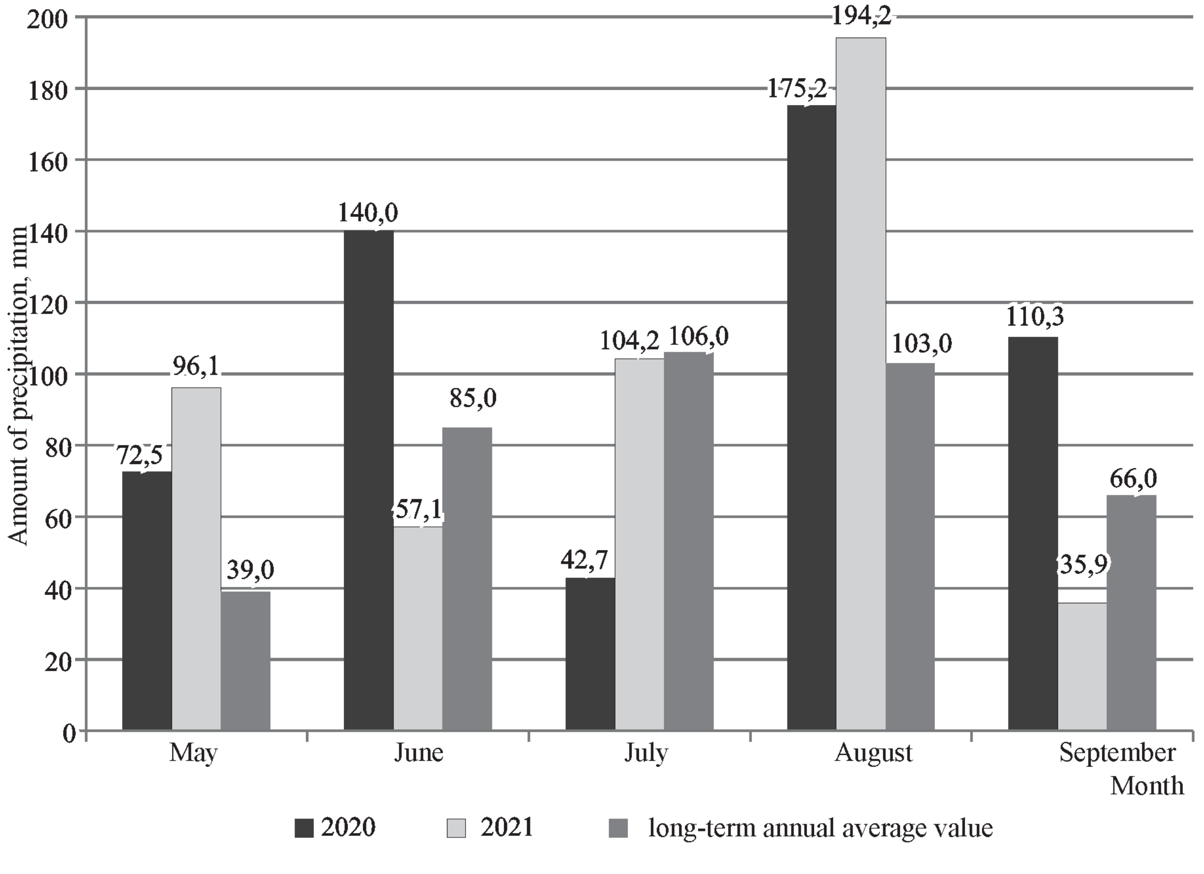

Рис. 2. Количество осадков за вегетационный период (с. Садовое)

Fig. 2. Precipitation for the growing season (Sadovoye village)

erage. The distribution of rainfall was uneven. May and August were characterized by excessive soil moisture, with precipitation exceeding the long-term norm by 57.1 mm and 91.2 mm, respectively.

The combination of temperature and precipitation during the vegetation period had both positive and negative effects on plant growth and development. Adequate heat and moisture promoted uniform germination of seedlings. In July (the flowering phase of soybeans), the temperature exceeded the long-term average, and the precipitation was at a normal level, resulting in abundant flowering and pod formation. The agrometeorological conditions in August were predominantly warm and rainy. The total precipitation for the month exceeded the climatic norm, leading to increased prevalence of phytopathogens and a decrease in crop quality. The temperature in September was 1.8 °C higher than the long-term average, while the precipitation was 45.6% below the norm.

RESULTS AND DISCUSSION

The main cause of poor soybean yield is weed infestation. To reduce yield losses in agricultural production, highly effective herbicides are actively used in combination with agronomic practices. It is well known that herbicides not only affect weeds but also the cultivated crop, making it highly relevant to combine their use with biological preparations that reduce the negative impact on plants, providing them with a boost for further growth and development [8–10].

One significant element determining seed yield is the number of productive stems that survive until harvest. To assess plant survival just before harvest, plant counting was conducted in each plot. The results showed that, on average, the highest plant survival rate was observed with the pre-sowing treatment of seeds using the Bio-Fish preparation, while the use of the herbicides promoted the survival of vegetative plants. The plant survival rate reached 93.9%, which was 6.4% higher than the control and 7.8% higher than the variant where only herbicide treatment was applied, indicating its particular importance in years with unfavorable weather conditions. When Bio-Fish was applied to the seeds before sowing without herbicide treatment the share of soybean plants survived at the moment of harvesting reached 88,4%, which is 1,4% higher than the control and 2,3% higher than in the variant with herbicides (see Fig. 3).

The study of crop structure revealed that the pre-sowing treatment of seeds with the biological preparation contributed to the reduction of herbicide toxicity on plants and had a positive impact on their growth and development. The use of only Bio-Fish seed treatment led to an increase in the number of pods by 5.8, seeds by 12.9, and seed weight by 2.47 grams per plant compared to the control. Additionally, when compared to herbicide treatment, the increase was 5.8 pods, 12.1 seeds, and 2.17 grams, respectively. The combined application of Bio-Fish and herbicide mixture resulted in a higher number of pods, seeds, and seed weight per plant compared to the control group. Treatment of vegetative plants with Bio-Algo and the herbicide mixture increased the number of pods by 2.9, seeds by 6.4, and seed weight by 1.22 grams per plant compared to the control (see Table 1).

The 2020 growing season was characterized by excessive soil moisture during certain stages of soybean plant development, which affected their growth and development. Under these conditions, the pre-sowing treatment of seeds with the studied biological preparation had the greatest positive impact on plant productivity. The yield in this variant reached 3.18 tons per hectare, which was 0.41 tons per hectare higher than the control and 0.51 tons per hectare higher than the herbicide treatment (LSD_{05} = 0.33 tons per hectare). In soybean crops where the vegetative plants were treated with herbicides Bizon and Stratos Ultra and the seeds were pre-sown treated with Bio-Fish, the yield increased by 0.20 and 0.30 tons per hectare, respectively, compared to the control (LSD_{05} = 0.33 tons per hectare).

The weather conditions in 2021 were generally favorable for the normal development of soybean plants. The use of bio-preparations contributed to the reduction of the negative im-

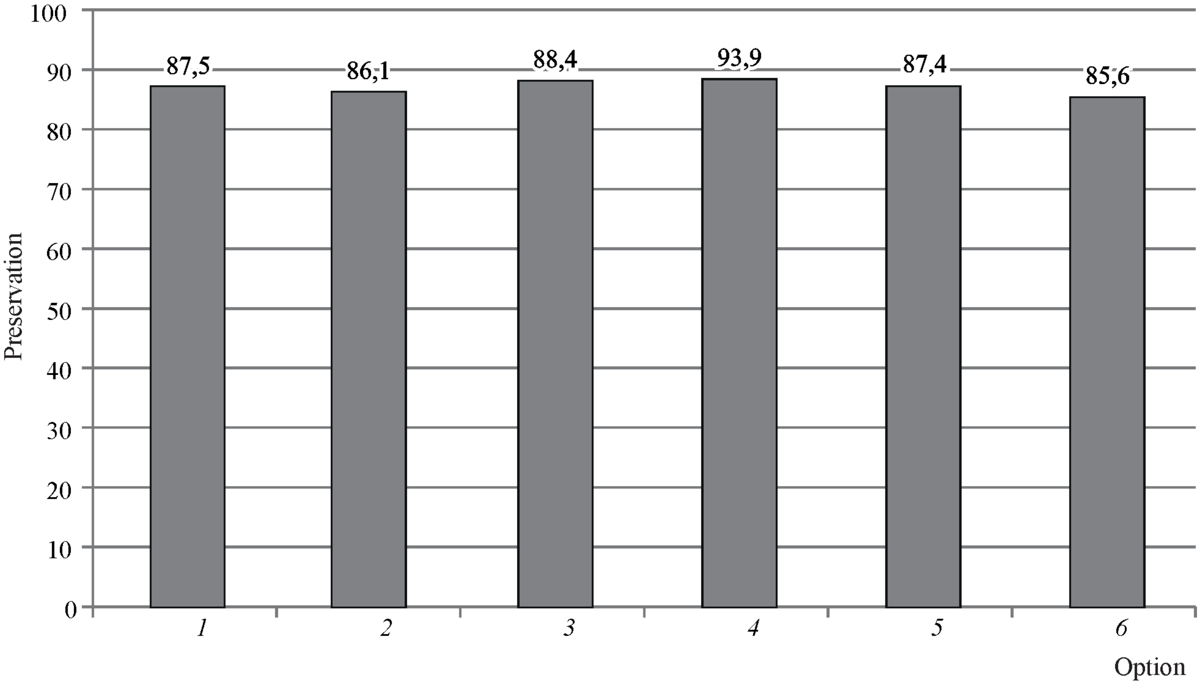

Рис. 3. Сохранность растений сои сорта Журавушка при разных вариантах обработки (средняя за 2020, 2021 гг.):

1 – контроль (без обработки); *2* – Стратос Ультра + Бизон (обработка вегетирующих растений); *3* – Био-Фиш (обработка семян); *4* – Био-Фиш (обработка семян) + Стратос Ультра и Бизон (обработка вегетирующих растений); *5* – Био-Фиш (обработка семян) + Био-Альго (обработка вегетирующих растений); *6* – Био-Фиш (обработка семян) + Био-Альго (обработка вегетирующих растений) + Стратос Ультра и Бизон (обработка вегетирующих растений)

Fig. 3. Preservation of the plants of soybean variety Zhuravushka at different treatment options (average for 2020, 2021):

1 – control (untreated); *2* – Stratos Ultra + Bizone (vegetating plant treatment); *3* – Bio-Fish (seed treatment); *4* – Bio-Fish (seed treatment) + Stratos Ultra and Bizone (vegetating plant treatment); *5* – Bio-Fish (seed treatment) + Bio-Algo (vegetating plant treatment); *6* – Bio-Fish (seed treatment) + Bio-Algo (vegetating plant treatment) + Stratos Ultra and Bizone (vegetating plant treatment)

pact of herbicides, resulting in an increase in biological yield by 0.85–1.09 tons per hectare (LSD_{05} = 0.49 tons per hectare) compared to the control and by 0.78–1.02 tons per hectare compared to the variant where herbicides were used for vegetative plant treatment (see Table 2).

It is known that most pre-sowing seed treatments increase the intensity of metabolic processes during germination with effective mobilization of reserve substances under the influence of corresponding active enzymes. As a result, seedlings emerge, and their quality influences further development, viability, and productivity of plants [11–14]. Laboratory studies of growth processes at the initial stages of plant development showed that seed treatment positively influenced their seeding qualities despite herbicide treatment (see Fig. 4).

The natural origin preparations Bio-Fish and Bio-Algo had a positive influence on the initial growth of soybean seedlings of the Zhuravushka variety. The length of seedlings was 1.2–2.7 cm greater with the combined treatment of bio-preparations and herbicide compared to the control, and it exceeded the data from the herbicide treatment variant by 4.0–5.5 cm (see Table 3).

The number of abnormally developed seedlings decreased by 6–8% compared to the variant where herbicides were used. The variation range, which characterizes the most complete and uniform seed germination, was 20.9% when Bio-Algo was used, which was 2.3% lower than the control.

Табл. 1. Биометрические показатели растений сои сорта Журавушка (в среднем за 2020, 2021 гг.)
Table 1. Biometric indicators of the plants of soybean variety Zhuravushka (on average for 2020, 2021)

Treatment		Number, pcs. per one plant		Seed weight per one plant, g
seeds before sowing	vegetative plants	beans	seeds	
Control (without treatment)		21,3	39,7	7,76
Distilled water	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha)	21,3	40,5	8,06
Bio-Fish (20 ml/t)	Distilled water	27,1	52,6	10,23
	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha)	24,3	47,4	9,31
	Distilled water + Bio-Algo (5 ml/l)	23,9	46,9	9,14
	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha) + Bio-Algo (5 ml/l)	23,9	46,1	8,98
LSD_{05}, pcs. per one plant		3,0	5,8	1,22
F_{fact}		5,6	5,1	
F_{theor}		2,9	2,9	

Note. Here and further in the tables the concentration of herbicides and biopreparations is given in brackets.

Табл. 2. Биологическая урожайность сои сорта Журавушка, т/га
Table 2. Biological yield of soybean variety Zhuravushka, t/ha

Treatment		2020	2021	Average for two years	Increment
of seeds before sowing	of vegetative plants				
Control (without treatment)		2,77	2,48	2,63	–
Distilled water	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha)	2,67	2,55	2,61	−0,02
Bio-Fish (20 ml/t)	Distilled water	3,18	3,33	3,26	0,63
	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha)	2,97	3,57	3,27	0,64
	Distilled water + Bio-Algo (5 ml/l)	2,65	3,48	3,07	0,44
	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha) + Bio-Algo (5 ml/l)	2,46	3,42	2,94	0,31
$LSD_{05,}$ t/ha		0,33	0,49		
F_{fact}		5,58	6,20		
F_{theor}		2,90	3,97		

CONCLUSION

Thus, over the course of two years of research, the use of natural-origin preparations had a positive influence on the initial growth of seedlings, germination vigor, and laboratory seedling emergence of the mid-ripening variety Zhuravushka. The length of the seedlings increased by 3.6-8.1% with combined treatment of bio-preparations and herbicides compared to the control, and it exceeded the herbicide treatment variant by 13.1-18.0%. Plant survival rate just before harvest, on average for 2020 and 2021, was highest when the Bio-Fish preparation was used for pre-sowing seed treatment in combination with herbicides, reaching 93.9%. This was 6.4% higher than the control and 7.8% higher than the variant where only herbicide treatment was applied.

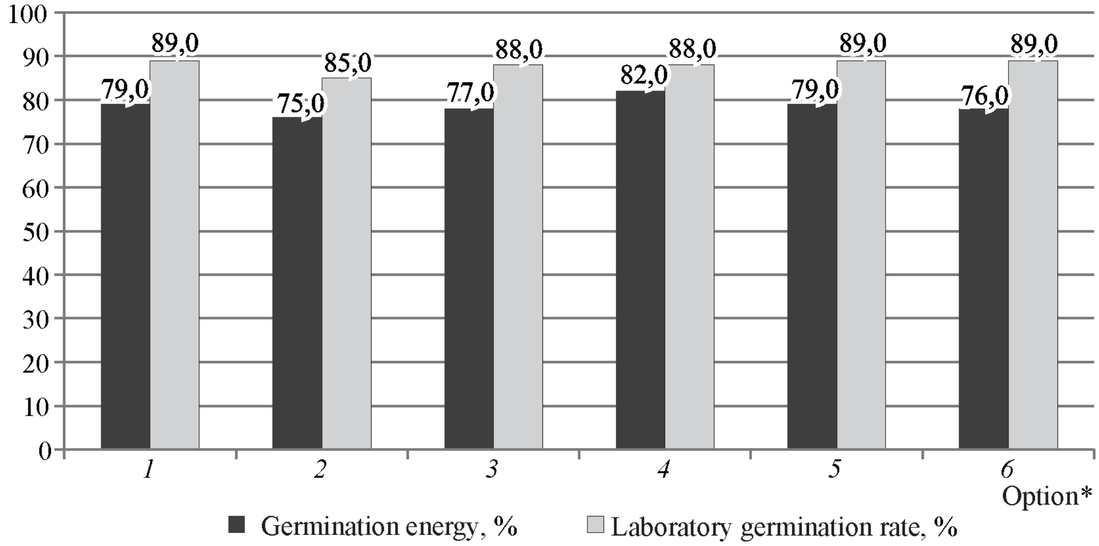

Рис. 4. Влияние разных вариантов обработки на посевные качества семян сои сорта Журавушка (2020, 2021 гг.)

*Описание вариантов обработки см. на рис. 3

Fig. 4. The impact of Bio-Fish on the sowing qualities of soybean seeds of the Zhuravushka variety (2020, 2021)

*See Figure 3 for the description of the treatment options

Табл. 3. Влияние биопрепаратов и гербицидов на первоначальный рост проростков сои сорта Журавушка (в среднем за 2020, 2021 гг.)

Table 3. The impact of Bio-Fish on the initial growth of soybean seedlings of the Zhuravushka variety (on average for 2020, 2021)

Treatment		Abnormally developed seedlings, %	Seedling length		
of seeds before sowing	of vegetative plants		Average value, cm	Variation range, %	Variation coefficient, %
Control (without treatment)		11,3	33,3	23,2	13,5
Distilled water	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha)	17,3	30,5	22,6	17,5
Bio-Fsh (20 ml/t)	Distilled water	10,0	35,2	23,2	12,5
	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha)	11,3	34,5	22,7	13,4
	Distilled water + Bio-Algo (5 ml/l)	9,3	36,0	20,9	13,1
	Stratos Ultra (1l/ha) + Bizon (1,5 l/ha) + Bio-Algo (5 ml/l)	9,3	35,2	26,3	17,4
LSD_{05}, cm			2,2		

The bio-preparations also had a significant influence on the formation of crop structure elements. Pre-sowing seed treatment with Bio-Fish, both without herbicide treatment and in combination with the herbicides, led to an increase in the number of pods by 3.0-5.8, seeds by 7.7-12.9, and seed weight by 1.55-2.47 grams per plant compared to the control. Moreover, the use of natural-origin preparations, Bio-Fish and Bio-Algo, helped reduce the negative impact on soybean plants, resulting in increased seed yield. Pre-sowing seed treatment with Bio-Fish increased grain yield by 0.31-0.64 tons per hectare compared to the control and by 0.33-0.66 tons per hectare compared to herbicide treatment (LSD_{05} = 0.45 tons per hectare).

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ИНФОРМАЦИЯ ОБ АВТОРАХ

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ПРОЯВЛЕНИЕ ПРИЗНАКА МНОГОКИСТНОСТИ СМОРОДИНЫ ЧЕРНОЙ

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Представлены результаты оценки генетической коллекции черной смородины по признаку многокистности для повышения продуктивности культуры в условиях Брянской области. Изучен показатель числа кистей с плодоношением на одном узле побега. Показано, что в условиях юго-западной части Нечерноземной зоны России (Брянская область) для культуры типично образование в пазухах листьев одной генеративной почки, однако встречаются формы, у которых часть узлов способна формировать 2–3 кисти с плодоношением. Установлено, что из 132 изученных сортов генетической коллекции 116 образцов (87,9%) формировали узлы с 1–2 генеративными почками. В результате исследований отобраны сорта с 3–4 соцветиями на узлах, способных к плодоношению (Дар Смольяниновой, Дебрянск, Брянский Агат, Селеченская 2, Ладушка, Орловский Вальс, Исток, Чудное Мгновение, Юбилейная Копаня, Вера, Чернавка и др.). Их использование в дальнейших скрещиваниях позволит получить более продуктивные генотипы. Выделены наиболее результативные комбинации скрещиваний по выходу потомства, формирующего 2–4 генеративных образования на одном узле (63-35-1 × Литвиновская, Свитязянка × Селеченская 2, Дебрянск × Дар Смольяниновой, Чудное Мгновение × Голубичка, 10-141-2 × Партизанка Брянская, Дебрянск × Литвиновская). Выделены перспективные отборные формы (3-63-01, 5-82-02, 8-69-01, 5-45-02, 4-18-01, 4-94-1, 4-18-02, 2-30-01 и др.), совмещающие признак многокистности с другими хозяйственно ценными показателями (устойчивость к патогенам, крупноплодность, десертный вкус плодов, количество ягод в кисти, их одномерность).

Ключевые слова: смородина черная, селекция, признак, многокистность

MANIFESTATION OF MULTIPLE RACEMES TRAIT OF BLACK CURRANT

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The results of the evaluation of the genetic collection of black currants on the multiple racemes trait for increasing the productivity of the crop in the conditions of the Bryansk region are presented. The index of the number of racemes with fruiting on one shoot node was studied. It has been shown that under the conditions of the southwestern part of the nonchernozem belt of Russia (Bryansk region), formation of one generative bud in the axils of leaves is typical for the crop, but there are forms in which some nodes are capable of forming 2-3 racemes with fructification. It has been found that out of 132 varieties of the genetic collection studied, 116 specimens (87.9%) formed nodes with 1-2 generative buds. As a result of the studies, varieties with 3-4 inflorescences on the nodes capable of bearing fruit were selected (Dar Smolyaninova, Debryansk, Bryansky Agat, Selechenskaya 2, Ladushka, Orlovsky Vals, Istok, Chudnoe Mgnovenie, Yubileinaya Kopanya, Vera, Chernavka, etc.). Their use in further crosses will produce more productive genotypes. The most productive

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combinations of the crosses have been identified according to the yield of progeny forming 2-4 generative formations on one node (63-35-1 × Litvinovskaya, Svityazyanka × Selechenskaya 2, Debryansk × Dar Smolyaninovoy, Chudnoe Mgnovenie × Golubichka, 10-141-2 × Partizanka Bryanskaya, Debryansk × Litvinovskaya). Promising selected forms (3-63-01, 5-82-02, 8-69-01, 5-45-02, 4-18-01, 4-94-1, 4-18-02, 2-30-01, etc.), which combine the multiple racemes feature with other economically valuable indicators (resistance to pathogens, large fruits, dessert taste of fruits, number of berries in the raceme, their one-dimensionality) are highlighted.

Keywords: black currant, selection, trait, multiple racemes

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INTRODUCTION

Blackcurrant (*Ribes nigrum* L.) is one of the most popular berry crops in domestic and international horticulture. The widespread cultivation of this crop is attributed to its ease of propagation, high winter hardiness, productivity, early fruiting, medicinal and nutritional value of the fruits. Its cultivation can be practically fully mechanized, including harvest operations[1].

The traditional use of the crop includes processing it into marmalade, juice, jam, preserves, wine, confectionery, and more [1].

The result of meticulous breeding work aimed at increasing the productivity of blackcurrants has been the development of varieties with an average berry weight of 1.5-2.0 grams. When combined with high self-fertility and adaptability of genotypes, these varieties can guarantee competitiveness in commercial production [2]. However, most breeding programs have focused on improving yield, while research on other productivity components, such as the number of fruiting nodes and generative buds on a single node, has been insufficient. Assessments of blackcurrant breeding achievements and directions in modern assortment formation for both commercial and amateur horticulture indicate that increased yield has been achieved through enhanced self-fertility, pathogen resistance, and larger fruit size [3-6]. One understudied component of blackcurrant yield formation is the number of racemes per node. While it is typical for the species to produce a single generative bud in the leaf axils, there are forms in which multiple buds develop, resulting in 2-3 fruit-bearing racemes per node.

Blackcurrant flowers are arranged in inflorescences (racemes) that form on one-year-old or older wood. The racemes hang down and are formed from primary and one or several secondary buds, depending on the variety's characteristics. Therefore, an important factor for increasing blackcurrant productivity is the abil-

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[1] *Panfilova O., Tsoy M., Golyaeva O.* Currant growing technology and mechanized harvesting-review // E3S Web of Conferences, Orel, 24–25 февраля 2021. Orel. 2021. P. 07002. DOI: 10.1051/e3sconf/202125407002.

ity to develop 2-3 generative buds per node, capable of developing into racemes[2]. Such forms have been previously identified among the subspecies of the European blackcurrant (*R. n.* subsp. *europaeum* Jancz.) and Siberian blackcurrant (*R. n.* subsp. *sibiricum* (Wolf.) Pav.) by N.M. Pavlova and V.L. Vitkovsky, as well as among *R. dikuscha* Fisch. by N.M. Bochkarnikova. It has been observed that the formation of 3-4 fruit-bearing buds per node is quite common in various forms of *R. dikuscha*[3].

According to the methodology, nodes that produce more than one raceme are considered multi-racemes nodes[4]. The manifestation of multi-racemes traits in modern cultivars is due to the extensive use of varieties such as Slozhnokistnaya and Primorsky Champion[5].

According to T.P. Ogoltsova (see footnote 2), blackcurrant plant productivity can be increased by branching the fruiting cluster, as in the case of the Slozhnokistnaya variety, or by forming main and additional buds on a single node capable of bearing fruit. The occurrence of multi-racemes nodes is associated with accelerated bud development and differentiation. Genotypes created with the participation of the Siberian subspecies of blackcurrant and R. dikuscha often develop several full-fledged generative buds in addition to the main bud by the end of the growing season. The biological mechanisms of multi-racemes formation on a single node in the representatives of the Scandinavian ecotype (*R. nigrum spp. scandinavicum*) differ. Typically, they form a single bud on the node in autumn, from which 5-6 mixed buds emerge in spring, each of which contains a flower cluster. In some buds, the development process does not reach completion, resulting in multiple clusters developing from a single bud.

V.L. Vitkovsky[6] describes deformations of fruit clusters in the variety "Blagodatnaya" as fasciations, which may be associated with changes in the conditions of differentiation of primordial-axillary growth apexes. Whorled arrangement of peduncles - formations in the form of a brush, forming 19 clusters with 129 fruits on one node - has been noted by him.

I.E. Buchenkov and I.V. Ryshkel[7] observe an increase in the length of the floral cluster and the formation of up to 2 buds in the leaf axils and 2 clusters per one raceme in *F1* hybrids obtained from interspecific crosses of *R. Nigrum* L. × *R. Rubrum* L. Similar results were obtained by I.P. Chuvashina[8] when studying offspring from the crosses between red and black currants. Seedlings were selected that were phenotypically similar to black currants, except that they formed multiple growth apexes instead of a single one, and a cluster of racemes grew from them in the spring of the following year, similar to red currants.

The formation of 2-3 racemes on one node[9] is typical for the varieties "Dikovinka," "Naryadnaya," "Seyanets Golubki," "Minai Shmyryov," "Brödtorp," "Stakhanovka Altaya," and "Öjebyn." Considering how actively these varieties were involved in the breeding programs implemented by domestic scientists, it becomes evident that multi- racemes trait should manifest in a number of their offspring. It is known

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[2] *Ogoltsova T.P.* Selection of black currant - past, present, future. Tula: Priokskoe book publishing house, 1992. 384 p.

[3] *Bochkarnikova N.M.* Black currants in the Far East. - Vladivostok: Far East Book Publishing House, 1973.183 p.

[4] *Knyazev S.D., Bayanova L.V.* Currant, gooseberry and their hybrids // Program and methodology of the varietal study of fruit, berry and nut crops. Orel: VNIISPK, 1999. pp. 351–373.

[5] *Ogoltsova T.P., Sedova Z.A.* Study of the Far Eastern forms of black currant as source material for selection in the middle zone of the RSFSR // Selection, varietal study, agrotechnics of fruit and berry crops. Orel: Orel Branch of the Priokskу Book Publishing House, 1979. Vol. 9, Part 2. pp. 59–73.

[6] *Vitkovsky V.L.* Budding neoplasms in black currant // Botanical Journal. Moscow, 1962. Vol. 47. N 3. pp. 35–40.

[7] *Buchenkov I.E., Ryshkel I.V.* Hybridization of black currant (*Ribesnigrum* L.) and red currant (*Ribesrubrum* L.) // Agriculture - problems and prospects. 2016. pp. 43–50.

[8] *Chuvashina I.P.* Neoformations in the structure of the mixed buds of distant currant hybrids // Morphogenesis of plants. Moscow, 1961. Vol. 2. pp. 256–258.

[9] *Kopan K.N., Kopan V.P.* Selection of black currants for productivity and fruitfulness // Collection of scientific articles. "Selection and varietal study of black currant". Michurinsk, 1988. pp. 57–63.

that the varieties "Labilnaya," "Orlovsky Vals," and "Nara"[10] are capable of forming 4-5 clusters on one node. Mention can be found in the literature about the French variety "Noirde Bourgogne," which is capable of forming up to 6 racemes on one node (see footnote 2). There is information that the maximum level of manifestation of this trait (up to 6 racemes on one node) is found in the variety "Ocharovanie" of the Orlovsky selection [7].

Some researchers[11] [8] believe that the manifestation of the multi-racemes trait in black currants largely depends on the fertility level of the site and compliance with agronomic requirements. V.F. Severin[12] demonstrated through experiments that properly balanced mineral nutrition and a high agrophone of a commercial plantation positively affect the length of the raceme and the formation of multi-racemes nodes on the shoot.

The purpose of the research is to assess the existing assortment and hybrid offspring of black currants in terms of the manifestation of the multi-racemes trait, as well as to search for donors and genetic sources of this productivity component.

MATERIAL AND METHODS

The work was carried out in the experimental plots of the Kokino experimental station (ES) of the Federal Horticultural Center for Breeding, Agrotechnology and Nursery (FRC of Horticulture) where 132 collection samples of foreign and domestic breeding have been studied from 2007 to 2022. The creation of the hybrid collection was carried out in accordance with the methodology[13]. Field observations and plant counts in collection plantings and hybrid seedlings were conducted according to the requirements of the methodology "Program and methodology for studying the varieties of fruit, berry, and nut crops" (see footnote 4). The statistical analysis of the obtained data was performed using Microsoft Office Excel.

The collection and breeding plots where the research was conducted are represented by gray forest soils. The soil-forming rocks are loess-like loams and loesses with a homogeneous coarse-grained granulometric composition. The content of available phosphorus in the soil is 25-35 mg/100 g of soil, potassium - 9.8-14.1 mg/100 g of soil, humus - 3.8%. The reaction of the soil solution varies from slightly acidic to acidic (pH = 4.9-6.1). The cultivation agronomy of black currants is the one that is generally accepted in the nonchernozem zone.

RESULTS AND DISCUSSION

The conducted evaluation of 132 black currant varieties in the collection plantings of the Kokino Experimental Station of the Federal Research Center of Horticulture allowed for differentiation of the original forms based on the studied trait. Despite the information found in scientific literature stating that the formation of only one raceme per node is typical for most black currant varieties[14], our research revealed that the group of varieties that do not produce multi-racemes nodes is small in number.

Thus, the group of varieties consistently maintaining the trait of single-raceme nodes throughout the entire research period includes Arabka, Gamma, Gamayun, Glarioza, Gracia, Gulliver, Dabradzea, Debut, Degtyarevskaya, Dessertnaya Ogoltsovoj, Divo Zvyaginoj, Diamant, Dobry Djinn, Dobrynya, Gold of the Incas, Kazkova, Carmelita, Klussonovskaya, Lybed, Mashenka, Nymfa, Nyura, Nezhdan-

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[10] Zatsepina I.V. Productivity of black currant varieties // Adaptive potential and quality of production of varieties and varietal-podstock combinations of fruit crops. Orel, 2012. pp. 100–106.

[11] *Shavyrkina M.A., Knyazev S.D.* Evaluation of black currant samples on morphostructural components of productivity // Bulletin of Orel State Agrarian University. 2015. N 5 (56). pp. 46–50.

[12] *Severin V.F.* Effect of mineral fertilizers on the laying of vegetative-generative buds, the formation of the number of brushes in the buds and flowers in the brushes of black currant // Siberian Herald of Agricultural Science, 1993. N 3. pp. 21–28.

[13] *Ogoltsova T.P., Kuminov E.P.* Selection of black currant // Program and methodology of selection of fruit, berry and nut crops / Under the general editorship of E.N. Sedov. Sedov. Orel: VNIISPK, 1995. pp. 314–340.

[14] *Kanshina M.V.* Black currants: selection, genetics, varieties. Chelyabinsk: NPO "Sad i ogorod". Chelyabinsk Press House,2013. 160 p.

chik, Nanny, Orlovskaya Serenada, Pamyati Potapenko, Pamyati Vavilova, Partizanka Bryanskaya, Gift of Kalinina, Ragneda, Snow Queen, Solomon, Trilena, Uslada, Charovnitsa, Chernookaya, Shaman, Shalunya, Elevesta, Ben Gairn, Ben Sarek, Big Ben, Bona, Black Magic, Black Magic Carbon.

The majority of the studied black currant varieties (87.9%) formed 1-2 racemes per node. When the number of the generative buds in the nodes changed, the formation of two-racemes formations was more frequently observed. The formation of 2 racemes per node was observed in 53% (70 varieties) of the studied varieties. These include Ametist, Amirani, Annadi, Bagira, Barmaley, Belorussotchka, Vernisazh, Voevoda (Fortuna-17), Vymplel, Galaktika, Zaglyadenie, Zelyonaya Dymka, Iskushenie, Katyusha, Kipiana, Kaskad, Krynichka, Delikates, Kudesnik, Kudmig, Kupalinka, Lentyay, Lider, Litvinovskaya, Malenkiy Prints, Minusinskaya Sladkaya, Myth, Mriya, Mriya-3, Mriya-5, Monisto, Dachnitsa, Nadina, Nadya, Sensei, Ocharovanie, Perun, Podarok Astakhova, Pamyati Ravkina, Tamerlan, Pigmy, Selechenskaya, Rita, Sevchanka, Podarok Veteranam, Slastena, Nara, Orloviya, Sudarushka, Solovinaya Noch, Azhurnaya, Oriana, Strelets, Tatyana's Day, Izyumnaya, Favorit, Fortuna, Charodey, Chereshneva, Cherny Zhemchug, Etude, Exotika, Sharovidnaya, Yadryonaya, Ben Alder, Ben Tirran, Ben Hope, Tiben, Tisel, Triton.

Much less frequently, genotypes forming up to 3 racemes on a single node were observed. Under favorable conditions for plant growth, such generative formations were noted on the shoots of the following varieties: Dar Smolyaninovoy, Debransk, Bryansky Agat, Selechenskaya 2, Slavyanka, Sokrovishche, Sofievskaya, Ladushka, Lukomorye, Orlovsky Vals, Istok, Chudnoe Mgnovenie, Yubileinaya Kopanya. The varieties Chernookaya and Sofievskaya form branched racemes similar to the variety Slozhnokistnaya, with elongated cluster-like inflorescences. Among the wide variety of studied samples, only the varieties Vera and Chernavka exhibited the formation of 4 inflorescences in the nodes.

If multi-racemes nodes are formed on a shoot, they account for a certain proportion of the total number of fruiting clusters on the fruiting wood. The table shows the level of manifestation of the multi-racemes trait using the genotypes that we most frequently used in breeding as the original forms based on a complex of economically significant traits. For example, for the Debransk variety, on average over the observation period, multi- racemes nodes accounted for 25.0% of their total number, Bryansky Agat – 23.2%, Kudmig – 22.6%, Selechenskaya 2 – 17.2%, Rita – 15.3%, and so on. At the same time, the assessment and recording of the number of inflorescences showed that for the Debransk variety, 20.8% of nodes were three-racemes, 25.0% were two- racemes, and 54.2% were single- raceme. The Bryansky Agat variety formed 15.7% three- racemes nodes, 23.5% two- racemes, and 60.8% single- raceme. On average, 22.6% of nodes for the Kudmig variety were two- racemes, and the remaining nodes were single- raceme. For the Charodey and Etude varieties, two- racemes nodes accounted for 7% of the total number. This indicates a significant variation of the studied trait among the different varieties.

The conducted series of crosses, carried out in 2009-2011, using the original forms that have the ability to develop multiple generative buds in a single node suitable for normal inflorescence development, allowed the identification of several combinations that produced multi- racemes seedlings in the offspring [9]. The majority of such hybrids (30.4-42.0%) were selected in the families Nara × Yadryonaya, Yadryonaya × Exotica, Nara × (Yadryonaya × Exotica), Kipiana × Glarioza, and Kipiana × Debransk. In the first three combinations, seedlings that formed up to 4 clusters on a single node were identified. These selections include 43-8-05 (Nara × Yadryonaya), 85-03-3 (Yadryonaya × Exotica), and 2-49-01 [8-4-1 (Yadryonaya × Exotica) I_1].

The best results in selecting multi-racemes offspring were obtained in the cross combination of Chudnoye Mgnoveniye × Golubichka, where up to 43.1% of seedlings formed more than one raceme on a single node. This can be

Оценка смородины черной по уровню проявления признака многокистности (2018–2022 гг.)
Evaluation of black currant by the level of manifestation of the multiple racemes trait (2018-2022)

Variety, selection	Number of nodes with fruiting on shoots		Number of racemes per node	Percentage of multi-racemes nodes on a fruiting shoot, %
	$X_{ср} \pm m$	V, %		
Barmalei	48,3 ± 5,7	10,3	1–2	14,5
Bryansky Agat	51,0 ± 8,0	12,6	1–3	23,2
Dar Smolyaninovoy	37,3 ± 8,7	23,4	1–3	10,7
Debryansk	48,0 ± 8,2	17,1	1–3	25,0
Kipiana	38,7 ± 5,5	14,8	1–2	13,2
Kudmig	44,3 ± 6,0	13,6	1–2	22,6
Lentyay	40,0 ± 4,0	10,0	1–2	7,5
Litvinovskaya	46,3 ± 6,0	13,0	1–2	12,9
Myth	53,0 ± 11,8	12,1	1–2	15,1
Nezhdanchik	45,3 ±7,6	16,7	1	–
Podarok Veterana	47,3 ± 7,6	19,9	1–2	12,7
Rita	39,3 ± 4,0	10,3	1–2	15,3
Selechenskaya 2	40,7 ± 10,1	24,8	1–3	17,2
Strelets	37,0 ± 5,0	14,3	1–2	10,8
Charodey	42,7 ± 3,8	8,9	1–2	7,0
Chereshneva	47,7 ± 8,1	17,0	1–2	10,5
Chernavka	39,0 ± 3,6	9,3	1–4	10,3
Etude	43,0 ± 7,6	17,6	1–2	7,0
BenHope	51,0 ± 7,9	9,0	1–2	9,8
BenTirran	31,0 ± 8,5	27,6	1–2	12,9
Tiben	42,0 ± 8,9	21,0	1–2	9,5
Tisel	37,3 ± 2,5	6,7	1–2	10,7
1–29–02	39,0 ± 4,4	12,5	1–3	10,3
4–18–01	36,3 ± 4,0	11,1	1–3	8,3
10–141–2	39,3± 9,5	24,5	1–3	12,7
20–69–1	41,7 ± 6,0	14,5	1–3	14,4
63–35–1	45,3 ± 7,1	9,1	1–3	15,5
5–37–02	49,7 ± 2,5	5,1	1–4	10,1
2–49–01	45,7 ± 5,1	11,2	1–4	10,2
43–8–05	36,0 ± 8,5	23,7	1–4	15,3
4–5–2	46,3 ± 5,0	10,9	1–4	15,1
$LSD_{0,05}$	9,87	–	–	–

explained by the fact that the Chudnoe Mgnovenie variety is a third-generation derivative (*F3*) of the Primorsky Champion variety, which has proven itself as a donor of multi- racemes, and an *F2* of a descendant of the Scandinavian subspecies variety Brödtorp, which also effectively transmits multi-racemes to the offspring, as repeatedly confirmed by domestic scientists (see footnote 14). The paternal form in this cross combination is represented by the Golubichka variety, which is also an *F3* descendant of the Brödtorp variety and an *F2* of the Primorsky Champion variety [10]. Among the studied forms selected for multi- racemes from this family, the best selections were 15-11/01 and 73-32-12, which formed up to 3 inflorescences on individual nodes and had aligned, non-shattering fruits with an average weight of 1.4 g.

The study of hybrid fund made it possible to select the forms combining multi-racemes trait with other economically valuable traits (large-fruitedness, one-dimensional berries, resistance to fungal diseases, etc.). For example, dessert selection No. 4-5-2, isolated in the family SC-7 × Exotica, forms on average 15.1% of multi-racemes nodes on the shoot, among which four-racemes nodes are found. Three-racemes nodes were observed in the forms 1-29-02 [(Dar Smolyaninovoy × Litvinovskaya) × Mriya-3], 10-141-2 (Sagittarius × Golubichka), and 20-69-1 (Nara I_1). A large-fruited hybrid 63-35-1, forming berries weighing more than 5.0 g and about 15% three-racemes nodes, was isolated in the family Lentyay × Debryansk, with the participation of large-fruited initial forms. Further inclusion of some of the presented selections in hybridization has allowed us to evaluate their donor qualities.

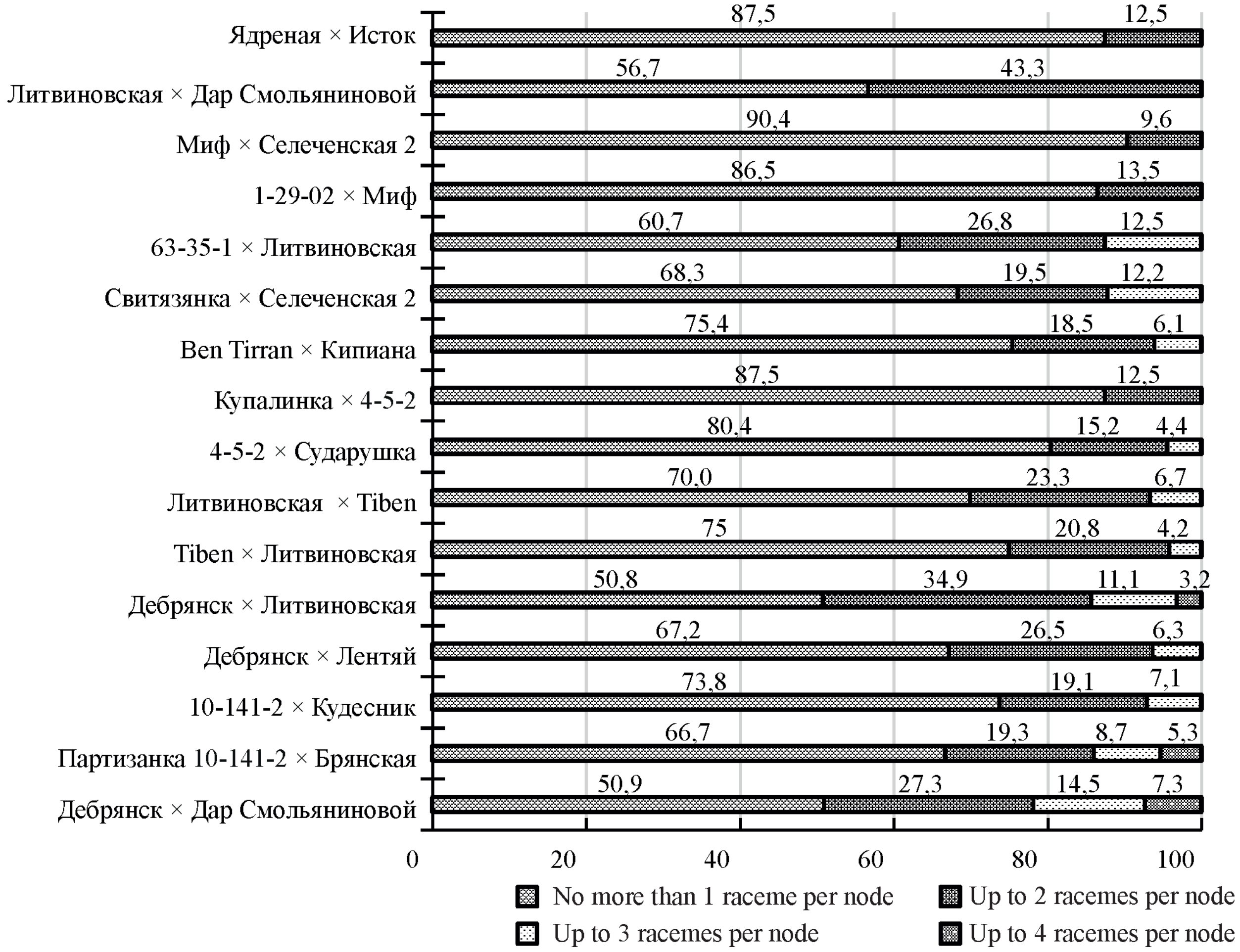
During the selection for multi-racemes traits, preference was given to the genotypes previously identified that combined this characteristic with other economically valuable traits such as large fruit size, long racemes, dessert-like berry taste, etc. Hybridological analysis of seedlings from varieties and selected forms that differed in the number of fruit-bearing clusters on a single node showed a predominance of offspring where multi-racemes nodes were not observed. Even in the families involving multi- racemes original forms, such as Tiben × Selechenskaya 2, Selechenskaya 2 × Dar Smolyaninovoy, Orlovsky Vals × Partizanka Bryanskaya, Mriya × Dar Smolyaninovoy, Istok × Dar Smolyaninovoy, Podarok Veteranam × Dar Smolyaninovoy, Bryansky Agat × Dar Smolyaninovoy, Tamerlan × Bryansky Agat, no hybrids capable of forming more than one raceme on a single node were selected in the offspring.

In the study of the hybrid gene pool, the families were identified in which seedlings with multi-racemes nodes on the shoots were selected. The successful combination of such multi-racemes varieties as Selechenskaya 2 and Debransk in the crossbreeding combinations like Svitzyanka × Selechenskaya 2 and Debransk × Lentyay allowed for the selection of the progeny with 31.7% to 32.8% of seedlings forming 2-3 racemes on a single node (see the figure). Productive combinations were found involving multi- racemes selected forms. For example, in the families 4-5-2 × Sudarushka, 10-141-2 × Partizanka Bryanskaya, and 63-35-1 × Litvinovskaya, 19.6% to 39.3% of hybrids capable of forming 2-3 racemes on a single node were identified.

The use of even less prominent multi-racemes parental forms in hybridization, in combinations such as Ben Tirran × Kipiana, Tiben × Litvinovskaya, and Litvinovskaya × Tiben, allowed the selection of 24.1%, 25.0%, and 30.0% respectively of multi-racemes seedlings, of which 4.2-6.7% of the hybrids formed up to 3 racemes per node. Reciprocal crosses between the varieties Litvinovskaya and Tiben resulted in the selection of promising forms 8-69-01 (Litvinovskaya × Tiben) and 5-82-02 (Tiben × Litvinovskaya) in their progeny, characterized by high resistance to powdery mildew, the formation of 2-3 generative buds per node, and synchronized ripening of the berries within the raceme. In the family of Ben Tirran × Kipiana, seedling No. 3-63-01 was selected, exhibiting 2-3 racemes per node and resistance to anthracnose and leaf spotting. Production of the hybrids exhibiting greater multi-racemes traits than the parental forms indicates the possibility of selecting genotypes with a higher expression of the studied trait in a large analyzed progeny.

However, hybridological analysis shows that the use of multi-racemes parental forms in crosses does not always guarantee the same progeny. The inclusion of varieties such as Selechenskaya 2, Istok, Dar Smolyaninovoy, and the form 1-29-02, capable of forming up to 3 racemes per a node, in certain combinations does not guarantee the segregation of multi-racemes seedlings. This is evident in the families such as Myth × Selechenskaya 2, Litvinovskaya × Dar Smolyaninovoy, Yadrenaya × Istok, 1-29-02 × Myth. In the progeny of the mentioned crosses, all hybrids were single- or double-racemes.

Among the studied cross combinations, the



Расщепление гибридного потомства в комбинациях скрещиваний по числу кистей на узлах, %
Splitting of hybrid offspring in combinations of crosses by the number of racemes at the nodes, %

best results in terms of multi-racemes trait were observed in the progeny of the following families: Debransk × Dar Smolyaninovoy, 10-141-2 × Partizanka Bryanskaya, and Debransk × Litvinovskaya. These families produced seedlings with three or four racemes on a single node. In the Debransk × Litvinovskaya and 10-141-2 × Partizanka Bryanskaya families, 11.1% and 8.7% of the seedlings, respectively, formed up to three racemes on a single node, while the proportion of the seedlings with four racemes was 3.2% and 5.3%, respectively. In the Debransk × Dar Smolyaninovoy family, 14.5% of the seedlings were capable of forming up to three racemes on a single node, and 7.3% of the hybrids had four-racemes nodes. In the presented families, 33.3% to 49.2% of the seedlings formed more than one generative bud on a single node. For example, the progeny of the Debransk × Dar Smolyaninovoy family included selections 5-37-02 and 5-37-03, which combined multi-racemes with dessert-flavored fruits. The form 7-136-3 from the Debransk × Litvinovskaya family not only formed up to 27% of multi-racemes nodes but also had large-sized fruits and uniform berries on the cluster.

Despite the fact that the variety Partizanka Bryanskaya does not form multi-racemes nodes on its shoots, its combination with the multi-racemes elite seedling 10-141-2 allowed for the selection of the genotypes that combined several valuable traits. This may be due to the fact that the selection 10-141-2 was obtained from a broad genetic basis, and its parental forms, Streltsy (Selenchenskaya 2 open pollination) and Golubichka [Izumnaya × (Alfa × Primorsky Champion)], are the derivatives of various subspecies of blackcurrant. From the 10-141-2 ×

Partizanka Bryanskaya family, large-fruited hybrids 4-18-01 and 4-18-02 were selected, which formed 3-4 racemes with dessert-flavored fruits on the nodes. This family also yielded the selection 4-94-1, characterized by multi-racemes, high field resistance to powdery mildew, and a compact and upright bush habitus.

The use of the method of seed sowing from open pollination proved to be effective in analytical selection. In such populations, individual seedlings with multi-racemes trait and the manifestation of several economically valuable traits were identified. These included hybrids resistant to Sphaerotheca, such as 2-26-02 (Chereshneva, open pollination), 3-10-02 (Mriya-5, open pollination), 9-5-01 (6-15-52, open pollination), 9-62-01 (Irmen, open pollination), and 8-10-1 (Izumnaya, open pollination); long-racemes forms 2-30-01 (Selenchenskaya 2, open pollination), 4-14-03 (Vera, open pollination), 5-45-02 (52-42-1, open pollination); selections with dessert-flavored fruits 1-17-01 (Dar Smolyaninovoy, open pollination), 1-9-02, 2-17-03 (Mriya-3, open pollination). The selected form 3-31-01 (Kudesnik, open pollination) was characterized by long racemes (up to 12 berries per cluster) and the ability to form up to 4 racemes on a single node.

Hybridological analysis shows that the Debransk variety is a promising donor of multi-racemes trait. It forms up to 3 generative buds on a single node, and in most cases, hybrids with multi- racemes are obtained in the crosses involving Debransk. In the populations derived from open pollination of the Debransk variety, large-fruited multi-racemes progeny combining this trait with other economically valuable characteristics were identified. For example, form 7-53-01 (Debransk, open pollination) exhibited resistance to fungal diseases (powdery mildew, leaf spotting); selection 37-27-4/05 was resistant to powdery mildew and leaf anthracnose; selected form 7-53-02 produced dessert-flavored fruits; the average berry weight of hybrid 36-27-8/05 was 2.2 g; the new large-fruited variety Kaskad was also derived from this population.

CONCLUSION

As a result of the conducted research, genetic sources and donors of the multi-racemes trait (Dar Smolyaninovoy, Debransk, Bryansky Agat, Selenchenskaya 2, Vera, Chernavka, Nara, Yadryonaya, Exotika, Kipiana, Orlovsky Vals, Istok, Chudnoe Mgnovenie, Litvinovskaya, etc.) have been identified, the use of which in further crosses will allow for the development of more productive forms. The most successful cross combinations in terms of obtaining multi-racemes progeny were 63-35-1 × Litvinovskaya, Svityazanka × Selenchenskaya 2, Debransk × Dar Smolyaninovoy, 10-141-2 × Partizanka Bryanskaya, Debransk × Litvinovskaya, and Debransk (open pollination). Of particular interest are the selected multi-racemes genotypes (63-35-1, 10-141-2, 20-69-1, 2-49-01, 43-8-05, 4-5-2, 4-18-01, 4-18-02, 4-94-1, etc.) from the hybrid population, which deserve active use in the breeding process to create more productive blackcurrant forms.

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МИРОВЫЕ ГЕНЕТИЧЕСКИЕ РЕСУРСЫ ЛЬНА КОЛЛЕКЦИИ ВИР В СОЗДАНИИ СОРТОВ ТОМСКОЙ СЕЛЕКЦИИ

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Представлены результаты изучения 30 образцов льна различного эколого-географического происхождения из коллекции Всероссийского института генетических ресурсов растений им. Н.И. Вавилова (ВИР). Исследованы сорта российской селекции – 14, китайской – 6, украинской – 5, французской – 4, белорусской – 1. Установлено влияние генотипов и погодных условий на проявление хозяйственных признаков многофакторным дисперсионным анализом. Полевые исследования проводили в подтаежной зоне Томской области в 2015–2017 гг. Природно-климатические условия соответствовали требованиям возделывания льна-долгунца. Лучшими по общей и технической длине стеблей отмечены сорта китайской селекции Heiya 4 (К-8485), Sxy 7 (К-8689), российский гибрид Томский 16*Успех (К-8544), французский сорт Drakkar (К-8493), украинский – Глазур (К-8695), 66–72 и 60–66 см соответственно, достоверно выше стандарта Томского 16. По содержанию волокна в технической части стеблей (38–40%) лидировали сорта: российской селекции П-3989 (К-8672), А-236 (К-8692), М-249 (К-8693), французской – Alizee (К-8494), Agatha (К-8492), Melina (К-8495), украинской – Вручий (К-8694), достоверно выше стандарта Томского 16. По массе волокна (91–104 мг) – французские сорта Drakkar (К-8493) и Alizee (К-8494), украинские – Вручий (К-8694) и Глазур (К-8695), российские – А-236 (К-8692) и М-249 (К-8693) – достоверно превосходили стандарт Томский 16 на 6–44 мг. Сорта льна российской селекции П-3989 (К-8672), Добрыня (К-8504), А-236 (К-8692), китайской – Heiya 4 (К-8485), Heiya 13 (К-8486), Tyy 13 (К-8687), французской – Agatha (К-8492), Drakkar (К-8493), Alizee (К-8494), Melina (К-8495), украинской – Гладиатор (К-8505) и Вручий (К-8694) – признаны перспективными и включены в селекционный процесс в качестве отцовских родительских форм. Полученный гибридный материал находится на испытании в питомнике отбора с 2017 г. и второго года селекции с 2021 г.

Ключевые слова: лен-долгунец (*Linum usitatissimum* L. *f. elongata*), селекция, коллекция, сорта, продуктивность, волокно, семена, мыклость

WORLD’S GENETIC RESOURCES OF THE VIR FLAX COLLECTION IN THE CREATION OF TOMSK SELECTION VARIETIES

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The results of the study of 30 flax samples of different ecological and geographical origin from the collection of the N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR) are presented. The varieties of the Russian selection - 14, Chinese - 6, Ukrainian - 5, French - 4, Belarusian - 1 have been investigated. The influence of genotypes and weather conditions on the manifestation of economic traits by multivariate analysis of variance has been established. Field studies were conducted in the sub taiga zone of the Tomsk region in 2015-2017. Natural and climatic conditions met the requirements for the cultivation of fiber flax. By total and technical stem length the best varieties of the Chinese selection Heiya 4 (K-8485), Sxy 7 (K-8689), the Russian hybrid Tomsky 16*Uspekh (K-8544), the French variety Drakkar (K-8493), the Ukrainian - Glazur (K-8695), 66-72 and 60-66 cm respectively, were significantly higher than the standard Tomsky 16. According to the fiber content in the technical part of the stems (38-40%) the following varieties were the leaders: the Russian selection P-3989 (K-8672), A-236 (K-8692), M-249 (K-8693), the French selection Alizee (K-8494), Agatha (K-8492), Melina (K-8495), and the Ukrainian selection Vruchy (K-8694), were significantly above the Tomsky 16 standard. By the fiber mass (91-104 mg) the French varieties Drakkar (K-8493) and Alizee (K-8494), the Ukrainian varieties Vruchii (K-8694) and Glazur (K-8695), the Russian varieties A-236 (K-8692) and M-249 (K-8693) reliably exceeded the Tomsky 16 standard by 6-44 mg. The flax varieties of the Russian selection P-3989 (K-8672), Dobrynya (K-8504), A-236 (K-8692), the Chinese - Heiya 4 (K-8485), Heiya 13 (K-8486), Tyy 13 (K-8687), the French - Agatha (K-8492), Drakkar (K-8493), Alizee (K-8494), Melina (K-8495), and the Ukrainian Gladiator (K-8505) and Vruchiy (K-8694) were recognized as promising and were included in the breeding process as male seed parents. The resulting hybrid material has been on trial in the selection nursery from 2017 and the second year of breeding from 2021.

Keywords: fiber flax (*Linum usitatissimum* L. *f. elongata*), breeding, collection, varieties, productivity, fiber, seeds, stem slenderness (the ratio between the stem length and the diameter)

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INTRODUCTION

Historically, flax has remained the main and leading fiber and oil crop in Russia for a long time, being highly adapted to cultivation in moderate climates and its specific soil and climatic conditions. Russia has been the largest global producer and exporter of natural flax fiber and fabrics for a significant period. To ensure the country's economic and strategic independence, it is important to preserve domestic cellulose fiber raw materials, which can significantly contribute to cotton import substitution [1]. In modern flax varieties, cellulose can account for up to 90% of the fiber content. Despite the annual decrease in flax cultivation, it remains the main source of annually renewable fibers in the Russian Federation [2, 3].

Modern flax breeding continues to focus on improving the quality of flax products. The success of the breeding work in creating new varieties relies on the effectiveness of a scientifically based approach to the selection of initial material and its evaluation under specific soil and climatic conditions[1].

To enrich the genetic material in flax breeding, the Siberian Research Institute of Agriculture and Peat - branch of the Siberian Federal Scientific Centre of Agro-BioTechnologies of the Russian Academy of Sciences (SibNIISHiT - SFSCA RAS) – is establishing a nursery for the ecological testing using the samples from the main Russian collections of the VIR and the Federal Research Center for Bast Fiber Crops (FRC BFC).

For a long time in Russian flax breeding, including during the development of the first Tomsk varieties, local thickset flax was used as the initial material [4]. In the early 20th century, high-fiber lines were selected from local Siberian flax, which served and continue to serve as genetic material in creating new varieties with increased fiber content. The drawback of the early Siberian varieties was that they had coarse, low-quality fiber, with a long fiber num-

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[1] *Pavlova L.N., Gerasimova E.G., Rumyantseva V.N.* Innovative techniques in the selection of fiber flax // Flax breeding: current state and prospects for development: materials of the interregional scientific-practical conference with international participation, dedicated to the 80th anniversary of the Tomsk school of fiber flax breeding. FASO, SibNIISKhit - branch of SFSCA RAS. Tomsk: LLC "Grafika", 2017. pp. 43–46.

ber of 9-10. In the second half of the 20th century, the inclusion of a set of collection samples and varieties from the VIR (N. I. Vavilov All-Russian Institute of Plant Genetic Resources) and the All-Russian Flax Research Institute (VNIIL) allowed for the expansion of genetic diversity and the development of a range of early-maturing Tomsk varieties[2].

The obtained varieties inherited a high fiber content and acquired improved fiber quality (long fiber number of 11-14). Modern Tomsk varieties of flax are included in the State Register of Breeding Achievements of the Russian Federation and are adapted to the Northwestern, Central, Volga-Vyatka, and West Siberian regions, with some varieties being suitable for all regions (for example, Tomich 3, indicating its high adaptive potential).

Modern flax varieties are subject to high requirements for fiber quality, resistance to biotic and abiotic environmental factors, and adaptive potential [5]. Many varieties with high fiber quality indicators have been developed in Russia[3].

The State Register of Breeding Achievements approved for use in the territory of the Russian Federation has been expanded with Tomsk varieties such as Pamyati Krepkova (included in 2012), Tomich (2017), Tomich 2 (2019), and Tomich 3 (2022)[4].

The development of flax varieties with a high fiber content has led to changes towards a deterioration of the structural and morphological qualities of the plants. The increased fiber productivity of the new varieties has resulted in a decrease in technological spinning indicators such as flexibility, fineness, strength, and uniformity of fiber distribution along the stem length, as well as a deterioration in the anatomical structure of the stem, including an increase in the diameter of elementary fibers by almost 50% and a reduction in their length[5] [5].

Researchers have noted a deterioration in the chemical composition of the fiber, as well as a decrease in pectin substances, which affects the spinning properties of the yarn. Therefore, improving the fiber quality in the new varieties is a top priority for Russian breeders.

In addition to these factors, changes in temperature trends have been observed in Siberia since the early 2000s. The climate in the entire subtaiga of the West Siberian Plain has been warming from 1936 to 2015 [6]. During the vegetative period of fiber flax, there is an increasing occurrence of temperature fluctuations and uneven precipitation, especially during critical growth phases. Heavy rains and gusty winds lead to soil overhydration, lodging of flax crops, and the development of diseases, which in turn reduce the quantity and quality of flax products.

The influence of growing conditions on the manifestation of economically valuable traits in flax has been thoroughly studied [7]. The majority of these studies focus on individual factors that affect the physiological processes of plant growth and development. The expression of most traits depends not on a single factor but on the overall system. It has been previously established that the geographical conditions during flax cultivation in different natural-climatic zones influence morphological characteristics. For example, increased temperature and insufficient moisture reduce plant height, fiber yield and quality, seed size, but increase inflorescence length and the number of capsules [8]. Fiber flax plants acquire the habitus of oil flax-intermediate type.

When developing new varieties, it is important to consider their ability to provide high and

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[2] Michkina G.A., Rogalskaya N.B., Popova G.A. History of breeding of Tomsk fiber flax. Development of N.I. Vavilov scientific heritage at the present stage: materials of the international scientific conference devoted to the 120th anniversary of the birth of Academician N.I. Vavilov (Novosibirsk, December 19, 2007). Rosselkhozakademia. Siberian Branch. Novosibirsk, 2009. pp. 148–155.

[3] *Kutuzova S.N., Brach N.B., Tikhvinsky S.F., Doronin S.V., Sharov I.Y., Pitko A.G.* Geographical variability of economically valuable traits of flax // Proceedings on applied botany, genetics and breeding. 1991. Vol. 144. pp. 40–48.

[4] The State Register of Breeding Achievements admitted to use (plant varieties): //gossortrf.ru/ wp-content/uploads/2022/06/ Реестр%20на%20допуск%202022.pdf (accessed on 18.11.2022).

[5] *Pavlova L.N.* Variety - the basis of successful development of flax production // The role of flax in improving the habitat and active longevity of man. Materials of the international seminar. Tver, 2012. pp. 51–55.

stable productivity, as well as ecological plasticity and resistance to a complex set of biotic and abiotic environmental factors under unfavorable agroclimatic conditions [8].

Analysis of the results of fiber flax breeding conducted by N.B. Brach[6] and colleagues from 1932 to 2000 demonstrated that increasing the diversity of the initial material allows overcoming undesirable correlations between the traits and achieving a combination of high economic indicators. It has been established that plant length is one of the key traits that influence the mass of technical fiber and fiber content [7]. The most stable indicator, least dependent on weather conditions, harvesting time, and primary processing methods, is the total fiber content (see footnote 3).

Extensive genetic collections of the VIR and the FRC BFC are the only accessible sources of new collection samples and varieties of flax with diverse eco-geographical origins.

The purpose of the research is to study high-fiber samples and varieties of fiber flax from the global collection of the VIR under the conditions of the subtaiga zone of the Tomsk region, focusing on the productivity of flax fiber and seeds, and to identify promising initial material for inclusion in the breeding process.

MATERIAL AND METHODS

The study utilized 30 samples of cultivated flax (*Linum usitatissimum* L.) from the global VIR collection with diverse eco-geographical origins. The samples consisted of 14 Russian varieties, 6 Chinese varieties, 5 Ukrainian varieties, 4 French varieties, and 1 Belarusian variety.

Field research was conducted from 2015 to 2017 at the Bogashevsk branch of the SibNIISHiT – branch of the SFSCA RAS, located in the subtaiga zone of the Tomsk district in the Tomsk region.

The Tomsk region is situated in the taiga zone of the southeastern part of the West Siberian Plain, and its climate is characterized as continental-cyclical [7, 8].

In the subtaiga zone, the frost-free period lasts on average 115 days, and the multi-year sum of average daily temperatures above 10 °C is 1700°; precipitation during the vegetation period amounts to 200-220 mm, approximately half of the annual norm. According to agroclimatic zoning, the research area belongs to the 5th agroclimatic zone and is characterized as moderately warm and moderately humid. The hydrothermal coefficient (HTC) according to T.K. Selyaninov ranges from 1.1 to 1.6 (see footnote 8) [6]. Despite being located in a region with excessive moisture, there can be periods of drought and dry winds. Overall, the agroclimatic resources of temperature and moisture are close to optimal conditions and meet the requirements for cultivating fiber flax.

The analyzed period of the research covers years with different meteorological conditions. In 2015, there was sufficient moisture and thermal resources (HTC - 1.38), while 2016 belonged to the moderately humid type (HTC – 1.14). The highest amount of precipitation occurred in 2017, indicating excessive moisture (HTC – 1.50). Overall, the moisture supply during the vegetation periods was characterized by sufficient moisture and heat for the growth of fiber flax (see fig. 1)[9]. The soil cover of the experimental plots consisted of medium-podzolic loamy soils[10]. The plowed horizon had a weakly acidic to near-neutral soil solution reaction (pH-water: 5.9 – 6.1), and as the horizons descended, the soil contained carbonates.

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[6] *Brutch N., Pavlov A., Porokhovinova E. et. al*. The role of initial material in the results flax breeding in Soviet Union and Russia from 1932 till 2000. // Innovative technologies for comfort: Proceedings of the 4th global workshop (general consultation) of the FAO/ESCORENA European co-operative research network on flax and other bast plants. 7–10 October 2007. Arad, Romania. pp. 43–44.

[7] Agroclimatic resources of the Tomsk region. Reference book. L.: Gidrometeoizdat, 1975. 148 p.

[8] *Azmuka T.I.* Climate Resources. Natural resources of the Tomsk region. Tomsk: Tomsk University Publishing House, 1991. pp. 83–103.

[9] http://www.pogodaiklimat.ru/ Weather and Climate.

[10] *Solovyova T.P., Makeeva E.A., Popova G.A.* The state of agrosulfurous old plowed soils of the Basandaika River / Flax growing: current state and prospects of development: materials of the interregional scientific-practical conference with international participation, dedicated to the 80th anniversary of the Tomsk school of fiber flax breeding. FASO, SibNIISKhit - branch of SFSCA RAS. Tomsk: LLC "Grafika", 2017. pp. 141–149.

The gross humus content in the plowed horizon varied from 4 to 6%. The main soil nutrients, available phosphorus and exchangeable potassium, were present in sufficient quantities for the cultivation of fiber flax (25-27 mg/100 g). Flax is grown in a seven-field crop rotation, with preceding crops being grains such as wheat, oats, and barley.

The analysis of morphological characteristics and determination of fiber content in stems were carried out on the plants grown under field conditions using a square planting method with a feeding area of 2.5 × 2.5 cm in a leveled agricultural background. To assess fiber productivity, the following morphological characteristics were determined: total stem length (distance from the attachment point of the cotyledonary leaves to the beginning of the inflorescence branching (cm), stem diameter (mm), fiber mass (mg), and fiber content (%) in the technical part, determined by the ratio of the fiber mass to the stem mass. The stem slenderness (cm/mm) was determined by dividing the technical stem length by its average diameter[11,12]. Seed productivity was evaluated based on the number of the capsules per plant (pcs.) and the seed mass within them (mg). Fiber extraction was carried out from the dam retting flax straw obtained by thermal retting[13]. The regionally adapted variety Tomsky 16 (T-16) was used as a standard for morphological characteristics that determine fiber or seed productivity. The normality of feature distributions was tested using the Kolmogorov-Smirnov test. One-way analysis of variance (ANOVA) and Duncan's test were used to compare morphological characteristics of hybrids. Multifactorial analysis of variance was conducted to determine the proportion of factor influence.

RESULTS AND DISCUSSION

Drought during critical periods of growth and development of the crop is one of the limiting factors in obtaining a guaranteed high-quality flax fiber yield. The vegetative period of flax from emergence to flowering is critical in terms of moisture requirements. It has been proven that conditions of increased moisture have a positive effect on the quantity and quality of fiber in fiber flax stems [9].

While overall the amount of heat and moisture for the flax crop during the observed years

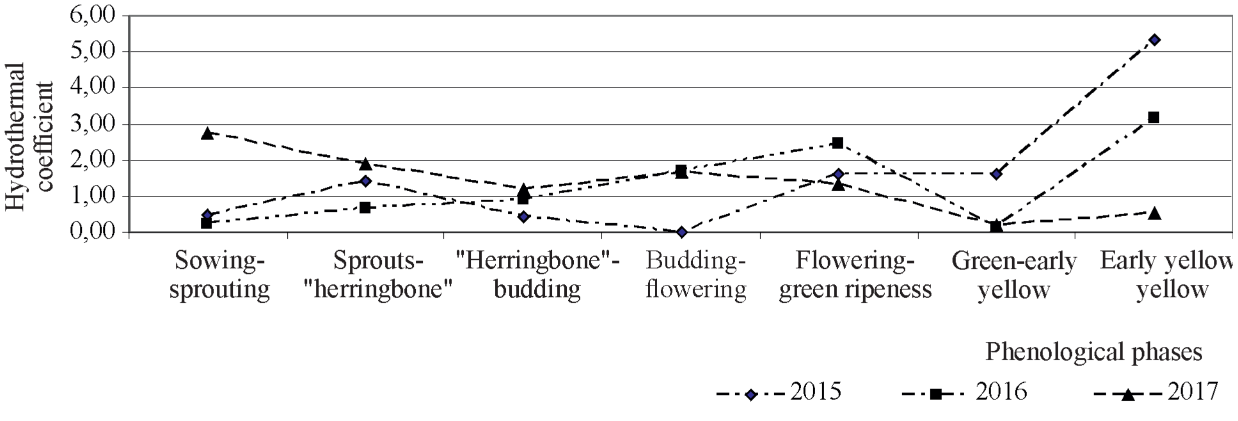

Рис. 1. Гидротермический коэффициент вегетационного периода по фазам роста льна-долгунца в 2015–2017 гг. в Томской области

Fig. 1. Hydrothermal coefficient of the growing season according to the growth phases of flax in 2015–2017 in the Tomsk region

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[11] GOST R 52784-2007. Fiber flax. Terms and definitions. Moscow: Standards Publishing House. 2009. 21 p.

[12] *Solov'ev A.Ya.* Flax growing. M.: Agropromizdat, 1989. 320 p.

[13] Methodological guidelines for technological evaluation of flax straw and experiments on primary processing of flax. Torzhok, 1972. 58 p.

(2015-2017) was considered sufficient, the specific distribution of precipitation and temperature regime showed a rather uneven nature. The integral indicator of plant moisture supply assessment (HTC) for the formation of high-stem fiber flax should be in the range of 1.3-1.6[14].

The 2015 vegetation period was characterized by the HTC value of 1.38, indicating sufficient moisture supply and thermal energy, but with an uneven distribution throughout the season during critical phases of flax water consumption. The period of active growth of flax during the "herring bone" stage – flower-bud formation stage, which is crucial for the potential formation of stems and fiber bundles, occurred under insufficient moisture. From sowing to flowering, only 68 mm of precipitation was recorded, with only 9 mm available during the phase of stem formation and fiber deposition, negatively affecting the linear dimensions of the stem and the yield of flax straw.

Optimal conditions for seed productivity are considered to be precipitation during the period after flowering and during the ripening phase (green-yellow ripeness), with a sufficient amount of 70-80 mm. However, there was an excess of precipitation with 120 mm actually recorded. Excessive moisture after flowering prolonged the ripening process and increased the duration of the vegetative period. The conditions of the year differed from the optimal moisture supply due to unfavorable distribution throughout the vegetative period.

In the moderately humid year of 2016, the HTC was 1.14, and the conditions for growth and yield formation of fiber and seeds were similar to the previous year of the study. Insufficient moisture and heat were noted prior to flowering. Elevated air temperatures and the absence of rainfall in June accelerated the passage of the "herring bone" – flower-bud formation stage, and the stem formation occurred under inadequate precipitation conditions. As a result, flax flowering started 5-7 days earlier than the average. The beginning of the first ten-day period of July was characterized by optimal air temperatures and sufficient rainfall, which further contributed to increased seed productivity. The weather conditions in the second ten-day period of July, with high air temperatures (up to 30°C) and almost daily precipitation, led to soil over moistening. Overall, the temperature and moisture conditions during the growth and development periods of flax in the vegetation period of 2016, similar to 2015, did not always correspond to optimal indicators.

The most favorable in terms of moisture should be considered the 2017 vegetation period. Overall, it was characterized as over moistened (HTC – 1.50) with an optimal distribution of temperature and water regimes. Precipitation from sowing to flowering amounted to 143 mm, and after flowering - 63 mm. The weather conditions during the study period allowed for the assessment of the collection material for its adaptability to environmental stress factors.

Frequently, unfavorable conditions occurred during important growth and development phases throughout the vegetation period, which reflected in the morphological characteristics that determine the productivity of flax plants and its linear parameters, such as total and technical plant length, fiber content in the technical part of the stem, flax straw and seed yield.

Important heritably stable morphological characteristics of fiber flax plants, such as total and technical stem length, largely determine the yield of flax straw and its fiber content. Based on the results of the 3-year observations, high-growing varieties of Chinese flax selection were identified, such as Heiya 4 (K-8485), Sxy 7 (K-8689), with a total stem length of 66-72 cm. The Russian hybrid Tomsky 16*Uspekh (K-8544), the French variety Drakkar (K-8493), and the Ukrainian variety Glazur (K-8695) with a total stem length of 67-68 cm significantly exceeded the standard Tomsky 16 (58 cm) by 9-10 cm (see Table 1).

Long fiber, the main product for which flax is cultivated, is formed and contained in the technical part of the stem, which is an important morphological characteristic that determines the linear size of the stem. The length of the technical part of the stem in 17 studied flax

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[14] Flax farmer reference book. Moscow: Rosselkhozizzdat, 1969. 215 p.

samples and varieties significantly exceeded the standard Tomsky 16 (52 cm) by 9-10 cm. As in the case with the total plant length, Chinese varieties Heiya 4 (K-8485) and Sxy 7 (K-8689) had the highest values for this important morphological characteristic (technical stem length), they reached the value of 60-62 cm. Russian hybrid Tomsky 16*Uspekh (K-8544), M-249 (K-8693) and the French variety Drakkar (K-8493) - 59-62 cm, the Ukrainian variety Glazur (K-8695) - 58 cm - by 6-10 cm significantly exceeded the standard Tomsky 16 (see Table 1).

An important morphological characteristic that can be used to assess the quality of flax straw and its fiber is the stem diameter. It has been empirically proven that the thinner the stem, the higher the fiber quality. Flax provides high-quality fiber with a stem length of at least 70 cm and a diameter of 1.0-1.2 mm (see footnote 12). All flax samples in the experiment exhibited thin stems (0.92-1.18 mm) and showed slight differences from the Tomsky 16 standard (0.95 mm). The stem diameter of the Russian hybrid Tomsky 16*Uspekh (K-8544), the French variety Drakkar (K-8493) (1.15 mm), and the Ukrainian varieties Vruchiy (K-8694) and Glazur (K-8695) (1.12-1.18 mm) were significantly larger than the standard (see Table 1).

The stem slenderness, which is the ratio of the stem's technical length to its diameter, reaches 600 in tall stems, while for most plants, it does not exceed 300 units. This is one of the significant characteristics that determine the yield and quality of the fiber [7]. As V.N. Ponazhev and E.G. Vinogradova [5] note, modern varieties of flax have experienced a decrease in stem slenderness from 620-650 to 420-450 units. In our case, based on a 3-year study (2015-2017), there were no significant differences from the Tomsky 16 standard (564 units) in the studied samples. All the samples exhibited sufficiently high levels of stem slenderness ranging from 485 to 620 units (see Table 1). Three samples showed a tendency to increase this characteristic compared to the standard: the Russian hybrid (K-8498) with 613 units, the variety Dobrynya (K-8504) with 576 units, and the sample from China, Heiya 4 (K-8485), with 620 units.

The main determining indicator of fiber productivity in flax is the hereditary trait of fiber content in the technical part of the stem, expressed as a percentage. The natural-climatic conditions of the 2017 growing season contributed to achieving the highest fiber productivity and proved to be the most favorable for fiber formation (see Figure 2). The regional variety of fiber flax, Tomsky 16, with high fiber content used as a standard in our case, had a fiber content in the technical part of the stem of 34.8% (see Figure 2a). The highest fiber content, exceeding the standard by 9.9%, was observed in the sample of Russian flax selection P-3989 (K-8692). The French varieties Alizee (K-8494) and Melina (K-8495) also ranked high with fiber content in the technical part of the stems exceeding 40% (Figure 2 в). Slightly lower values (over 38%) were observed in the Russian varieties A-236 (K-8692), M-249 (K-8693), and the Ukrainian variety Vruchiy (K-8694) (see Figure 2a, b). During our 3-year observation period, 14 samples of flax had fiber content in the stems (30-37%) reaching or exceeding the standard level, while 15 samples had significantly lower fiber content (less than 30%) (see Figure 2).

The evaluation of fiber productivity in flax was conducted based on the fiber mass in the technical part of the stem, which ultimately determines the fiber yield. In our case, based on the observations, the majority of the samples and varieties significantly exceeded the Tomsky 16 standard in terms of fiber mass in the technical part of the stem by 6-44 mg (see Table 1). The highest values (91-104 mg) were observed in the French varieties Drakkar (K-8493) and Alizee (K-8494), the Ukrainian varieties Vruchiy (K-8694) and Glazur (K-8695), and the Russian varieties A-236 (K-8692) and M-249 (K-8693).

The conducted analysis of flax productivity showed that the highest values in terms of the number of bolls per plant (2.7-3.3) were observed in the samples of the Ukrainian selection, specifically the variety Kamenyar (K-8556), the Russian hybrid Tomsky 16*Uspekh Uspekh (K-8544), the Belarusian variety Fort (K-8507), and the Chinese varieties Heiya

Табл. 1. Результаты морфолого-структурного анализа образцов льна-долгунца коллекции ВИР в Томской области (среднее за 2015–2017 гг.)

Table 1. Results of the morphological and structural analysis of the flax samples yield from the VIR collection in the Tomsk region (average for 2015–2017)

Number according to VIR catalog	Name	Total length, cm	Technical length, cm	Diameter, mm	Stem slenderness, cm/mm	Fiber weight in the technical part of the stem, mg	Fiber content, %	Number of bolls	Seed weight per plant, mg
Tomsky 16 standard		58	52	0,95	564	60	30	2,1	63
Russian varieties									
К-8498	l-4к-5512*l1-к-5523	62*	55*	0,92	613	43*	24*	1,6	43*
К-8499	к-6083*l-1к-550	64*	56*	1,02	557	56*	23*	2,5	87*
К-8500	l-1к-550*к-6084	57*	50	0,92	555	44*	29*	2,2	67*
К-8504	Dobrynya	59	52	1,04	576	76*	32*	2,4	74*
К-8539	Toast 4* Zaryanka	57*	49	0,98	510	56*	30	2,4	65
К-8540	l 2 Toast*Zaryanka	56*	49	1,00	495	56*	29*	2,5	59*
К-8544	Tomsky 16*Uspekh	67*	59*	1,15*	537	69*	22*	3	116*
К-8557	Alexandrit	62*	55*	1,09	507	87*	33*	2,3	64*
К-8558	Gorizont	64*	56*	1,09	527	84*	30	2,4	69*
К-8671	Vesnichka	61*	53	1,01	537	57*	26*	2,1	52*
К-8672	P-3989	61*	53	1,03	523	84*	37*	2,3	66
К-8673	L-205	62*	54	1,11	500	63*	25*	2,6	83*
К-8692	A-236	64*	57*	1,09	532	91*	33*	2,2	56*
К-8693	M-249	66*	59*	1,07	560	91*	31*	2,4	68*
Chinese varieties									
К-8485	Heiya 4	72*	62*	1,09	620	77*	24*	2,9	76*
К-8486	Heiya 13	61*	51	1,11	485	59	23*	2,6	92*
К-8667	Sxy 20	66*	57*	1,09	543	75*	27*	2,5	73*
К-8687	Tyy 13	62*	55*	1,06	527	58	25*	2,7	82*
К-8688	Lu 1	60*	53	1,04	546	66*	28*	2,2	79*
К-8689	Sxy 7	67*	60*	1,09	565	76*	26*	2,4	69*
Ukrainian varieties									
К-8505	Gladiator	65*	58*	1,08	547	84*	31*	2,3	78*
К-8506	Globus	64*	55*	1,09	512	81*	32*	2,5	88*
К-8556	Kamenyar	61*	53	1,09	497	60	24*	3,3	108*
К-8694	Vruchiy	65*	58*	1,12*	536	97*	32*	2,6	76*
К-8695	Glazur	68*	60*	1,18*	534	96*	28*	2,7	76*
French varieties									
К-8492	Agatha	58	52	1,04	512	84*	34*	2,2	77*
К-8493	Drakkar	67*	61*	1,15*	541	104*	32*	2,1	55*
К-8494	Alizee	64*	58*	1,10	542	99*	33*	2,2	86*
К-8495	Melina	59	53	0,99	542	83*	35*	2,2	72*
Belorussian varieties									
К-8507	Fort	61	53	1,04	523	74*	29*	2,9	76*
mean		62,6	55	1,06	538	74,1	28,9	2,4	74,2
LSD$_{05}$		0,06	1,8	0,16	88	3,09	0,07	0,25	3,98

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* Differences with the standard are reliable at 5% significance level by the Duncan test.

4 (K-8485) and Tyy 13 (K-8687). No statistically significant differences were found among the samples (see Table 1).

The maximum seed productivity values, in terms of seed mass per plant, were recorded for the Russian hybrid Tomsky 16*Uspekh (K-8544) with 116 g, the Ukrainian variety Kamenyar (K-8556) with 108 g, and the Chinese variety Heiya 13 (K-8486) with 92 g. In comparison, the standard variety Tomsky 16 exhibited a much lower value of only 63 g (see Table 1).

The analysis of variance of flax collection samples revealed that the factor "year" significantly influenced the morphological characteristics. It had the greatest impact on the overall length, technical length, and stem diameter, accounting for 75.0%, 69.5%, and 52.6% respectively (see Table 2). The thinnest stems of flax plants were obtained in 2017.

Based on the analysis of field observations of the morphological characteristics of the studied flax samples and varieties, it was determined that the "year" factor had a significant influence (44%) on the stem slenderness trait (see Table 2). Therefore, under the most favorable conditions for the growth and development of flax, which were observed in 2017, samples of flax from China, specifically Lu 1 (K-8688), Sxy 7 (K-8689), Heiya 4 (K-8485), and Sxy 20 (K-8667), exhibited excellent stem slenderness values ranging from 728 to 789 cm/mm.

The Ukrainian varieties Glazur (K-8695) and Vruchiy (K-8694), the French varieties Drakkar (K-8493) and Alizee (K-8494), and the Russian hybrids Tomsky 16*Uspekh (K-8544) and l-4k-5512*l-1 k-5523 (K-8498) exhibited values exceeding 700 cm/mm. Among the samples, 12 had high values (at the level of or above the standard) ranging from 658 to 700 cm/mm. These included the Russian varieties M-249 (K-8693) and A-236 (K-8692), as well as the hybrids l-4k-5512*l-1k-5523 (K-8498) and k-6083*l-1k-550 (K-8499). On the other hand, 10 samples had values below the standard of Tomsky 16 (ranging from 571 to 650 cm/mm).

The analysis of variance indicated that the factors "year" and "genotype" had a strong influence on the characteristics of stem mass and fiber content in the technical part of the stem (see Table 2). These traits were relatively stable and more resistant to the impact of weather conditions.

Furthermore, it was observed that seed productivity, as indicated by the number of bolls and the seed mass per plant, was more dependent on weather conditions (38.8-38.3%) than on genotype (5-8%).

Based on the three-year observations, it was found that the best fiber characteristics were obtained in 2017. Optimal moisture supply from germination to flowering facilitated stem development, the formation of bast fiber bundles, and consequently, increased flax straw and fiber yield. This finding confirms the commonly accepted notion that flax is a moisture-demanding plant, especially during the period from germination to flowering. Optimal moisture conditions are considered to be when precipitation during this period exceeds 100 mm [4]. In 2015 and 2016, the moisture supply during the vegetation period from sowing to flowering was only 68 mm, while in 2017, it was twice as high at 143 mm. According to A.P. Krepkov [4], with a precipitation level of 120 mm and an average temperature of 16.6 °C in July, the maximum straw yield (up to 70 c/ha) and fiber content in the technical part of the stem (38.3%) were achieved.

A.I. Sizov's research [7] demonstrated that ancient varieties of flax, with their wide cultivation range, exhibited less variation in different conditions in terms of morphological characteristics that characterize flax productivity.

Modern flax researchers note that new breeding varieties, despite their high yield potential, have weak genetic protection and adaptability to local soil and climatic conditions, as well as various environmental stresses, resulting in a decrease in the quantity and quality of flax products[15] [8]. Previously, it was believed that

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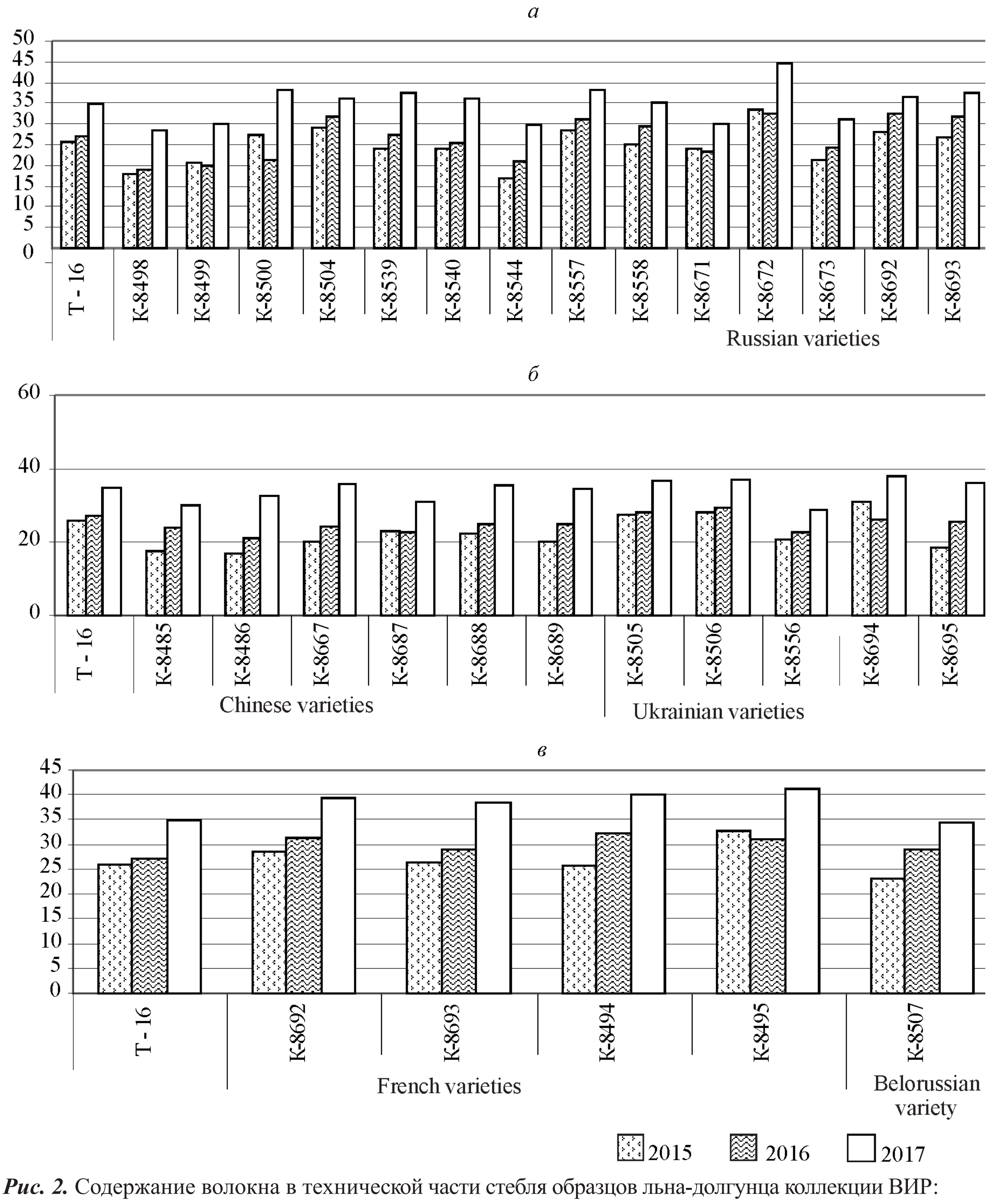

Рис. 2. Содержание волокна в технической части стебля образцов льна-долгунца коллекции ВИР:
а – российской, *б* – китайской, украинской, *в* – французской и белорусской селекции в 2015–2017 гг., %

Fig. 2. Fiber content (%) in the technical part of the stem of flax specimens from the VIR collection:
а – Russian, *б* – Chinese, Ukrainian, *в* – French and Belarusian selection in 2015–2017, %

Табл. 2. Влияние факторов «год» и «генотип» на изменение значений морфологических характеристик коллекционных сортов льна-долгунца луночного посева в 2015–2017 гг.

Table 2. Influence of factors "year" and "genotype" on the change in values of morphological characteristics of flax collection cultivars in 2015–2017

Factor	*df*	SS	*F*	*p*	Factor contribution, %
Total stem length, cm					
Genotype	30	37 374	49,7	< 0,05	7,2
Year	2	390 829	7792,1	< 0,05	75,0
Genotype *Year	60	25 127	16,7	< 0,05	4,8
Error	2697	67 637			
Total	2789	520 968			
Technical stem length, cm					
Genotype	30	32 284	46,1	< 0,05	7,6
Year	2	293 493	6285,3	< 0,05	69,5
Genotype *Year	60	33 783	24,1	< 0,05	8
Error	2697	62 969			
Total	2789	422 527			
Diameter, mm					
Genotype	30	10,608	20,2	< 0,05	7,8
Year	2	71,159	2035	< 0,05	52,6
Genotype *Year	60	6,25	6	< 0,05	4,6
Error	2697	47,153			
Total	2789	135,169			
Stem slenderness, cm/mm					
Genotype	30	2 526 481	6,11	< 0,05	3,2
Year	2	34 436 839	1249,48	< 0,05	44,0
Genotype *Year	60	4 075 446	4,93	< 0,05	5,2
Error	2697	37 165 836			
Total	2789	78 204 602			
Fiber weight of the technical part, mg					
Genotype	30	728 716	70,46	< 0,05	19,8
Year	2	1 657 501	2404,02	< 0,05	45,1
Genotype *Year	60	361 288	17,47	< 0,05	9,8
Error	2697	929 751			
Total	2789	3 677 257			
Fiber content, %					
Genotype	30	41 189	181,9	< 0,05	30,8
Year	2	65 222	4319,6	< 0,05	48,7
Genotype *Year	60	7 137	15,8	< 0,05	5,3
Error	2697	20 361			
Total	2789	133 908			
Number of bolls per plant					
Genotype	30	283,91	10,13	< 0,05	5,6
Year	2	1954,4	1046,31	< 0,05	38,8
Genotype *Year	60	282,06	5,03	< 0,05	5,6
Error	2697	2518,87			
Total	2789	5039,24			
Seed weight per plant, g					
Genotype	30	625 400	15,85	< 0,05	8,3
Year	2	2 874 215	1092,62	< 0,05	38,3
Genotype *Year	60	463 214	5,87	< 0,05	6,2
Error	2697	3 547 312			
Total	2789	7 510 140			

Note. *df* - degrees of freedom, SS - sum of squared deviations, *F* - criterion of the ratio of the effect mean squares to the error mean square, *p* - significance of differences.

there was a negative correlation between fiber content in the flax stem and its quality[16,17] [10]. However, based on the observations in 2017, the studied flax samples and varieties exhibited high fiber content and sufficiently high stem slenderness values, suggesting a positive influence of favorable weather conditions during the vegetation period. Previous studies have shown that plant length, both overall and technical, was almost entirely dependent on the sample genotype[18].

The technical stem length parameter has a dual significance. On the one hand, varieties with longer stems can yield higher-grade fibers, but on the other hand, there is a high risk of lodging, leading to a decrease in fiber quality [10]. Grain crop breeding focuses on cultivating dwarf varieties due to their vulnerability to lodging[19] [11]. However, flax breeding is not aimed at reducing plant height. On the contrary, relatively tall plants are desirable to achieve higher yield since fibers are extracted from the stem [12].

In 2016 and 2017, the Russian selection samples l-4k-5512*l-1k-5523 (K-8498), k-6083*l-1k-550 (K-8499), l-1k-550*k-6084 (K-8500), Dobrynya (K-8504), Vesnichka (K-8671), P-3989 (K-8672), L-205 (K-8673), A-236 (K-8692), the Chinese variety Tyy 13 (K-8687), and the Ukrainian variety Gladiator (K-8505) were involved in hybridization as paternal parental forms. The resulting progeny is currently being studied in the hole breeding nursery at the F_5–F_6 selection stage. Over 40 promising hybrids have been advanced to subsequent stages of the breeding process in the second-year nursery from 2021 to 2023.

CONCLUSION

As a result of the conducted research, valuable and adaptable breeding material has been identified for creating varieties with high productivity traits. Chinese selection varieties, namely Heiya 4 (K-8485) and Sxy 7 (K-8689), the Russian hybrid Tomsky 16*Uspekh (K-8544), the French variety Drakkar (K-8493), and the Ukrainian variety Glazur (K-8695) stood out in terms of overall and technical stem length, with measurements ranging from 66-72 cm and 60-66 cm, respectively, significantly exceeding the standard of Tomsky 16 by 9-10 cm.

In terms of fiber content in the technical part of the stem, the leading samples were the Russian selection varieties P-3989 (K-8672), A-236 (K-8692), and M-249 (K-8693), the French selection varieties Alizee (K-8494), Agatha (K-8492), and Melina (K-8495), and the Ukrainian variety Vruchiy (K-8694), with percentages ranging from 38-40%, significantly surpassing the standard of Tomsky 16 (34.8%) by 7.0-9.9%.

The highest fiber mass in the technical part of the stem was observed in the French varieties Drakkar (K-8493) and Alizee (K-8494), the Ukrainian varieties Vruchiy (K-8694) and Glazur (K-8695), and the Russian varieties A-236 (K-8692) and M-249 (K-8693), ranging from 91-104 mg. They significantly exceeded the standard of Tomsky 16 by 6-44 mg.

The flax varieties P-3989 (K-8672) and Dobrynya (K-8504) from the Russian selection, A-236 (K-8692) from the Ukrainian selection, Heiya 4 (K-8485) and Heiya 13 (K-8486) from the Chinese selection, Agatha (K-8492), Drakkar (K-8493), Alizee (K-8494), and Melina (K-8495) from the French selection, as well as Gladiator (K-8505) and Vruchiy (K-8694) from the Ukrainian selection, have been recognized as promising and included in the breeding process as paternal parental forms in hybridization. The obtained hybrid material is currently under evaluation in the breeding nursery since 2017 and the second-year selection nursery since 2021.

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ОЦЕНКА КОМБИНАЦИОННОЙ СПОСОБНОСТИ ЛИНИЙ КУКУРУЗЫ НА СОДЕРЖАНИЕ КРАХМАЛА

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Представлены результаты исследования содержания крахмала в гибридных комбинациях кукурузы. В результате изучения экспериментальных гибридов, созданных на основе коллекционного материала ВИР, выявлена селекционная и комбинационная ценность линий по содержанию в зерне и выходу крахмала с 1 га. Приведены результаты по сбору крахмала с единицы площади. В эксперимент включены простые гибриды (30 комбинаций), полученные по полной топкроссной схеме скрещиваний. В исследовании в качестве тестеров использованы линии РСК 7, Б 293 и синтетическая популяция РНИИСК 1. Интервал варьирования содержания крахмала в зерне за изучаемый период изменялся от низких значений до среднего показателя. В 2020 г. он составил от 60,9 до 65,2%, в 2021 г. – от 59,3 до 66,1%. Выделены линии с высоким эффектом общей комбинационной способности по содержанию крахмала в зерне (Х 46, Вз 6, Ом 12, ЮВ 106), а также гибридные комбинации ЮВ 25 / РСК 7 (63,3–64,2%), КС 75 / РСК 7 (62,7–64,4), ХЛГ 948 / РСК 7 (63,5–64,1), Кин 073 / РСК 7 (63,4–63,8), ЮВ 106 / РСК 7 (63,6–66,1), КС 25 / Б 293 (63,0–63,5), ХЛГ 182 / Б 293 (63,5–63,6), КС 75 / Б 293 (63,1–63,5), ХЛГ 182 / РНИИСК 1 (62,9–63,6%). Выявлены экспериментальные гибриды, формирующие наибольший выход крахмала с единицы площади: ХЛГ 182 / РСК 7 (3,12–3,58 т/га), ЮВ 106 / РСК 7 (2,77–3,11), Х 46 / Б 293 (3,22–3,39), Ом 12 / Б 293 (2,72–3,85 т/га).

Ключевые слова: гибрид, общая комбинационная способность, специфическая комбинационная способность, тестер, скрещивание, дисперсия

EVALUATION OF COMBINATION ABILITY OF CORN LINES FOR STARCH CONTENT

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The results of the study of starch content in corn hybrid combinations are presented. As a result of the study of experimental hybrids created on the basis of VIR collection material, the breeding and combinational value of the lines in terms of grain content and starch yield per 1 ha was revealed. The results of starch harvesting per unit area are given. The experiment includes simple hybrids (30 combinations) obtained using the full topcross crossing scheme. In the study, the RCK 7, B 293 lines and the synthetic population of RNIISK 1 were used as testers. The interval of variation of starch content in the grain during the study period varied from low values to the average indicator. It was 60.9% to 65.2% in 2020, and 59.3% to 66.1% in 2021. The lines with high effect of total combining ability by starch content in the grain (X 46, Bz 6, Om 12, YuV 106), and hybrid combinations of YuV 25 / RSK 7 (63, 3-64.2%), KS 75 / RSK 7 (62.7-64.4), KhLG 948 / RSK 7 (63.5-64.1), Kin 073 / RSK 7 (63.4-63.8), YuV 106 / RSK 7 (63.6-66, 1), KS 25 / B 293 (63.0-63.5), KhLG 182 / B 293 (63.5-63.6), KS 75 / B 293 (63.1-63.5), KhLG 182 / RNIISK 1 (62.9-63.6%) were identified. The experimental hybrids that form the highest yield of starch per unit area were identified: KhLG 182 / RSK 7 (3,12-3,58 t/ha), YuV 106 / RSK 7 (2,77-3,11), X 46 / B 293 (3,22-3,39), Om 12 / B 293 (2,72-3,85 t/ha).

Keywords: hybrid, general combining ability, specific combining ability, tester, crossing, dispersion

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The authors declare no conflict of interest.

INTRODUCTION

Self-pollinated lines are the basis for the breeding process [1]. The breeding value of the lines used determines the quantitative and qualitative traits of the hybrids created, which must meet the specific requirements of modern agricultural production [2]. The production of starch from corn grain holds significant economic and food value [3]. Therefore, it is necessary to identify lines capable of producing hybrids with high starch content in the grain and high yield per unit area [4, 5].

The evaluation of the combining ability at a later stage of selection is usually conducted based on testing hybrids using a complete diallel cross scheme [6, 7]. However, this scheme requires obtaining a large number of hybrids and becomes challenging when dealing with a large number of the lines under study [8]. When selecting the best samples from a large population, the topcross method is more appropriate [9]. In this case, instead of crossing lines with each other, two to three common parents with broad genetic backgrounds (lines, varieties, synthetic populations) are used [10, 11]. This is necessary to fully capture the genetic variability present among the lines and identify the best combinations for specific traits [12]. Crossing lines with testers allows for obtaining information about both their general combining ability (GCA) and specific combining ability (SCA) without resorting to diallel crosses, provided that several good inbred lines are used as testers [13]. If the magnitude of heterosis in the hybrid combination of a line with a tester is significantly higher than expected based on the line's general combining ability, it is possible to infer high specific combining ability. High SCA effects can be achieved when crossing lines not only with high GCA but also with low GCA [14, 15].

The purpose of this study is to evaluate the general and specific combining ability of inbred corn lines based on test crosses using a complete topcross scheme and identify the best parental lines for use in selection to improve starch yield.

MATERIAL AND METHODS

The research was conducted in 2020 and 2021 at the experimental field of the Russian Research Institute for Sorghum and Maize (RosNIISK "Rossorgo") according to the methodology[1]. The climate of the region is characterized as sharply continental. The average annual temperature during the study years ranged from 0.56 to 1.05. The soil of the experimental site is a moderately heavy, low-humus, southern chernozem. The experiment included simple hybrids (30 combinations) obtained through a complete topcross breeding scheme. The testers used were the RSK 7 lines, B 293, and the synthetic population RNIISK 1, which have a wide genetic basis. The selection of testers was based on their different origins and corresponding genotypic diversity, which allowed for a more comprehensive evaluation of the expression of combinatorial ability parameters. The experiment was replicated three times. The size of the plot was 7.7 m^2, with a length of 5.5 m. The plant density was 50,000 plants/ha. The agricultural techniques used in the experiment were zonal and developed at RosNIISK "Rossorgo". The corresponding methodolo-

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[1] *Dospekhov B.A.* Methodology of field experience. Moscow: Agropromizdat, 1985. 351 p.

gies[2, 3] were employed for data collection, observations, and determination of combinatorial ability. Data analysis was performed using the Agros-2.09 computer program.

RESULTS AND DISCUSSION

Starch is the main biochemical indicator that characterizes the quality of grain intended for the production of food starch. The expansion of food usage of maize grain is driven by the need to create and study the initial material for breeding hybrids with high starch content suitable for application in the starch industry [16]. Additionally, the majority of energy obtained by livestock through feeding comes from carbohydrates.

The obtained data indicate significant differences between hybrids in terms of starch content in the grain (see Table 1). The range of starch content variation in the grain over the study period ranged from low to moderate values, with values ranging from 60.9% to 65.2% in 2020 and from 59.3% to 66.1% in 2021. The skewness coefficient indicates a nearly symmetric distribution of the trait in 2020 and a right-skewed distribution in 2021. However, the coefficients of variation indicate insignificant differences among hybrids in terms of starch content in the grain.

The evaluation of the biochemical composition of the grain allowed for the identification of starch content in the grain (see Table 2). It is considered justified to cultivate maize for feed purposes when the starch content in whole plants is no less than 35-40% [17]. The amount of starch in the grain varied depending on the composition of the combinations and averaged for hybrids including the testers: RSK 7 - 62.3-62.8%, B 293 - 62.5-63.2%, RNIISK 1 - 61.8-63.3%. The highest starch content was observed in the following combinations: YuV 25 / RSK 7 (63.3-64.2%), KS 75 / RSK 7 (62.7-64.4%), KhLG 948 / RSK 7 (63.5-64.1%), Kin 073 / RSK 7 (63.4-63.8%), YuV 106 / RSK 7 (63.6-66.1%), KS 25 / B 293 (63.0-63.5%), KhLG 182 / B 293 (63.5-63.6%), KS 75 / B 293 (63.1-63.5%), KhLG 182 / RNIIISK 1 (62.9-63.6%).

Табл. 1. Параметры статистической оценки гибридов по содержанию крахмала в зерне

Table 1. Parameters of statistical evaluation of hybrids by starch content in grain

Parameter	2020	2021
Mean value, %	63,1	62,2
Min, %	60,9	59,3
Max, %	65,2	66,1
LSD_{05}	2,57	2,41
Error of the mean value	0,14	0,20
Dispersion	0,85	1,58
Standard deviation	0,92	1,37
Coefficient of variation	1,46	2,20
Skew coefficient	0,084 ns	0,397 ns
Skew coefficient error	0,354	0,354
Coefficient of excess	–0,167 ns	0,419 ns
Coefficient of excess error	0,693	0,693

The range of starch yield per unit area over the study period varied from 1.74 to 3.85 t/ha. The skewness coefficients indicate a right-skewed distribution of the trait in the sample in 2020 and 2021 (0.311-0.709), while the coefficients of variation suggest a moderate degree of variation among hybrids in terms of starch yield per 1 ha (13.8%).

The evaluation of grain yield and biochemical composition allowed for the identification of starch yield per 1 ha (see Figure 1). Starch collection from the grain varied depending on the composition of combinations and averaged for hybrids including the tester: RSK 7 - 2.28-2.63 t/ha, B 293 - 2.39-2.56 t/ha, RNIIISK 1 - 2.32-2.58 t/ha. The highest starch yield was obtained in the following combinations: KhLG 182 / RSK 7 (3.12-3.58 t/ha), YuV 106 / RSK 7 (2.77-3.11 t/ha), X 46 / B 293 (3.22-3.39 t/ ha), Om 12 / B 293 (2.72-3.85 t/ha). The range of variation in GCA effects for starch content in

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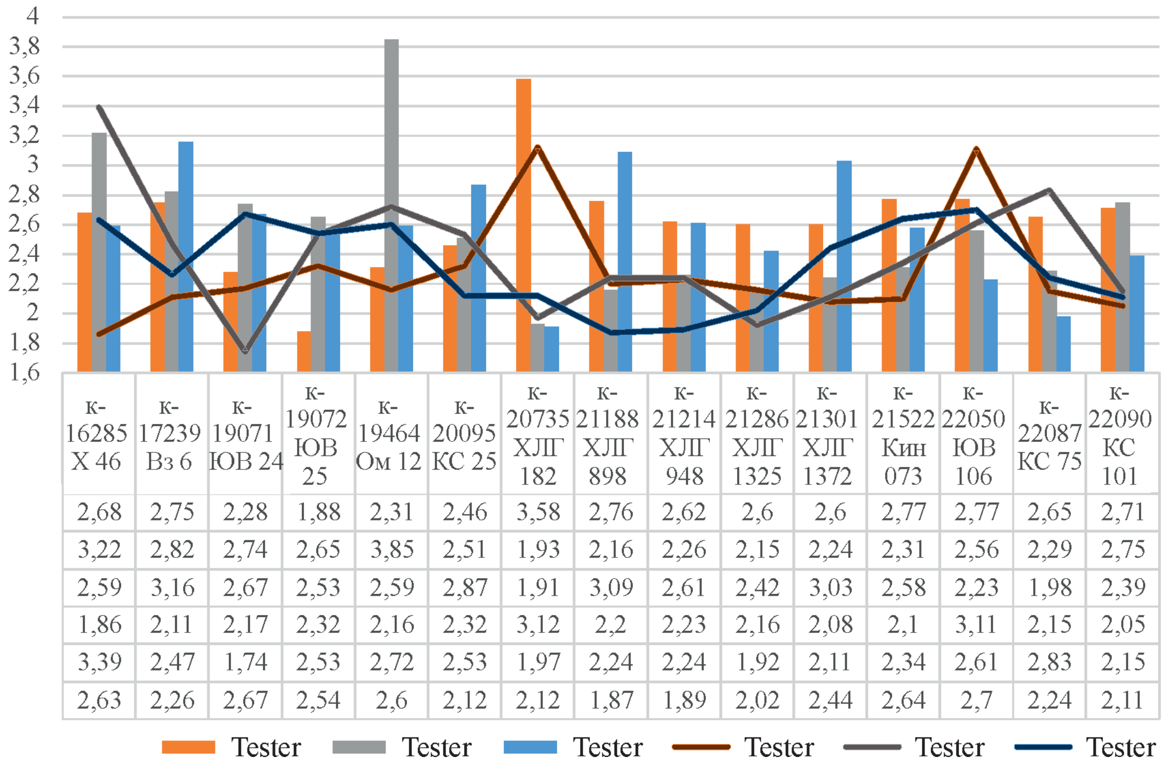
[2] Methods of state variety testing of agricultural crops. Crops, cereals, legumes, corn and fodder crops // Gosagroprom of the USSR. State Commission for variety testing of agricultural crops. Moscow, 1989.Vol. 2. 194 p.

[3] Fedin M.A., Silis D.Y., Smiryaev A.V. Statistical methods of genetic analysis. Moscow: Kolos, 1980. 208 p.

Табл. 2. Содержание крахмала в зерне гибридов кукурузы, %
Table 2. Starch content in corn hybrids grain, %

Line	Tester					
	RSK7		B293		RNIISK 1	
	2020	2021	2020	2021	2020	2021
к-16285 X 46	62,0	62,6	63,0	62,6	62,0	61,8
к-17239 Vz 6	62,0	61,6	62,5	62,5	64,3	62,2
к-19071 YuV 24	62,0	61,8	62,0	61,7	64,8	60,2
к-19072 YuV 25	63,3	64,2	62,9	61,9	64,3	62,6
к-19464 Om 12	63,2	61,1	64,4	62,1	62,1	62,4
к-20095 KS 25	62,7	64,4	63,5	63,0	63,8	61,3
к-20735 KhLG 182	63,1	60,6	63,5	63,6	62,9	63,6
к-21188 KhLG 898	63,4	61,6	64,0	63,1	62,7	62,3
к-21214 KhLG 948	63,5	64,1	65,2	62,3	62,6	60,2
к-21286 KhLG 1325	60,9	60,6	63,0	60,7	64,4	63,2
к-21301 KhLG 1372	63,2	61,1	63,1	63,3	64,4	60,0
к-21522 Kin 073	63,8	63,4	62,2	64,5	63,0	62,2
к-22050 YuV 106	63,6	66,1	63,3	60,4	61,5	61,5
к-22087 KS 75	62,8	59,3	63,1	63,5	62,3	61,7
к-22090 KS 101	62,3	61,7	62,8	61,9	64,4	61,3
Mean value	62,8	62,3	63,2	62,5	63,3	61,8



к-16285 Х 46	к-17239 Вз 6	к-19071 ЮВ 24	к-19072 ЮВ 25	к-19464 Ом 12	к-20095 КС 25	к-20735 ХЛГ 182	к-21188 ХЛГ 898	к-21214 ХЛГ 948	к-21286 ХЛГ 1325	к-21301 ХЛГ 1372	к-21522 Кин 073	к-22050 ЮВ 106	к-22087 КС 75	к-22090 КС 101
2,68	2,75	2,28	1,88	2,31	2,46	3,58	2,76	2,62	2,6	2,6	2,77	2,77	2,65	2,71
3,22	2,82	2,74	2,65	3,85	2,51	1,93	2,16	2,26	2,15	2,24	2,31	2,56	2,29	2,75
2,59	3,16	2,67	2,53	2,59	2,87	1,91	3,09	2,61	2,42	3,03	2,58	2,23	1,98	2,39
1,86	2,11	2,17	2,32	2,16	2,32	3,12	2,2	2,23	2,16	2,08	2,1	3,11	2,15	2,05
3,39	2,47	1,74	2,53	2,72	2,53	1,97	2,24	2,24	1,92	2,11	2,34	2,61	2,83	2,15
2,63	2,26	2,67	2,54	2,6	2,12	2,12	1,87	1,89	2,02	2,44	2,64	2,7	2,24	2,11

Рис. 1. Выход крахмала зерна у гибридов кукурузы с 1 га (2020, 2021 гг.), т/га
Fig. 1. Grain starch yield of corn hybrids from 1 ha (2020, 2021), t/ha

the grain ranged from -0.89 to 0.54 in 2020 and from -1.25 to 0.88 in 2021 (see Table 3). High GCA values were observed for lines in 2020 - YuV 25, KhLG 948, KhLG 1372, and in 2021 - YuV 25, KS 25, Kin 073.

The variance of SCA for starch content in the grain in 2020 ranged from 0.09 to 3.06, and in 2021, it ranged from 0.14 to 9.81. The highest positive SCA variance in 2020 was observed for the variety samples k-17239 Vz 6, k-19071 YuV 24, k-19464 Om 12, k-21214 KhLG 948, k-21286 KhLG 1325, and in 2021 - k-20095 KS 25, k-20735 KhLG 182, k-21214 KhLG 948, k-21301 KhLG 1372, k-22050 YuV 106, k-22087 KS 75. The ratio of mean squares of GCA to SCA deviations in 2020 was 2.38, and in 2021, it was 1.16. It can be concluded that there is a predominance of additive gene interaction in the formation and content of starch.

The range of variation in GCA effects for starch yield per hectare in 2020 ranged from -0.34 to 0.26, and in 2021, it ranged from -0.33 to 0.44 (see Figure 2). High GCA effects were observed in 2020 for the lines X 46, Vz 6, Om 12, and in 2021 for Kh 46, YuV 106. The variance of SCA for the lines ranged from 0.03 to 0.82 in 2020, and from 0.01 to 0.53 in 2021. The highest positive SCA variance in 2020 was observed for the variety samples k-19464 Om 12, k-20735 KhLG 182, and in 2021 for k-16285 X 46, k-20735 KhLG 182, k-19071 YuV 24. The ratio of mean squares of GCA to SCA deviations in 2020 was 1.16, and in 2021 it was 2.90, indicating the influence of additive gene effects on the amount of harvested starch.

The effects of general and specific combining ability are associated with the genetic diversity of the specific breeding material reflected in the gene effects. Gene effects can vary depending on the growth conditions. Thus, the parameters of GCA and SCA are also subject to ecological variability[4]. This parameter characterizes individual combinations and is measured by the deviation of the trait in a specific cross based on the average quality of the studied parental forms. In 2020 and 2021, the following hybrids were characterized by high SCA effects for starch content in the grain: Kin 073 / RSK 7, YuV 106 / RSK 7, X 46 / B 293, Om 12 / B 293, KhLG 182 / B 293, KhLG 898 / B 293, KS 75 / B 293, KhLG 1325 / RNIISK 1 (see Table 4).

Табл. 3. Эффекты ОКС и дисперсия СКС линий по признаку «содержание крахмала в зерне», %

Table 3. Effects of GCA and variance of SCA lines according to the "starch content in grain", %

Line	GCA effect		SCA dispersion	
	2020	2021	2020	2021
к-16285 X 46	–0,89	–0,15	0,33	0,32
к-17239 Вз 6	–0,29	–0,38	1,44	0,14
к-19071 YuV 24	–0,29	–1,25	2,59	1,00
к-19072 YuV 25	0,27	0,42	0,52	1,64
к-19464 Om 12	0,01	–0,62	1,32	0,31
к-20095 KS 25	0,10	0,42	0,31	2,80
к-20735 KhLG 182	–0,06	0,12	0,09	2,61
к-21188 KhLG 898	0,14	–0,15	0,42	0,46
к-21214 KhLG 948	0,54	–0,28	1,74	4,30
к-21286 KhLG 1325	–0,46	–0,98	3,06	1,90
к-21301 KhLG 1372	0,34	–1,02	0,51	2,90
к-21522 Kin 073	–0,23	0,88	0,66	1,44
к-22050 YuV 106	–0,43	0,18	1,31	9,81
к-22087 KS 75	–0,49	–0,98	0,16	4,08
к-22090 KS 101	–0,06	–0,85	1,18	0,15

The hybrids characterized by high SCA effects for starch yield per 1 ha in 2020 and 2021 were: KhLG 182 / RSK 7, YuV 106 / RSK 7, X 46 / B 293, Om 12 / B 293, KhLG 1372 / RNIISK 1, YuV 24 / RNIISK 1 (see Figure 3).

CONCLUSION

The study of experimental hybrids created based on the VIR germplasm revealed their breeding and combining value in terms of starch content in the grain and starch yield per hectare. Lines with high GCA effects for starch content in the grain were identified (X 46, Vz 6, Om 12, YuV 106), as well as hybrid combinations YuV 25 / RSK 7 (63.3-64.2%), KS 75 / RSK 7

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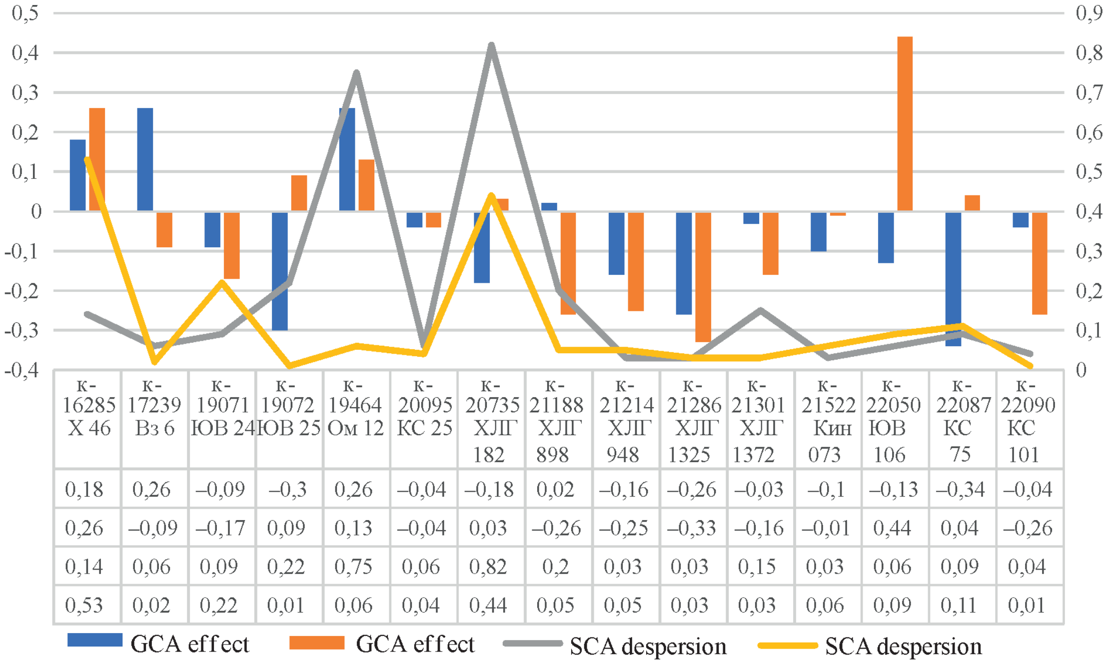
[4] Smiryaev A.V., Kilchevsky A.V. Genetics of populations and quantitative traits. Moscow: KolosS, 2007. 272 p.



к-16285 Х 46	к-17239 Вз 6	к-19071 ЮВ 24	к-19072 ЮВ 25	к-19464 Ом 12	к-20095 КС 25	к-20735 ХЛГ 182	к-21188 ХЛГ 898	к-21214 ХЛГ 948	к-21286 ХЛГ 1325	к-21301 ХЛГ 1372	к-21522 Кин 073	к-22050 ЮВ 106	к-22087 КС 75	к-22090 КС 101
0,18	0,26	–0,09	–0,3	0,26	–0,04	–0,18	0,02	–0,16	–0,26	–0,03	–0,1	–0,13	–0,34	–0,04
0,26	–0,09	–0,17	0,09	0,13	–0,04	0,03	–0,26	–0,25	–0,33	–0,16	–0,01	0,44	0,04	–0,26
0,14	0,06	0,09	0,22	0,75	0,06	0,82	0,2	0,03	0,03	0,15	0,03	0,06	0,09	0,04
0,53	0,02	0,22	0,01	0,06	0,04	0,44	0,05	0,05	0,03	0,03	0,06	0,09	0,11	0,01

Рис. 2. Эффекты ОКС и дисперсии СКС линий по признаку «выход крахмала с 1 га», т/га
Fig. 2. Effects of GCA and variance of SCA lines according to the "starch yield per 1 ha", t/ha

Табл. 4. Эффекты СКС гибридов по признаку «содержание крахмала в зерне», %
Table 4. Effects of SCA of hybrids according to the "starch content in grain", %

Line	Tester					
	RSK7		B 293		RNIISK 1	
	2020	2021	2020	2021	2020	2021
к-16285 X 46	–0,32	0,40	0,66	0,24	–0,34	–0,64
к-17239 Vz 6	–0,92	–0,36	–0,44	0,37	1,36	–0,01
к-19071 YuV 24	–0,92	0,70	–0,94	0,44	1,86	–1,14
к-19072 YuV 25	–0,18	1,44	–0,61	–1,03	0,79	–0,41
к-19464 Om 12	–0,02	–0,63	1,16	0,21	–1,14	0,42
к-20095 KS 25	–0,62	1,64	0,16	0,07	0,46	–1,71
к-20735 KhLG 182	–0,05	–1,86	0,33	0,97	–0,27	0,89
к-21188 KhLG 898	0,05	–0,60	0,63	0,74	–0,67	–0,14
к-21214 KhLG 948	–0,25	2,03	1,43	0,07	–1,17	–2,11
к-21286 KhLG 1325	–1,85	–0,77	0,23	–0,83	1,63	1,59
к-21301 KhLG 1372	–0,35	–0,23	–0,47	1,81	0,83	–1,58
к-21522 Kin 073	0,82	0,17	–0,81	1,11	–0,01	–1,28
к-22050 YuV 106	0,82	3,57	0,49	–2,29	–1,31	–1,28
к-22087 KS 75	0,08	–2,07	0,36	1,97	–0,44	0,09
к-22090 KS 101	–0,85	0,20	–0,37	0,24	1,23	–0,44

(62.7-64.4%), KhLG 948 / RSK 7 (63.5-64.1), Kin 073 / RSK 7 (63.4-63.8), YuV 106 / RSK 7 (63.6-66.1), KS 25 / B 293 (63.0-63.5), KhLG 182 / B 293 (63.5-63.6), KS 75 / B 293 (63.1-63.5), KhLG 182 / RNIISK 1 (62.9-63.6%). The results of the study allowed for the identification of experimental hybrids that showed the highest starch yield per unit area: KhLG 182 / RSK 7 (3.12-3.58 t/ha), YuV 106 / RSK 7 (2.77-3.11), X 46 / B 293 (3.22-3.39), Om 12 / B 293 (2.72-3.85 t/ha).

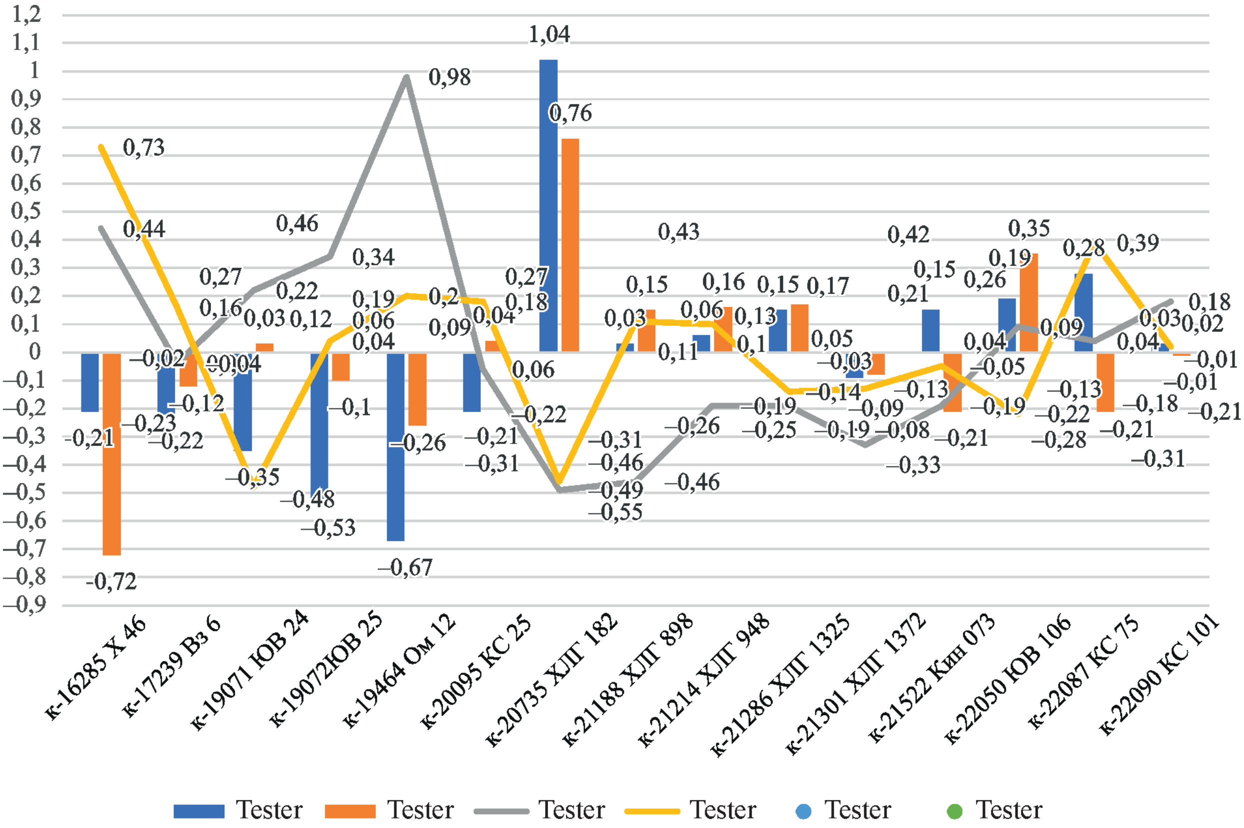


Рис. 3. Эффекты СКС гибридов по признаку «выход крахмала с 1 га» (2020, 2021 гг.), т/га

Fig. 3. Effects of SCA hybrids according to the "starch yield per 1 ha" (2020, 2021), t/ha

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РАСПРОСТРАНЕНИЕ АДВЕНТИВНЫХ ВИДОВ *GALINSOGA PARVIFLORA* И *G. GUADRIRADIATA* (ASTERACEAE) НА ЮГЕ ДАЛЬНЕГО ВОСТОКА

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Представлены результаты изучения заносных американских видов *Galinsoga parviflora* и *G. guadriradiata* на юге Приморского края (Россия). Полевые исследования проведены в 2018–2022 гг. на территории Приморского края в городских и сельских поселениях, на особо охраняемых природных территориях (Уссурийский заповедник им. В.Л. Комарова). Проанализированы литературные данные, информация с интернет-ресурсов, исследованы гербарные образцы. Исследованиями установлено, что за последние 30 лет инвазионный ареал видов рода *Galinsoga* на юге Дальнего Востока значительно увеличился. В настоящее время в Приморском крае эти адвентивные виды активно расселяются по антропогенно трансформированным территориям (обочины автомобильных дорог, заброшенные поля и луга, городские парки и скверы, придомовые территории, строительные карьеры и т.д.) и отмечены в большинстве административно-территориальных районов региона. В северных и восточных районах края виды *Galinsoga* имеют спорадическое распространение. В районах с развитым сельским хозяйством (западные и центральные районы Приморского края) *G. guadriradiata* и *G. parviflora* произрастают массово. Во Владивостоке отмечено несколько крупных травянистых сообществ с доминированием *G. guadriradiata*, площадью до 100 м^2 с проективным покрытием 90–100%. Большую настороженность вызывает проникновение видов рода *Galinsoga* на особо охраняемые природные территории. Поэтому необходим дальнейший мониторинг инвазионного ареала данных видов на юге Дальнего Востока России.

Ключевые слова: инвазивные виды, *Galinsoga parviflora*, *G. guadriradiata*, Дальний Восток, Приморский край

DISTRIBUTION OF THE ADVENTIVE SPECIES *GALINSOGA PARVIFLORA* AND *G. GUADRIRADIATA* (ASTERACEAE) IN THE SOUTH OF THE FAR EAST

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The results of the study of the stranger American species *Galinsoga parviflora* and *G. guadriradiata* in the south of the Primorsky Territory (Russia) are presented. Field studies were conducted in 2018-2022 on the territory of the Primorsky Territory in urban and rural settlements, in specially protected natural areas (V.L. Komarov Ussurisky Nature Reserve). Literary data, information from Internet resources, herbarium specimens have been analyzed. Studies have found that over the past 30 years, the invasive range of species of the genus *Galinsoga* in the south of the Far East has increased significantly. At present, in the Primorsky Territory, these adventive species actively disperse over anthropogenically transformed territories (roadsides, abandoned fields and meadows, city parks and squares, adjacent territories, construction pits, etc.) and are noted in most administrative-territorial districts of the region. *Galinsoga* species have a sporadic distribution in the northern and eastern parts of the region. *G. guadriradiata* and *G. parviflora* grow en masse in the areas with developed agriculture (western and central Primorsky Territory). In Vladivostok, several large herbaceous communities are noted with dominance of *G. guadriradiata*, up to 100 m^2 in area with projective coverage of 90-100%. The penetration of species of the genus *Galinsoga* into specially protected natural areas is of great concern. Therefore, further monitoring of the invasive range of these species in the south of the Russian Far East is necessary.

Keywords: invasive species, *Galinsoga parviflora*, *G. guadriradiata*, Far East, Primorsky Territory

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INTRODUCTION

The introduction of invasive alien plant species poses a threat to regional biodiversity and contributes to the alteration of natural ecosystems. They cause economic and ecological damage, and some of these invaders are unsafe for human health. Therefore, identifying the foci of their invasion, monitoring their spread, and controlling their population are crucial ecological tasks [1-3].

Currently, one of the significant phytosanitary problems is the widespread distribution of two American species - *Galinsoga parviflora* Cav. (small-flower galinsoga) and *G. Guadriradiata* Ruiz et Pav. (galinsoga quadriradiata), which have been introduced as weeds in almost all countries worldwide due to human activities. The natural range of these species is Central and South America. Their secondary range includes most countries in America, Europe, Asia, Africa, as well as Australia and New Zealand [4-6]. As widely spread adventive species, *G. parviflora* and *G. guadriradiata* are included in the Black Books of Western Russia and the Black Book of the Flora of the Far East[1] [7, 8]. *G. guadriradiata* is listed as invasive and potentially invasive species in Siberia and in the Black Book of the Flora of Siberia[2, 3].

Species of the genus *Galinsoga* Ruiz et Pav. are host plants for many insect pests of field crops. Their numerous leaves (with a large total leaf surface area) shade cultivated plants, leading to yield reductions of 10-50%. In landscape compositions and flower beds, these weed species significantly diminish their aesthetic perception[4]. The biological characteristics of *Galinsoga* plants allow them to compete successfully with other weeds and become dominant in disturbed habitats.

In the Far East, the first *Galinsoga* species to appear was *G. parviflora*. It was first mentioned as follows: "Primorskaya Province, Vladivostok District, Golden Horn Bay, Buff Garden, covers clearings in the shade of trees. August 20, 1925. Alisova E." (VLA). This species was introduced with the goods from America to

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[1] *Vinogradova Y.K., Antonova L.A., Darman G.F., Devyatova E.A., Kotenko O.V., Kudryavtseva E.P., Lesik (Aistova) E.V., Marchuk E.A., Nikolin E.G., Prokopenko S.V., Rubtsova T.A., Khoreva M.G., Chernyagina O.A., Chubar E.A., Sheiko V.V., Krestov P.V.* Black book of the flora of the Far East: invasive plant species in ecosystems of the Far Eastern Federal District. Moscow: Partnership of scientific publications KMK, 2021. 510 p.

[2] *Ebel A.L., Strelnikova T.O., Kupriyanov A.N., Anenkhonov O.A., Ankipovich E.S., Antipova E.M., Verkhozina A.V., Efremov A.N., Zykova E.Y., Mikhailova S.I., Plikina N.V., Ryabovol S.V., Silantieva M.M., Stepanov N.V., Terekhina T.A., Chernova O.D., Shaulo D.N.* Invasive and potentially invasive species of Siberia // Bulletin of the Main Botanical Garden. 2014. Iss. 200. N 1. pp. 52–61.

[3] Black Book of the Flora of Siberia. Novosibirsk: Geo Publishing House, 2016. 440 p.

[4] *Vinogradova Yu.K., Mayorov S.R., Khorun L.V.* Black Book of the Flora of the Middle Russia. MOSCOW: GEOS, 2010. 512 p.

Vladivostok and became one of the most common plants in wastelands, slopes, and gardens in the early 20th century. *G. guadriradiata* was first collected by P.G. Gorov and D.P. Vorobyov in 1962 in the Soviet District of Vladivostok, in the vicinity of Akademgorodok (VLA). In the Primorsky Territory, there are also records of *Galinsoga* species growing in specially protected natural areas (SPNAs): *G. parviflora* is registered in Lazovsky, Far Eastern Marine, and Sikhote-Alin Nature Reserves[5-7]. *G. guadriradiata* is found in the following reserves: Lazovsky, Ussurisky, and Kedrovaya Pad [8, 9][9].

MATERIAL AND METHODS

Field studies were conducted from 2018 to 2022 using traditional route reconnaissance methods in urban and rural settlements of the Primorsky Territory and in specially protected natural areas (Ussurisky Nature Reserve named after V.L. Komarov). Literature data were analyzed, herbarium specimens stored at the Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch of the Russian Academy of Sciences (FSC Biodiversity of Terrestrial Biota FEB RAS) in Vladivostok (VLA), and at the Botanical Garden-Institute FEB RAS (VBGI) were examined. Data from the iNaturalist website[10] and Plantarium[11] were also taken into account.

RESULTS AND DISCUSSION

For the area of the Primorsky Territory, the summary "Vascular Plants of the Far East" previously indicated (1992) that *G. parviflora* occurs frequently, and this species is given in the sources only for the southern part of the region; *G. guadriradiata* is mentioned as a rarely occurring species[12].

Nearly 30 years later, A.E. Kozhevnikov [10] characterizes the distribution of both species in this area as common. In the Primorsky Territory, Galinsoga species have an invasive status (2) - alien species that colonize and naturalize in disturbed, semi-natural, and natural habitats [7]. In terms of their distribution, *G. guadriradiata* and *G. parviflora* in the Primorsky Territory are epiphytes - introduced species that colonize one or several types of anthropogenic habitats (see footnote 4).

In the Ussurisky Nature Reserve, *G. guadriradiata* was first recorded in 2004 in the Suvorov Forestry near a remote wintering site "in a flowering state, a single specimen, 8.09.2004, L.A. Fedina" [9]. Fifteen years later, starting from 2019, the replacement of *Ambrosia artemisiifolia* L. (common ragweed) with *G. guadriradiata* plants was observed along the roadside of public dirt roads. In recent years, *G. guadriradiata* has also spread widely in the settlements in the southern part of the Primorsky Territory. In the villages of Kaymanovka and Kamenushka of the Ussurisky Urban District (UUD), located in close proximity to the Ussurisky Nature Reserve, this species is the predominant weed in the gardens of the residents of these villages, and it grows abundantly in the backyard plots and other settlements in UUD (see the table). The occurrence of *Galinsoga* species in the Oktyabrsky, Chuguevsky, and Krasnoarmeisky districts was recorded for the first time. Our findings also expand the list

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[5] *Taran A.A.* New species of vascular plants for the flora of the Lazovsky Reserve (Primorsky Territory) // Botanical Journal. 1987. Vol. 72. N 12. pp. 1673.

[6] *Chubar E.A.* Adventive species of vascular plants in the flora of small marine islands: types of strategies, cenotic activity, level of adventitization (on the example of the Far Eastern Marine Reserve, Primorsky Territory) // Komarov Readings. 2015. Iss. 18. pp. 127–163.

[7] *Pimenova L.A., Medvedeva L.A., Cherdantseva V.Ya., Bulakh E.M., Bukharova N.V., Bogacheva A.V., Egorova L.N., Skirina I.F., Malysheva V.F., Malysheva E.F., Morozova O.V., Gromyko M.N., Gracheva R.G., Rebriev Yu. A., Svetasheva T. Yu.* Plants, fungi and lichens of the Sikhote-Alin Reserve. Vladivostok: Dalnauka, 2016. 557 p.

[8] *Chubar E.A.* Addition to the flora of the islands of the Far Eastern Marine Reserve // Botanical Journal. 1992.Vol. 77. N 12. pp. 131.

[9] *Korkishko R.I.* Vascular plants of the reserve "Kedrovaya Pad". Flora and fauna of nature reserves. M: IPEE RAS, 2000. Iss. 82. 84 p.

[10] https://www.inaturalist.org

[11] https://www.plantarium.ru

[12] Vascular Plants of the Soviet Far East / Edited by S.S. Kharkevich. St. Petersburg: Nauka, 1992. Vol. 6. 428 p.

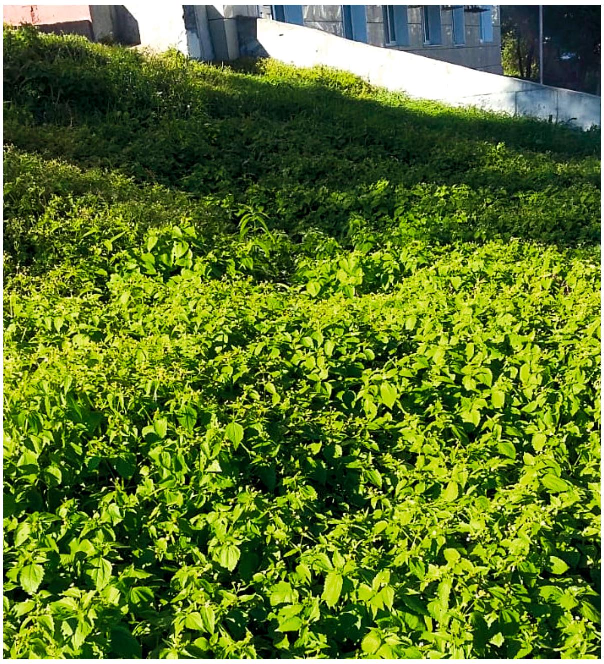
of settlements where these weed plants occur in previously known areas listed in the Black Book of the Flora of the Russian Far East [7].

In Vladivostok, Galinsoga species are found in all areas of the city, as well as along the seaside. In several locations in the city, particularly on the slopes and embankments, monodominant stands of *G. guadriradiata* have been observed, covering an area ranging from 10 to 100 square meters, with a projected cover of 90-100% and an average density of 350 individuals of different ages per square meter. Examples include the following: Pervomaysky District, Grizodubova Street, 53 (43°5′53″, 131°56′46″), N 43°5′53″, E 131°56′46″, 2022; Pervomaysky District, Elochnaya Street, 1, N 43°5′41″, E 131°53′35″, 2022 (see the figure).

The relatively new microdistrict of "Snegovaya Pad" (Pervomaysky District) is also populated by *Galinsoga* species, with one species predominating near certain new buildings and the other near others. Often, both species grow together. Dense communities measuring 3 × 2 meters are formed on the embankments along Anna Shchetinina Street, 15 (43°9′38″, 131°57′20″) and Anna Shchetinina Street, 35 (43°9′48″, 131°57′10″).

Находки и характеристика местопроизрастаний видов рода *Galinsoga* в Приморском крае
Findings and Characteristics of the species of the genus *Galinsoga* in the Primorsky Territory

Location name	Position data	Soil-site characteristics	Data origin
UUD, Kaimanovka village	N43°63'399" E132°23'709"	Field road shoulder, vegetable gardens, en masse	Author's findings 2010–2022
UUD, Kamenushka village	N43°61'695" E132°23'056"	The same	The same
UUD, Kondratenovka village	N 43°37′58″ E 132°9′57″	Vegetable gardens, en masse	»
UUD, Dubovy Klyuch village	N 43°39′45″ E 132°7′52″	The same	»
UUD, Gorno-Taezhnoe village	N 43°41′52″ E 132°9′26″	»	Author's findings 2022
Ussuriisk	N 43°28′54″ E 131°34′3″	Courtyard areas, flower beds, a large number	The same
Khasansky district, Slavyanka settlement	N 42°51′44 E ″131°23′34	The same	»
Khasansky district, hotel complex "Teploe more"	N 42°51′18″ E 131°25′16″	Landscape plantings, slopes, hillsides, a large number	»
Vladivostok, Pervomaisky district, Patrokl Bay	N 43°4′24″ E 131°56′52″	Along the road and exits to the sea, a large number	»
Vladivostok, Leninsky district, Gornostay Bay	N 43°6′55″ E 132°0′51″	The same	»
Vladivostok, Soviet district, Steklyanukha Bay	N 43°6′55″ E 132°0′51″	»	»
Krasnoarmeysky district, Roshchino village	N 45°54′40″ E 134°53′20″	On the building surrounding grounds, vegetable gardens, flower beds, a large number	»
Mikhailovsky district, Mikhailovka village	N 43°56′27″ E 132°0′40″	The same	»
Oktyabrsky district, Pokrovka village	N 43°57′19″ E 131°37′45″	»	»
Chuguevsky district, Uborka village	N 44°23′52″ E 134°5′20″	»	»
Shkotovsky District, Ussuriysky Nature Reserve	N43°64'965" E132°53'156"	The shoulder of a dirt public road, a large number	Author's findings 2004 – 2022



Владивосток, ул. Елочная, 1 – заросли *G. guadriradiata* с проективным покрытием 90–100%.

1, Elochnaya St., Vladivostok – *G. guadriradiata* thickets with a projective coverage of 90-100%.

Large areas of continuous growth of *G. guadriradiata* are noted on the following territories according to the Plantarium website: Vladivostok, Leninsky District, Pushkinskaya Street, 12 (Polytechnic Park), 2016; on the iNaturalist website: Vladivostok, Sovetsky District (Kirova Street, 27), 2020.

On the iNaturalist website, *G. guadriradiata* in the Primorsky Territory is mentioned in the following locations: Vladivostok, Leninsky District, 2021; Vladivostok, Pervorechensky District, 2021; Vladivostok, Sovetsky District, 2021; Vladivostok, Frunzensky District, 2021, 2022; Spassk-Dalny, 2020; Partizansky District (Novitskoye village), 2020; Nakhodka, 2020; Shkotovsky District (Gribanovka village), 2020, 2021; Khasansky District (Lake Lotus), 2021; Ussuriysky Urban District (Kamenushka village), 2021; Arsenyev, 2022; Olginsky District, Olga village, 2022; Shkotovsky District (Shkotovo village), 2022.

On the Plantarium website, *G. guadriradiata* is listed for the following territories: Spassky District (Kvalynka village), 2008; Terny District (Zabolochennaya River valley), 2012; Vladivostok, Leninsky District, 2016.

G. parviflora is indicated on the iNaturalist website in the following locations in the Primorsky Territory: Vladivostok, Sovetsky District, 2018-2020, 2022; Vladivostok, Pervorechensky District, 2019-2022; Vladivostok, Frunzensky District, 2021; Dalnegorsk, 2019; Partizansky District, Nikolaevka village, 2020; Partizansky District, Novaya Sila village, 2020; Partizansky District, Novitskoye village, 2020; Spassk-Dalny, 2020; Spassky District (Knorring village), 2020; Artem, 2021; Dalneretchensk, 2021; Ussuriysky Urban District (Gornotaezhnoye village), 2021; Olginsky District, Olga village, 2022.

On the Plantarium website, the occurrence of *G. parviflora* is noted in the following locations: Nakhodkinsky Urban District (Avangard village), 2016; Artem (Artemovskaya CHP area), 2019.

A comprehensive analysis of author's findings, herbarium specimens (VLA, VBGI), literature data (see footnote 1), and information from internet resources has shown that the distribution range of the *Galinsoga* species has expanded over the past 30 years due to their colonization of the northern regions of the Primorsky Territory, coastal areas, islands, as well as the spread of these ruderal plants to new territories in the southern and central regions. The results of this study confirm the occurrence of the *Galinsoga* species in the following districts and cities of the Primorsky Territory: *G. parviflora* occurs in the districts of Hasan, Nadezhdinsky, Oktyabrsky, Mikhailovsky, Hankai, Pogranichny, Khorolsky, Kirovsky, Spassky, Shkotovsky, Lazovsky, Partizansky, Dalnegorsk, Kavalerovsky, Terny, Olga, Chuguevsky, Krasnoarmeysky, Ussuriysky Urban District, Nakhodkinsky Urban District, Artemovsky Urban District, as well as in the cities of Vladivostok, Artem, Nakhodka, Ussuriysk, Dalnegorsk, Dalneretchensk. *G. parviflora* is found on the islands of Peter the Great Gulf: Bolshoy Pelis, Popova, Putyatin, Russky, Falshivy, Furugelma.

G. guadriradiata occurs in the districts of Hasan, Oktyabrsky, Mikhailovsky, Spassky, Shkotovsky, Lazovsky, Partizansky, Olginsky, Chuguevsky, Terny, Krasnoarmeysky, Ussuriysky Urban District, Nakhodkinsky Urban District, Artemovsky Urban District, and in the cities of Vladivostok, Arsenyev, Nakhodka, Spassk-Dalny, Ussuriysk. *G. guadriradiata* is found on the islands of Peter the Great Gulf: Popova, Reineke, and Furugelma.

CONCLUSION

The conducted research has shown that *G. guadriradiata* and *G. parviflora* have significantly expanded their invasive range in the southern part of the Russian Far East over the past 30 years. Currently, these weed plants are found in almost all administrative districts of the Primorsky Territory, including the northern districts (Krasnoarmeysky, Dalneretchensky, Terny). It has been established that in recent years, *G. guadriradiata* has become the predominant weed in the gardens of rural residents of the Ussuriysk Urban District, and within the territory of the Ussuriysky Nature Reserve, this species actively colonizes new areas. Thus, the biological characteristics of *Galinsoga* species (rapid growth, high seed productivity, long flowering period until the second ten-day period of November) and their high ecological plasticity contribute to further spread of these adventive species across the area of the Primorsky Territory.

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БЕЛЬСКАЯ – НОВЫЙ СОРТ СМОРОДИНЫ ЧЕРНОЙ

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Климатические условия Республики Башкортостан требуют создания сортов с высокой устойчивостью к комплексу биотических и абиотических стрессоров региона возделывания. Изложены данные по хозяйственно ценным признакам нового сорта смородины черной Бельская (селекционный номер 4-46). Сорт смородины черной Бельская выведен в Республике Башкортостан в 1997 г. от опыления сортов Валовая (Крупная × Бредторп × Хлудовская) и Караидель (Память Мичурина × Компактная). Год посева – 1998, начало плодоношения – 2002 г., отбор элитного сеянца – 2003 г., передача на госсортоиспытание – 2013 г. Первичное изучение сортообразцов начато в 2005 г. по схеме посадки 3 × 1 м. Контрольным был сорт Валовая, широко распространенный и районированный по всем регионам Российской Федерации. Сорт Бельская характеризуется высокой зимостойкостью. Признаков подмерзания в суровые зимы не обнаружено, у контрольного сорта Валовая повреждения отмечены до 1 балла с подмерзанием верхушек однолетнего прироста. Листовой аппарат сорта устойчив к солнечным ожогам. В годы жаркого и сухого лета (2010, 2011) выделился высокой засухоустойчивостью, при этом продуктивность его была выше контрольного сорта. Новый сорт отличается высокой продуктивностью (урожайность в среднем 12,7 т/га), устойчив к осыпанию. Обладает полевой устойчивостью к американской мучнистой росе, слабо поражается антракнозом. Ягоды одномерные, черные, кругло-овальной формы, массой 2,3 г (максимальная – 2,6 г), кисло-сладкого нежного вкуса. Срок созревания средний. В 2022 г. сорт Бельская включен в Государственный реестр селекционных достижений Российской Федерации по Уральскому региону.

Ключевые слова: черная смородина, урожайность, зимостойкость, жаростойкость, засухоустойчивость

BELSKAYA – A NEW VARIETY OF BLACK CURRANT

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The climatic conditions of the Republic of Bashkortostan require the creation of varieties with high resistance to a complex of biotic and abiotic stressors of the region of cultivation. The data on economically valuable characteristics of a new variety of black currant Belskaya (breeding number 4-46) are presented. The black currant variety Belskaya was bred in the Republic of Bashkortostan in 1997 from pollination of the Valovaya (Krupnaya × Bredtorp × Khludovskaya) and Karaidel (Pamyati Michurina × Compactnaya). The year of sowing is 1998, the beginning of fruiting is 2002, the selection of an elite seedling is 2003, the transfer to the state varietal testing is

2013. The primary study of varietal samples was started in 2005 according to the planting scheme of 3 × 1 m. The control variety was Valovaya which is widespread and zoned across all regions of the Russian Federation. The Belskaya variety is characterized by high winter hardiness. There were no signs of freezing in severe winters, in the control variety Valovaya damage was noted up to 1 point with freezing of the tops of the annual growth. The leaf apparatus of the variety is resistant to sunburns. During the hot and dry summers (2010, 2011), it was distinguished by high drought resistance, while its productivity was higher than the control variety. The new variety is characterized by high productivity (yield on average 12.7 t / ha), and is resistant to shedding. It has field resistance to American powdery mildew, weakly affected by anthracnose. Berries are one-dimensional, black, round–oval shape, weighing 2.3 g (maximum - 2.6 g), sweet and sour delicate taste. The maturation period is average. In 2022, the Belskaya variety was included in the State Register of Breeding Achievements of the Russian Federation in the Ural region.

Keywords: black currant, yield, winter hardiness, heat resistance, drought resistance

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Конфликт интересов

Авторы заявляют об отсутствии конфликта интересов.

Conflict of interest

The authors declare no conflict of interest.

INTRODUCTION

Berry crops are highly adapted to the harsh climatic conditions of the Bashkir Pre-Urals: they have early fruiting, their yield is comparable to that of fruit crops, they are easily propagated, and they contain a high concentration of microelements essential for the normal functioning of various enzymes, vitamins, and free acids (malic acid, citric acid, succinic acid, etc.) and BAS [1]. Berries have a positive impact on metabolism, enhance the immune system during colds and infectious diseases[1-6], and serve as preventive and therapeutic agents for hypertension, atherosclerosis, and other cardiovascular diseases [2-7].

Black currant has a wide distribution in the Republic of Bashkortostan. The variety adapted to the local climatic conditions of the region plays a significant role in increasing the productivity of plantations of this crop.

Breeding work on black currant in the republic began in the early 1930s. It involved collecting and propagating the most interesting forms of wild black currant, mainly represented by the European variety. The next stage was analytical breeding, where seeds from open pollination were sown.

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Currently, intervarietal crosses are the main approach in black currant breeding[7–11]. Artificial or natural crossing of cultivars is carried out by selecting parental forms with more pronounced positive traits [8-14].

The hybrid collection of black currants at the Bashkir Scientific Research Institute of Agriculture, a separate structural unit of the Ufa Federal Research Center of the Russian Academy of Sciences, consists of over 4,000 plants. Currently, eight black currant varieties developed by the Bashkir Scientific Research Institute of Agriculture are listed in the State Register of Breeding Achievements of the Russian Federation.

The purpose of the research is to create new varieties that combine high productivity with good taste and technological qualities of berries, as well as resistance to major diseases.

MATERIAL AND METHODS

The research was conducted at the Kushnarenkovsky Breeding Center for Fruit and Berry Crops and Grapes of the Bashkir Scientific Research Institute of Agriculture, following commonly accepted methodologies. The variety under study was Belskaya (breeding number 4-46). The control variety used was Valovaya, which is recognized in all the regions of the Russian Federation. The primary variety evaluation was carried out from 2005 using a planting scheme of 3 × 1 meters.

RESULTS AND DISCUSSION

The black currant variety Belskaya was developed at the Kushnarenkovsky Breeding Center through cross-pollination in 1997 using the varieties Valovaya (Krupnaya × Bredtorp × Khludovskaya) and Karaidel (Pamyati Michurina × Kompaktnaya). The seeds were planted in 1998, and the onset of fruiting occurred in 2002. Elite seedlings were selected in 2003, and the variety was submitted for state variety testing in 2013.

The seedling successfully withstood severe winters in 2005/06, 2014/15, and hot and dry summers in 2009, 2010, and 2020. In February with temperature fluctuations and in January 2006, the temperature dropped to -42 °C. No signs of freezing were observed in the Belskaya variety, while the control variety Valovaya showed damage up to 1 point with freezing of the tips of the one-year growth.

Brief morphological description of the new variety Belskaya*:* Medium-sized bush, moderately spreading, compact form. Buds are medium-sized, green, pointed, elongated, with weak anthocyanin coloration. The shoots are straight, medium-sized, dark green, and not pubescent. The leaves are medium-sized, light green, three-lobed, with small notches. Leaf blades are open. Fruit clusters are medium-sized, and the berries are arranged in the cluster at an average density. Flowers are medium-sized with bright coloration. Sepals are medium-sized with bright coloration, moderately hairy on the outer side, bent upwards. Budbreak and the beginning of ripening occur at an average simultaneous time. The onset of flowering is average.

Fruiting begins in the third year after the planting. The average yield over 4 years is 3 kg per bush, with a maximum of 4 kg.

During the years of hot and dry summers (2010, 2011), the Belskaya variety demonstrated high resistance, while maintaining higher productivity compared to the control variety Valovaya.

The new variety exhibits field resistance to American powdery mildew, is slightly affected

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by anthracnose, has an upright bush form, and its foliage is resistant to sunburn. It is resistant to fruit drop, heat-tolerant, and drought-resistant.

The berries are uniform, large, black, round, with an average weight of 2.3 g and a maximum weight of 2.6 g (see Figure 1). The calyx is open. The skin is of medium thickness. The fuzz is weak and simple. The berries have a dry detachment, and the ripening period is average. The taste evaluation is 5 out of 5 points. The variety has a versatile use of the berries.

The optimal planting scheme for Belskaya currant plants is 3.0–4.5 × 1.0–1.5 meters.

The Belskaya variety has good self-fertility (over 45%), ensuring high fruit set in plantings where there may be single-variety crops.

For shaping and sanitation purposes, it is recommended to remove shoots older than 5–7 years from the lower part of the bush. After sanitary or rejuvenating pruning of the shoots, the bush quickly recovers. It propagates easily through green cuttings using a mist propagation system in greenhouses.

The berries contain bioactive substances, with over 21.6% of dry soluble matter, 10.0% sugars, 0.6% free acids, and 181.2 mg/% of vitamin C (maximum 200 mg/%). In terms of average and maximum yield, the Belskaya variety surpasses the control variety Valovaya (see the table, Figure 2).

CONCLUSION

In conclusion, extensive research has shown that the Belskaya variety combines high biological adaptability to environmental factors and pathogens in the conditions of the Bashkir Pre-Ural region. It is a large-fruited variety with high productivity and yield, heat and drought resistance, and resistance to fruit drop. In 2022, the Belskaya blackcurrant variety was included in the State Register for the Ural (9) region of the Russian Federation.

Рис. 1. Ягоды смородины сорта Бельская (фото Р.А. Нигматзянова)
Fig. 1. Currants of the Belskaya variety (photo R.A. Nigmatzyanov)

Основные хозяйственно-биологические признаки смородины (2013–2022 гг.)
The main commercial-biological traits of currant (2013–2022)

Trait	Variety	
	Belskaya	Valovaya (control)
Winter hardness	Strong	Strong
Drought resistance	»	Medium
Heat resistance	»	Weak
Major diseases and pests, point:		
anthracnose	1,0	1,5
grass moth	1,0	1,5
aphides	2,0	2,0
American mildew	0,0	0,0
Beginning and end of flowering (mean dates)	1–5.05, 7–12.05	1–5.05, 7–12.05
Fruit shedding, %	10	20
Yield, t/ha:		
medium	12,9	11,21
maximum	15,3	15,3
Weight of berries, g:		
medium	2,3	1,5
maximum	2,6	2,3
Berry detachment	Dry	Dry
Content of biologically active substances in berries:		
dry soluble solids, %	21,6	21,3
sugars, %	10,0	10,0
free acids, %	0,6	0,8
ascorbic acid (vitamin C), mg%	181,2	147,9
Tasting assessment in fresh form, score	5,0	4,8
Transportability of berries	Good	Good
Main purpose of the variety	Universal	Universal

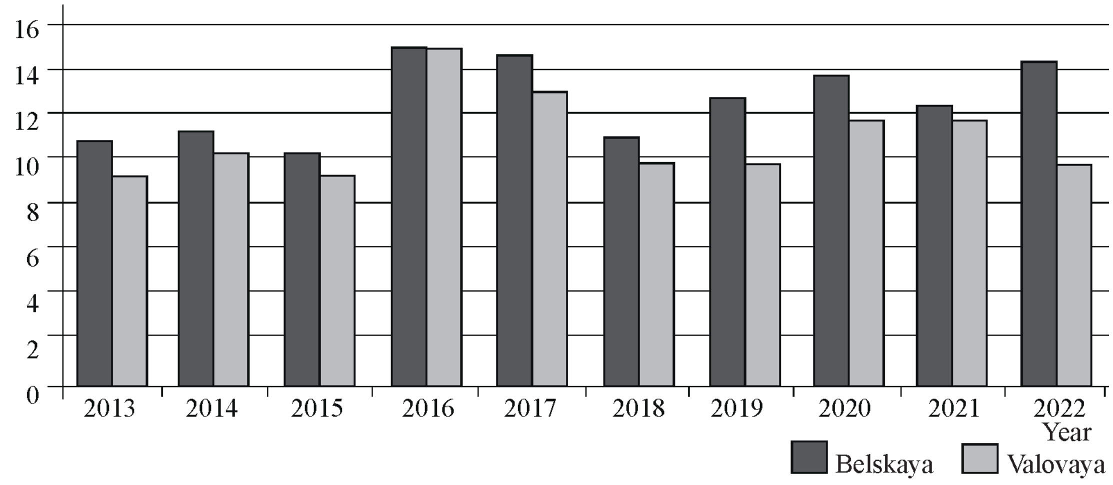

Рис. 2. Урожайность смородины черной по годам (Кушнаренково)
Fig. 2. Black currant yield (Kushnarenkovo)

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ВСПЫШКА БОЛЕЗНИ СЛИЗИСТЫХ ОБОЛОЧЕК У КРУПНОГО РОГАТОГО СКОТА, ВЫЗВАННАЯ *PESTIVIRUS H*

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Описана вспышка инфекции, вызванной *Pestivirus H* (вирус вирусной диареи – болезни слизистых оболочек третьего вида, BVDV-3), в молочном хозяйстве, сопровождающаяся высокой заболеваемостью и летальностью животных разных возрастов. У части больных животных зарегистрировали полный комплекс ярко выраженных симптомов, характерных для «классической» болезни слизистых оболочек крупного рогатого скота: эрозии и язвы на носовом зеркальце и языке, выделение пены из ротовой полости, серозные выделения из носа, геморрагическое воспаление и выраженные продольные эрозии на слизистой пищевода, сычуга и кишечника. Коровы абортировали на разных стадиях стельности. Коэффициент плодотворного осеменения снизился до 20%. Течение болезни осложнилось вовлечением в инфекционный процесс вируса герпеса крупного рогатого скота 4-го типа, бактерий семейства Pasteurellaceae и *Clostridium* spp. Геном BVDV-3 обнаружили в широком спектре внутренних органов абортированных плодов, телят и взрослых животных. По данным секвенирования возбудитель отнесли к субтипу 3а. Филогенетический анализ участка 5'-нетранслируемой области генома вируса (5'-UTR) показал близкое его родство со штаммами, выделенными в Италии и Бразилии, большинство из которых ранее идентифицированы как контаминанты эмбриональной сыворотки и живых вакцин против вирусных инфекций крупного рогатого скота. В настоящее время средства специфической профилактики против инфекции, вызванной BVDV-3, не разработаны, поэтому необходимы обновление и совершенствование методов диагностики, оптимизация противоэпизоотических мероприятий для недопущения распространения вирулентных штаммов возбудителя, контроль безопасности используемых вакцин.

Ключевые слова: крупный рогатый скот, болезнь слизистых оболочек, *Pestivirus H*, ПЦР, филогенетический анализ

AN OUTBREAK OF MUCOSAL DISEASE IN CATTLE CAUSED BY *PESTIVIRUS H*

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An outbreak of infection caused by *Pestivirus H* (virus of bovine viral diarrhea – mucosal disease of the third kind, BVDV-3) in a dairy farm with high morbidity and mortality in animals of different ages is described. In some sick animals a full complex of pronounced symptoms characteristic of "classical" bovine mucosal disease was registered: erosions and ulcers on the nasal mirror and tongue, foaming from the mouth, serous discharge from the nose, hemorrhagic inflammation and pronounced longitudinal erosions on the mucosa of the esophagus, rennet stomach and intestine. Cows miscarried at different stages of pregnancy. The coefficient of effective insemination decreased to 20%. The course of the disease was complicated by the involvement of the bovine herpes virus type 4, bacteria of the family Pasteurellaceae and *Clostridium* spp. in the infectious process. The BVDV-3 genome was found in a wide range of internal organs of aborted fetuses, calves, and adult animals. According to sequencing data, the pathogen was classified as subtype 3a. Phylogenetic analysis of the 5'-untranslated region of the virus genome (5'-UTR) showed its close relationship to the strains isolated in Italy and Brazil, most of which were previously identified as contaminants of fetal bovine serum and live vaccines against viral infections of cattle. No specific prophylaxis against BVDV-3 infection has been developed at this time, therefore, it is necessary to update and improve diagnostic methods, optimize control measures to prevent the spread of virulent strains of the pathogen, and control the safety of the vaccines used.

Keywords: cattle, *pestivirus H*, mucosal disease, PCR, phylogenetic analysis

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Conflict of interest

The authors declare no conflict of interest.

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INTRODUCTION

Pestiviruses of cattle are the causative agents of bovine viral diarrhea, a disease of the mucous membranes (BVD-MD), which is characterized by a variety of clinical manifestations including immunosuppression, respiratory and reproductive pathologies, erosive-ulcerative lesions of the mucous membranes of the oral cavity and gastrointestinal tract, enteritis, acute infections with hemorrhagic syndrome, and mucous membrane disease[1–3] [1, 2].

The disease is widespread worldwide. The economic consequences of the infection are mainly associated with the impact of the pathogen on the reproductive system of animals, resulting in reduced fertility rates, abortions, the birth of persistently infected calves, or young animals with developmental defects[4] [3].

Since 2017, representatives of the genus *Pestivirus* in the family Flaviviridae have been classified into 11 genetically distinct types. Three antigenically and genetically distinct species infect cattle: Pestivirus A (bovine viral diarrhea virus type 1, BVDV-1), *Pestivirus B* (bovine viral diarrhea virus type 2, BVDV-2), and *Pestivirus H* (Hobi-like pestivirus, bovine viral diarrhea virus type 3, BVDV-3). Each of them is further subdivided into subgenotypes: *Pestivirus A* has 23 subtypes (1a to 1w), and *Pestivirus B* and *Pestivirus H* have four sub-

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types[5] each (a to d) [4]. All BVDV types cause similar pathologies in animals. The forms of infection vary from subclinical to severe, acute cases with hemorrhagic syndrome and high mortality. The course of the disease depends on the immune status and age of the animal, virulence of the strain, as well as the conditions of housing and feeding [6–13] [2, 5–8]. BVD-MD in cattle is often enzootic, which hinders efforts to eradicate it.

Pestivirus A is widespread worldwide, while *Pestivirus B* is more virulent and less common. These two types are typical representatives of their genus and have been well studied. *Pestivirus H*, on the other hand, was identified relatively recently and classified as an atypical bovine pestivirus. Until now, its role as an etiological agent of BVD-MD in cattle has been poorly understood. It was first discovered in Germany in 2004 in a batch of embryonic bovine blood serum for the biological industry manufactured in Brazil (see footnote 11) [8]. A year later, it was detected in South America in an infected cell culture and buffalo blood[14]. In 2010, the virus was isolated from calves during a respiratory disease outbreak and in cases of persistent infection in Italy (see footnote 9). Subsequently, cases of respiratory disease in calves caused by *Pestivirus H* [9] were reported in Brazil and China, accompanied by gastrointestinal symptoms and high mortality rates [10].

BVDV-3 can be transmitted through airborne droplets, fecal-oral route, and vertical transmission from dam to fetus. In addition to infected animals, live vaccines made using virus-contaminated embryonic bovine blood serum for cell culture cultivation can serve as a source of the virus[15] [10, 11].

Italian researchers have conducted *in vitro* studies showing that BVDV-3 can replicate in the same cell cultures as typical bovine pestiviruses without showing cytopathic effects [7].

On the territory of the Russian Federation, infection of animals caused by *Pestivirus H* was first registered in 2022 [11].

The purpose of this study is to describe a case of an outbreak of mucous membrane disease in cattle caused by *Pestivirus H* in a dairy farm, examine the characteristics of the infection, and provide a phylogenetic analysis of the pathogen.

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MATERIAL AND METHODS

The research was conducted in a livestock farm with a total population of 1750 cattle, including 740 cows. Samples of biomaterial were collected from diseased, deceased, and euthanized animals of different age and sex groups exhibiting characteristic clinical signs. They were tested for the presence of infectious bovine rhinotracheitis virus (IBR), viral diarrhea-mucosal disease (VD-MD) of three types, respiratory syncytial virus (RSV), bovine herpesvirus type 4 (BHV-4), and bacteria of the *Clostridium* genus, as well as *Salmonella dublin*, *Pasteurella multocida*, and *Mannheimia haemolytica*, using PCR-based real-time assay systems developed by us [12].

Pestivirus H was detected using primers and probe sequences: PVspF-5-ccatrcccttag-taggackagc-3; PVHR-5-tccttgatgcgtcgaacca-3; PVHZ-5-(FAM) tagtggtagca-gtgagctccttggat (BHQ1)-3, targeting a 110 bp fragment. The reaction mixture consisted of PCR buffer (60 mM Tris-HCl, pH 8.5; 1.5 mM MgCl2; 25 mM KCl; 10 mM 2-mercaptoethanol; 0.1% Triton X-100), 0.2 mM dNTPs, 0.2 µg of each primer, 0.1 µg of the probe, 1.25 U of Taq DNA polymerase, and 5 µl of DNA template. The PCR temperature profile was as follows: 95 °C for 5 min - 1 cycle; 95 °C for 10 sec, 55 °C for 15 sec, 72 °C for 30 sec - 45 cycles. The experiments were performed using the CFX96 amplification system (Bio-Rad, USA). Fluorescence was measured at 55 °C using the FAM channel. Samples with a Ct value not exceeding 40 were considered positive.

The target fragments were purified from non-specific reaction products and reagents using Agencourt AMPure XP magnetic beads (Beckman Coulter, USA). Subsequently, the concentration of the samples was assessed using the NanoDrop One/OneC Microvolume UV Spectrophotometer (Thermo Scientific, USA). For sequencing, 10 ng of the purified product was used in the reaction with BrilliantDye™ Terminator v1.1 Kit (NimaGen, Netherlands) following the manufacturer's instructions on the Applied Biosystems 310 Genetic Analyzer (Applied Biosystems, USA). Nucleotide sequences were determined for both DNA strands. The primary sequencing data were analyzed using the Sequencer 4.0.5 software (Gene Codes, USA).

The nucleotide sequences of the synthesized fragments were aligned with published sequences of other pestivirus strains using the BioEdit 7.0.0 program. The maximum evolution method in MEGA v.7 software was used to construct a dendrogram. The reliability of the topology was assessed by a bootstrap test (1000 replicates)[16, 17].

RESULTS AND DISCUSSION

The outbreak of BVD-MD in cattle in the farm began in February 2020. The first affected animals were 18-month-old calves housed in the same facility. They showed signs of feed refusal, foamy oral discharge, hyperemia and ulcers on the oral mucosa, excessive salivation, white plaque and erosions on the tongue (see Fig. 1a), erosions on the nasal tapetum (see Figure 1b), conjunctivitis, and diarrhea.

Respiratory symptoms then appeared, including serous nasal discharge (see Figure 2a), rhinitis, and frothy discharge from the oral cavity (see Figure 2b), accompanied by a dry and wet cough. Later, erosive lesions were observed on the skin of the neck and the inner surface of the thighs.

During post-mortem examination, hemorrhagic inflammation of the esophageal and intestinal mucosa was observed, and in some animals, well-defined longitudinal erosions were found on the abomasum mucosa (see Figure 3).

Within 6 months, the morbidity rate reached 90% among the animals, with a 100% fatality rate based on the number of clinically affected individuals. Treatment was ineffective, so all the calves were culled over several months. From 2021 to 2022, animals of various ages (from a few days to several years) housed in

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different facilities also became ill. They showed symptoms such as feed refusal, conjunctivitis, prolonged diarrhea, and weight loss. Cows aborted at various stages of gestation.

Using PCR, genomes of BVDV-3, herpesvirus type 4, and DNA of *Pasteurella multocida* and *Clostridium* spp. were detected in the samples of pathological material collected from the animals. The table presents the results of the examination of samples from internal organs of deceased and culled animals, as well as from aborted fetuses.

Pestivirus H was detected in a wide range of internal organs (spleen, lymph nodes, lungs, intestines, brain) of the animals of different age groups, including aborted fetuses.

Analyzing the data of the epizootiology, clinical manifestations of the disease, pathological autopsy, and laboratory research results, it was concluded that the primary etiological agent of the disease in the farm was *Pestivirus H*. Its role in the occurrence of abortions, reduced fertility rate, manifestation of systemic infection and enteritis in calves and adult animals, as well as mucosal diseases, was identified.

The characteristic feature of all pestiviruses is their immunosuppressive effect on the animal's body, which increases susceptibility to secondary infections (see footnotes 2, 3) [2]. In this farm, the course of the disease was complicated by the involvement of bovine herpesvirus type 4, bacteria of the *Pasteurellaceae* family, and *Clostridium* spp. in the infectious process.

Based on the sequencing results, the investigated strain of BVDV-3 was classified as subtype 3a. Phylogenetic analysis showed that it is most closely related to strains of the Italian-Brazilian group (see Figure 4). It is known that the severe manifestation of mucosal diseases with a fatal outcome in animals occurs as a result of the mutation of the circulating non-cytopathic variant of the virus into a cytopathic variant, which further superinfects virus carriers, creating a so-called "viral pair"[18]. Another cause may be the introduction of a virulent strain of the virus into a non-immune herd from an external source, resulting in infected animals exhibiting the full spectrum of clinical symptoms described in the literature. Regarding the investigated farm, animals from other sources

Рис. 1. Клинические признаки заболевания, вызванного BVDV3 у телят:
а – эрозии на языке; *б* – эрозии на носовом зеркальце

Fig. 1. Clinical signs of the disease caused by BVDV3 in calves:
а – erosions on the tongue; *б* – erosions on the nasal speculum

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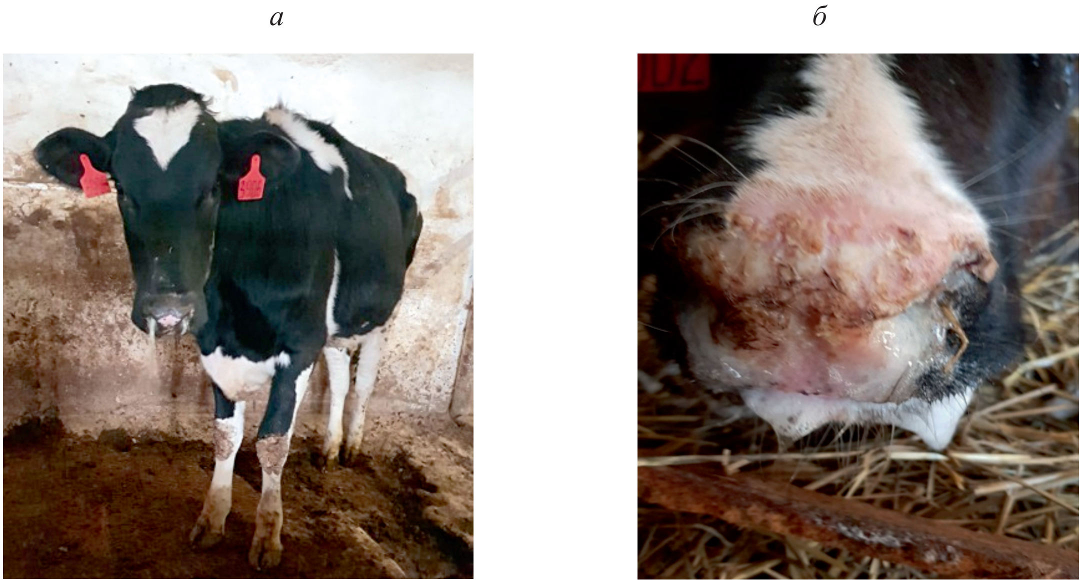

Рис. 2. Клинические признаки респираторного заболевания у телят:
а – серозные выделения из носа; *б* – ринит и выделение пены из ротовой полости

Fig. 2. Clinical signs of respiratory disease in calves:
а – serous nasal discharge; *б* – rhinitis and foaming from the mouth

Рис. 3. Эрозии на слизистой оболочке сычуга теленка

Fig. 3. Erosions on the mucous membrane of the abomasum of a calf

have not been introduced there in the past five years, and clinical signs of BVD-MD in cattle have not been previously recorded. It is possible that the introduction of the virulent strain of BVDV-3 could be associated with the use of contaminated live vaccines[19] [13]. Previously, we detected *Pestivirus H* in the samples of imported embryonic serum used for cell culture

Выявление инфекционных агентов во внутренних органах животных при вспышке заболевания
Detection of infectious agents in the internal organs of animals during a disease outbreak

Organ	Viruses		Bacteria	
	Pestivirus H	ВГ-4	*P. multocida*	*Clostridium*
	Calves and cows			
Spleen	+	+	–	+
Lymphatic nodes	+	+	+	+
Lungs	+	+	+	–
Kidney	–	+	–	+
Liver	–	–	+	+
Intestine	+	–	–	+
	Aborted fetuses			
Visceral organs	+	–	–	–
Brain	+	–	–	–

Note: Pestivirus H - viral diarrhea virus type 3 (BVDV-3); VH-4 - cattle herpesvirus type 4.

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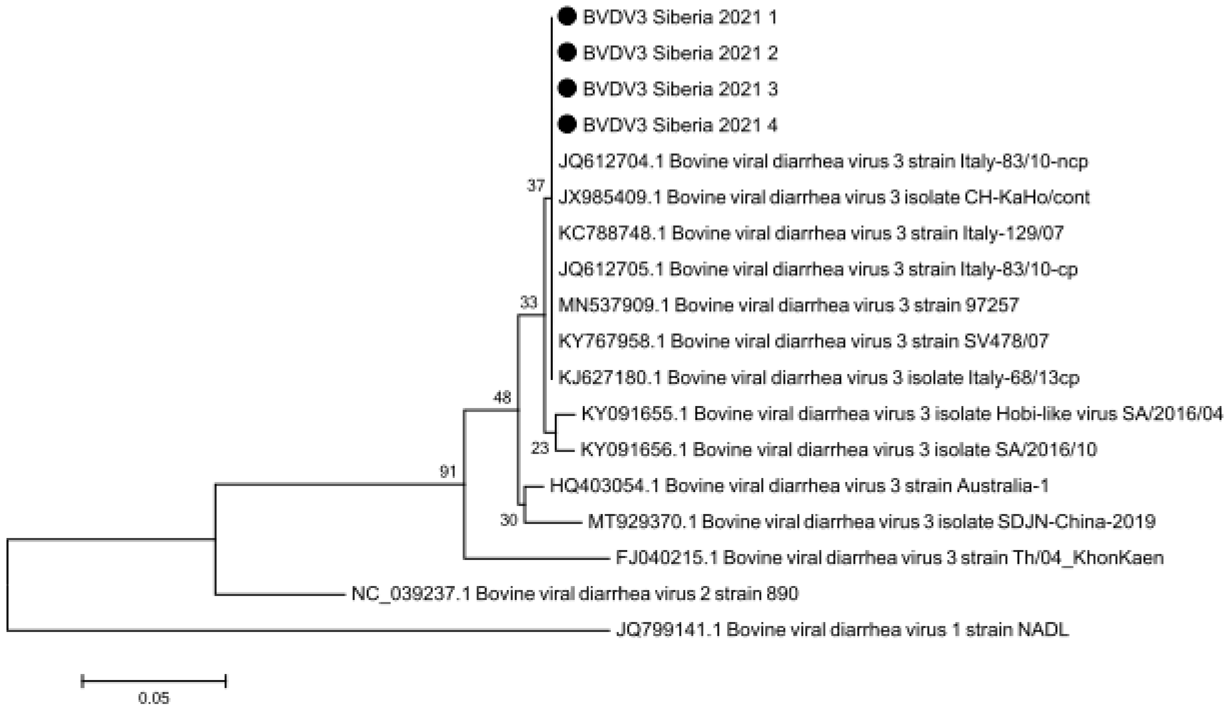

Рис. 4. Филогенетическое дерево, построенное на основе нуклеотидной последовательности области генома 5´UTR *Pestivirus H*; матрица генетических расстояний рассчитана методом максимальной эволюции; указаны индексы статистической поддержки узлов; бутстреп-тест рассчитан для 1000 реплик

Fig. 4. Phylogenetic tree built on the basis of the nucleotide sequence of the 5´UTR *Pestivirus H* genome region, the genetic distance matrix was calculated by the maximum evolution method; indexes of statistical node support are indicated, bootstrap test is calculated for 1000 replicas

cultivation. Based on phylogenetic research results, the isolates were classified as subtype 3a of the Italian-Brazilian group, similar to the strain of BVDV-3 identified in this study [13, 14]. Similar reports exist in the international literature regarding contamination of biological preparations with this virus (embryonic serum, continuous cell culture lines, vaccines for human and veterinary medicine, interferons, trypsin, biotechnological preparations, embryos, stem cells, semen of bull sires, etc.) (see footnotes 12, 15)[20]. Confirmed cases of BVDV-3 spread have been described in relation to the mass use of live vaccines manufactured using contaminated embryonic serum (see footnote 15) [10]. Italian researchers, based on the data on the low frequency of *Pestivirus H* detection in Italy and its absence in circulation in other European countries, concluded that the source of the pathogen was indeed contaminated live vaccines rather than infected animals. Moreover, the isolated BVDV-3 strains belonged to subtype 3a [15].

In Russia, as well as worldwide, specific prophylactic measures against BVDV-3 have not yet been developed, and the use of contaminated biological products may contribute to the spread of the pathogen to different regions of the country. Therefore, strict systematic control of the safety of biological products produced for veterinary purposes is necessary, as well as the updating and improvement of methods for diagnosing and preventing pestivirus infections. The spread of this strain of BVDV-3 in Russia may have significant economic consequences for the domestic livestock industry.

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CONCLUSION

The outbreak of viral diarrhea caused by the virulent strain of *Pestivirus H*, belonging to subtype 3a, with characteristic manifestations of "classical" bovine mucosal disease, has been described. According to phylogenetic analysis of the 5'-UTR genome sequence segment, the isolated virus strain was found to be most closely related to the strains from Italy and Brazil, the majority of which were previously detected in biological preparations for vaccine production. Considering the severe course of the infection, it is necessary to update and improve diagnostic methods, optimize preventive measures to prevent the spread of virulent BVDV-3 strains, and ensure the safety of the vaccines used.

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МАТЕМАТИЧЕСКОЕ МОДЕЛИРОВАНИЕ УРОВНЯ МАРГАНЦА В МЫШЕЧНОЙ ТКАНИ КРУПНОГО РОГАТОГО СКОТА

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Представлены результаты определения наиболее эффективной модели прогноза уровня марганца в мышечной ткани герефордского скота для прижизненной оценки элементного статуса животных малоинвазивными методами. Эксперимент проведен с помощью гематологического и биохимического исследования крови и атомно-абсорбционного анализа мышечной ткани крупного рогатого скота. Полученные данные использованы для подгонки регрессионной модели методом наименьших квадратов. Для анализа отобраны пробы скелетной мускулатуры массой 100 г с диафрагмальной мышцы от герефордского скота, разводимого в южной части Западной Сибири в условиях промышленного комплекса. Оценку концентрации марганца в тканях осуществляли методом атомно-абсорбционного анализа на спектрометре МГА-1000. Определение содержания эритроцитов, лейкоцитов и гемоглобина проводили на автоматическом гематологическом анализаторе PCE-90VET. Уровень протеина, альбуминов, глобулинов, мочевины, мочевой кислоты и холестерина определяли фотометрическими методами на полуавтоматическом биохимическом анализаторе Photometer-5010. Расчет эффектов регрессионных моделей осуществляли методом наименьших квадратов. Селекция лучшей модели по эффективности и точности оценки модели базировалась на комплексной оценке значений внутренних и внешних критериев качества. Между зависимой и независимыми переменными выявлены статистически значимые ассоциации ($p < 0,05$). Внутри пула предикторов отмечена скоррелированность ($p < 0,05$). В результате подгонки моделей получено оптимальное регрессионное уравнение, включающее два показателя (скорость оседания эритроцитов и уровень глобулинов), для прогноза уровня марганца в мышечной ткани крупного рогатого скота. Между главными эффектами модели отсутствуют признаки мультиколлинеарности, что подтверждает значения фактора инфляции дисперсии – 1,2. Полученная модель удовлетворяет необходимым допущениям в отношении остатков. Распределения остатков модели входят в доверительные интервалы кривой нормального распределения. Коэффициент автокорреляции был равен 0,039 ($p > 0,05$), что указывает на независимость остатков. Полученная модель может быть использована для прижизненной оценки концентрации марганца в мышечной ткани крупного рогатого скота.

Ключевые слова: марганец, крупный рогатый скот, герефордская порода, прогнозирование, регрессия

MATHEMATICAL MODELING OF THE MANGANESE LEVEL IN THE MUSCLE TISSUE OF CATTLE

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The results of determining the most effective model for predicting the level of manganese in the muscle tissue of Hereford cattle for in vivo assessment of the elemental status of animals by low invasive methods are presented. The experiment was carried out using hematological and biochemical blood tests and atomic absorption analysis of the muscle tissue of cattle. The data obtained are used to fit the regression model using the least square method. Skeletal muscle samples weighing 100 g from the diaphragm muscle of the Hereford cattle bred in the southern part of Western Siberia in the conditions of industrial complex were taken for analysis. Manganese concentration in tissues was assessed by atomic absorption analysis on an MGA-1000 spectrometer. The content of erythrocytes, leukocytes, and hemoglobin was determined on an automatic hematology analyzer

PCE-90VET. Protein, albumin, globulin, urea, uric acid, and cholesterol levels were determined by photometric methods on a Photometer-5010 semi-automatic biochemical analyzer. The effects of regression models were calculated using the least square method. Selection of the best model for efficiency and accuracy of model estimation was based on a comprehensive assessment of the values of internal and external quality criteria. Statistically significant associations ($p < 0.05$) were found between the dependent and independent variables. Within the pool of predictors, correlation ($p < 0.05$) was observed. As a result of model fitting, an optimal regression equation including two indicators (erythrocyte sedimentation rate and globulin level) for predicting manganese levels in bovine muscle tissue was obtained. There are no signs of multicollinearity between the main effects of the model, which confirms the values of the variance inflation factor - 1.2. The resulting model satisfies the necessary assumptions about the residuals. The distributions of the model residuals fall within the confidence intervals of the normal distribution curve. The autocorrelation coefficient was 0.039 ($p > 0.05$), indicating the independence of the residuals. The resulting model can be used for in vivo assessment of manganese concentration in bovine muscle tissue.

Keywords: manganese, cattle, Hereford breed, prediction, regression

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INTRODUCTION

Manganese is an essential micronutrient, with a requirement of 20 mg of manganese/kg of feed for beef cattle [1–3]. Deficiency of this element results in disturbances in carbohydrate and lipid metabolism, growth retardation, dermatitis, impaired synthesis of bone tissue and the reproductive system [4, 5]. It has been established that the key enzymes sensitive to manganese deficiency in the diet are glycosyltransferases and xylosyltransferases (enzymes activated by manganese and involved in the synthesis of proteoglycans and, consequently, in bone formation), as well as arginase and mitochondrial superoxide dismutase (manganese metalloenzymes) [6–9]. Decreased fertility due to manganese deficiency is a result of impaired synthesis of cholesterol and related compounds (ergosterol, ergosteryl sitosterol, stigmasterol, etc.) necessary for the synthesis of sex hormones and other steroids [10–12]. Replenishing manganese deficiency in ruminant animals can be achieved through the use of multicomponent mineral feed supplements [13, 14]. As a preventive measure, manganese-containing additives are used when there is only unconfirmed suspicion of micronutrient deficiency [15].

The elemental status is associated with biochemical processes occurring in the organism [16–18]. Identifying these patterns will allow for the development of the methods for assessing the levels of micronutrients in animal tissues during their lifetime. Hematological and biochemical blood parameters can serve as predictors and biomarkers of manganese levels.

The purpose of this study was to identify the most effective predictive model for manganese levels in the muscle tissue of the Hereford cattle, which would allow for non-invasive assessment of the animals' elemental status during their lifetime.

The research objectives were achieved through hematological and biochemical analysis of blood samples and atomic absorption analysis of muscle tissue in beef cattle. The obtained data were used to fit the regression models using the least squares method.

MATERIAL AND METHODS

Samples of skeletal muscle (*n* = 22) were taken from the diaphragm muscle of the Hereford cattle bred in the southern part of Western Siberia. The animals were kept under standard conditions of an industrial complex, complying with veterinary and zootechnical requirements (GOST 32855-2014, GOST 26090-84, GOST R 52254-2004). At the time of slaughter, the animals were clinically healthy. Blood samples were taken from the jugular vein of the animals and stabilized with 5% sodium citrate. Analysis of the muscle tissue samples was performed according to GOST R 55484-2013 using an electrothermal atomic absorption spectrometer MGA-1000. Hemoglobin level, red blood cell count, and leukocyte count were determined using a PCE-90VET hematological analyzer. Biochemical analysis of serum was conducted using a Photometer-5010 biochemical analyzer.

Statistical analysis of the raw data was performed in the R environment. Model fitting was done using the least squares method according to the exploratory data analysis protocol [19]. The Shapiro-Wilk test was used to assess the normality of residual distributions. Spearman's rank correlation coefficient was calculated to assess the correlation between model variables. The presence of multicollinearity in the parameters of the candidate models was assessed based on the variance inflation factor values and visual inspection of the scatterplot matrix. Influential observations in the model residuals were identified using the Grubbs' test. Multiple comparisons of influential observations in the model residuals were conducted using Bonferroni correction. The Durbin-Watson test was used to assess the independence of the model residuals.

For convenience of analysis and description, the names of the original variables have been changed (see Table 1).

Табл. 1. Обозначение и расшифровка для комплекса независимых переменных, используемых для селекции регрессионных моделей

Table 1. Designation and interpretation for the complex of independent variables used for the selection of regression models

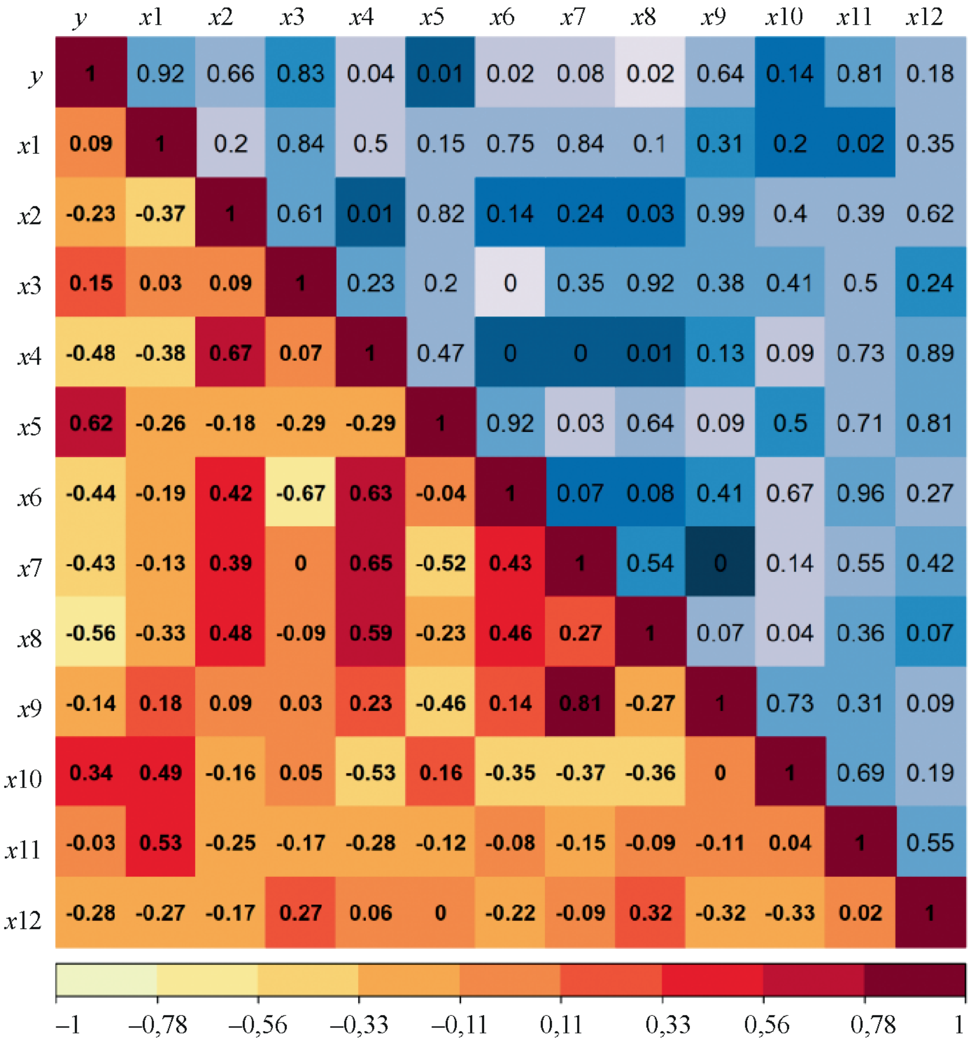
Indicator	Unit of measurement	Variable in the model
Fe level in the blood	mmol/L	*x*1
Leukocytes	$\times 10^9$ units	*x*2
Erythrocytes	$\times 10^{12}$ units	*x*3
Hemoglobin	g/l	*x*4
ESR	мм/ч	*x*5
Blood color index	Ratio	*x*6
Protein	g/l	*x*7
Albumin	g/l	*x*8
Globulin	g/l	*x*9
Urea	mmol/L	*x*10
Uric acid	μmol/L	*x*11
Cholesterol	mmol/L	*x*12

RESULTS AND DISCUSSION

In order to fit the regression models using the least squares method, it is necessary to assess the correlation between the predictors. When multicollinearity is detected among the model parameters, the coefficient values will be unstable, and the analysis of the contribution of each effect to the variance of the dependent variable will be difficult. Therefore, Spearman correlation coefficients were calculated to assess the associations between the variables (see Figure 1), and scatter plots were constructed (see Figure 2).

Four statistically significant correlations were found between the dependent and independent variables: hemoglobin, blood color index, albumin, and erythrocyte sedimentation rate (ESR). Hemoglobin concentration is associated with albumin and blood color index values, while ESR level is not related to these variables. In the selection of the models, it is necessary to choose a set of predictors that will allow for the calculation of the most effective and compact model, where the parameters do not duplicate each other's influence on the variance of the dependent variable.

Selection of the candidate models was based



	y	$x1$	$x2$	$x3$	$x4$	$x5$	$x6$	$x7$	$x8$	$x9$	$x10$	$x11$	$x12$
y	1	0.92	0.66	0.83	0.04	0.01	0.02	0.08	0.02	0.64	0.14	0.81	0.18
$x1$	0.09	1	0.2	0.84	0.5	0.15	0.75	0.84	0.1	0.31	0.2	0.02	0.35
$x2$	-0.23	-0.37	1	0.61	0.01	0.82	0.14	0.24	0.03	0.99	0.4	0.39	0.62
$x3$	0.15	0.03	0.09	1	0.23	0.2	0	0.35	0.92	0.38	0.41	0.5	0.24
$x4$	-0.48	-0.38	0.67	0.07	1	0.47	0	0	0.01	0.13	0.09	0.73	0.89
$x5$	0.62	-0.26	-0.18	-0.29	-0.29	1	0.92	0.03	0.64	0.09	0.5	0.71	0.81
$x6$	-0.44	-0.19	0.42	-0.67	0.63	-0.04	1	0.07	0.08	0.41	0.67	0.96	0.27
$x7$	-0.43	-0.13	0.39	0	0.65	-0.52	0.43	1	0.54	0	0.14	0.55	0.42
$x8$	-0.56	-0.33	0.48	-0.09	0.59	-0.23	0.46	0.27	1	0.07	0.04	0.36	0.07
$x9$	-0.14	0.18	0.09	0.03	0.23	-0.46	0.14	0.81	-0.27	1	0.73	0.31	0.09
$x10$	0.34	0.49	-0.16	0.05	-0.53	0.16	-0.35	-0.37	-0.36	0	1	0.69	0.19
$x11$	-0.03	0.53	-0.25	-0.17	-0.28	-0.12	-0.08	-0.15	-0.09	-0.11	0.04	1	0.55
$x12$	-0.28	-0.27	-0.17	0.27	0.06	0	-0.22	-0.09	0.32	-0.32	-0.33	0.02	1

Рис. 1. Корреляционная матрица (на красном фоне значения коэффициентов корреляции, на синем – их уровней значимости)

Fig. 1. Correlation matrix (on the red background are the values of the correlation coefficients, on the blue background are their significance levels)

on the assessments of internal quality criteria, including the Akaike information criterion (AIC), adjusted coefficient of determination (R2 adj), Mallow's criterion (Cp), and Bayesian information criterion (BIC). Based on the evaluations of the first two quality criteria, a model with four predictors was constructed (see Table 2). By considering the latter two criteria, a more compact model with two predictors was obtained (see Figure 3).

The evaluation of the obtained models and their effects is presented in Tables 3 and 4. Although the estimation of the residual standard deviation was slightly lower for the model with four predictors, only one coefficient (x9) was statistically significant, even though the value of the F-statistic was below the critical value, allowing us to reject the hypothesis of all coefficients being equal to zero (see Table 3). On the other hand, the model with two independent variables had a higher F-statistic value, leading to an improvement in the level of significance by a factor of two compared to the previous model (see Table 4).

Calculation of the variance inflation factor for the full model and candidate models is presented in Table 5. It is evident that the candidate models do not exhibit multicollinearity among the predictors, unlike the full model, where more than half of the coefficients are highly correlated.

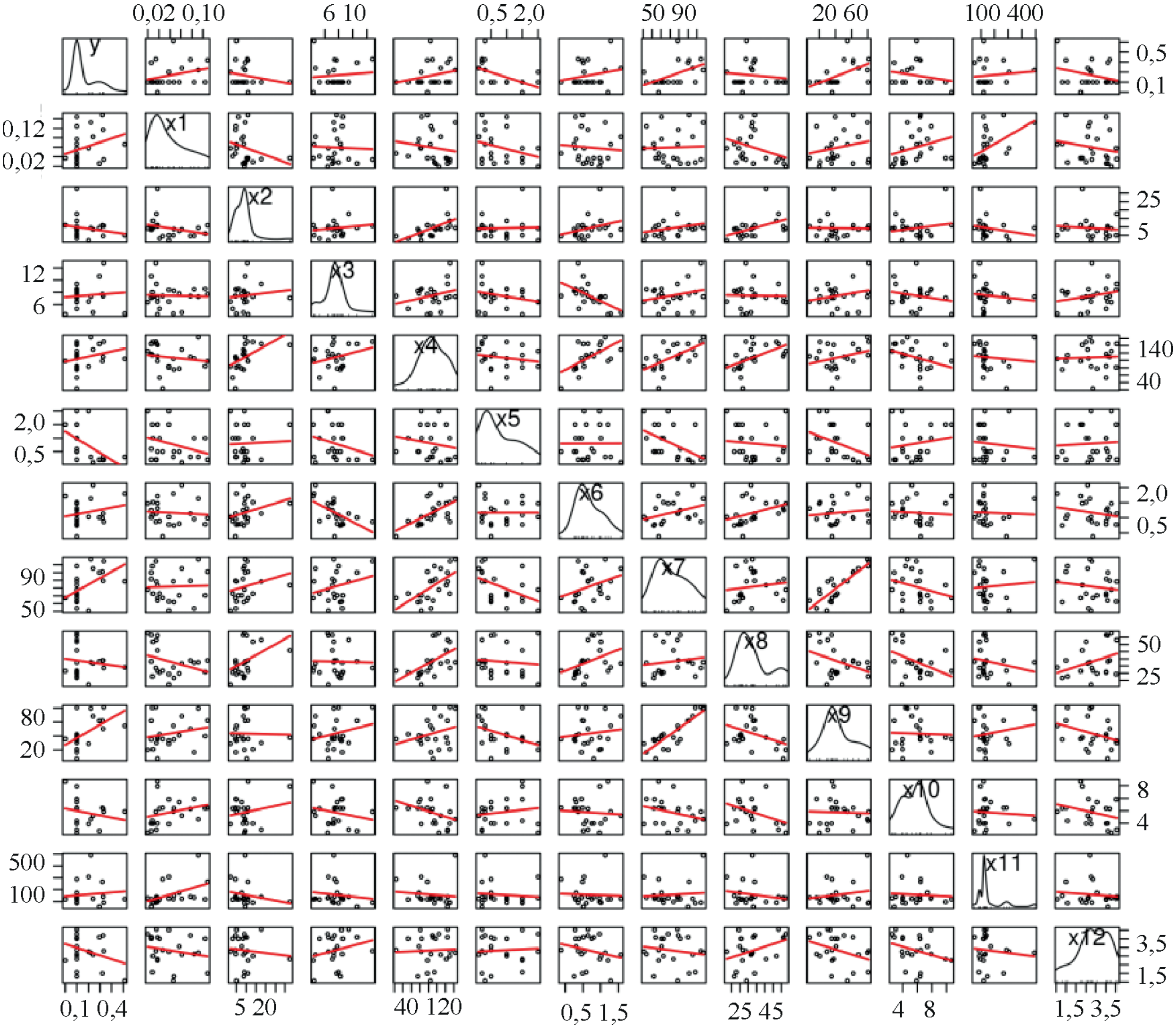


Рис. 2. Матрица диаграмм рассеяния параметров регрессионных моделей

Fig. 2. Matrix of scatterplots of regression models parameters

Табл. 2. Внутренние критерии оценки качества моделей-кандидатов прогноза уровня марганца в мышечной ткани, мг/кг

Table 2. Internal criteria for assessing the quality of candidate models for predicting the level of manganese in muscle tissue, mg/kg

Model formula	*df*	*p*	SSE	MSE	R^2	R^2_{adj}	AIC	BIC
$y \sim 1 + x1 + x3 + x9 + x10$	17	4	0,079	0,005	0,573	0,472	–49,358	–37,242
$y \sim 1 + x5 + x9$	19	2	0,097	0,005	0,478	0,423	–48,932	–38,998

Henceforward: SSE – square sum error; MSE – mean square error; R^2 – coefficient of determination; R^2_{adj} – adjusted coefficient of determination (ACD); AIC – Akaike information criterion; BIC – Bayesian information criterion.

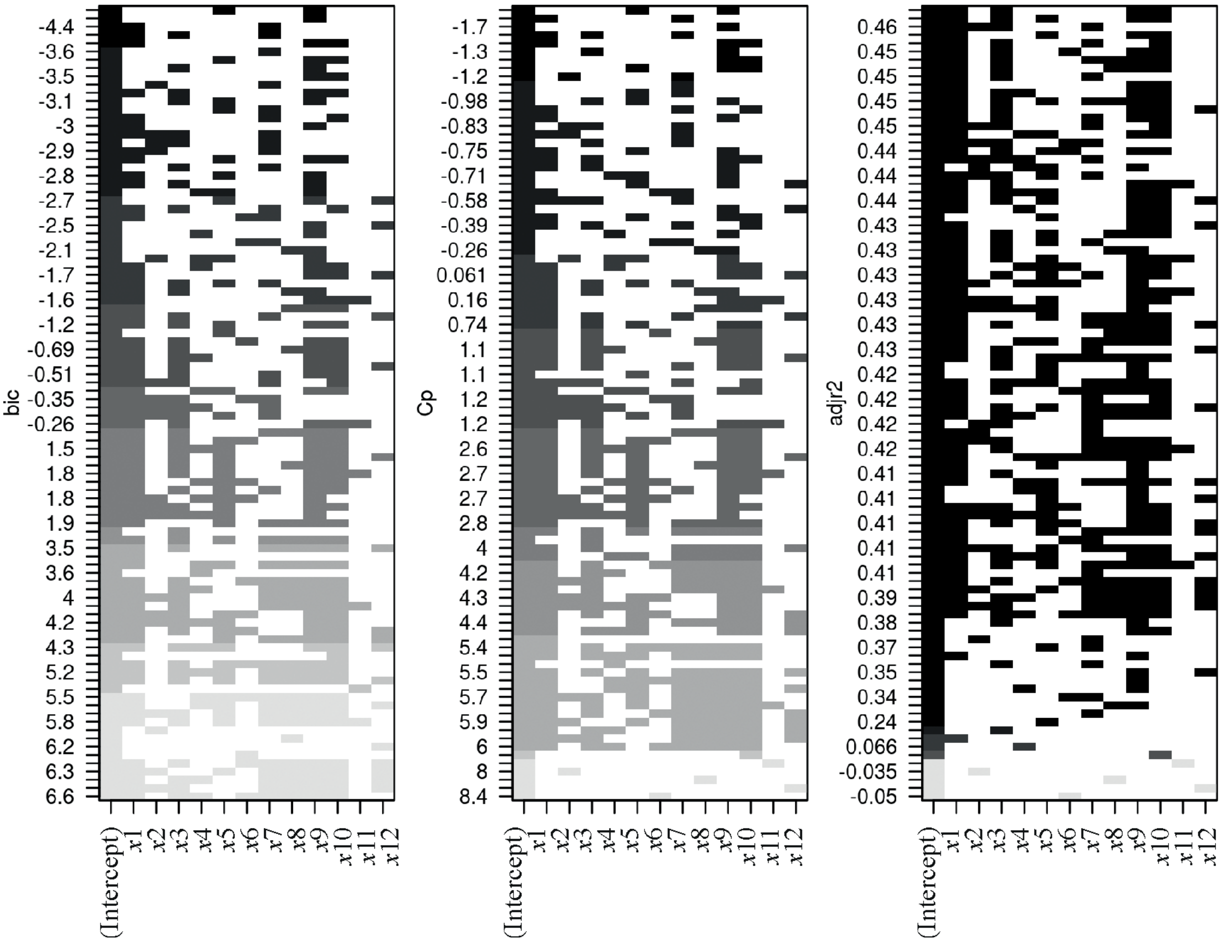


Рис. 3. Ранжирование моделей (слева направо) по BIC, критерию Мэллоу и R^2_{adj}

Fig. 3. Ranking of models (from left to right) according to the BIC, the Mallow criterion and R^2_{adj}

The choice of the best model was based on an external quality criterion for regression models – cross-validation. The visualization of cross-validation with the original dataset divided into 3 blocks is presented in Figure 4. The left graph shows that one of the regression lines deviates significantly from the overall trend, unlike the model with two predictors (on the right).

The forecast quality of the candidate models can be assessed using the unbiased value of the coefficient of determination and the mean square for each of the candidate models (see Table 6). The obtained data indicate a significant superiority of the compact model, as it provides a significantly more accurate forecast and explains the variance of manganese levels in muscle tissue nearly three times better than the closest competing model.

Thus, as a result of the selection, it can be concluded that the best model for predicting the level of manganese in cattle muscle tissue contains two predictors (x5 and x9).

To consider the selected model sufficiently effective for forecasting, it is necessary to check the assumptions regarding its residuals. Formal tests, such as the Anderson-Darling test ($A = 0.5$; $p = 0.2$) and the Shapiro-Wilk test ($W = 0.9$; $p = 0.2$), indicate the conformity of the residual distribution to normality. The visualization of the probability density values of the residuals falls within the confidence interval for the normal distribution curve (see Figure 5).

The plot of standardized residual quantiles and theoretically expected quantiles also shows that their values are normally distributed (see Figure 6, top-left plot).

The top-left and bottom plots indicate the relative homogeneity of residual variances (see Figure 6). The detection of the potentially influential observations using Cook's distance is

Табл. 3. Параметры оценки коэффициентов модели-претендента прогноза уровня марганца в мышечной ткани от показателей крови, мг/кг

Table 3. Parameters for estimating the coefficients of the candidate model for predicting the level of manganese in the muscle tissue from blood parameters, mg/kg

Coefficient designation	Coefficient estimates	Standard errors of the coefficients	t-statistics	p_t
Integer[1]	0,090	0,084	1,115	0,280
$x1$	0,889	0,463	1,919	0,072
$x3$	0,011	0,009	1,323	0,203
$x9$	0,002	0,001	2,759	0,013
$x10$	–0,013	0,007	–1,738	0,100

Note. RSE = 0,068, F-statistic = 5,7, p = 0,004.

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[1] Absolute term of an equation.

Табл. 4. Параметры оценки коэффициентов модели-претендента прогноза уровня марганца в мышечной ткани от показателей крови, мг/кг

Table 4. Parameters for estimating the coefficients of the candidate model for predicting the level of manganese in the muscle tissue from blood parameters, mg/kg

Coefficient designation	Coefficient estimates	Standard errors of the coefficients	t- statistics	p_t
Integer[1]	0,200	0,050	3,983	0,001
$x5$	–0,052	0,028	–1,873	0,077
$x9$	0,002	0,001	2,711	0,014

Note. RSE = 0,71, F-statistic = 8,7, p = 0,002.

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[1] Absolute term of an equation.

Табл. 5. Значения фактора инфляции дисперсии для коэффициентов регрессионных моделей оценки уровня марганца в мышечной ткани

Table 5. Values of the dispersion inflation factor for the coefficients of regression models for estimating the level of manganese in the muscle tissue

Predictor	Full model	$y \sim x1 + x3 + x9 + x10$	$y \sim x3 + x5$
$x1$	2,1	1,1	–
$x2$	4,2	–	–
$x3$	24	1,1	1,2
$x4$	33,8	–	–
$x5$	2,3	–	1,2
$x6$	33,3	–	–
$x7$	595,9	–	–
$x8$	162,6	–	–
$x9$	658,6	1,2	–
$x10$	3,3	1,1	–
$x11$	1,8	–	–
$x12$	1,8	–	–

shown in the bottom-right plot of Figure 6. The ordinal numbers of three observations with high influence potential are displayed. However, visually, these instances align with the model on the previous graphs of Figure 6. A formal check of the most influential observation's conformity to the overall population was conducted with Bonferroni correction. In the selected model, the maximum value of the studentized residual was 2.52 and corresponded to an adjusted significance level of 0.47. The obtained results indicate that this maximum value does not differ from the other observations in the population. To test the hypothesis of independence of the residuals, the autocorrelation coefficient was calculated as 0.039 (p = 0.32), confirming the null hypothesis of independence of the residuals in the model.

Thus, to forecast the level of manganese in Hereford cattle muscle tissue, it is necessary to determine the globulin concentration and erythrocyte sedimentation rate and build a regression equation based on the obtained data:

$$y = 0.2 - 0.052 \times \text{ESR} + 0.002 \times \text{G},$$

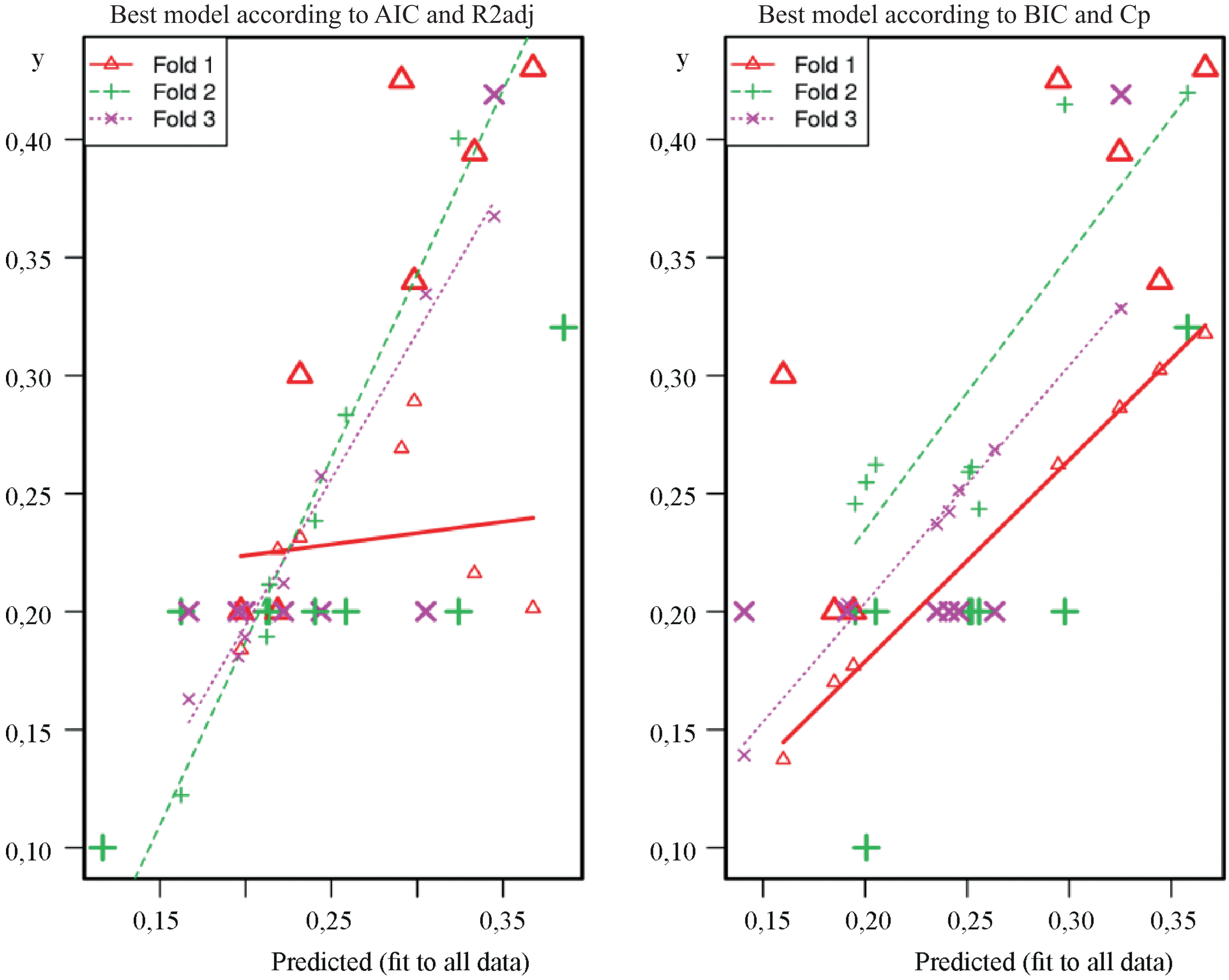

Рис. 4. Визуализация моделей-претендентов методом кросс-валидации с разбитием на 3 блока

Fig. 4. Visualization of candidate models for assessing by the cross-validation method divided into 3 blocks

Табл. 6. Кросс-валидация оценок регрессионных моделей прогноза уровня марганца в мышечной ткани

Table 6. Cross-validation of estimates of regression models for predicting the level of manganese in the muscle tissue

Model formula	SSE	*df*	MS	R^2	Cross-validation R^2
$y \sim 1 + x5 + x9$	0,2200	22	0,00996	0,478	0,227
$y \sim 1 + x1 + x3 + x9 + x10$	0,2242	22	0,01019	0,573	0,0826

where y is the manganese concentration in muscle tissue (mg/kg), ESR is the erythrocyte sedimentation rate (mm/h), and G is the globulin level (g/L).

Although the obtained results have demonstrated a sufficient level of statistical significance for the model and its coefficients, as well as the absence of outliers, this model requires training on new data as the precision of the forecast for manganese levels in muscle tissue will have wide confidence intervals with the available data. Therefore, additional data is needed to improve the model.

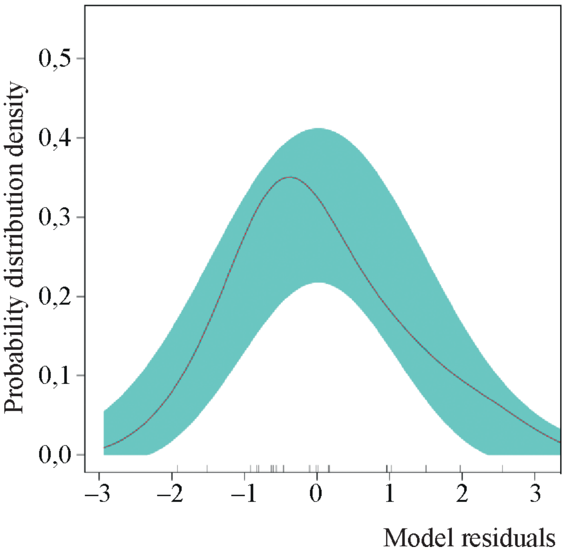

Рис. 5. Распределение остатков регрессионной модели оценки уровня марганца в мышечной ткани, мг/кг

Fig. 5. Residual distribution of the regression model for estimating the level of manganese in the muscle tissue, mg/kg

CONCLUSION

The obtained model can be used for the in vivo assessment of manganese levels in the Hereford cattle muscle tissue. The data obtained can be utilized for the purpose of ecological monitoring of elemental load on animals. The application of this method will enable the timely detection of Mn imbalances in muscle tissue and, through changes in diets, reduce or increase the concentration of this metal. Further training of the model is necessary to find a broader set of predictors to enhance the accuracy of the dependent variable estimates.

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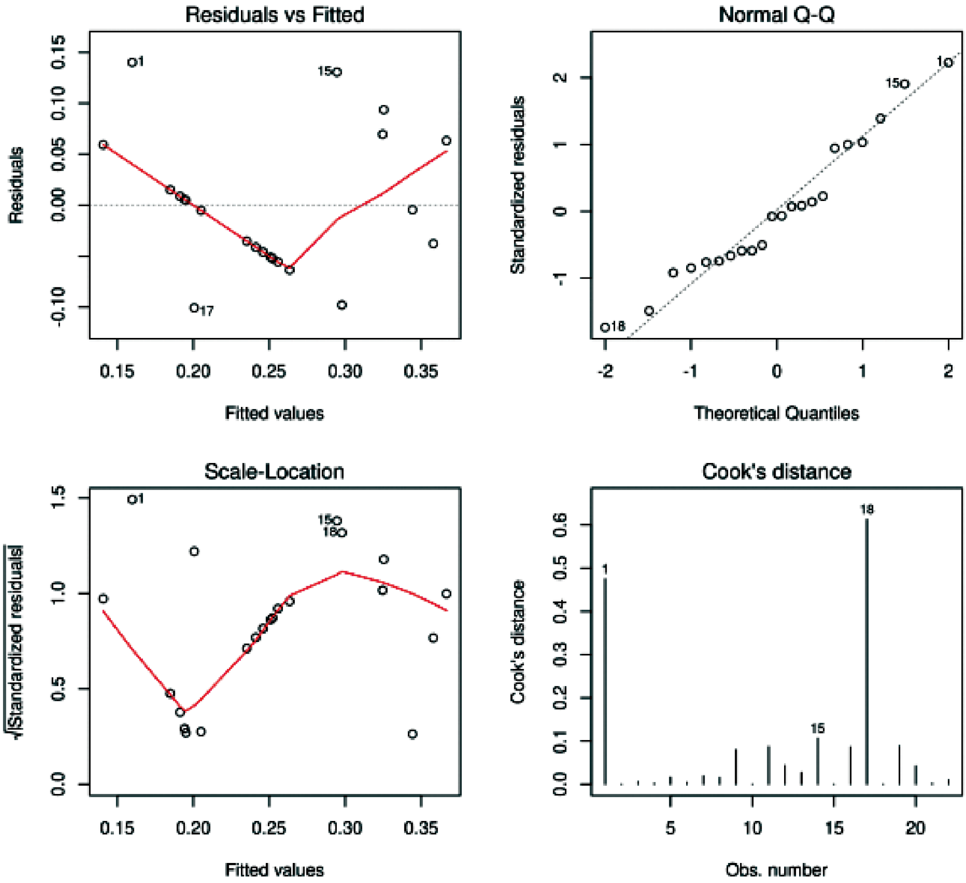

Рис. 6. Слева направо: остатки в зависимости от отклика, график квантилей, квадратный корень стандартизированных остатков в зависимости от отклика и дистанций Кука

Fig. 6. From left to right: residuals versus response, quantile plot, square root of standardized residuals versus response, and Cook's distances

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БИОРАЗНООБРАЗИЕ СВИНЕЙ РАЗЛИЧНЫХ ПОРОД НА ОСНОВЕ АНАЛИЗА D-ПЕТЛИ мтДНК

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Полиморфизм митохондриальной ДНК, представляющий собой один из наиболее распространенных генетических маркеров, активно применяется при изучении различных видов животных. Так как в пределах того или иного вида митохондриальный геном развивался на протяжении многих лет, это повлияло на фиксацию мутаций и образование митохондриальных линий, имеющих общее происхождение и формирующих митохондриальные геномы, называемые гаплогруппами мтДНК. Целями работы являлись оценка генетического разнообразия свиней двух материнских пород отечественной репродукции на основании анализа полиморфизма D-петли мтДНК, а также сравнение полученных результатов с идентичными последовательностями из базы данных NCBI в разрезе пород и их географического распространения. Были изучены 39 свиней породы ландрас и 49 – крупной белой породы. Митохондриальную ДНК выделяли из образцов тканей (ушной выщип). Для оценки генетического разнообразия определяли количество гаплотипов, гаплотипическое и нуклеотидное разнообразие, среднее число замен нуклеотидов на сайт. Обнаружено 23 полиморфных участка: 21 – у свиней породы ландрас, 17 – у представителей породы крупная белая. Всего в исследуемой популяции выявлено десять гаплотипов. В базе данных NCBI найдено 75 идентичных последовательностей, характерных для свиней различных пород, разводимых в разных странах мира. После определения нуклеотидных последовательностей фрагмента D-петли мтДНК свиней пород ландрас и крупная белая отечественной репродукции и их сравнения с последовательностями из базы данных NCBI было установлено наличие идентичных последовательностей у изучаемых нами животных и представителей европейских и азиатских пород, в том числе коммерческих и локальных. Полученные материалы показывают, что оценка полиморфизма мтДНК способствует идентификации филогенетических связей между популяциями, отслеживанию породообразовательных процессов и может быть рассмотрена как дополнительный критерий селекционно-племенной работы.

Ключевые слова: генетические маркеры, генетика, свиньи, мтДНК

BIODIVERSITY OF PIGS OF VARIOUS BREEDS BASED ON THE ANALYSIS OF mtDNA D-LOOP

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Mitochondrial DNA polymorphism, which is one of the most common genetic markers, is actively used in the study of various animal species. Since the mitochondrial genome has evolved over many years within a species, this has influenced the fixation of mutations and the formation of mitochondrial lineages that share a common origin and form mitochondrial genomes, called mtDNA haplogroups. The objectives of the work were to evaluate the genetic diversity of pigs of two maternal breeds of domestic reproduction based on the analysis of mtDNA D-loop polymorphism and to compare the results obtained with identical sequences from the NCBI database by breed and their geographic distribution. 39 Landrace pigs and 49 Large White pigs were used for the study. MtDNA was isolated from tissue samples (ear notch). The number of haplotypes, haplotypic and nucleotide diversity, and the average number of nucleotide substitutions per site were determined to assess the genetic diversity. 23 polymorphic sites were found: 21 in Landrace pigs, 17 in Large White pigs. A total of ten haplotypes were identified in the study population. The NCBI database found 75 identical sequences for pigs of different breeds bred around the world. After determining the nucleotide sequences of the D-loop fragment of the mtDNA of Landrace and Large White pigs of domestic reproduction and comparing them with the sequences from the NCBI database, the presence of identical sequences in the animals we studied and in the representatives of European and Asian breeds, including commercial and local was established. The materials obtained show that the assessment of mtDNA polymorphism contributes to the identification of phylogenetic relationships between populations, tracing of pedigree processes, and can be considered as an additional criterion of selection and breeding work.

Keywords: genetic markers, genetics, pigs, mtDNA

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INTRODUCTION

Mitochondrial DNA (mtDNA) polymorphism, as one of the most common genetic markers, is widely used in the study of various animal species. This is due to its maternal inheritance and the high frequency of occurrence of mutational processes. Mitochondrial DNA is inherited through cytoplasmic inheritance and is not subject to recombination. Within a species, the mitochondrial genome has evolved over many years, leading to the fixation of mutations and the formation of different mitochondrial lineages that share a common origin, forming mitochondrial genomes known as mtDNA haplogroups. mtDNA haplotypes not only confer the advantages and disadvantages on organisms[1, 2] (e.g., influencing the growth and physical performance of animals, adaptation to warm and cold climates, sperm motility), but also determine economically important traits such as milk quality [1]. Furthermore, it has been shown that embryonic stem cell lines of different mtDNA haplotypes, with identical

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nuclear DNA, exhibit different levels of gene expression during cell differentiation [2], which may be influenced by the impact of mtDNA on phenotype realization.

Currently, both Asian (A, B, and C) and European (D and E) haplogroups have been identified in pigs. Pig breeds developed in China, Korea, and Japan are largely similar to each other but significantly differ from the European-type pigs. Commercial breeds of the European origin, such as Landrace, Large White, and Duroc, are bred worldwide, and their mtDNA may belong to either the Asian or non-Asian type depending on their origin and further improvement by individual breeding centers.

For domestic selection purposes, studies on mtDNA of pigs from breeding farms in the Russian Federation are of particular interest. In this regard, the objectives of our work were to assess the genetic diversity of two domestically reproduced maternal pig breeds based on the analysis of mtDNA D-loop polymorphism and to compare the obtained materials with identical sequences from the National Center for Biotechnology Information (NCBI) database in terms of the breeds and their geographical distribution.

MATERIALO AND METHODS

The study was conducted on the domestically reproduced Landrace pigs (*n* = 39) and Large White pigs (*n* = 49). DNA was extracted from tissue samples using the "K-Sorb-100" reagent kit (Syntol, Russia). The D-loop region (1046 bp) was amplified by PCR using the primers FW 5'-TGCAAACCAAAACGCCAAGT-3' and RW 3'-TTTTTGGGGTTTGGCAAGGC-5'. Gel-purification of the amplified fragments was performed using the Cleanup Mini kit (Eurogene, Russia). Sequencing was outsourced to Eurogene company. Editing and alignment of the sequences were performed using BioEdit 7.2.6 and MEGA 7 software. mtDNA haplotypes were denoted as Hap. The number of the haplotypes (H), haplotype diversity (HD), nucleotide diversity (π), and average number of nucleotide substitutions per site (k) were calculated using DnaSP 5.10. Calculations and construction of the phylogenetic tree were performed using the maximum likelihood method. The sequence number NC000845 (NCBI) was considered as the reference. Sequences were assigned to specific haplogroups based on comparison with known haplogroup sequences from the NCBI database (A-KT279758, B-KT261429, C-KT279759, D-KT279760, E-KT261430).

RESULTS AND DISCUSSION

During the study, nucleotide sequences of the variable D-loop region of mtDNA were determined for 88 tissue samples from Landrace and Large White pigs. For further analysis, a 638 bp fragment located within the range of 87-724 bp according to the reference sequence was used. Table 1 presents the parameters of genetic diversity in the studied pig groups.

The haplotype diversity for the Landrace breed was recorded at a level of 0.839, while for the Large White breed, it was 0.041 (see Table 1). Landrace pigs exhibited a higher number of nucleotide substitutions (k = 8.640) compared to Large White pigs (k = 0.735). The average nucleotide diversity was 0.013 (mostly due to the Landrace breed).

A total of 23 mutations were detected in the studied group, with 21 in Landrace pigs and 17 in Large White pigs. Ten haplotypes were identified in total (see Table 2).

Out of the 49 Large White pigs, 48 had the Hap-10 haplotype, while only one individual had the Hap-9 haplotype. Landrace pigs showed greater genetic diversity, with eight haplotypes identified. The most frequent haplotypes were Hap-1 and Hap-4 (see the figure).

Табл. 1. Генетическое разнообразие свиней пород ландрас и крупная белая

Table 1. Genetic diversity of Landrace and Large White pigs

Breed	N	S	H	HD	k	π
Landrace	39	21	9	0,839	8,640	0,0139
Large White	49	18	2	0,041	0,735	0,0012
On average	88	23	10	0,674	8,328	0,0134

The assignment of the identified haplotypes to haplogroups A, C, D, and E is shown on the phylogenetic tree (see figure). No individuals belonging to haplogroup B were found.

A search for identical sequences in the NCBI database revealed 75 sequences belonging to the representatives of different breeds (see Table 3). Out of these, 30 sequences were assigned to the Hap-10 haplotype, which we identified in Large White pigs. Previously, two sequences were found in wild Asian boars, 27 in Asian pig breeds[3, 4] [1–9], and one in a Spanish-origin Large White pig (see footnote 2). The individuals of the Asian origin with the Hap-10 haplotype were associated with local Chinese breeds [2, 5, 6, 8, 9]. This haplotype was also found in Mong Cai pigs [4, 8] and Kunekune pigs bred in New Zealand.

According to the NCBI data, identical Hap-1 haplotypes were identified in Landrace and Duroc pigs bred in Australia [1] and Japan[5], Iberian pigs (see footnote 2), and French wild boars (see footnote 1). Sequences identical to the Hap-2 haplotype were found in wild boars (see footnote 2) and Mangalica pigs [10]. Carriers of the Hap-5 haplotype are similar to the Landrace pigs of Chinese origin[6], Canadian pigs [11], and Japanese pigs[7]. The Hap-8 haplotype is fixed in Duroc pigs in Spain[8] and China (see footnote

Табл. 2. Гаплотипы свиней пород ландрас и крупная белая
Table 2. Haplotypes in Landrace and Large White pigs

n	Haplo-type	Mutation																						
		109	124	131	145	153	158	180	185	241	248	279	294	306	323	390	405	452	560	575	640	692	704	706
												Landrace												
9	1H	T	T	G	C	C	A	C	T	T	G	C	A	C	C	C	T	C	T	A	C	G	A	A
2	2H	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	A	–	–
5	3H	–	–	–	–	–	–	T	–	–	–	–	–	–	–	–	–	–	–	G	–	A	–	–
11	4H	C	A	A	T	T	G	–	–	C	–	T	G	T	T	T	–	–	C	G	–	A	G	G
2	5H	–	–	–	–	–	–	–	C	–	A	–	–	–	T	–	–	–	–	–	–	–	–	–
6	6H	–	A	–	–	–	–	T	–	–	–	–	–	–	T	–	–	–	–	–	T	–	–	–
2	7H	–	–	–	–	–	–	T	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
2	8H	–	–	–	–	–	–	T	–	–	–	T	–	–	–	–	–	–	–	–	–	–	–	–
												Large White												
1	9H	C	A	A	T	T	G	–	–	C	–	T	G	T	T	T	–	–	C	G	–	A	–	–
48	10H	C	A	A	T	T	G	–	–	C	–	–	G	T	T	T	–	–	–	G	–	–	G	G

Note. Positions are listed in accordance with Sequence No. NC000845.

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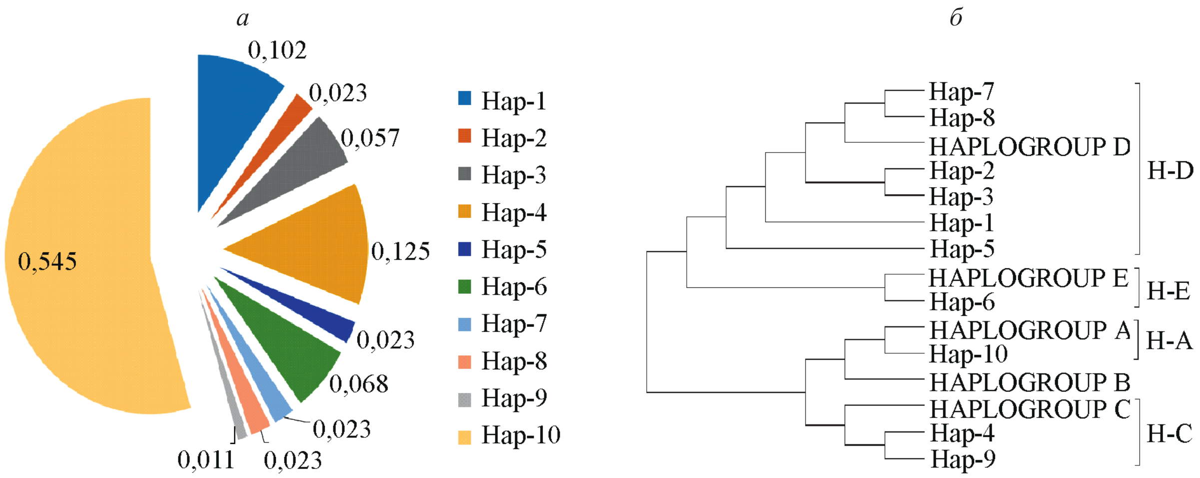
Табл. 3. Идентичные гаплотипы из базы данных NCBI

Table 3. Identical haplotypes from the NCBI database

Haplotype	Number in the NCBI	Breed	Country	Haplotype	Number in the NCBI	Breed	Country
Hap-1	KT279760	Commercial	Australia	Hap-8	KF569218	F2	Vietnam
Hap-1	FJ236997	Duroc	Spain	Hap-8	KC250275	Large White	China
Hap-1	AM040631	»	Taiwan	Hap-8	FJ236996	Duroc	Spain
Hap-1	AM040613	Landrace	»	Hap-8	EU660148	»	China
Hap-1	AM040615-AM040620	»	»	Hap-9	Hap-9 sequences are absent		
Hap-1	D42170	Commercial	Japan	Hap-10	MG250567	Yudong black	China
Hap-1	HM747198	Wild boar	Portugal	Hap-10	MG250564	Wuzhishan	»
Hap-1	AY232858	Iberian	Spain	Hap-10	MG250562	Wuzhishan	»
Hap-2	KJ746666	Mangalitsa	China	Hap-10	MG250556	Tunchang	»
Hap-2	HM747198	Wild boar	France	Hap-10	MG250532	Huizhong	»
Hap-2	JN601068	Mangalitsa	USA	Hap-10	MG250529	Huizhong	»
Hap-3	Hap-3 sequences are absent			Hap-10	MG250518	Bamaksyang	»
Hap-4	EU979134	Dapulian	China	Hap-10	KF913287	Kwangbaihai	»
Hap-5	EU660147	Landrace	»	Hap-10	KF913276	Cunjiangxiang	»
Hap-5	MH113791	Yorkshire and Landrace	»	Hap-10	KF913275	Cunjiangxiang	»
Hap-5	AB041499	Landrace	Japan	Hap-10	KF913271	Cunjiangxiang	»
Hap-6	Hap-6 sequences are absent			Hap-10	KF913253	Baixi	»
Hap-7	KC469587	Pietren	China	Hap-10	KF913252	Baixi	»
Hap-7	EU660181	Yorkshire	»	Hap-10	KX982643	Wild boar	Vietnam
Hap-7	EU660154	Duroc	»	Hap-10	KX982646	» »	»
Hap-7	EU660151	»	»	Hap-10	KX982647	» »	»
Hap-7	EU660150	»	»	Hap-10	KX982651	» »	»
Hap-7	EU660140	Landrace	»	Hap-10	KX982652	» »	»
Hap-7	AF034253	»	Taiwan	Hap-10	KX147100	Mong Cai	»
Hap-7	D16483	»	Japan	Hap-10	KU556691	Mong Cai	China
Hap-7	AM040625-AM040629	Duroc	Taiwan	Hap-10	KT279758	Large White	Australia
Hap-7	AM040612	Landrace	»	Hap-10	KP681243	Wuzhishan	China
Hap-7	AM040614	»	»	Hap-10	KM094194	Sandu black	»
Hap-7	AM040619	»	»	Hap-10	KF767443	Wuzhishan	»
Hap-7	AM040621	»	»	Hap-10	KC250274	Lantang	»
Hap-7	AM040622	»	»	Hap-10	FM244684	Wild boar	Thailand
Hap-7	HM747216	Bisaro	Portugal	Hap-10	FM244685	» »	»
Hap-7	AY232856	Iberian	Spain	Hap-10	EU979182	Chunghwai White	China
Hap-7	GQ169779	Duroc	Taiwan	Hap-10	AY884824	Kunekune	United Kingdom
Hap-7	AB041494	Large White	Japan	Hap-10	AY232882	Large White	Spain



Частота встречаемости гаплотипов мтДНК (*а*) и их распределение в соответствии с гаплогруппами A, B, C, D, E (*б*)

Frequencies of mtDNA haplotypes in the studied pigs (*a*). Distribution of haplotypes according to haplogroup A, B, C, D, E (*б*)

3) [4], as well as in Large White pigs in China [3]. It has been established that the divergence of European and Asian pig breeds based on mtDNA differences occurred long before their domestication [12]. Pigs and boars from China, Korea, and Japan demonstrate close relationships among themselves and are significantly different from European pigs in the maternal lineage [3].

CONCLUSION

As a result of the study, nucleotide sequences of the most variable fragment of the D-loop region of mtDNA in Landrace and Large White pigs have been determined. Comparison of these sequences with the variants deposited in the NCBI database revealed the presence of identical sequences among pigs of various Asian and European breeds. Thus, the assessment of mtDNA polymorphism contributes to the identification of phylogenetic relationships between populations, tracking breed formation processes, and can be considered as an additional criterion in breeding and breeding work.

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ПРОДУКТИВНОСТЬ ПОТОМСТВА БЫКОВ-ПРОИЗВОДИТЕЛЕЙ С РАЗНОЙ ИНДЕКСНОЙ ОЦЕНКОЙ

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Проблема изучения степени влияния индекса «Период продуктивной жизни/продуктивное долголетие» быков-производителей на продолжительность продуктивного использования их потомства недостаточно освещена в научной литературе, что и обосновывает актуальность проведенных исследований. Осуществлена сравнительная оценка хозяйственно-полезных признаков дочерей быков-производителей с величиной индекса от 103 до 117. Динамика выбытия опытных животных определена в период от рождения до завершения второй лактации, уровень молочной продуктивности – по данным за первую и вторую лактации. Установлено, что выбытие среди дочерей быков-производителей с индексом, равным103 и 105, было наибольшим во все физиологические периоды и составило на конец опыта 80,0 и 78,1% соответственно. В группах дочерей быков-производителей с величиной индекса 109 и 117 доля выбывших животных достигала 62,9 и 65,6%. Наименьшая продуктивность за первую и вторую лактации зафиксирована у дочерей быка-производителя с величиной индекса 103 – 6760,2 и 7100,7 кг молока. Дочери быка-производителя с индексом, равным 117, отличались наибольшей молочной продуктивностью – 7475,9 и 8158,3 кг молока за две лактации. Анализ полученных данных показывает, что закрепление быков-производителей за маточным стадом с учетом индекса «Период продуктивной жизни/продуктивное долголетие» позволит получать более крепкое потомство с хорошими продуктивными качествами.

Ключевые слова: быки-производители, индекс оценки, продуктивное долголетие, выбытие, сохранность поголовья

PRODUCTIVITY OF THE SERVICING BULLS PROGENY WITH DIFFERENT INDEX SCORES

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The problem of studying the degree of influence of the index "Period of productive life/productive longevity" of the servicing bulls on the duration of productive use of their progeny is not sufficiently covered in the scientific literature, which substantiates the relevance of the research. A comparative assessment of economically useful features of the daughters of servicing bulls with the index value from 103 to 117 has been carried out. Dynamics of the experimental animals' mortality is determined in the period from birth to the end of the second lactation, the level of milk productivity - according to the data for the first and second lactations. It was found that mortality among the daughters of the servicing bulls with an index equal to 103 and 105 was the highest in all physiological periods and amounted to 80.0 and 78.1% at the end of the experiment, respectively. In the groups of the daughters of the servicing bulls with index values of 109 and 117, the proportion of animals that died out reached 62.9 and 65.6%. The lowest productivity for the first and second lactations was recorded in the daughters of the servicing bull with the index value of 103 - 6760.2 and 7100.7 kg of milk. The daughters of the servicing bull with the index equal to 117 were distinguished by the highest milk productivity - 7475.9 and 8158.3 kg of milk in two lactations. Analysis of the obtained data shows that fixation of servicing bulls to the breeding herd taking into account the "Period of productive life/productive longevity" index will make it possible to obtain more robust progeny with good productive qualities.

Keywords: servicing bulls, assessment index, productive longevity, mortality, livestock viability

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Конфликт интересов

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Conflict of interest

The authors declare no conflict of interest.

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INTRODUCTION

The profitability of dairy cattle farming directly depends on the productivity of the animals. In the Russian Federation, the task of increasing milk productivity is solved through the extensive use of the Holstein breed gene pool. Although the Holstein breed ranks second in terms of population size in our country, representatives of other breeds of dairy cattle carry a certain proportion of Holstein blood[1] in their genotype [1–3]. However, high productivity is an antagonist to animal health indicators. Holsteinized cattle have a low potential for immune defense, which results in the productive lifespan of Holsteinized dairy cows being less than three lactations[2, 3] [4, 5]. Recently, great attention has been paid to animal health, their reproductive ability, and productive longevity [6–8]. The productive longevity of dairy cows is determined not only by their genotype but also by the influence of the environment. Among the genetic factors influencing the productive longevity of dairy cattle, the genotype of the sire plays a decisive role[4–6]. Рентабельность молочного скотоводства напрямую зависит от продуктивности животных.

In the last 20 years, selection and breeding of animals based on selection indexes have been successfully used in dairy breeding. Genetic indexes facilitate the work of breeders in cattle breeding and increase production profitability[7] [9]. Sire evaluation is based not only on the productive traits of their daughters but also on health indicators, particularly the "Productive Life (PL)/Longevity" index. Offspring of sire bulls with this index evaluation exhibit high indicators of nonspecific immunity and reproductive ability [10]. It is assumed a priori that any sire bull with an index evaluation above 100 can improve this indicator in its

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offspring. However, there is no data in the scientific literature on how the magnitude of the aforementioned sire bull index is related to the productive longevity of its progeny.

The purpose of the study is to determine the influence of the magnitude of the "Productive Life/Longevity" index of sire bulls on the survival and productive qualities of their daughters.

MATERIAL AND METHODS

The work was conducted from 2017 to 2021 at the agricultural production cooperative "Kazminsky" in the Kochubeyevsky municipal district of the Stavropol Territory, Russia. This farm is a breeding facility specializing in Holstein dairy cattle. Through years of targeted selection for increasing the quantitative and qualitative indicators of milk productivity, milk yields have been raised to 8056 kg per cow, but the duration of productive use for most animals still remained within one to two lactations.

In 2017, the Black-and-White dairy cows were used for artificial insemination by the Holstein bulls Alta-Red 66726504, Mirok-M 5226675598, Allhard 65431789, and Memory-M 54215651. The magnitude of the "Productive Life/Longevity" index for these bulls was 103, 105, 109, and 117, respectively. In 2018, a total of 815 daughters were obtained from these bulls and divided into four experimental groups: Group 1 - offspring of Alta-Red, Group 2 - offspring of Mirok-M, Group 3 - offspring of Allhard, and Group 4 - offspring of Memory-M. All experimental animals were kept on the same farm under identical feeding and management conditions that met their physiological and technological needs.

Observations on the animals were conducted from birth until the completion of the second lactation. Exclusion was recorded during the following life periods: from birth to 9 and 18 months of age, and from birth to the completion of the first and second lactations. The information and analytical system "SELEX. Dairy Cattle" was used as the data source.

RESULTS AND DISCUSSION

The dynamics of exclusion and the level of daughter retention of bulls with different "Productive Life/Longevity" index values over the entire observation period are presented in Table 1.

Among the heifers up to 9 months of age, the highest percentage of exclusion was recorded in the 1st and 2nd experimental groups, at 17.0% and 17.9% respectively, which is 7.5% and 8.6% higher than the 3rd group and 10.1% and 11.0% higher than the 4th group.

During the period from birth to 18 months of age, the superiority also remained with the representatives of the 3rd and 4th experimental groups. Compared to the 1st and 2nd groups, the difference was 13.0% and 12.8% in favor of the 3rd group, and 12.5% and 13.2% in favor of the 4th group.

The greatest difference in the exclusion rate was observed during the period from birth to the completion of the first and second lactations,

Табл. 1. Выбытие и сохранность опытных животных

Table 1. Mortality and preservation of experimental animals

Indicator	Experimental group			
	1st (*n* = 100)	2nd (*n* = 501)	3rd (*n* = 54)	4th (*n* = 160)
The number of excluded animals, heads:				
from birth to 9 months	17 (17,0%)	90 (18,0%)	5 (9,3%)	11 (6,9%)
from birth to 18 months	30 (30,0%)	154 (30,7%)	7 (13,0%)	28 (17,5%)
from birth to the end of the first lactation	56 (56,0%)	232 (46,3%)	19 (35,2%)	54 (33,8%)
from birth to the end of the second lactation	80 (80,0%)	390 (77,8%)	34 (63,0%)	105 (65,6%)
Herd retention after completion of the second lactation, %	20,0	22,2	37,0	34,4

which is when the cost of rearing non-milking animals is recovered. During this period, the attrition rate of daughters from the bull Alta-Red 66726504, who had the lowest "Productive Life/Longevity" index, reached 56.0% and 80.0%. In the group of daughters from the bull Mirok-M 5226675598 (index value 105), the percentage of animals excluded before completing the first lactation was 46.3%, which is 9.7% lower than in the 1st experimental group. However, after completing the second lactation, the differences between these groups decreased to 1.9%.

Among the daughters of the bulls Allhard 65431789 and Memory-M 54215651 (index values 109 and 117, respectively), the exclusion rate from birth to the completion of the first lactation was 20.8% and 22.3% lower than in the 1st experimental group, and 11.1% and 12.6% lower than in the 2nd group. During the period from birth to the completion of the second lactation, the difference between the 1st and 3rd groups, and the 1st and 4th groups, was 17.1% and 14.4%, while between the 2nd and 3rd groups, and the 2nd and 4th groups, it was 15.2% and 12.5%, respectively.

After completing the second lactation, the lowest exclusion rate was observed in the 1st experimental group (20.0%), while the highest was in the 3rd group (37.1%). In the 4th group, where the bull had the highest index, the daughter retention was 2.7% lower than in the 3rd group. Possibly, the level of milk productivity had a negative influence on this indicator, as the animals in the 4th experimental group had higher milk yields in both the first and second lactations compared to the 3rd experimental group (see Table 2).

During the first lactation, the highest milk yield was obtained from the animals in the 4th experimental group - 7475.9 kg (a 24.1 kg difference compared to the 2nd group).

The lowest amount of milk was obtained from the 1st experimental group - 6760.2 kg, which was 715.7 kg less than from the animals in the 4th group. In terms of milk yield, the animals in the 2nd, 3rd, and 4th groups significantly outperformed those in the 1st experimental group (p > 0.999). However, the animals in the 1st group had better milk quality characteristics: fat content was 4.06% (p > 0.99), and protein content was 3.18%.

The same trend was observed in the results of the second lactation. The animals in the 4th experimental group also had the highest milk yield - 8158.3 kg. The difference in this indicator compared to the 2nd and 3rd groups was 14.3 kg and 524.2 kg respectively. The largest difference in milk yield was observed between the 1st and 4th groups - 1057.6 kg (p > 0.999).

Thus, the daughters of the bull Alta-Red, who had an index value of 103, not only had the lowest retention rate but also showed lower milk yield performance in both completed lac-

Табл. 2. Молочная продуктивность опытных животных

Table 2. Milk productivity of experimental animals

Indicator	Experimental group			
	1st (n = 100)	2nd (n = 501)	3rd (n = 54)	4th (n = 160)
First lactation				
Number of heads	44	269	35	106
Milk yield, kg	6760,2 ± 52,0	7451,8 ± 44,6**	7294,1 ± 49,6**	7475,9 ± 5 0,9**
Milk fat content, %	4,06 ± 0,09*	3,91 ± 0,10	3,92 ± 0,08	3,87 ± 0,07
Milk protein content, %	3,18 ± 0,09	3,16 ± 0,08	3,16 ± 0,08	3,12 ± 0,07
Second lactation				
Number of heads	15	78	13	41
Milk yield, kg	7100,7 ± 206,1	8144,0 ± 151,3*	7634,1 ± 318,0	8158,3 ± 115,6**
Milk fat content, %	3,99 ± 0,01	3,9 ± 0,01	3,93 ± 0,02	3,95 ± 0,01
Milk protein content, %	3,17 ± 0,02	3,15 ± 0,01	3,19 ± 0,01	3,18 ± 0,02

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*$p > 0,99$.

**$p > 0,999$.

tations. The daughters of the bull Memory-M with an index value of 117 were the milk yield leaders and only slightly differed in retention rate from the animals in the 3rd experimental group.

The difference in the milk yield between the 2nd and 4th groups, both in the first and second lactations, was minimal, indicating that the use of bulls with a "Productive Life/Longevity" index value of at least 105 in breeding has a positive influence on the productive qualities of the offspring.

CONCLUSION

Based on the conducted research, reliable results have been obtained, proving that the selection of sire bulls taking into account the "Productive Life/Longevity" index value contributes to the improvement of offspring retention and productive qualities. The highest heifer survival rate was observed in the 2nd and 3rd experimental groups in all evaluated age periods. By the end of the second lactation, the retention rate of animals in these groups was on average 15% higher than that of their counterparts. Therefore, the offspring of the bulls with high values of this index exhibits high indicators of nonspecific immunity. Significantly lower productivity indicators were recorded only in the animals of the 1st group. Since the first two lactations are when the cost of rearing non-milking animals is recovered the most, the application of the studied breeding approach will increase the profitability of milk production.

Thus, we recommend using the method of selecting sire bulls based on the "Productive Life/Longevity" index value (≥ 109) in the breeding process, which will result in obtaining more robust offspring and increasing the profitability of milk production.

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АССОЦИАЦИИ ПОЛИМОРФИЗМА ГЕНА СОМАТОТРОПИНА (GH) С ПОКАЗАТЕЛЯМИ МОЛОЧНОЙ ПРОДУКТИВНОСТИ КОРОВ

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Исследования проведены в лаборатории молекулярно-генетической экспертизы в 2018 и 2019 гг. в рамках государственного задания по теме «Разработка селекционно-генетических и теоретических основ сохранения и эффективного использования генофонда крупного рогатого скота в Уральском регионе с применением современных биотехнологий». Объект исследования – крупный рогатый скот голштинизированной черно-пестрой породы. Основная задача – анализ степени влияния полиморфизма гена соматотропина (GH) на показатели молочной продуктивности. В процессе изучения выделено ДНК 270 коров, на основе полученных данных определен полиморфизм гена соматотропина, установлена взаимосвязь различных генотипов с показателями живой массы, удоя, массовой доли белка и массовой доли жира в молоке. Результаты биометрически обработаны при помощи программы IBM SPSS Statistics 23. Выявлено, что *LL* является основным генотипом гена GH среди представителей голштинизированной черно-пестрой породы (частота встречаемости 77,0%). Доля генотипов *LV* и *VV* в популяции составляет 21,9 и 1,1% соответственно. Во время наблюдения коровы – носительницы генотипа *LL* – показывали более высокие удои по первой и третьей лактациям. Разница со сверстницами у них составила 202–2334 кг ($p \leq 0,05$). Зафиксирована тенденция к увеличению содержания белка в молоке у животных с генотипом *VV*. По первой лактации разница с носительницами генотипов *LL* и *LV* достигала 0,03 и 0,06% соответственно. По третьей лактации особи с генотипом *VV* превосходили сверстниц по содержанию белка на 0,07 и 0,12% соответственно.

Ключевые слова: крупный рогатый скот, соматотропин, полиморфизм, удой, массовая доля жира, массовая доля белка, живая масса, первая лактация, третья лактация

ASSOCIATIONS OF SOMATOTROPIN (GH) GENE POLYMORPHISM WITH LACTATION PERFORMANCE OF COWS

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The research was conducted in the laboratory of molecular genetic expertise in 2018 and 2019 within the framework of the state assignment on the topic "Development of genetic-selection and theoretical foundations for the conservation and effective use of the gene pool of cattle in the Ural region with the use of modern biotechnologies". The object of the study is the cattle of Holsteinized black-and-white breed. The main task is to analyze the degree of influence of the somatotropin (GH) gene polymorphism on lactation performance indicators. In the course of the study, DNA from 270 cows was isolated, the polymorphism of the somatotropin gene was determined based on the obtained data, and the relationship between different genotypes and indicators of live weight, milk yield, protein mass fraction and fat mass fraction in milk was established. The results were biometrically processed using IBM SPSS Statistics 23 software program. It was revealed that *LL* is the main genotype of the GH gene among the representatives of the Holsteinized black-and-white breed (frequency of occurrence 77.0%). The proportion of *LV* and *VV* genotypes in the population is 21.9 and 1.1%, respectively. During the observation period, cows carrying the *LL* genotype showed higher milk yields in the first and third lactations. The difference with their peers was 202-2334 kg

($p \leq 0.05$). A tendency towards increased protein content in milk was recorded in animals with the *VV* genotype. In the first lactation, the difference with *LL* and *LV* genotype carriers was 0.03 and 0.06%, respectively. In the third lactation, individuals with the *VV* genotype surpassed their female counterparts in protein content by 0.07 and 0.12%, respectively.

Keywords: cattle, somatotropin, polymorphism, milk yield, MFF, MFP, live weight, first lactation, third lactation

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Conflict of interest

The authors declare no conflict of interest.

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INTRODUCTION

The expansion of marker selection in livestock breeding has contributed to the improvement of dairy and meat product supply in our country. Studying candidate genes such as kappa-casein, lactoglobulin, calpain, and somatotropin allows us to use selection to obtain animals with high milk yields, protein content in milk, meat tenderness, and so on. Additionally, the investigation of the genetic structure of populations of Bos taurus cattle of different breeds is of significant importance[1, 2]. For example, it has been found that the GHLL genotype and GHL allele are predominant in the Holstein and Holsteinized cattle [1], while the L allele is more characteristic of the Ayrshire breed (occurring in 61.5% of individuals). Among the Yaroslavl breed, 65% of animals have the LL genotype [2, 3]. The Hereford breed predominantly exhibits the LL genotype of the somatotropin gene [4]. Furthermore, studies have been conducted on the Simmental and Ukrainian Red Steppe breeds of Bos taurus cattle[3] [5].

Since somatotropin (GH) is a growth hormone, it can be assumed that its gene is associated with the body weight of cattle[4, 5]. There is also evidence of a correlation between the somatotropin gene and milk productivity [6–9]. Similar studies have been conducted in Russia,

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Indonesia, Turkey, China, and India[6-9] [10-12].

The purpose of our research was to determine the extent of the influence of somatotropin gene polymorphism on milk productivity and body weight of the Holsteinized Black-and-White cattle. The objectives included analyzing the prevalence of different genotypes and alleles of somatotropin in the population, as well as assessing the specific genotypes' impact on milk yield, milk fat content (MFC), and milk protein content (MPC).

MATERIAL AND METHODS

For the first time in the Urals region, genetic material from Holsteinized Black-and-White cattle was used to study the polymorphism of the somatotropin gene and its association with economically valuable traits. The research was conducted in 2018 and 2019 at the Laboratory of Molecular Genetic Expertise. Blood samples were collected from 270 representatives of the Black-and-White Holsteinized cattle for DNA diagnostics. Blood samples were taken from the tail vein and collected in tubes containing 100 mM EDTA (ethylenediaminetetraacetic acid) to a final concentration of 10 mM. DNA extraction was performed according to the protocol of "Sintol" company (Russia). Genotyping of the animals for the GH gene was carried out using the PCR-RFLP method based on the technique developed by S.V. Tyulkina et al. (see footnote 1) with the Bio-Rad PTC-225 DNA Engine Tetrad Cycler (Bio-Rad Lab., USA).

The list of economically valuable traits (milk yield, MFC, MPC, body weight) was compiled based on the "SELEX. Dairy Cattle" program. The study utilized the data from the first and third lactations (305 days each), as cows typically have an average productive lifespan of three lactations. This approach allows for observing the influence of the genotypes throughout the entire period of animal use.

The frequency of the genotype occurrence was calculated using the formula

$$p = n/N,$$

where p is the frequency of the genotype, n is the number of individuals with a specific genotype, and N is the total number of the animals. Mean values of the studied traits and their standard errors were determined. The results were analyzed using the IBM SPSS Statistics 23 software.

RESULTS AND DISCUSSION

First, the genotypes of the somatotropin gene present in the population were determined (see Figure 1). It was found that the *LV* polymorphism of the growth hormone gene is represented by two alleles - *L* and *V*, resulting in three genotypes: *LL*, *LV*, and *VV*. The *LL* genotype is represented by a single lower band at position 159 bp, the *VV* genotype is represented by a single upper band at position 211 bp, and the *LV* genotype is represented by two bands at positions 159 bp and 211 bp.

Next, the frequency of occurrence of the *LV* polymorphism of the somatotropin gene in the studied animals was determined (see Figure 2).

The most common genotype was found to be *LL*, with a frequency of occurrence of 77.0%. The *LV* genotype ranked second with a frequency of 21.9%. The *VV* genotype was extremely rare, observed only in 1.1% of the animals. The frequency of the *L* allele was 0.883%, while the *V* allele frequency was 0.117%. Similar data have been reported by other researchers [2, 12].

Table 1 presents the results of studying the association between somatotropin genotypes and economically valuable traits of cows based on data from the first lactation.

Thus, cows with the *LL* genotype produced 602 kg more milk compared to the animals with the *LV* genotype ($p \leq 0.01$) and 2334 kg more

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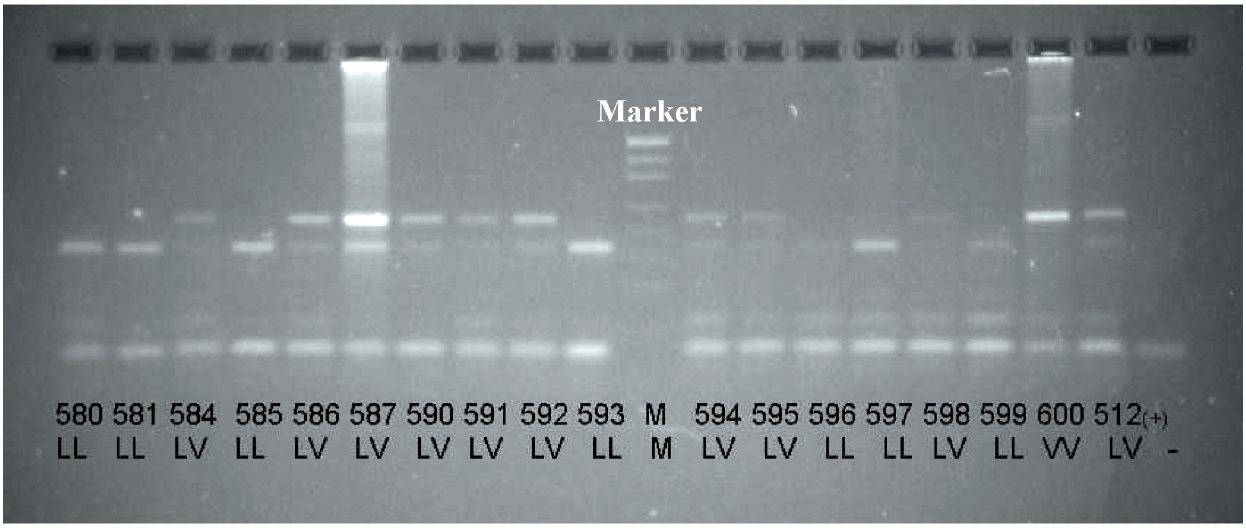

Рис. 1. Фореграмма *LV*-полиморфизма гена соматотропина:

М – маркер молекулярного веса; 580, 581, 585, 593, 596, 597, 599 – генотип *LL*; 584, 586–592, 594, 595, 598, 512 (положительный контроль) – генотип *LV*

Fig. 1. Foregram of *LV*-polymorphism of the somatotropin gene:

M – molecular weight marker; 580, 581, 585, 593, 596, 597, 599 – *LL* genotype; 584, 586-592, 594, 595, 598, 512 (positive control) – *LV* genotype

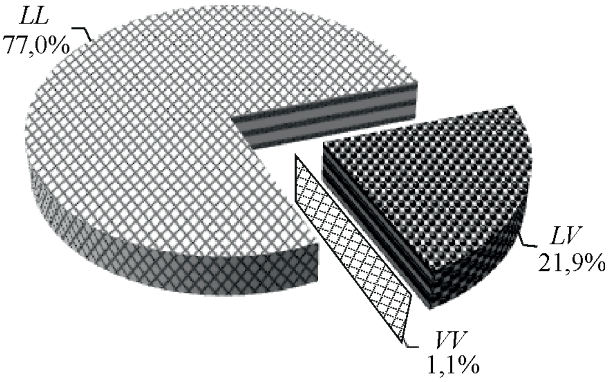

Рис. 2. Частота встречаемости различных генотипов гормона роста в выборке

Fig. 2. The occurrence of growth hormone genotypes in the sample

milk compared to individuals with the VV genotype ($p \leq 0.05$). In terms of the body weight, individuals with the *LL* genotype exceeded carriers of the *LV* genotype by 17 kg ($p \leq 0.01$) and carriers of the *VV* genotype by 2 kg.

Regarding milk fat content, cows with the *VV* genotype outperformed animals with the *LL* genotype by 0.16%. Carrier cows of the *LL* genotype had a 0.03% higher milk protein content compared to carriers of the *LV* genotype ($p \leq 0.05$). Additionally, cows with the *VV* genotype had the highest protein content at 3.12%.

Table 2 presents the results of studying the association between cow body weight, milk

Табл. 1. Молочная продуктивность и живая масса коров с различными генотипами соматотропина в период первой лактации ($n = 270$; $X \pm S_x$)

Table 1. Indicators of milk productivity and live weight of cows for the first lactation with different genotypes of somatotropin ($n = 270$; $X \pm S_x$)

Genotype	Number of heads	Milk yield, kg	MFF, %	MFP, %	Live weight, kg
LL	206	8008 ± 103	3,99 ± 0,01	3,09 ± 0,01	577 ± 2
LV	62	7406 ± 165	3,96 ± 0,03	3,06 ± 0,01	560 ± 5
VV	2	5674 ± 875	4,15 ± 0,20	3,12 ± 0,10	575 ± 177
LV–LL	–	−602**	−0,03	−0,03*	−17**
VV–LL	–	−2334*	0,16	0,03	−2

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*$p \leq 0{,}05$.
**$p \leq 0{,}01$.

Табл. 2. Молочная продуктивность и живая масса коров с различными генотипами соматотропина в период третьей лактации ($n = 270$; $X \pm S_x$)

Table 2. Indicators of milk productivity and live weight of cows for the third lactation with different genotypes of somatotropin ($n = 270$; $X \pm S_x$)

Genotype	Number of heads	Milk yield, kg	MFF, %	MFP, %	Live weight, kg
LL	206	9297 ± 132	3,95 ± 0,01	3,17 ± 0,01	644 ± 4
LV	62	9095 ± 264	3,98 ± 0,03	3,12 ± 0,02	644 ± 9
VV	2	7106 ± 537	3,96 ± 0,52	3,24 ± 0,15	661 ± 69
LV–LL	–	−202	0,03*	−0,05	0
VV–LL	–	−2191*	0,01	0,07	17

*$p \leq 0{,}001$.

productivity during the third lactation, and the *LV* polymorphism of the somatotropin gene.

It was found that animals with the *LL* genotype had a milk yield that was 202 kg higher than animals with the *LV* genotype and 2191 kg higher than animals with the *VV* genotype ($p \leq 0.001$). Cows carrying the *VV* genotype had a higher milk protein content, with a difference of 0.07% to 0.12% compared to their counterparts. In terms of milk fat content, individuals with the *LV* genotype surpassed carriers of the *LL* and *VV* genotypes by 0.03% and 0.02%, respectively. Animals with the *VV* genotype had a higher body weight compared to animals with the *LL* and *LV* genotypes, with a difference of 17 kg. Due to the low prevalence of the *VV* genotype, it is difficult to draw conclusions about its influence on body weight and economically valuable traits.

CONCLUSION

Thus, it has been established that in the population of Holsteinized Black and White cattle carriers of the *LL* genotype significantly predominate, while individuals with the *VV* genotype are rare. The *L* allele is present in 88% of the animals.

Based on the results of the first lactation, milk productivity of cows with the *LL* genotype was found to be 600-2000 kg higher compared to the carriers of other genotypes. Differences in milk fat and protein content were observed in the carriers of the *VV* genotype, which is associated with low milk productivity.

In the results of the third lactation, cows with the *LL* genotype produced 200-2000 kg more milk compared to the carriers of other genotypes. Animals with the *VV* genotype had lower milk yield but higher protein content in the milk.

Based on the conducted research, it can be concluded that the *LL* genotype contributes to high milk production in Holsteinized Black and White cows, while animals with the *VV* genotype tend to have higher protein content in the milk. Therefore, it is recommended for agricultural organizations to conduct selective breeding work to increase the number of the cows carrying the *LL* genotype in order to enhance the milk productivity of their herds.

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*МЕХАНИЗАЦИЯ, АВТОМАТИЗАЦИЯ, МОДЕЛИРОВАНИЕ
И ИНФОРМАЦИОННОЕ ОБЕСПЕЧЕНИЕ*
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УБОРКА МЕТОДОМ ОЧЕСА КАК СПОСОБ СНЕГОЗАДЕРЖАНИЯ В УСЛОВИЯХ СТЕПИ ЗАПАДНОЙ СИБИРИ

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Изучен процесс формирования снежного покрова на полях с различным состоянием поверхности. Исследования проведены весной 2022 г. в степной зоне земледелия Омской области. Рассмотрено влияние высокого стеблестоя зерновых культур, оставшегося после уборки методом очеса на корню, на величину снежного покрова и объемы весеннего влагонакопления в почве как резерва для увеличения урожайности в степных районах Западной Сибири. Представлены результаты определения высоты снежного покрова на паровом поле (чистый пар), на полях под зерновыми культурами, убранными разными способами: с помощью жатки для прямого комбайнирования с последующей плоскорезной обработкой почвы; с использованием жатки для прямого комбайнирования без последующей обработки; с применением очесывающей жатки при высоте стеблестоя во время уборки до 0,55 м. В ходе исследования установлено, что при уборке методом очеса запасы влаги в снежном покрове оказались в 2,2 раза больше по сравнению со стерневым фоном, в 3,7 раза выше относительно стерневого фона, обработанного плоскорезом, в 4,1 раза больше по сравнению с паровым полем (контроль). На основе полученных данных сделан вывод о возможности применения указанного метода с целью формирования условий для влагонакопления в засушливой степной зоне без проведения дополнительных мероприятий по снегозадержанию, что должно положительно сказаться не только на урожайности возделываемых культур, но и на агроэкономических показателях.

Ключевые слова: степная зона, снегозадержание, уборка зерновых методом очеса, запасы влаги в снеге, продуктивная влага

STRIPPING AS A SNOW RETENTION METHOD IN THE STEPPE CONDITIONS OF WESTERN SIBERIA

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The process of snow cover formation on the fields with different surface conditions was studied. The research was conducted in the spring of 2022 in the steppe farming zone of the Omsk region. The effect of high plant stand of cereal crops remaining after harvesting by standing crop stripping on the amount of snow cover and the volume of spring moisture accumulation in the soil as a reserve for increasing the yield in the steppe regions of Western Siberia is considered. The results of determining the height of snow cover on a fallow field (complete fallow), on fields under grain crops harvested by different methods: with a direct harvester followed by flat tillage; with a direct harvester without subsequent tillage; with a combing harvester at the height of the stem during harvesting up to 0.55 m are presented. In the course of the study it was found that during harvesting by the stripping method, the moisture reserves in the snow cover were 2.2 times higher compared to the stubble background, 3.7 times higher compared to the stubble background treated with a flat cutter, and 4.1 times higher compared to the fallow field (control). Based on the data obtained, the conclusion is made about the possibility of using this method to form the conditions for moisture accumulation in the arid steppe zone without additional measures for snow retention, which should have a positive impact not only on the yield of cultivated crops, but also on the agro-economic indicators.

Keywords: steppe zone, snow retention, grain harvesting by stripping, snow depth, moisture reserves in snow, productive moisture

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INTRODUCTION

Western Siberia is one of the main regions traditionally ensuring Russia's food security through the cultivation of grains, legumes, and other agricultural crops. This region accounts for 10 to 22% of the total grain harvest in Russia. In this context, the Omsk region occupies the second place in the Siberian Federal District in terms of the area under grain cultivation and the volume of the annual grain harvest, second only to the Altai Territory. The average annual grain yield in the Omsk region is 14.8 quintals per hectare, ranking it fifth among the top ten regions in the Siberian Federal District[1].

The cultivation of grain crops in the Omsk region is predominantly concentrated in the steppe and southern forest-steppe zones. The main factor limiting higher yields in the region is insufficient precipitation. This situation is aggravated by the uneven distribution of rainfall during the growing season and high evaporation rates (up to 2-4 mm per day in the spring). Non-vegetative precipitation accounts for about 30-50% of the annual volume, of which only 25-40%[2] is retained in the soil. Moisture losses in the steppe and forest-steppe zones reach 80-120 mm, resulting in a yield reduction of 0.8-1.2 tons per hectare[3].

Accumulation and preservation of soil moisture are among the major challenges in agriculture in the steppe zone of Western Siberia[4] [1]. Creating conditions for winter precipitation accumulation on the field surface and preventing its removal by winds in the arid areas is an effective method for replenishing limited water reserves.

It is known that the uniform distribution and increased height of the snow cover on the fields can be achieved through sowing of mustard or sunflower stubble, leaving tall stubble, con-

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ducting snow retention measures in the winter period, and others[5-7].

A significant amount of research has been devoted to solving the problem of snow retention, water accumulation, and preservation in the soil[8, 9] [2–4]. The effectiveness of a complex of measures for moisture accumulation has been established by the authors of these studies. Over a long period (1970-1980s), various machines and a complex of forestry measures aimed at snow retention and water accumulation were used in Russia. However, the economic situation in the agricultural industry subsequently led producers to minimize their expenses [5], resulting in the abandonment of certain water storage techniques. The fallacy of such an approach has been confirmed by research conducted after the widespread abandonment of snow retention operations in the territory of Western Siberia [6–10].

Insufficient attention paid to water accumulation and snow retention techniques leads to insufficient yields as a result of reduced water accumulation, melt water inflow into the soil over-compacted by energy-intensive equipment[10].

In current conditions, alternative methods to specialized tools used during snow retention operations can be combing reapers that leave over 80% of the stubble undamaged after harvest. The use of combing reapers is one of the methods that can increase snow reserves without additional snow retention operations.

In 2021 and 2022, research was conducted on the fields of the Novouralskoe Scientific and Production Farm of the Omsk Agricultural Research Center. The purpose of the research was to study the influence of high stubble remaining after harvest using the undercutting method on the height of the snow cover and the magnitude of spring moisture accumulation in the soil as a reserve for increasing crop yields in the steppe zone of Western Siberian agriculture.

The objectives of the research included determining the soil moisture levels in the autumn period, comparing the height of the snow cover in spring and the productive moisture reserves before sowing on the plots after direct combining and undercutting methods, and assessing the potential use of these methods to increase crop yields in the Western Siberian region.

MATERIAL AND METHODS

In autumn 2021, plots were marked out on the fields with different conditions of the surface layer in the steppe zone of the Omsk region for conducting spring measurements. The experiment included the following variants: bare fallow (control), the field after one-phase grain harvesting with subsequent flat cutting, the field after grain harvesting by direct combining without treatment, and the field of grain harvested using the combing method at a stem height of 0.55 m during harvesting. The soil was ordinary medium-loamy chernozem with a humus content of 5.4%.

In spring 2022, before the snowmelt, measurements of the snow cover depth formed during the winter period were taken on the marked plots. Later (before sowing), the reserves of productive soil moisture in the one-meter soil layer were determined. The need for repeated measurements of snow cover depth arose after a portion of snowfall occurred a few days after the initial measurements. Snow sampling was carried out in fields with different surface layer characteristics.

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RESULTS AND DISCUSSION

Measurement of the snow cover depth was conducted on March 9 and March 29, 2022, using a weight snow gauge VS-43, according to the procedure described in the device manual, diagonally across the field in 15 repetitions (see Table 1).

The analysis of the data presented in Table 1 indicates that the lowest snow cover height was formed on the fallow background during the spring period. At the same time, the snow cover height increased with the amount and height of crop residues on the surface. Thus, considering the snow cover depth, the variants can be arranged in the following order (ascending): 1) bare fallow; 2) the field harvested by direct combining with subsequent flat cutting; 3) the field with grain stubble on the surface after direct combining; 4) the field with wheat stubble height up to 55 cm after combing harvesting.

To determine the resulting impact of the remaining stubble on the field after grain harvesting using the combing method on the soil's productive moisture content, moisture reserves were measured in the variants with direct combining and spreading of chopped straw, as well as with combing harvesting. The obtained results are presented in Table 2 and the figure.

Based on the analysis of the moisture reserve indicators, it can be noted that in the experimental area in 2022, from snowmelt to sowing, there was no rainfall in the form of rain.

A comparison of data on autumn (during harvesting) and spring (before sowing) reserves of productive soil moisture indicates intensive moisture loss by the soil in the spring period. Thus, the spring reserves of productive soil moisture in the one-meter soil layer on the field with stubble after direct combining amounted to only 48.6 mm, or 60.5%. On the plot where harvesting was carried out using the combing method, 96.6 mm of productive moisture, or 120.3%, was preserved in the 100 cm of soil by the time of sowing. Here, the resulting effect of moisture infiltration into the soil from winter precipitation and its evaporation from the soil surface, mainly in the spring period, is observed.

The indicators presented in Table 2 indicate that in the one-meter soil layer by the time of sowing, the plot harvested using the combining method retained almost twice as much productive moisture compared to the plot harvested by direct combining. This difference is even more significant for the lower soil layer (50-100 cm). In this layer, the moisture content on the plot harvested by the combining method exceeds the moisture content on the plot harvested by direct combining by more than 2.6 times.

A larger amount of productive moisture was

Табл. 1. Высота снежного покрова и запасы влаги в снеге на полях с различным состоянием поверхностного слоя почвы

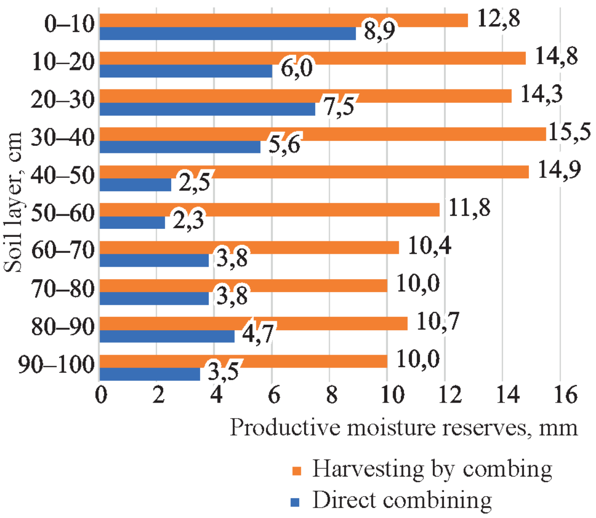
Table 1. The height of the snow cover and the moisture reserves in the snow in the fields with different conditions of the surface soil layer

Option	09.03.2022		29.03.2022		Excess relative to the control, %	
	Snow cover depth, cm	Moisture reserves in snow, mm	Snow cover depth, cm	Moisture reserves in snow, mm	as measured by snow depth	as measured by snow moisture reserves
Complete fallow (control)	8,1	21,3	10,4	28,7	–	–
Stubble after direct combining with subsequent flat-cutting cultivation	11,1	23,1	12,8	31,6	23,1	10,1
Stubble after direct harvesting without treatment	19,9	37,5	19,3	47,1	85,6	64,1
Plant stand after harvesting by a combing method	51,3	111,6	49,3	116,3	374,0	305,2

Табл. 2. Запасы продуктивной влаги в почве на 30.09.2021 г. и 19.05.2022 г., мм

Table 2. Reserves of productive moisture in the soil as of 30.09.2021and 19.05.2022, mm

Option	Soil layer, cm		
	0–50	50–100	0–100
30.09.2021			
Plantings before harvesting	35,4	44,9	80,3
19.05.2022			
Stubble after harvesting with a conventional reaper with spreading of the chopped straw (cutting height 12-15 cm)	30,5	18,1	48,6
Plant stand after harvesting by combing (stem height 55 cm)	49,2	47,4	96,6
Increase on the plot harvested by the combing standing crop method, compared to a traditionally harvested plot, %	61,3	161,9	98,8



Распределение запасов продуктивной влаги по 10-сантиметровым слоям

Distribution of productive moisture reserves in 10-cm layers

recorded in all horizons of the one-meter soil layer on the plot where wheat was harvested using the combing method (see the Figure). The greatest difference was observed in the 40-50 cm and 50-60 cm layers: 12.4 mm and 9.5 mm, respectively, or 496% and 413% of the moisture level on the plot harvested by one-phase harvesting.

CONCLUSION

Harvesting grains using the combing method contributes to snow accumulation on the field surface. During the study, it was found that by the time the snow melted, the moisture reserves in the snow cover after swathing were 2.2 times higher compared to the combing background, 3.7 times higher compared to the swath background treated with a blade, and 4.1 times higher compared to the fallow field (control).

The results of the experiment showed that the stubble left after combing grains at ground level has advantages over direct combining in terms of not only forming a higher snow cover but also accumulating and preserving moisture in the soil. During the period from harvesting to spring sowing, the productive moisture reserves in the one-meter soil layer on the combing plot decreased to 48.6 mm (60.5% of the fall moisture reserves), while the same indicator on the stubble after combing reached 96.6 mm (120.3% of the fall moisture reserves).

The obtained data indicate that conditions are created on the surface of the combing grain fields that hinder the removal of the snow cover from the field surface and promote the preservation of soil moisture until sowing. Thus, harvesting grains using the combing method allows for the creation of more favorable conditions for increasing spring moisture reserves and, as a result, crop yield, without additional financial expenses for mechanized snow retention.

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ПРАВИЛА ДЛЯ АВТОРОВ

Правила для авторов составлены на основе этических принципов, общих для членов научного сообщества, и правил публикации в международных и отечественных научных периодических изданиях, а также в соответствии с требованиями ВАК для периодических изданий, включенных в Перечень российских рецензируемых научных журналов, в которых должны быть опубликованы основные научные результаты диссертаций на соискание ученой степени доктора и кандидата наук.

Журнал публикует оригинальные статьи по фундаментальным и прикладным проблемам по направлениям:

- общее земледелие и растениеводство;
- селекция, семеноводство и биотехнология растений;
- агрохимия, агропочвоведение, защита и карантин растений;
- кормопроизводство;
- инфекционные болезни и иммунология животных;
- частная зоотехния, кормление, технологии приготовления кормов и производства продукции животноводства;
- разведение, селекция, генетика и биотехнология животных;
- технологии, машины и оборудование для агропромышленного комплекса;
- пищевые системы.

Статья, направляемая в редакцию, должна соответствовать тематическим разделам журнала «Сибирский вестник сельскохозяйственной науки»:

Наименование рубрики	**Шифр и наименование научной специальности в соответствии с Номенклатурой научных специальностей, по которым присуждаются ученые степени**
Земледелие и химизация	4.1.1. Общее земледелие и растениеводство 4.1.3. Агрохимия, агропочвоведение, защита и карантин растений
Растениеводство и селекция	4.1.1. Общее земледелие и растениеводство 4.1.2. Селекция, семеноводство и биотехнология растений
Защита растений	4.1.3. Агрохимия, агропочвоведение, защита и карантин растений
Кормопроизводство	4.1.1. Общее земледелие и растениеводство 4.1.2. Селекция, семеноводство и биотехнология растений 4.1.3. Агрохимия, агропочвоведение, защита и карантин растений
Зоотехния и ветеринария	4.2.3. Инфекционные болезни и иммунология животных 4.2.4. Частная зоотехния, кормление, технологии приготовления кормов и производства продукции животноводства 4.2.5. Разведение, селекция, генетика и биотехнология животных
Механизация, автоматизация, моделирование и информационное обеспечение	4.3.1. Технологии, машины и оборудование для агропромышленного комплекса
Переработка сельскохозяйственной продукции	4.3.3. Пищевые системы
Проблемы. Суждения Научные связи Из истории сельскохозяйственной науки Краткие сообщения Из диссертационных работ	4.1.1. Общее земледелие и растениеводство 4.1.2. Селекция, семеноводство и биотехнология растений 4.1.3. Агрохимия, агропочвоведение, защита и карантин растений 4.2.3. Инфекционные болезни и иммунология животных 4.2.4. Частная зоотехния, кормление, технологии приготовления кормов и производства продукции животноводства 4.2.5. Разведение, селекция, генетика и биотехнология животных 4.3.1. Технологии, машины и оборудование для агропромышленного комплекса 4.3.3. Пищевые системы

В журнале также публикуются обзоры, краткие сообщения, хроника, рецензии, книжные обозрения, материалы по истории сельскохозяйственной науки и деятельности учреждений и ученых.

Число публикаций одного автора в номере журнала не должно превышать двух, при этом вторая статья допустима лишь в соавторстве.

К рассмотрению принимаются материалы от различных категорий исследователей, аспирантов, докторантов, специалистов и экспертов в соответствующих областях знаний.

Все статьи рецензируются и имеют зарегистрированный в системе CrossRef индекс DOI.

Публикации для авторов **бесплатны**.

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РЕКОМЕНДАЦИИ АВТОРУ ДО ПОДАЧИ СТАТЬИ

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- статья не находится на рассмотрении в другом журнале;
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2. Все поступающие в редакцию рукописи статей регистрируются через систему электронной редакции. В личном кабинете автора отражается текущий статус рукописи.

3. Нерецензируемые материалы (материалы научной хроники, рецензии, книжные обозрения, материалы по истории сельскохозяйственной науки и деятельности учреждений и ученых) направляются на e-mail: **sibvestnik@sfsca.ru** и регистрируются ответственным секретарем.

ПОРЯДОК ОФОРМЛЕНИЯ СТАТЬИ

Текст рукописи оформляется шрифтом Times New Roman, кеглем 14 с интервалом 1,5, все поля 2,0 см, нумерация страниц внизу. Объем статьи не более 15 страниц (включая таблицы, иллюстрации и библиографию); статей, размещаемых в рубриках «Из диссертационных работ» и «Краткие сообщения», – не более 7 страниц.

Структура оформления статьи:

1. **УДК**
2. **Заголовок статьи на русском и английском языках (не более 70 знаков).**
3. **Фамилии и инициалы авторов, полное официальное название научного учреждения, в котором проведены исследования, на русском и английском языках.**

Если в подготовке статьи принимали участие авторы из разных учреждений, необходимо указать принадлежность каждого автора к конкретному учреждению с помощью надстрочного индекса.

4. **Реферат на русском и английском языках.** Объем реферата не менее 200–250 слов. Реферат является кратким и последовательным изложением материала статьи по основным разделам и должен отражать основное содержание, следовать логике изложения материала и описания результатов в статье с приведением конкретных данных. Не следует включать впервые введенные термины, аббревиатуры (за исключением общеизвестных), ссылки на литературу. В реферате не следует подчеркивать новизну, актуальность и личный вклад автора; место исследования необходимо указывать до области (края), не упоминать конкретные организации.
5. **Ключевые слова на русском и английском языках.** 5–7 слов по теме статьи. Желательно, чтобы ключевые слова дополняли реферат и название статьи.
6. **Информация о конфликте интересов либо его отсутствии.** Автор обязан уведомить редактора о реальном или потенциальном конфликте интересов, включив информацию о конфликте интересов в соответствующий раздел статьи. Если конфликта интересов нет, автор должен также сообщить об этом.

Пример формулировки: «Автор заявляет об отсутствии конфликта интересов».

7. **Благодарности на русском и английском языках.** В этом разделе указываются все источники финансирования исследования, а также благодарности людям, которые участвовали в работе над статьей, но не являются ее авторами.
8. **Основной текст статьи.** При изложении оригинальных экспериментальных данных рекомендуется использовать подзаголовки:

ВВЕДЕНИЕ (постановка проблемы, цели, задачи исследования)

МАТЕРИАЛ И МЕТОДЫ (условия, методы (методика) исследований, описание объекта, место и время проведения)

РЕЗУЛЬТАТЫ И ОБСУЖДЕНИЕ

ЗАКЛЮЧЕНИЕ или **ВЫВОДЫ**

СПИСОК ЛИТЕРАТУРЫ. Количество источников не менее 15. В список литературы включаются только рецензируемые источники: статьи из научных журналов и монографии. Самоцитирование не более 10% от общего количества. Библиографический список должен быть оформлен в виде общего списка в порядке упоминания в тексте, желательны ссылки на источники 2–3-летнего срока давности. Правила оформления списка литературы – в соответствии с ГОСТ Р 7.05–2008 (требования и правила составления библиографической ссылки). В тексте ссылка на источник отмечается порядковой цифрой в квадратных скобках, например [1]. Литература в списке дается на тех языках, на которых она издана. В библиографическое описание публикации необходимо вносить всех авторов, не сокращая их одним, тремя и т.п. Недопустимо сокращение названий статей, журналов, издательств.

Если необходимо сослаться на авторефераты, диссертации, сборники статей, учебники, рекомендации, учебные пособия, ГОСТы, информацию с сайтов, статистические отчеты, статьи в общественно-политических газетах и прочее, то такую информацию следует оформить в *сноску* в конце страницы. Сноски нумеруются арабскими цифрами, размещаются постранично сквозной нумерацией.

Внимание! Теоретические, обзорные и проблемные статьи могут иметь произвольную структуру, но обязательно должны содержать реферат, ключевые слова, список литературы.

ПРИМЕРЫ ОФОРМЛЕНИЯ СПИСКА ЛИТЕРАТУРЫ, REFERENCES И СНОСОК

СПИСОК ЛИТЕРАТУРЫ:

Монография

Климова Э.В. Полевые культуры Забайкалья: монография. Чита: Поиск, 2001. 392 с.

Часть книги

Холмов В.Г. Минимальная обработка кулисного пара под яровую пшеницу при интенсификации земледелия в южной лесостепи Западной Сибири // Ресурсосберегающие системы обработки почвы. М.: Агропромиздат, 1990. С. 230–235.

Периодическое издание

Пакуль А.Л., Лапшинов Н.А., Божанова Г.В., Пакуль В.Н. Технологические качества зерна мягкой яровой пшеницы в зависимости от системы обработки почвы // Сибирский вестник сельскохозяйственной науки. 2018. Т. 48. № 4. С. 27–35. DOI: 10.26898/0370-8799-2018-4-4.

REFERENCES:

Составляется в том же порядке, что и русскоязычный вариант, по следующим правилам:

Фамилии И.О. авторов в устоявшемся способе транслитерации, англоязычное название статьи, *транслитерация названия русскоязычного источника (например, через сайт: https://antropophob.ru/translit-bsi) = англоязычное название источника.* Далее оформление для монографии: город, англоязычное название издательства, год, количество страниц; для журнала: год, том, номер, страницы. (In Russian).

Пример: Avtor A.A., Avtor B.B., Avtor C.C. Title of article.

Транслитерация авторов. Англоязычное название статьи

Zaglavie jurnala = Title of Journal, 2012, vol. 10, no. 2, pp. 49–54.

Транслитерация источника = Англоязычное название источника

Монография

Klimova E.V. *Field crops of Zabaikalya*. Chita, Poisk Publ., 2001, 392 p. (In Russian).

Часть книги

Kholmov V.G. Minimum tillage of coulisse-strip fallow for spring wheat with intensification of arable agriculture in southern forest-steppe of Western Siberia. *Resource-saving tillage systems*, Moscow, Agropromizdat Publ., 1990, pp. 230–235. (In Russian).

Периодическое издание

Pakul A.L., Lapshinov N.A., Bozhanova G.V., Pakul V.N. Technological grain qualities of spring common wheat depending on the system of soil tillage. *Sibirskii vestnik sel'skokhozyaistvennoi nauki = Siberian Herald of Agricultural Science*, 2018, vol. 48, no. 4, pp. 27–35. (In Russian). DOI: 10.26898/0370-8799-2018-4-4.

СНОСКИ:

Цитируемый текст[1].

[1] *Климова Э.В., Андреева О.Т., Темникова Г.П.* Пути стабилизации кормопроизводства Забайкалья // Проблемы и перспективы совершенствования зональных систем земледелия в современных условиях: материалы науч.-практ. конф. (Чита, 16–17 октября 2008 г.). Чита, 2009. С. 36–39.

Цифровой идентификатор Digital Object Identifier – DOI (когда он есть у цитируемого материала) необходимо указывать в конце библиографической ссылки.

Пример:

Chu T., Starek M.J., Brewer M.J., Murray S.C., Pruter L.S. Assessing lodging severity over an experimental maize (Zea mays L.) field using UAS images // Remote Sensing. 2017. Vol. 9. P. 923. DOI: 10.3390/rs9090923.

Наличие DOI статьи следует проверять на сайте http://search.crossref.org/ или https://www.citethisforme.com. Для этого нужно ввести в поисковую строку название статьи на английском языке.

РИСУНКИ, ТАБЛИЦЫ, СКРИНШОТЫ И ФОТОГРАФИИ

Рисунки должны быть хорошего качества, пригодные для печати. Все рисунки должны иметь подрисуночные подписи. Подрисуночную подпись необходимо перевести на английский язык. Рисунки нумеруются арабскими цифрами по порядку следования в тексте. Если рисунок в тексте один, то он не нумеруется. Отсылки на рисунки оформляются следующим образом: «На рис. 3 указано, что …» или «Указано, что … (см. рис. 3)». Подрисуночная подпись включает порядковый номер рисунка и его название: «Рис. 2. Описание жизненно важных процессов». Перевод подрисуночной подписи следует располагать после подрисуночной подписи на русском языке.

Таблицы должны быть хорошего качества, пригодные для печати. Предпочтительны таблицы, пригодные для редактирования, а не отсканированные или в виде рисунков. Все таблицы должны иметь заголовки. Название таблицы должно быть переведено на английский язык. Таблицы нумеруются арабскими цифрами по порядку следования в тексте. Если таблица в тексте одна, то она не нумеруется. Отсылки на таблицы оформляются следующим образом: «В табл. 3 указано, что …» или «Указано, что … (см. табл. 3)». Заголовок таблицы включает порядковый номер таблицы и ее название: «Табл. 2. Описание жизненно важных процессов». Перевод заголовка таблицы следует располагать после заголовка таблицы на русском языке.

Фотографии, скриншоты и другие нерисованные иллюстрации необходимо загружать отдельно в виде файлов формата *.jpeg (*.doc и *.docx – в случае, если на изображение нанесены дополнительные пометки). Разрешение изображения должно быть >300 dpi. Файлам изображений необходимо присвоить название, соответствующее номеру рисунка в тексте. В описании файла следует отдельно привести подрисуночную подпись, которая должна соответствовать названию фотографии, помещаемой в текст.

Следует обратить внимание на написание формул в статье. Во избежание путаницы необходимо греческие (α, β, π и др.), русские (А, а, Б, б и др.) буквы и цифры писать прямым шрифтом, латинские – курсивным (W, Z, m, n и др.). Математические знаки и символы нужно писать также прямым шрифтом. Необходимо четко указывать верхние и нижние надстрочные символы (W^1, F_1 и др.).

ВЗАИМОДЕЙСТВИЕ МЕЖДУ ЖУРНАЛОМ И АВТОРОМ

Редакция просит авторов при подготовке статей руководствоваться изложенными выше правилами.

Все поступающие в журнал «Сибирский вестник сельскохозяйственной науки» статьи проходят предварительную проверку на соответствие формальным требованиям. На этом этапе редакция оставляет за собой право:

- принять статью к рассмотрению;
- вернуть статью автору (авторам) на доработку с просьбой устранить ошибки или добавить недостающие данные;
- вернуть статью автору (авторам) без рассмотрения, оформленную не по требованиям журнала;
- отклонить статью из-за несоответствия ее целям журнала, отсутствия оригинальности, малой научной ценности.

Переписка с авторами рукописи ведется через контактное лицо, указанное в рукописи.

Все научные статьи, поступившие в редакцию журнала «Сибирский вестник сельскохозяйственной науки», проходят обязательное двухстороннее «слепое» рецензирование (double-blind – автор и рецензент не знают друг о друге). Рукописи направляются по профилю научного исследования на рецензию членам редакционной коллегии. В спорных случаях редактор может привлечь к процессу рецензирования нескольких специалистов, а также главного редактора. При положительном заключении рецензента статья передается редактору для подготовки к печати.

При принятии решения о доработке статьи замечания и комментарии рецензента передаются автору. Автору дается 2 месяца на устранения замечаний. Если в течение этого срока автор не уведомил редакцию о планируемых действиях, статья снимается с очереди публикации.

При принятии решения об отказе в публикации статьи автору отправляется соответствующее решение редакции.

Ответственному (контактному) автору принятой к публикации статьи направляется финальная версия верстки, которую он обязан проверить.

ПОРЯДОК ПЕРЕСМОТРА РЕШЕНИЙ РЕДАКТОРА/РЕЦЕНЗЕНТА

Если автор не согласен с заключением рецензента и/или редактора или отдельными замечаниями, он может оспорить принятое решение. Для этого автору необходимо:

- исправить рукопись статьи согласно обоснованным комментариям рецензентов и редакторов;
- ясно изложить свою позицию по рассматриваемому вопросу.

Редакторы содействуют повторной подаче рукописей, которые потенциально могли бы быть приняты, однако были отклонены из-за необходимости внесения существенных изменений или сбора дополнительных данных, и готовы подробно объяснить, что требуется исправить в рукописи для того, чтобы она была принята к публикации.

ДЕЙСТВИЯ РЕДАКЦИИ В СЛУЧАЕ ОБНАРУЖЕНИЯ ПЛАГИАТА, ФАБРИКАЦИИ ИЛИ ФАЛЬСИФИКАЦИИ ДАННЫХ

Редакция научного журнала «Сибирский вестник сельскохозяйственной науки» в своей работе руководствуется традиционными этическими принципами научной периодики и сводом принципов «Кодекса этики научных публикаций», разработанным и утвержденным Комитетом по этике научных публикаций, требуя соблюдения этих правил от всех участников издательского процесса.

ИСПРАВЛЕНИЕ ОШИБОК И ОТЗЫВ СТАТЬИ

В случае обнаружения в тексте статьи ошибок, влияющих на ее восприятие, но не искажающих изложенные результаты исследования, они могут быть исправлены путем замены pdf-файла статьи. В случае обнаружения в тексте статьи ошибок, искажающих результаты исследования, либо в случае плагиата, обнаружения недобросовестного поведения автора (авторов), связанного с фальсификацией и/или фабрикацией данных, статья может быть отозвана. Инициатором отзыва статьи может быть редакция, автор, организация, частное лицо. Отозванная статья помечается знаком «Статья отозвана», на странице статьи размещается информация о причине ее отзыва. Информация об отзыве статьи направляется в базы данных, в которых индексируется журнал.

УВАЖАЕМЫЕ ПОДПИСЧИКИ!

Подписку на журнал «Сибирский вестник сельскохозяйственной науки»
(как на годовой комплект, так и на отдельные номера)
можно оформить одним из следующих способов:

- в агентстве подписки ГК «Урал-Пресс» по индексу 014973. Ссылка на издание https://www.ural-press.ru/catalog/97210/8707659/?sphrase_id=392975. В разделе контакты зайти по ссылке http://ural-press.ru/contact/, где можно выбрать филиал по месту жительства;
- в редакции журнала (телефон 7-383-348-37-62; e-mail: sibvestnik@sfsca.ru).

Полнотекстовая версия журнала
«Сибирский вестник сельскохозяйственной науки»
размещена на сайте Научной электронной библиотеки:
http://www.elibrary.ru.