

AL-FARABI KAZAKH  
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INFORMATION  
about publication activity  
FACULTY OF BIOLOGY AND BIOTECHNOLOGY

№	Наименование публикации	Выходные данные (doi статьи)	Аннотация статьи	Ссылка для цитирования (Ф.И.О., название статьи, название, номер и/или выпуск, том журнала, страницы, doi статьи)
1	Rice Plants ( <i>Oryza sativa</i> L.) under Cd Stress in Fe Deficiency Conditions	<a href="https://doi.org/10.1155/2022/7425085">https://doi.org/10.1155/2022/7425085</a>	<p>Due to the environment pollution by cadmium (Cd) near industrial metallurgic factories and the widespread use of phosphorus fertilizers, the problem of toxic Cd effect on plants is well discussed by many authors, but the phytotoxicity of Cd under iron (Fe) deficiency stress has not been sufficiently studied. The aim of the work was to study comprehensively the effect of Cd under Fe deficiency conditions on physiological, biochemical, and anatomical parameters of rice varieties, to identify varietal differences in plant response to the effect of double stress. Relative resistance and sensitivity to the joint effect of Cd and Fe deficiency stress rice varieties have been identified. Double stress decreased a linear growth and biomass accumulation of roots and</p>	<p>S.D. Atabayeva, A.B. Rakhymgozhina , A.S. Nurmahanova , S.S. Kenzhebayeva , B.N. Usenbekov , R.A. Alybayeva , S.Sh.Asrandina , B.M.Тыныбеков , and A.K. Amirova</p> <p>Hindawi BioMed Research International Volume 2022, Article ID 7425085, 23 pages</p>

			<p>shoots (by 36-50% and 33-46% and 32-56% and 32-48%, accordingly), content of photosynthetic pigments (Chla, Chlb, and carotenoids by 36-51%, 32-47%, and 64-78%, accordingly), and relative water content (by 18-26%). Proline content increased by 28-103% in all rice varieties, but to a lesser extent in sensitive varieties. The thickness of the lower and upper epidermis and the diameter of vascular bundles of leaves decreased by 18-50%, 46-60%, and 13-48%, accordingly. The thickness of the root endodermis and exodermis and diameter of the central cylinder mainly decreased. The thickness of the exodermis increased slightly by 7%, and the diameter of the central cylinder remained at the control level in resistant Madina variety while in sensitive Chapsari variety, these indicators decreased significantly by 50 and 45%, accordingly. Thus, the aggravation of adverse effect of Cd under Fe deficiency conditions and the varietal specificity of plants' response to double stress were shown. It creates the need for further study of these rice varieties using Fe to identify mechanisms for reducing the toxic effect of Cd on plants as well as the study of Fe and Cd transporter genes at the molecular level.</p>	
2	Organ-specific expression of genes involved in iron homeostasis in wheat mutant lines with increased grain iron and zinc content	DOI 10.7717/peerj.13515	<p>Iron deficiency is a well-known nutritional disorder, and the imbalance of trace-elements, specifically iron, is the most common nutrient deficiency of foods across the world, including in Kazakhstan. Wheat has significant nutritional relevance, especially in the provision of iron, however many bread wheat varieties have low iron despite the need for human nourishment. In this study, the expression profiles of wheat homologous genes related to iron homeostasis were investigated. The work resulted in the development of two new M5 mutant lines of spring bread wheat through gamma-irradiation (200 Gy) with higher grain iron and zinc content, lower phytic acid content, and enhanced iron bioavailability compared to the parent variety. Mutant lines were also characterized by higher means of yield associated traits such as grain number per main spike, grain weight per main spike, grain weight per plant, and thousand-grain weight. Methods: The homologous genes of bread wheat from several groups were selected for gene expression studies exploring the</p>	S. Kenzhebayeva, S. Atabayeva, F. Sarsu, A. Abekova, S. Shoinbekova, N. Omirbekova, G. Doktyrbay, A. Beisenova, Y. Shavrukov PeerJ, 2022, DOI 10.7717/peerj.13515

			<p>tight control of iron uptake, translocation rate and accumulation in leaves and roots, and comprised the following: (1) S-adenosylmethionine synthase (SAMS), nicotianamine synthase (NAS1), nicotianamine aminotransferase (NAAT), deoxymugineic acid synthetase (DMAS), involved in the synthesis and release of phytosiderophores; (2) transcription factor basic helix-loop-helix (bHLH); (3) transporters of mugineic acid (TOM), involved in long-distance iron transport; (4) yellow stripe-like (YSIA), and the vacuolar transporter (VIT2), involved in intracellular iron transport and storage; and lastly (5) natural resistance-associated macrophage protein (NRAMP) and ferritin (Fer1A).</p> <p>Results: The wheat homologous genes TaSAMS, TaNAS1, and TaDMAS, were significantly up-regulated in the roots of both mutant lines by 2.1–4.7-fold compared to the parent variety. The combined over-expression of TaYSIA and TaVIT2 was also revealed in the roots of mutant lines by 1.3–2.7-fold. In one of the mutant lines, genes encoding intracellular iron transport and storage genes TaNRAMP and TaFer1A-D showed significant up-regulation in roots and leaves (by 1.4- and 3.5-fold, respectively). The highest expression was recorded in the transcription factor TabHLH, which was expressed 13.1- and 30.2-fold in the roots of mutant lines.</p> <p>Our research revealed that genotype-dependent and organ-specific gene expression profiles can provide new insights into iron uptake, translocation rate, storage, and regulation in wheat which aid the prioritization of gene targets for iron biofortification and bioavailability.</p>	
3	The protein and amino acid content in seeds of Kazakhstani soybean varieties	<a href="https://doi.org/10.52081/bkaku.2022.v62.i3.087">https://doi.org/10.52081/bkaku.2022.v62.i3.087</a>	The article presents results of determining the content of proteins and amino acids in seeds of Kazakhstani soybean varieties. Soybean, being a high-protein crop, contains from 30 to 50% protein. The advantage of soybean protein among other plant proteins is the optimal ratio of amino acids. These are, first of all, essential amino acids, the main source of which are animal proteins. Soy protein, when consumed at the recommended dose, most fully satisfies the daily intake of essential amino acids of an adult. It is important to identify varieties with the highest	Kh.S. Yevloyeva, S.D. Atabayeva, A.B. Rakhymgozhina, S.V. Didorenko, G.K.Kamshybayeva. The protein and amino acid content in seeds of Kazakhstani soybean varieties. Вестник КУ им. Кокрыт Ата, №3(62), стр

			protein content and essential amino acids. In this study, protein determination was carried out by the Bradford (1976) spectrophotometric method. The amino acid content was determined by high-performance liquid chromatography. The objects of the study were domestic soybean varieties: «Lastochka», «Almaty» and «Vita» from the collection of LLP «Kazakh Research Institute of Agriculture and Plant growing», Almalybak v., Almaty region, Republic of Kazakhstan. According to the results obtained, the Lastochka variety has the highest content of protein, and also the amino acid composition of the «Lastochka» variety differs by existing of essential amino acids, which makes it possible to recommend it both for food and in the production of biologically active additives.	121-128. <a href="https://doi.org/10.52081/bkaku.2022.v62.i3.087">https://doi.org/10.52081/bkaku.2022.v62.i3.087</a>
4	Identification and characterization of bluetongue virus in <i>Culicoides</i> spp. and clinically healthy livestock in southeastern Kazakhstan	<a href="https://doi.org/10.1016/j.cimid.2022.101895">https://doi.org/10.1016/j.cimid.2022.101895</a>	Bluetongue is an arthropod-borne disease of ruminants. Here, we investigated the seroprevalence of bluetongue virus (BTV) in livestock and performed the first genetic characterization of BTV isolated from sheep and <i>Culicoides</i> midges in the southeastern region of Kazakhstan.	Zhigailov AV, Perfilyeva YV, Maltseva ER, Ostapchuk YO, Cherusheva AS, Naizabayeva DA, Nizkorodova AS, Berdygulova ZA, Mashzhan AS, Bissenbay AO, Kuatbekova SA, Koshemetov ZK, Abdolla N, Skiba YA, Mamadaliyev SM. Identification and characterization of bluetongue virus in <i>Culicoides</i> spp. and clinically healthy livestock in southeastern Kazakhstan. <i>Comp Immunol Microbiol Infect Dis.</i> P. 90-91:101895. doi: 10.1016/j.cimid.2022.101895.
5	Prevalence and genetic diversity of <i>coronaviruses</i> , <i>astroviruses</i> and <i>paramyxoviruses</i> in wild birds in southeastern Kazakhstan	<a href="https://doi.org/10.1016/j.heliyon.2022.e11324">https://doi.org/10.1016/j.heliyon.2022.e11324</a>	Wild birds are natural reservoirs of many emerging viruses, including some zoonoses. Considering that the territory of Kazakhstan is crossed by several bird migration routes, it is important to know pathogenic viruses circulating in migratory birds in this region. Therefore, the aim of this study was to identify the host range, diversity and spatial distribution of avian paramyxoviruses, coronaviruses, and astroviruses in free-ranging wild birds in the southeastern region of Kazakhstan. For this purpose, we collected tracheal and cloacal swabs from 242 wild birds belonging to 51 species and screened them using	Zhigailov AV, Maltseva ER, Perfilyeva YV, Ostapchuk YO, Naizabayeva DA, Berdygulova ZA, Kuatbekova SA, Nizkorodova AS, Mashzhan A, Gavrilov AE, Abayev AZ, Akhmetollayev IA, Mamadaliyev SM, Skiba YA. Prevalence and genetic diversity of coronaviruses, astroviruses and

			<p>conventional PCR assays. Overall, 4.1% (10/242) and 2.9% (7/242) of all examined birds tested positive for coronaviruses and astroviruses, respectively. Coronaviruses were found in the orders Pelecaniformes (30%; 3/10), Charadriiformes (30%; 3/10), Columbiformes (20%; 2/10), Anseriformes (10%; 1/10), and Passeriformes (10%; 1/10). All detected strains belonged to the genus <i>Gammacoronavirus</i>. Astroviruses were detected in birds representing the orders Passeriformes (57%; 4/7), Coraciiformes (14%; 1/7), Charadriiformes (14%; 1/7), and Columbiformes (14%; 1/7). Paramyxoviruses were observed in only two birds (0.8%; 2/242). Both strains were closely related to the species APMV-22, which had not been previously detected in Kazakhstan. Phylogenetic analysis of the partial <i>RdRp</i> gene sequences of the virus strains revealed three different clades of astroviruses, two clades of coronaviruses, and one clade of paramyxoviruses. The results of this study provide valuable information on the diversity and spatial distribution of paramyxoviruses, coronaviruses, and astroviruses in wild birds in southeastern Kazakhstan and highlight the importance of further thorough monitoring of wild birds in this region.</p>	<p>paramyxoviruses in wild birds in southeastern Kazakhstan. <i>Heliyon</i>. 31;8(11):e11324. doi: 10.1016/j.heliyon.2022.e11324.</p>
6	<p>Распространенность лихорадки Ку в южном регионе Казахстана</p>	<p><a href="https://doi.org/10.26577/EJE.2022.v73.i4.010">https://doi.org/10.26577/EJE.2022.v73.i4.010</a></p>	<p>Лихорадка Ку (коксииеллез) - зоонозная инфекция, вызываемой бактерией <i>Coxiella (C.) burnetii</i>, которая может инфицировать многие виды млекопитающих, включая человека. Эта работа направлена на исследование распространённости <i>C. burnetii</i> среди домашнего скота и людей, проживающих в южном регионе Казахстана с помощью иммуноферментного анализа (ИФА). Для серологического мониторинга проведен сбор образцов сыворотки у 100 жителей Жамбылской области в эпидемиологический сезон 2021 г. Выявлено, что общая серопревалентность IgG к <i>C. burnetii</i> равна 3,3%. Также проведен серологический анализ 282 образцов сыворотки крови от <i>Capra hircus</i>, <i>Ovis aries</i> и <i>Bos taurus</i>, собранных в Туркестанской и Жамбылской областях. Показано, что общая серопревалентность антител к <i>C. burnetii</i> у сельскохозяйственных животных составляет 32,2% и 23,0% в Туркестанской и Жамбылской областях, соответственно. Проведен эпидемиологический анализ данных серомониторинга домашнего скота. Показано, что видовая</p>	<p>Перфильева Ю.В., Машжан А.С., Жигайлов А.В., Остапчук Е.О., Мальцева Э.Р., Найзабаева Д.А., Бердыгулова Ж.А., Бисенбай А.О., Скиба Ю.А., Дмитровский А.М., Мамадалиев С.М. Распространенность лихорадки Ку в южном регионе Казахстана. Вестник КазНУ. Серия «экологическая» №4(73). 2022. С. 99-110 <a href="https://doi.org/10.26577/EJE.2022.v73.i4.010">https://doi.org/10.26577/EJE.2022.v73.i4.010</a></p>

			<p>принадлежность к <i>Capra hircus</i>, женский пол и обитание в Байдибекском, Сайрамском, Казыгуртском районах Туркестанской области и в районе Т. Рыскулов Жамбылской области являются факторами риска инфицирования <i>S. burnetii</i> в южном регионе Казахстана. Полученные результаты говорят о необходимости проведения дальнейшего исследования в этом направлении для выделения возбудителя и идентификации его основных резервуаров. Ключевые слова: <i>Coxiella (C.) burnetii</i>, коксиеллез, эпидемиология, иммуноферментный анализ, сыворотка.</p>	
7	<p>Детекция <i>Bacillus anthracis</i> по генам профага lambda_Ba03 посредством ПЦР в реальном времени</p>	<p><a href="https://doi.org/10.21055/0370-1069-2022-3-170-172">https://doi.org/10.21055/0370-1069-2022-3-170-172</a></p>	<p>Цель исследования – разработка набора праймеров и флуоресцентных зондов для детекции двух хромосомных мишеней <i>Bacillus anthracis</i> методом ПЦР в реальном времени на основе генов профага lambda_Ba03. При BLAST-анализе хромосомной ДНК <i>B. anthracis</i> в качестве мишеней определены два гена профага lambdaBa03: BA_5358 (AE016879.1: 4852332..4853642) и BA_5361 (AE016879.1: 4855298..4856278). Разработанные праймеры и флуоресцентные гидролизуемые пробы TaqMan для одновременной детекции хромосомной ДНК <i>B. anthracis</i> по двум указанным генам проверены в реакциях ПЦР в реальном времени на чувствительность и специфичность. Проведенные исследования на образцах хромосомной ДНК близкородственных бактерий (<i>B. cereus</i>, <i>B. thuringiensis</i>, <i>B. subtilis</i>, <i>B. clausii</i>) показали 100 % специфичность разработанных сетов праймеров/зондов. Чувствительность разработанного мультиплексного набора, исследованная на образцах ДНК вакцинного штамма м55-ВНИИВВиМ и архивных образцах ДНК <i>B. anthracis</i>, составила 100 фг бактериальной ДНК, что в пересчете определяет предел чувствительности в 16,72 бактериального генома на реакцию. Разработанный мультиплексный набор позволяет использовать его как отдельный инструмент для исследовательских лабораторий, изучающих сибирскую язву.</p>	<p>Низкородова А.С., Мальцева Э.Р., Бердыгулова Ж.А., Найзабаева Д.А., Куатбекова С.А., Жигайлов А.В., Абдолла Н., Машжан А.С., Ахметоллаев И.А., Скиба Ю.А., Мамадалиев С.М. Детекция <i>Bacillus anthracis</i> по генам профага lambda_Ba03 посредством ПЦР в реальном времени. Проблемы особо опасных инфекций. 2022;(3):170-172. <a href="https://doi.org/10.21055/0370-1069-2022-3-170-172">https://doi.org/10.21055/0370-1069-2022-3-170-172</a></p>

8	Анализ рисков распространения катаральной лихорадки овец в Казахстане	<a href="https://doi.org/10.31489/2022BMG1/71-81">https://doi.org/10.31489/2022BMG1/71-81</a>	<p>Казахстан считается страной, благополучной по катаральной лихорадке овец (КЛО). В то же время мокрецы рода <i>Culicoides</i>, являющиеся основными переносчиками вируса, вызывающего КЛО, распространены в стране практически повсеместно. На юге Казахстана сложились идеальные условия для распространения КЛО в случае заноса вируса из других стран, включающие оптимальный для размножения мокрецов климат, высокую плотность восприимчивого к вирусу скота и постоянный приток импортируемого племенного скота из районов, где инфекция является эндемичной. Неконтролируемое распространение КЛО на территории Казахстана может быть сопряжено с колоссальными экономическими потерями в силу того, что овцеводство имеет чрезвычайно важное значение для отечественного животноводства. Экономические затраты в этом случае не будут ограничиваться лишь падежом животных: существенный ущерб может быть нанесен имиджу нашей страны как экспортёру баранины. В настоящем обзоре приведены сведения, подчеркивающие значимость программ по контролю КЛО в Казахстане и эпидемиологический анализ рисков распространения данной инфекции в стране.</p>	<p>Жигайлов А.В., Остапчук Е.О., Перфильева Ю.В., Абдолла Н., Мальцева Э.Р., Найзабаева Д.А., Куатбекова С., Машжан А., Низкородова А.С., Бердыгулова Ж.А., Скиба Ю.А., Мамадалиев С.М. Вестник КарГУ. Серия «Биология. Медицина. География» №2(106) 2022. С. 71-81  <a href="https://doi.org/10.31489/2022BMG1/71-81">https://doi.org/10.31489/2022BMG1/71-81</a></p>
9	Анализ рисков распространения оспы верблюдов в Казахстане	<a href="https://doi.org/10.26577/EJE.2022.v71.i2.09">https://doi.org/10.26577/EJE.2022.v71.i2.09</a>	<p>Верблюдоводство является важным направлением отечественного животноводства. Значительные территории Казахстана заняты пустынями, а верблюды – одни из немногих домашних животных, способных к жизни на таких землях. Оспа верблюдов является самой важной в экономическом плане вирусной болезнью мозолоногих. Ранее на территории страны происходили эпизоотии этой инфекции. Важно, что последнее десятилетие поголовье верблюдов в стране постоянно увеличивается, поэтому риски, связанные с возникновением новых эпизоотий, многократно возрастают. Для обеспечения эффективных мер по контролю этой опасной болезни верблюдов необходимо провести тотальный мониторинг всей территории страны. Спорадические серологические</p>	<p>Жигайлов А.В., Машжан А.С., Бисенбай А.О., Остапчук Е.О., Перфильева Ю.В., Мальцева Э.Р., Найзабаева Д.А., Бердыгулова Ж.А., Скиба Ю.А., Мамадалиев С.М. Вестник КазНУ. Серия «экологическая» №2(71). 2022. С. 93-102  <a href="https://doi.org/10.26577/EJE.2022.v71.i2.09">https://doi.org/10.26577/EJE.2022.v71.i2.09</a></p>

			<p>исследования проводились прежде только в Мангистауской области, уровень серопревалентности к возбудителю оспы верблюдов для других областей страны не определен. Критично, чтобы такой мониторинг был проведен до старта компании по вакцинации верблюдов вакциной отечественного производства, чтобы можно было оценить эффективность проводимой вакцинации. В статье приводятся данные по анализу рисков, связанных с распространением оспы верблюдов в Казахстане, а также результаты подготовительных работ для проведения мониторинга территории страны в отношении оспы верблюдов.</p>	
10	<p>Identification of microorganisms isolated from oil reservoir water of the Akingen field, Kazakhstan</p>	<p><a href="https://doi.org/10.26577/eb.2022.v90.i1.11">https://doi.org/10.26577/eb.2022.v90.i1.11</a></p>	<p>Currently, there is a continuous growth of deposits in Western Kazakhstan that are in the late stage of development. Deposits often have a complex heterogeneous structure with hard-to-recover reserves, so for their effective development it is necessary to apply methods of increasing oil recovery. One of the most effective methods of enhanced oil recovery is microbial enhanced oil recovery (MEOR). Microorganisms of the developed oil-reservoir waters, adapted to the extreme underground conditions of the reservoirs, are promising objects for the development of microbiological methods for increasing oil recovery, based on their ability to displace and dilute oil. The article presents the identification of aero-bic microorganisms, waterlogged oil reservoir waters of the Akingen field. The aim of this study was to identify microorganisms of oil-reservoir waters of the Akingen field isolated under aerobic conditions. Traditional microbiological and genetic methods of identification of microorganisms are used in the research work. The enzymatic activity of the isolated strains (lipase, amylolytic, proteolytic activity) was evaluated. The emulsification index was carried out according to the Cooper method. As a result of microbiological and genetic studies of the nucleotide sequence of the 16S rRNA gene fragment, 14 aerobic strains of microorganisms were identified as representatives of the genus <i>Pseudomonas</i> and <i>Bacillus</i>, in particular, <i>Bacillus paramycoides</i>-M1; <i>B. subtilis</i> subsp. <i>spizizenii</i>-S1; <i>Bacillus</i> sp. – M2, A1, A2, A3, A4, A5, S2, S3, D-1X; <i>P. aeruginosa</i>-D5, D6, D7. The evaluation of emulsifying activity allowed us to identify 4 strains of</p>	<p>Kaiyrmanova G. K., Tapeshova Sh. Zh., Shaimerdenova U. T., Magmiyayev R. B., Yernazarova A.K. Вестник КазНУ. Серия биологическая – №1 (90). – 2022. – 126-136 с.  <a href="https://doi.org/10.26577/eb.2022.v90.i1.11">https://doi.org/10.26577/eb.2022.v90.i1.11</a></p>



			microorganisms with a high oil emulsification index: <i>P. aeruginosa</i> -D5, D6, D7 (40-49 %) and <i>Bacillus</i> sp. D1X (32 %). Isolates <i>P. aeruginosa</i> – D5, D6, D7 and <i>Bacillus</i> sp. D1X are promising objects for use in enhanced oil recovery technologies	
11	Biotechnology of Microorganisms from Coal Environments: From Environmental Remediation to Energy Production.	<a href="https://doi.org/10.3390/biology11091306">https://doi.org/10.3390/biology11091306</a>	It was generally believed that coal sources are not favorable as live-in habitats for microorganisms due to their recalcitrant chemical nature and negligible decomposition. However, accumulating evidence has revealed the presence of diverse microbial groups in coal environments and their significant metabolic role in coal biogeochemical dynamics and ecosystem functioning. The high oxygen content, organic fractions, and lignin-like structures of lower-rank coals may provide effective means for microbial attack, still representing a greatly unexplored frontier in microbiology. Coal degradation/conversion technology by native bacterial and fungal species has great potential in agricultural development, chemical industry production, and environmental rehabilitation. Furthermore, native microalgal species can offer a sustainable energy source and an excellent bioremediation strategy applicable to coal spill/seam waters. Additionally, the measures of the fate of the microbial community would serve as an indicator of restoration progress on post-coal-mining sites. This review puts forward a comprehensive vision of coal biodegradation and bioprocessing by microorganisms native to coal environments for determining their biotechnological potential and possible applications.	Akimbekov NS, Digel I, Tastambek KT, Marat AK, Turaliyeva MA, Kaiyrmanova GK. Biotechnology of Microorganisms from Coal Environments: From Environmental Remediation to Energy Production. <i>Biology</i> . 2022; 11(9):1306. <a href="https://doi.org/10.3390/biology11091306">https://doi.org/10.3390/biology11091306</a>
12	Feasibility of waste-free use of microalgae in aquaculture	Journal of Applied Phycology. 2022, Q-2, процентиль–88.	Following the circular bioeconomy approach, this study shows the possibility of effective microalgal bioremediation of aquaculture wastewater integrated with the production of protein-rich biomass, which can be used as a feed additive. Screening was carried out among strains of <i>Chlorella vulgaris</i> BB-2, <i>Parachlorella kessleri</i> Bh-2 and <i>Chlamydomonas reinhardtii</i> C-124 with the aim of selecting the strain which is characterized by high indicators of growth in the fish farms wastewaters. Among these three strains, <i>C. vulgaris</i> BB-2 was selected due to its increased growth rate in aquaculture wastewater with ammonia, nitrite, and nitrate and phosphate removal. In addition, in the water when cultivating microalgae in it the coliform index and total microbial number decreased to 5 and $1.8 \times 10^3$ colony-forming unit $\text{cm}^{-3}$ . Large-scale microalgae cultivation utilizing	Akmukhanova, N.R., Sadvakasova, A.K., Torekhanova, M.M., Chang, J.-S., Allakhverdiev, S.I. Feasibility of waste-free use of microalgae in aquaculture Journal of Applied Phycology, 2022, 34(5), стр. 2297–2313 DOI 10.1007/s10811-022-02787-y

			<p>aquaculture wastewater gave biomass production of 43.5 mg L<sup>-1</sup> day<sup>-1</sup>. The biochemical composition analysis of the aquaculture wastewater phycoremediation-derived biomass of <i>C. vulgaris</i> BB-2 revealed that the content of 57.0 ± 1.2% protein, 16 ± 1.2% lipid, and 11.4 ± 1.4% carbohydrate. The obtained data indicate that the lipid extract of microalgae <i>C. vulgaris</i> BB-2 contained saturated 30.7% and polyunsaturated fatty acids 69.3%. The main fraction of amino acids consisted of glutamic acid, lysine, aspartic acid and leucine. The utilization of 25% microalgal biomass as a feed additive in the diet of fish has shown a positive effect on the morpho-physiological and biochemical growth parameters and intestinal microflora of Nile tilapia (<i>Oreochromis niloticus</i>).</p>	
13	<p>Determination of the Promising Microalgal Strain for Bioremediation of the Aquaculture Wastewater</p>	<p>Microbiology. Том 91, Выпуск 5, Страницы 533 - 54, Q-3, процентиль-32.</p>	<p>Applicability of three strains of green microalgae (<i>Chlorella vulgaris</i> SP BB-2, <i>Parachlorella kessleri</i>, and <i>Chlamydomonas reinhardtii</i> Dangeard CC-124) for bioremediation (contaminants removal) of aquaculture wastewater was investigated. <i>C. vulgaris</i> strain SP BB-2 exhibited the highest growth rate and biomass accumulation. This strain was found to utilize nitrogen and phosphorus from wastewater for growth and development and showed high efficiency according to chemical oxygen demand (COD). Moreover, among the studied strains, <i>C. vulgaris</i> SP BB-2 produced biomass with the highest protein content, which may be recommended as a feed additive for the aquaculture. Analysis of the induction and rapid light curves of chlorophyll fluorescence revealed alterations in the energy storage photosynthetic processes of <i>C. vulgaris</i> SP BB-2 cells when grown on the aquaculture wastewater. Thus, high values of the maximum quantum yield of primary photochemistry in photosystem II (PSII) (<math>F_V/F_M</math>), quantum yield of electron transport (<math>\phi_{E0}</math>), PSII performance index on absorption basis (<math>PI_{ABS}</math>), and the light utilization coefficient (<math>\alpha</math>) were observed. <i>C. vulgaris</i> strain SP BB-2 may be recommended for wastewater treatment, while its highly sensitive parameters of chlorophyll fluorescence induction (<math>PI_{ABS}</math>, <math>\phi_{E0}</math>) may be used as indicators of the state of the microalgae. © 2022, Pleiades Publishing, Ltd.</p>	<p>Akmukhanova, N.R., Zayadan, B.K., Sadvakasova, A.K., ...Todorenko, D.A., Matorin, D.N. Determination of the Promising Microalgal Strain for Bioremediation of the Aquaculture Wastewater Microbiology (Russian Federation), 2022, 91(5), стр. 533–541 DOI 10.1134/S0026261722601166</p>

14	Peculiarities of adsorption of Cr (VI) ions on the surface of <i>Chlorella vulgaris</i> ZBS1 algae cells.	Heliyon, 2022, 8(9), e10468 <a href="https://doi.org/10.1016/j.heliyon.2022.e10468">https://doi.org/10.1016/j.heliyon.2022.e10468</a>	<p>Cr (VI) compounds are the most dangerous for human health and the environment, therefore, the study of their adsorption features is of great interest. A comprehensive study of the adsorption of Cr (VI) ions on the surface of <i>Chlorella vulgaris</i> ZBS1 algae cells was carried out evaluating the effect of the pH of the medium on the degree of removal of Cr (VI) ions from solutions and on the <a href="#">zeta potential</a> of the cell surface was. The highest values of the degree of removal of Cr (VI) ions equal to 94.6–95.4% are achieved in the pH range of 1–2, being the result of the <a href="#">electrostatic attraction</a> of <math>\text{HCrO}_4^-</math> groups to protonated amino groups of the cell surface and the possibility of reducing Cr (VI) ions to Cr (III) in an acidic medium, followed by the formation of Cr (III) ions of coordination bonds with amine and <a href="#">carboxyl groups</a> of algae cells.</p> <p>The adsorption data were processed within the framework of Langmuir, Freundlich, Dubinin-Radushkevich and Temkin models. It was shown that the maximum <a href="#">Langmuir adsorption</a> value was 74.63 mg/g. The values of the adsorption parameters <math>1/n</math> and <math>K_f</math> in the Freundlich model were equal to 0.713 and 2.82 mg/g. In the Dubinin-Radushkevich model, the maximum <a href="#">adsorption capacity</a> (<math>q_m</math>) and free energy (E) were equal to 39.73 mg/g and 2.604 kJ/mol, respectively. Whereas, according to the Temkin model, the constant A was equal to 18.215 L/mg, and <math>b_T</math> was equal to 0.023 kJ/mol. Taking into account the low values of free energy, it is concluded that adsorption is caused by non-covalent interactions.</p> <p>The study of <a href="#">adsorption kinetics</a> showed that the adsorption of Cr (VI) ions on the surface of <i>Chlorella vulgaris</i> ZBS1 algae cells is described in the framework of the pseudo-second order model. The kinetic behavior of the process is discussed in the framework of the IPDM and ELM models. With increasing temperature, the constant of intraparticle diffusion of Cr (VI) ions decreases, which is explained with increasing of <a href="#">hydrophobic interactions</a> between nonpolar sites of <a href="#">protein macromolecules</a> and <a href="#">polysaccharides</a> in the composition of algae cells. The increase in the adsorption of Cr (VI) ions at pH 8.62 in the temperature range of 298–353 K is</p>	Tattibayeva, Z., Tazhibayeva, S., Kujawski, W., Zayadan, B., Musabekov, K. Peculiarities of adsorption of Cr (VI) ions on the surface of <i>Chlorella vulgaris</i> ZBS1 algae cells. Heliyon, 2022, 8(9), e10468 <a href="https://doi.org/10.1016/j.heliyon.2022.e10468">https://doi.org/10.1016/j.heliyon.2022.e10468</a>
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			justified by the shrinkage of the biosorbent volume, which leads to the blocking of a part of the <a href="#">anionic groups</a> on the surface of algae cells. Therefore, the decrease in the <a href="#">electrostatic repulsion</a> between the <a href="#">negatively charged surface</a> of the adsorbent and Cr (VI) <a href="#">oxyanions</a> is observed.	
15	Strategies and economic feasibilities in cyanobacterial hydrogen production	International Journal of Hydrogen Energy, 2022	Due to the side effects of greenhouse gases, interest in <a href="#">alternative energy sources</a> is growing, and research into hydrogen (H <sub>2</sub> ) production from cyanobacteria has become a promising direction for the industry. The article provides an overview of cyanobacterial <a href="#">hydrogen production</a> strategies and their current economic efficiency. It also describes metabolic, genetic and technical methods for obtaining H <sub>2</sub> from cyanobacteria. Cyanobacteria are considered potential producers of <a href="#">hydrogen energy</a> that will be economically viable shortly, as they only need cheap salts, water and solar energy to grow. However, <a href="#">producing hydrogen</a> from cyanobacteria still requires extensive work, and the main problem is the small amount of hydrogen energy obtained. To produce large amounts of cyanobacterial hydrogen, the most active wild-type strains must be selected and technological, modular and genetic research must be carried out simultaneously. The low energy efficiency of hydrogen from cyanobacteria also shows the need for comprehensive research through international programs.	Kamshybayeva, G.K., Kossalbayev, B.D., Sadvakasova, A.K., Zayadan B.K., ...Alwasel, S., Allakhverdiev, S.I. <a href="#">Strategies and economic feasibilities in cyanobacterial hydrogen production. International Journal of Hydrogen Energy, 2022</a>
16	A Novel Antimicrobial Metabolite Produced by Paenibacillus apiarius Isolated from Brackish Water of Lake Balkhash in Kazakhstan., Microorganisms,	<i>Microorganisms</i> 2022, 10(8), 1519; <a href="https://doi.org/10.3390/microorganisms10081519">https://doi.org/10.3390/microorganisms10081519</a>		Meene, A., Herzer, C., Schlüter, R., Zayadan B.K., ... Urich, T., Mikolasch, A. A Novel Antimicrobial Metabolite Produced by Paenibacillus apiarius Isolated from Brackish Water of Lake Balkhash in Kazakhstan., <i>Microorganisms</i> , 2022, 10(8), 1519

17	Biohydrogen production by novel cyanobacterial strains isolated from rice paddies in Kazakhstan	International Journal of Hydrogen Energy. Q-1, процентиль – 90. <a href="https://doi.org/10.1016/j.ijhydene.2022.03.126">https://doi.org/10.1016/j.ijhydene.2022.03.126</a> .	A limited supply of oil prompts the search for non-traditional energy sources to replace traditional ones. This makes <a href="#">hydrogen gas</a> an appealing alternative source. <a href="#">Photosynthetic organisms</a> capture sunlight very efficiently and convert it into organic molecules. A promising wild strain was isolated for the first time, from the rice paddies of Kazakhstan (Kyzylorda and Almaty regions), which can be considered as one of the most active hydrogen producers compared to the literature. The result showed that among the 13 isolated and collection cyanobacterial strains, <i>Synechocystis</i> sp. S-1 is the most active H <sub>2</sub> producer (2.35 μmol H <sub>2</sub> mg <sup>-1</sup> Chl a h <sup>-1</sup> ) in the light. In contrast, the wild-type cyanobacterium <i>Anabaena variabilis</i> A-1 had higher productivity, <a href="#">nitrogenase</a> activity, and a stronger capacity to <a href="#">produce hydrogen</a> in the dark (8.67 μmol H <sub>2</sub> mg <sup>-1</sup> Chl a h <sup>-1</sup> ), which matched the maximum yield obtained in the research. The metabolic modulation performed significantly increased <a href="#">hydrogen production</a> . The highest photohydrogen production rate was observed in cells incubated with 25 μmol HEPES and 50 μmol sodium bicarbonate (NaHCO <sub>3</sub> ).	Bekzhan D. Kossalbayev, Ardak B. Kakimova, Kenzhegul Bolatkhan, Bolatkhan K. Zayadan, Sandugash K. Sandybayeva, Ayshat M. Bozieva, Asemgul K. Sadvakasova, Saleh Alwasel, Suleyman I. Allakhverdiev. Biohydrogen production by novel cyanobacterial strains isolated from rice paddies in Kazakhstan//International Journal of Hydrogen Energy. Q-1, процентиль – 90. <a href="https://doi.org/10.1016/j.ijhydene.2022.03.126">https://doi.org/10.1016/j.ijhydene.2022.03.126</a> .
18	Influence of Mo and Fe on Photosynthetic and Nitrogenase Activities of Nitrogen-Fixing Cyanobacteria under Nitrogen Starvation Cells	<i>Cells</i> 2022, 11(5), 904; <a href="https://doi.org/10.3390/cells11050904">https://doi.org/10.3390/cells11050904</a>	The potential of cyanobacteria to perform a variety of distinct roles vital for the biosphere, including nutrient cycling and environmental detoxification, drives interest in studying their biodiversity. Increasing soil erosion and the overuse of chemical fertilizers are global problems in developed countries. The option might be to switch to organic farming, which entails largely the use of biofertilisers. Cyanobacteria are prokaryotic, photosynthetic organisms with considerable potential, within agrobiotechnology, to produce biofertilisers. They contribute significantly to plant drought resistance and nitrogen enrichment in the soil. This study sought, isolated, and investigated nitrogen-fixing cyanobacterial strains in rice fields, and evaluated the effect of Mo and Fe on photosynthetic and nitrogenase activities under nitrogen starvation. Cyanobacterial isolates, isolated from rice paddies in Kazakhstan, were identified as <i>Trichormus variabilis</i> K-31 (MZ079356), <i>Cylindrospermum badium</i> J-8 (MZ079357), <i>Nostoc</i> sp. J-14 (MZ079360), <i>Oscillatoria brevis</i> SH-12 (MZ090011), and <i>Tolypothrix tenuis</i> J-1 (MZ079361). The study of the influence of various concentrations of Mo and Fe on photosynthetic and nitrogenase activities under conditions of	Sadvakasova, A.K., Kossalbayev, B.D., Token, A.I., Zayadan, B.K., ... Chang, J.-S., Allakhverdiev, S.I. Influence of Mo and Fe on Photosynthetic and Nitrogenase Activities of Nitrogen-Fixing Cyanobacteria under Nitrogen Starvation Cells, 2022, 11(5), 904

			nitrogen starvation revealed the optimal concentrations of metals that have a stimulating effect on the studied parameters.	
19	A Novel Antimicrobial Metabolite Produced by <i>Paenibacillus apiarius</i> Isolated from Brackish Water of Lake Balkhash in Kazakhstan	<i>Microorganisms</i> 2022, 10, 1519. <a href="https://doi.org/10.3390/microorganisms10081519">https://doi.org/10.3390/microorganisms10081519</a>	Abstract: Four aerobic bacteria with bacteriolytic capabilities were isolated from the brackish water site Strait Uzynaral of Lake Balkhash in Kazakhstan. The morphology and physiology of the bacterial isolates have subsequently been analyzed. Using matrix assisted laser desorption ionization-time of flight mass spectrum and partial 16S rRNA gene sequence analyses, three of the isolates have been identified as <i>Pseudomonas veronii</i> and one as <i>Paenibacillus apiarius</i> . We determined the capability of both species to lyse pre-grown cells of the Gram-negative strains <i>Pseudomonas putida</i> SBUG 24 and <i>Escherichia coli</i> SBUG 13 as well as the Gram-positive strains <i>Micrococcus luteus</i> SBUG 16 and <i>Arthrobacter citreus</i> SBUG 321 on solid media. The bacteriolysis process was analyzed by creating growth curves and electron micrographs of co-cultures with the bacteriolytic isolates and the lysis sensitive strain <i>Arthrobacter citreus</i> SBUG 321 in nutrient-poor liquid media. One metabolite of <i>Paenibacillus apiarius</i> was isolated and structurally characterized by various chemical structure determination methods. It is a novel antibiotic substance.	Alexander Meene 1,†, Christiane Herzer 1,†, Rabea Schlüter 2 , Bolatkhan Zayadan 3 , Ruediger Pukall 4 , Peter Schumann 4 , Frieder Schauer 1 , Tim Urich 1 and Annett Mikolasch 1,*
20	Prospects of cyanobacterial pigment production: Biotechnological potential and optimization strategies.	<i>Biochemical Engineering Journal</i> , 187 doi:10.1016/j.bej.2022.108640	Increasing awareness of the harmful effects of synthetic colorants has led consumers to favor the use of natural alternatives such as plant or microbial pigments in food and cosmetics. Cyanobacteria are a rich source of many natural biopigments that are of high commercial value. In the market, bio-based pigments are usually sold as extracts to reduce purification costs. Various cell disruption methods are used for pigment extraction, such as sonication, homogenization, high pressure, supercritical CO <sub>2</sub> extraction, enzymatic extraction, as well as other promising novel extraction methods that make the production of cyanobacterial pigments economically viable. In addition, a continuous cultivation system is considered the most suitable cultivation mode for large-scale biomass production. However, a major limitation in the large-scale production of cyanobacterial pigments is the installation and operation costs. Thus, basic and applied research is still needed to overcome such limitations and enable cyanobacteria to enter the global market. This review focuses on various cyanobacterial pigments, their applications, and current	Sandybayeva, S. K., Kossalbayev, B. D., Zayadan, B. K., Sadvakasova, A. K., Bolatkhan, K., Zadneprovskaya, E. V., . . . Chang, J.

			<p>biotechnological approaches to increase the production of biopigments for their potential use in the pharmaceutical, food, and cosmetic industries. The current state of production technologies based on either open pond systems or closed photobioreactors was compared. The potential of scientific and technological advances to increase yield and reduce production costs of cyanobacteria biomass-based pigments was also discussed.</p>	
21	<p>Prospects of cyanobacterial pigment production: Biotechnological potential and optimization strategies</p>	<p><a href="https://doi.org/10.1016/j.bej.2022.108640">https://doi.org/10.1016/j.bej.2022.108640</a>  IF 4.446  Q1  Percentile 81%  H-index 130</p>	<p>Increasing awareness of the harmful effects of synthetic colorants has led consumers to favor the use of natural alternatives such as plant or microbial pigments in food and cosmetics. Cyanobacteria are a rich source of many natural biopigments that are of high commercial value. In the market, bio-based pigments are usually sold as extracts to reduce purification costs. Various cell disruption methods are used for pigment extraction, such as sonication, homogenization, high pressure, supercritical CO<sub>2</sub> extraction, enzymatic extraction, as well as other promising novel extraction methods that make the production of cyanobacterial pigments economically viable. In addition, a continuous cultivation system is considered the most suitable cultivation mode for large-scale biomass production. However, a major limitation in the large-scale production of cyanobacterial pigments is the installation and operation costs. Thus, basic and applied research is still needed to overcome such limitations and enable cyanobacteria to enter the global market. This review focuses on various cyanobacterial pigments, their applications, and current biotechnological approaches to increase the production of biopigments for their potential use in the pharmaceutical, food, and cosmetic industries. The current state of production technologies based on either open pond systems or closed photobioreactors was compared. The potential of scientific and technological advances to increase yield and reduce production costs of cyanobacteria biomass-based pigments was also discussed.</p>	<p>Sandugash K. Sandybayeva, Bekzhan D. Kossalbayev, Bolatkhan K. Zayadan, Asem K. Sadvakasova, Kenzhegul Bolatkhan, Elena V. Zadneprovskaya, Ardak B. Kakimova, Saleh Alwasel, Yoong Kit Leong, Suleyman I. Allakhverdiev, Jo-Shu Chang, Prospects of cyanobacterial pigment production: Biotechnological potential and optimization strategies, Biochemical Engineering Journal, Volume 187, 2022, 108640, ISSN 1369-703X, <a href="https://doi.org/10.1016/j.bej.2022.108640">https://doi.org/10.1016/j.bej.2022.108640</a> . (<a href="https://www.sciencedirect.com/science/article/pii/S1369703X22003096">https://www.sciencedirect.com/science/article/pii/S1369703X22003096</a> )</p>



22	Biohydrogen production by novel cyanobacterial strains isolated from rice paddies in Kazakhstan	<a href="https://doi.org/10.1016/j.ijhydene.2022.03.126">https://doi.org/10.1016/j.ijhydene.2022.03.126</a> International Journal of Hydrogen Energy. Q-1, процентиль – 90.	A limited supply of oil prompts the search for non-traditional energy sources to replace traditional ones. This makes hydrogen gas an appealing alternative source. Photosynthetic organisms capture sunlight very efficiently and convert it into organic molecules. A promising wild strain was isolated for the first time, from the rice paddies of Kazakhstan (Kyzylorda and Almaty regions), which can be considered as one of the most active hydrogen producers compared to the literature. The result showed that among the 13 isolated and collection cyanobacterial strains, <i>Synechocystis</i> sp. S-1 is the most active H <sub>2</sub> producer (2.35 μmol H <sub>2</sub> mg <sup>-1</sup> Chl a h <sup>-1</sup> ) in the light. In contrast, the wild-type cyanobacterium <i>Anabaena variabilis</i> A-1 had higher productivity, nitrogenase activity, and a stronger capacity to produce hydrogen in the dark (8.67 μmol H <sub>2</sub> mg <sup>-1</sup> Chl a h <sup>-1</sup> ), which matched the maximum yield obtained in the research. The metabolic modulation performed significantly increased hydrogen production. The highest photohydrogen production rate was observed in cells incubated with 25 μmol HEPES and 50 μmol sodium bicarbonate (NaHCO <sub>3</sub> ).	Bekzhan D. Kossalbayev, Ardak B. Kakimova, Kenzhegul Bolatkhan, Bolatkhan K. Zayadan, Sandugash K. Sandybayeva, Ayshat M. Bozieva, Asemgul K. Sadvakasova, Saleh Alwasel, Suleyman I. Allakhverdiev. Biohydrogen production by novel cyanobacterial strains isolated from rice paddies in Kazakhstan//International Journal of Hydrogen Energy. Q-1, процентиль – 90. <a href="https://doi.org/10.1016/j.ijhydene.2022.03.126">https://doi.org/10.1016/j.ijhydene.2022.03.126</a> .
23	Equine lactoferrin: Antioxidant properties related to divalent metal chelation	DOI 10.1016/j.lwt.2022.113426 LWT Том 1611 May 2022 Номер статьи 113426 Q1, процентиль – 87%	Lactoferrin is a minor whey protein known for its multifunctionalities, particularly for its role in regulation of immune system and for its antimicrobial activities. Although bovine lactoferrin has been extensively studied, very few information exists on lactoferrin from mare's milk. This article studies the antioxidant properties via metal chelation of purified lactoferrin from Kazakhstan mare's milk. Equine lactoferrin shows free radical-scavenger activity when tested with radical DPPH and ABTS and has reducing capacities testing by FRAP. Moreover, the ferrous(II) and copper(II) ion-chelating power is highlighted by chemical colorimetric tests. Finally, the newly introduced biophysics switchSENSE® technology allowed to measure in real time the molecular interactions between equine lactoferrin and divalent cations. The order of magnitude of the KD values was tens or so μM for the four metal ions tested: Zn <sup>2+</sup> (KD = 23.9 ± 4.0 μM), Ca <sup>2+</sup> (KD = 28.2 ± 4.4 μM), Cu <sup>2+</sup> (KD = 43.5 ± 5.1 μM) and Fe <sup>2+</sup> (KD = 54.1 ± 8.9 μM). According to these results, we can conclude that equine lactoferrin shows antioxidant activity by radical-scavenging mechanism, reducing capacities and divalent pro-oxidant metals chelation ability	Narmuratova, Zhanar; Hentati, Faiez; Girardet, Jean-Michel; Narmuratova, Meyramkul; Cakir-Kiefer, Céline



24	Technological Process of Anaerobic Digestion of Cattle Manure in a Bioenergy Plant	Journal of Ecological Engineering, 2022, 23(7), стр. 131–142	<p>Anaerobic digestion consists of the biological decomposition of organic waste under anaerobic conditions by various types of microorganisms. The purpose of this study was to evaluate the effect of the fermentation starter of methanogenic bacteria on the anaerobic digestion of cattle manure in a bioenergy plant. The effect of various methods (physical, microbiological and chemical) on the digestion of cattle manure was studied under mesophilic (35°C) and thermophilic (50°C) modes. The results of the study showed that the content of volatile fatty acids and the pH of the medium was in the optimal range, the yield of methane biogas (CH<sub>4</sub>) during anaerobic digestion at t-35°C was 0.45 m<sup>3</sup>/kg and at t-50°C 0.58 m<sup>3</sup>/kg. The data obtained indicate that the thermophilic mode (50°C) of anaerobic digestion of manure effectively affects the yield of methane biogas. Based on anaerobic digestion in mesophilic mode, a fermentation starter of methanogenic cultures adapted to thermophilic conditions was obtained. According to cultural and morphological characteristics, the cultures were assigned to the genera Methanopyrus and Methanococcus. The results of a study on the effect of the fermentation starter of methanogenic bacteria in fermented manure at t-50°C showed that with an increase in the dose of the fermentation starter, the methane-forming ability of anaerobic bacteria increased and the process of methane biogas release intensified (from 0.36 m<sup>3</sup>/kg to 0.79 m<sup>3</sup>/kg). Besides, the dose of methanogenic fermentation starter based on Methanopyrus and Methanococcus isolates (28 kg) was determined. When the bioenergy plant is launched in thermophilic mode, the release of biogas increases by 2.2 times, and the digestion period decreases to 10 days.</p>	<p><u>Gulnar Dauletbaevna Ultanbekova</u> ,  <u>Gaukhar Madykhanovna Salkhozhayeva</u>,  <u>Karlygash Mamytbekovna Abdiyeva</u>,  <u>Sholpan Yescuatovna Arystanova</u></p> <p>Technological Process of Anaerobic Digestion of Cattle Manure in a Bioenergy Plant</p> <p>Journal of Ecological Engineering, 2022, 23(7), стр. 131–142</p> <p><a href="https://doi.org/10.12911/22998993/149516">DOI: https://doi.org/10.12911/22998993/149516</a></p> <p>Оглавление: <a href="http://www.jeeng.net/Issue-7-2022,10562">http://www.jeeng.net/Issue-7-2022,10562</a>  Статья: <a href="http://www.jeeng.net/Technological-Process-of-Anaerobic-Digestion-of-Cattle-Manure-in-a-Bioenergy-Plant,149516,0,2.html">http://www.jeeng.net/Technological-Process-of-Anaerobic-Digestion-of-Cattle-Manure-in-a-Bioenergy-Plant,149516,0,2.html</a></p>
25	GENES AND MIRNAS INVOLVED IN THE DEVELOPMENT OF ATHEROSCLEROSIS	Вестник КазНУ. Серия экологическая No4 (73). 2022 <a href="https://doi.org/10.26577/EJE.2022.v73.i4.07">https://doi.org/10.26577/EJE.2022.v73.i4.07</a>	<p>Atherosclerosis is a complex multifactorial disease. miRNAs, single-stranded RNA molecules may play an important role in the regulation genes expression which involved in atherosclerosis. The work studied binding of miRNAs with mRNA of genes responsible for development of human atherosclerosis. Based on the literature data of PubMed, a database of 14 genes sequences associated with development of atherosclerosis was created. The miRNA binding sites in mRNAs of the studied genes were found using the miRWalk, miRTarBase, TargetScan, miRDB, and MirTarget programs. 94 binding sites of</p>	<p>O.Yu. Yurikova, T.I.Abdullayeva, Sh.A. Atambayeva, A. Bekenkali</p> <p>GENES AND MIRNAS INVOLVED IN THE DEVELOPMENT OF ATHEROSCLEROSIS</p> <p>Вестник КазНУ. Серия экологическая No4 (73). 2022</p>

			<p>51 miRNAs were revealed in mRNA of genes responsible for the development of atherosclerosis. Of the studied binding sites, 15 sites are located in CDS, 17 in 5'UTR, and 62 in 3'UTR. It was defined that some mRNAs of genes have several binding sites with miRNAs. Thus, TNFRSF9 has 15, LDLR – 11 binding sites, TGFB1 – 14 binding sites. It was shown that miR-619-5p more frequently than others binds to mRNA of genes responsible for the development of atherosclerosis. miR-619-5p binds to CD36 with a <math>\Delta G/\Delta G_m</math> ratio of 100%, miR-5096 with a <math>\Delta G/\Delta G_m</math> equal to 100% binds to IL18. Among the studied genes, TGFB1 is the most preferred target of miRNA with high values of interaction, indicating the degree of miRNA binding to mRNA. Thus, using miRWalk, miRTarBase, TargetScan, and miRDB programs, it was shown that mRNA of TGFB1 is a target for many miRNAs in CDS, 5'UTR, and 3'UTR regions. Key words: miRNA, mRNA, binding sites, atherosclerosis, CDS, 5'UTR, 3'UTR, and nucleotide sequences.</p>	<p><a href="https://doi.org/10.26577/EJE.2022.v73.i4.07">https://doi.org/10.26577/EJE.2022.v73.i4.07</a></p>
26	<p>Phytoremediation of Soil Contaminated by Organochlorine Pesticides and Toxic Trace Elements: Prospects and Limitations of Paulownia tomentosa</p>	<p>Toxics Том 10, Выпуск 8 August 2022 Номер статьи 465  DOI 10.3390/toxics10080465 Q3 62-й перцентиль</p>	<p>Paulownia tomentosa (Thunb.) Steud is a drought-resistant, low-maintenance and fast-growing energy crop that can withstand a wide range of climatic conditions, provides a high biomass yield (approximately 50 t DM ha<sup>-1</sup> yr<sup>-1</sup>), and develops successfully in contaminated sites. In Kazakhstan, there are many historically contaminated sites polluted by a mixture of xenobiotics of organic and inorganic origin that need to be revitalised. Pilot-scale research evaluated the potential of P. tomentosa for the phytoremediation of soils historically contaminated with organochlorine pesticides (OCPs) and toxic trace elements (TTEs) to minimise their impact on the environment. Targeted soils from the obsolete pesticide stockpiles located in three villages of Talgar district, Almaty region, Kazakhstan, i.e., Amangeldy (soil A), Beskainar (soil B), and Kyzylkairat (soil K), were subjected to research. Twenty OCPs and eight TTEs (As, Cr, Co, Ni, Cu, Zn, Cd, and Pb) were detected in the soils. The phytoremediation potential of P. tomentosa was investigated for OCPs whose concentrations in the soils were significantly different (aldrin, endosulfans, endrin aldehyde, HCB, heptachlor, hexabromobenzene, keltan, methoxychlor, and <math>\gamma</math>-HCH) and for TTEs (Cu, Zn, and Cd) whose concentrations exceeded</p>	<p>Mamirova A.; Baubekova, Almagul; Pidlisnyuk, Valentina Shadenova, Elvira; Djansugurova, Leyla; Jurjanz, Stefan</p>

			<p>maximum permissible concentrations. Bioconcentration (BCF) and translocation (TLF) factors were used as indicators of the phytoremediation process. It was ensured that the uptake and translocation of contaminants by <i>P. tomentosa</i> was highly variable and depended on their properties and concentrations in soil. Besides the ability to bioconcentrate Cr, Ni, and Cu, <i>P. tomentosa</i> demonstrated very encouraging results in the accumulation of endosulfans, keltan, and methoxychlor and the phytoextraction of <math>\gamma</math>-HCH (TLFs of 1.9–9.9) and HCB (BCFs of 197–571). The results of the pilot trials support the need to further investigate the potential of <i>P. tomentosa</i> for phytoremediation on a field scale</p>	
27	<p>The Coal Humic Product EldORost Shows Fertilizing and Growth Stimulating Properties on Diverse Agricultural Crops</p>	<p>Agronomy Том 12, Выпуск 12December 2022 Номер статьи 3012 DOI 10.3390/agronomy 12123012 Q2 73-й процентиль</p>	<p>The use of environmentally safe products of natural origin is a global trend today. A particular point of interest is the use of humic fertilizers. This is due to the growing awareness of the positive impact of humic substances on plant growth and development as well as on the quality of agricultural products and soil fertility. Humates are physiologically active substances. As a result, they regulate and intensify metabolic processes in plants and soil, and contribute to the bioavailability of nutrients to plants. EldORost is a new-generation humic product that contains humic substances with a high humification degree. In addition to humates, this product contains a complex of amino acids, macro-, and microelements in a bioavailable form for plants. The product is eco-friendly and completely soluble in water, which is a substantial advantage for drip irrigation systems. It can be used for all types of agricultural crops on a wide diversity of soils and climatic zones. It displays the properties of plant hormones while its optimum concentration is as low as 0.0001% (wt). The efficiency of this novel humic product was tested in laboratory and field tests conducted on potatoes and vegetable crops (tomatoes, cucumbers, cabbage, carrots, onions, beets). The obtained results showed high efficiency displayed in the significantly improved sowing quality of vegetable seeds, nominally increased the germination degree and seed germination energy, intensively stimulated the side root development in plants, accelerated the growth of biomass, increased the fruiting period, and reduced maturation on the yield of potatoes and vegetable crops. The obtained data allowed us to characterize this novel humic product</p>	<p>Zhilkibayev, Oral T.; Aitbayev, Temirzhan E.; Zhirkova, Anastasiya M.; Perminova, Irina V.; Popov, Alexander I., Shoinbekova, Sabina A. Kudaibergenov, Mukhtar S.; Shalmaganbetov, Kairzhan M.</p>

			from the perspective of an eco-friendly fertilizer and growth promoter	
28	Organ-specific expression of genes involved in iron homeostasis in wheat mutant lines with increased grain iron and zinc content	PeerJ Том 10 June 2022 Номер статьи e13515 DOI 10.7717/peerj.13515	Iron deficiency is a well-known nutritional disorder, and the imbalance of trace-elements, specifically iron, is the most common nutrient deficiency of foods across the world, including in Kazakhstan. Wheat has significant nutritional relevance, especially in the provision of iron, however many bread wheat varieties have low iron despite the need for human nourishment. In this study, the expression profiles of wheat homologous genes related to iron homeostasis were investigated. The work resulted in the development of two new M5 mutant lines of spring bread wheat through gamma-irradiation (200 Gy) with higher grain iron and zinc content, lower phytic acid content, and enhanced iron bioavailability compared to the parent variety. Mutant lines were also characterized by higher means of yield associated traits such as grain number per main spike, grain weight per main spike, grain weight per plant, and thousand-grain weight. Methods: The homologous genes of bread wheat from several groups were selected for gene expression studies exploring the tight control of iron uptake, translocation rate and accumulation in leaves and roots, and comprised the following: (1) S-adenosylmethionine synthase (SAMS), nicotianamine synthase (NAS1), nicotianamine aminotransferase (NAAT), deoxymugineic acid synthetase (DMAS), involved in the synthesis and release of phytosiderophores; (2) transcription factor basic helix-loop-helix (bHLH); (3) transporters of mugineic acid (TOM), involved in long-distance iron transport; (4) yellow stripe-like (YSIA), and the vacuolar transporter (VIT2), involved in intracellular iron transport and storage; and lastly (5) natural resistance-associated macrophage protein (NRAMP) and ferritin (Fer1A). Results: The wheat homologous genes TaSAMS, TaNAS1, and TaDMAS, were significantly up-regulated in the roots of both mutant lines by 2.1-4.7-fold compared to the parent variety. The combined over-expression of TaYSIA and TaVIT2 was also revealed in the roots of mutant lines by 1.3-2.7-fold. In one of the mutant lines, genes encoding intracellular iron transport and storage genes TaNRAMP and TaFer1A-D showed significant up-regulation in roots and leaves (by 1.4- and 3.5-fold, respectively). The highest expression was recorded in the transcription factor TabHLH,	Kenzhebayeva S.; Atabayeva, Saulea; Sarsu, Fatma; Abekova, Alfiya; Shoinbekova, Sabina; Omirbekova, Nargul; Doktyrbay, Gulina; Beisenova, Aizhan; Shavrukov, Yuri

			which was expressed 13.1- and 30.2-fold in the roots of mutant lines. Our research revealed that genotype-dependent and organ-specific gene expression profiles can provide new insights into iron uptake, translocation rate, storage, and regulation in wheat which aid the prioritization of gene targets for iron biofortification and bioavailability	
29	Plant Probiotic Endophytic <i>Pseudomonas flavescens</i> D5 Strain for Protection of Barley Plants from Salt Stress	<a href="https://doi.org/10.3390/su142315881">https://doi.org/10.3390/su142315881</a>	Soil salinity has become a global issue that is directly related to land degradation and results in many changes in climate, ecosystem services, and biodiversity. The present study focuses on the investigation of beneficial properties of a plant probiotic bacterial strain as an eco-friendly and sustainable approach to promote crop growth in saline soil. The endophytic halotolerant strain <i>Pseudomonas flavescens</i> D5 isolated from common chicory ( <i>Cichorium intybus</i> L.) was able to grow on a medium containing 15% NaCl; produced indole-3-acetic acid (45.2 $\mu\text{g mL}^{-1}$ ) and polyhydroxyalkanoate (1.72 $\text{g L}^{-1}$ ); and had amylolytic, cellulolytic, and proteolytic activities. Polyhydroxyalkanoate had a pronounced antifungal activity against <i>Fusarium graminearum</i> , <i>F. solani</i> , <i>F. oxysporum</i> , and <i>Alternaria alternata</i> .	Ignatova L., Usmanova A., Brazhnikova Y., Omirbekova A. et al. Plant Probiotic Endophytic <i>Pseudomonas flavescens</i> D5 Strain for Protection of Barley Plants from Salt Stress // Sustainability. – 2022. – Vol. 14 (23). - 15881. <a href="https://www.mdpi.com/2071-1050/14/23/15881">https://www.mdpi.com/2071-1050/14/23/15881</a>
30	Скрининг эффективных микроскопических грибов, способствующих улучшению роста и развития растений	<a href="https://doi.org/10.26577/EJE.2022.v73.i4.09">https://doi.org/10.26577/EJE.2022.v73.i4.09</a>	В статье представлены данные по отбору штаммов микромицетов, выделенных из агроценозов зерновых и кормовых культур Казахстана, улучшающих рост растений и обладающих способностью повышать доступность для них элементов питания. В результате проведенного скрининга из 44 штаммов было отобрано 2, показавших наибольшую активность и обладающих сразу несколькими ценными свойствами. Отобранные эффективные микромицеты оказывали положительное влияние на физиологические процессы растений (морфометрические показатели и фотосинтез), а также повышали доступность элементов питания (фосфор и калий).	Игнатова Л., Усманова А., Бражникова Е., Омирбекова А. и др. Скрининг эффективных микроскопических грибов, способствующих улучшению роста и развития растений // Вестник КазНУ, Серия экологическая. – 2022. – Том 73, № 4, с. 90 - 98
31	Review Nutritional factors influencing microbiota-mediated colonization resistance of the oral cavity	<a href="https://doi.org/10.3389%2Ffnut.2022.1029324">https://doi.org/10.3389%2Ffnut.2022.1029324</a>	The oral cavity is a key biocenosis for many distinct microbial communities that interact with both the external environment and internal body systems. The oral microbiota is a vital part of the human microbiome. It has been developed through mutual interactions among the environment, host physiological state, and microbial community composition. Indigenous microbiota of the oral cavity is one of the factors that prevent adhesion and invasion of pathogens on the mucous membrane, i.e., the	Akimbekov, N. S., Digel, I., Yerezhepov, A. Y., Shardarbek R. S. (2022). Nutritional factors influencing microbiota-mediated colonization resistance of the oral cavity. <i>Frontiers in Nutrition.</i> ; 9: 1029324.

			development of the infectious process and thereby participating in the implementation of one of the mechanisms of local immunity–colonization resistance. The balance between bacterial symbiosis, microbial virulence, and host resistance ensures the integrity of the oral cavity. In this review we have tried to address how nutritional factors influence integrity of the oral indigenous microbiota and its involvement in colonization resistance.	
32	Review  Lysostaphin: Engineering and Potentiation toward Better Applications	<a href="https://doi.org/10.1021/acs.jafc.2c03459">https://doi.org/10.1021/acs.jafc.2c03459</a>	Lysostaphin is a potent bacteriolytic enzyme with endopeptidase activity against the common pathogen <i>Staphylococcus aureus</i> . By digesting the pentaglycine crossbridge in the cell wall peptidoglycan of <i>S. aureus</i> including the methicillin-resistant strains, lysostaphin initiates rapid lysis of planktonic and sessile cells (biofilms) and has great potential for use in agriculture, food industries, and pharmaceutical industries. In the past few decades, there have been tremendous efforts in potentiating lysostaphin for better applications in these fields, including engineering of the enzyme for higher potency and lower immunogenicity with longer-lasting effects, formulation and immobilization of the enzyme for higher stability and better durability, and recombinant expression for low-cost industrial production and in situ biocontrol. These achievements are extensively reviewed in this article focusing on applications in disease control, food preservation, surface decontamination, and pathogen detection. In addition, some basic properties of lysostaphin that have been controversial and only elucidated recently are summarized, including the substrate-binding properties, the number of zinc-binding sites, the substrate range, and the cleavage site in the pentaglycine crossbridge. Resistance to lysostaphin is also highlighted with a focus on various mechanisms. This article is concluded with a discussion on the limitations and future perspectives for the actual applications of lysostaphin.	Zha, J., Li, J., Su, Z., Akimbekov, N. S., & Wu, X. (2022). Lysostaphin: Engineering and Potentiation toward Better Applications. <i>Journal of Agricultural and Food Chemistry</i> , 70, 37, 11441–11457.
33	Book chapter  Vitamin D and Phosphate Interactions in Health and Disease	<a href="https://doi.org/10.1007/978-3-030-91623-7_5">https://doi.org/10.1007/978-3-030-91623-7_5</a>	Vitamin D plays an essential role in calcium and inorganic phosphate (Pi) homeostasis, maintaining their optimal levels to assure adequate bone mineralization. Vitamin D, as calcitriol (1,25(OH)2D), not only increases intestinal calcium and phosphate absorption but also facilitates their renal reabsorption, leading to elevated serum calcium and phosphate levels. The interaction of 1,25(OH)2D with its receptor (VDR) increases the	Akimbekov, N. S., Digel, I., Sherelkhan, D. K., & Razzaque, M. S. (2022). Vitamin D and Phosphate Interactions in Health and Disease. In M. S. Razzaque (Ed.), <i>Phosphate Metabolism: From Physiology</i>

			<p>efficiency of intestinal absorption of calcium to 30–40% and phosphate to nearly 80%. Serum phosphate levels can also influence 1,25(OH)<sub>2</sub>D and fibroblast growth factor 23 (FGF23) levels, i.e., higher phosphate concentrations suppress vitamin D activation and stimulate parathyroid hormone (PTH) release, while a high FGF23 serum level leads to reduced vitamin D synthesis. In the vitamin D-deficient state, the intestinal calcium absorption decreases and the secretion of PTH increases, which in turn causes the stimulation of 1,25(OH)<sub>2</sub>D production, resulting in excessive urinary phosphate loss. Maintenance of phosphate homeostasis is essential as hyperphosphatemia is a risk factor of cardiovascular calcification, chronic kidney diseases (CKD), and premature aging, while hypophosphatemia is usually associated with rickets and osteomalacia. This chapter elaborates on the possible interactions between vitamin D and phosphate in health and disease.</p>	<p>to Toxicity (pp. 37-46). Springer International Publishing.</p>
34	<p>Original article</p> <p>Antimicrobial Properties of the Triclosan-Loaded Polymeric Composite Based on Unsaturated Polyester Resin: Synthesis, Characterization and Activity</p>	<p><a href="https://doi.org/10.3390/polym14040676">https://doi.org/10.3390/polym14040676</a></p>	<p>The manufacturing of sanitary and household furniture on a large scale with inherently antimicrobial properties is an essential field of research. This work focuses on the synthesis of polymer composites based on the unsaturated polyester of resin loaded with 5 wt.-%-Triclosan produced by a co-mixing approach on automated technological complex with a potential for broad applications. According to findings, the polymer composite has a non-porous structure (surface area &lt; 1.97 m<sup>2</sup>/g) suitable for sanitary applications to reduce the growth of bacteria. The chemical composition confirmed the presence of major elements, and the inclusion of Triclosan was quantitatively confirmed by the appearance of chlorine on XRF (1.67 wt.%) and EDS (1.62 wt.%) analysis. Thermal analysis showed the difference of 5 wt.-% in weight loss, which confirms the loading of Triclosan into the polymer matrix. The polymer composite completely inhibited the strains of <i>S. aureus</i> 6538-P, <i>S. aureus</i> 39, <i>S. epidermidis</i> 12228, and <i>Kl. Pneumoniae</i> 10031 after 5-min contact time. The antimicrobial effects against <i>Kl. pneumoniae</i> 700603, <i>Ps. aeruginosa</i> 9027 and <i>Ps. aeruginosa</i> TA2 strains were 92.7%, 85.8% and 18.4%, respectively. The inhibition activity against <i>C. albicans</i> 10231 and <i>C. albicans</i> 2091 was 1.6% and 82.4%, respectively; while the clinical strain of <i>C. albicans</i> was inhibited by 92.2%. The polymer composite loaded with 5 wt.-%-Triclosan</p>	<p>Tauanov, Z., Zakiruly, O., Baimenova, Z., Baimenov, A., Akimbekov, N. S., &amp; Berillo, D. (2022). Antimicrobial Properties of the Triclosan-Loaded Polymeric Composite Based on Unsaturated Polyester Resin: Synthesis, Characterization and Activity. <i>Polymers</i>, 14(4).</p>



			displayed a stability over the period that illustrates the possibility of washing the composite surface.	
35	Role of Vitamins in Maintaining Structure and Function of Intestinal Microbiome  Book chapter	<a href="https://doi.org/10.1016/B978-0-12-819265-8.00043-7">https://doi.org/10.1016/B978-0-12-819265-8.00043-7</a>	The recent advances in microbiology have shed light on understanding the role of vitamins beyond the nutritional range. Vitamins are critical in contributing to healthy biodiversity and maintaining the proper function of gut microbiota. The sharing of vitamins among bacterial populations promotes stability in community composition and diversity; however, this balance becomes disturbed in various pathologies. Here, we overview and analyze the ability of different vitamins to selectively and specifically induce changes in the intestinal microbial community. Some schemes and regularities become visible, which may provide new insights and avenues for therapeutic management and functional optimization of the gut microbiota.	Akimbekov, N. S., Digel, I., & Razzaque, M. S. (2022). 1.24 – Role of Vitamins in Maintaining Structure and Function of Intestinal Microbiome. In M. Glibetic (Ed.), <i>Comprehensive Gut Microbiota</i> (pp. 320-334). Elsevier.
36	Biotechnology of Microorganisms from Coal Environments: From Environmental Remediation to Energy Production	<a href="https://doi.org/10.3390/biology11091306">https://doi.org/10.3390/biology11091306</a>	It was generally believed that coal sources are not favorable as live-in habitats for microorganisms due to their recalcitrant chemical nature and negligible decomposition. However, accumulating evidence has revealed the presence of diverse microbial groups in coal environments and their significant metabolic role in coal biogeochemical dynamics and ecosystem functioning. The high oxygen content, organic fractions, and lignin-like structures of lower-rank coals may provide effective means for microbial attack, still representing a greatly unexplored frontier in microbiology. Coal degradation/conversion technology by native bacterial and fungal species has great potential in agricultural development, chemical industry production, and environmental rehabilitation. Furthermore, native microalgal species can offer a sustainable energy source and an excellent bioremediation strategy applicable to coal spill/seam waters. Additionally, the measures of the fate of the microbial community would serve as an indicator of restoration progress on post-coal-mining sites. This review puts forward a comprehensive vision of coal biodegradation and bioprocessing by microorganisms native to coal environments for determining their biotechnological potential and possible applications.	Akimbekov, N.S., Digel, I., Tastambek, K.T., Turaliyeva, M.A., Kaiyrmanova, G.K. (2022). <i>Biotechnology of Microorganisms from Coal Environments: From Environmental Remediation to Energy Production</i> <i>Biology</i> , 11(9), 1306.
37	Изучение содержания хлорофилла и каротиноидов в	10.26577/EJE.2022.v71.i2.010	Натуральный каучук – это растительный биополимер, который используется во многих отраслях промышленности, например, в медицине, машиностроении и т.д. Тау-сагыз (лат. <i>Scorzonera tau-saghyz</i> Lipsch et Bosse) – полукустарник,	М.С. Муталханов, А.А. Альнурова, К.Р. Сисемали, А.И. Акильбекова, М.К. Таусарова, Ж.М. Басыгараев,



	<p>листьях тау-сагыза (<i>Scorzonera tau-saghyz</i> Lipsch et Bosse) из различных эколого-географических мест обитания в горах Каратау для определения связи с накоплением каучука в корнях</p>		<p>произрастающий на территории Южного Казахстана, способный производить и накапливать натуральный каучук в корнях. Экономическая ценность тау-сагыза определяется количеством и качеством синтезируемого натурального каучука. Соответственно, для введения тау-сагыза в культуру и создания экономически жизнеспособной культуры каучуконоса, определение факторов, связанных с повышенным содержанием каучука является первоочередной задачей. По утверждению М.В. Культиасова «Чем больше развита листовая масса, тем большая корневая масса должна ей соответствовать, т.е. листовая масса является косвенным критерием урожая корневой массы. Отсюда следует вывод: лист может служить критерием оценки накопления каучука в корневой массе». Поскольку основная функция листьев - фотосинтез, то в связи с этим в наших экспериментах количество фотосинтетических пигментов в листьях было выбрано в качестве фактора, возможно, определяющего уровень накопления каучука в корнях. Таким образом нами было выбрано 3 группы растений из различных мест обитания (северный склон, восточный склон, южный склон хребта Терис-аккан). Из отобранных образцов листьев ацетоном экстрагировали фотосинтетические пигменты, а из корней этих же образцов с использованием гексана экстрагировали каучук. Полученные данные количественного анализа проверяли с использованием следующих статистических методов: t-критерия Стьюдента и коэффициента корреляции Пирсона. Результаты показали наличие статистически значимой разницы между группами в количестве фотосинтетических пигментов, а также отсутствие разницы между группами в количестве каучука. Корреляционный анализ показал очень слабую связь между количеством пигментов в листьях и процентным содержанием каучука в корнях во всех трех группах. Таким образом, показано, что количество фотосинтетических пигментов не влияет на процессы накопления каучука в корнях.</p>	<p>К.К. Богуспаев. Изучение содержания хлорофилла и каротиноидов в листьях тау-сагыза (<i>Scorzonera tau-saghyz</i> Lipsch et Bosse) из различных эколого-географических мест обитания в горах Каратау для определения связи с накоплением каучука в корнях. Вестник Серия экологическая. №2 (71). 103-111. DOI: 10.26577/EJE.2022.v71.i2.010</p>
38	Earthworms: biology, scientific	ISBN: 978-601-7667-58-0	The book "Earthworms: biology, scientific and practical basis of vermiculture" is the most comprehensive practical guide on	I.N. Titov, K.K. Boguspayev, R.K. Sinha, S. Singh, B.M.

	<p>and practical basis of vermotechnology</p>		<p>earthworms and vermiculture technology and has been written to reflect the latest scientific and practical developments in the field. the book is divided into 12 chapters. Each chapter provides an analytical overview of current scientific data and achievements and priorities for future research. The book contains scientific and practical information about the place and role of the earthworms in the global ecosystems, different types of earthworm species present in soil their anatomy, biology, physiology and biochemistry.</p> <p>All known technologies of vermicomposting of different organic wastes using different types and species of waste eater earthworms in the world are described in detail. The criteria for determining the quality and standards of vermicompost as a nutritive organic fertilizer giving high productivity of nutritive organic foods are described, and the results of modern physio-chemical, biological and molecular biological research methods to determine the quality and maturity of vermicompost are also analyzed. Methods of obtaining and using various earthworms &amp; vermicompost-based biological compounds such as vermiwash (body fluid of earth worms) and vermicompost tea (fermented solution of vermicompost) for their use as safe biopesticides to protect the crops from pests and diseases have also been described. .</p> <p>The benefits &amp; advantages of the new and innovative vermifiltration technology for wastewater treatment by earthworms and reuse of the vermifiltered clean (disinfected and detoxified) nutritive water (rich in NKP) in farm and garden irrigation saving huge groundwater of earth which are fast depleting are also described. The book also inform that earthworms are a unique and fast multiplying organism for producing large amount of complete animal proteins rich in all essential amino acids tor use as vermi-meals cattle, poultry &amp; fish farming and also as an anti-pathogenic and biologically active substances for use as vermi-medicines in pharmaceutical industries.</p> <p>The book will inspire the students, teachers and researchers in earthworms &amp; vermiculture for increasing their scientific knowledge. It will also also inspire inspire the the farmers (the</p>	<p>Djumakhanov. Earthworms: biology, scientific and practical basis of vermotechnology. "Asyl kitap" publishing house. 2022. ISBN: 978-601-7667-58-0</p>
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			feeders of nations) and the gardeners and the producers of organic fertilizers to promote organic farming in world for production of chemical-free, nutritive and health protective foods for the global human society.	
39	Evaluation of the impact of varied biochars produced from <i>M. x giganteus</i> waste and application rate on the soil properties and physiological parameters of <i>Spinacia oleracea</i> L.	<a href="https://doi.org/10.1016/j.eti.2022.102898">https://doi.org/10.1016/j.eti.2022.102898</a>	The use of <i>M. x giganteus</i> in phytoremediation requires treatment of the contaminated biomass, which can be done by pyrolysis to produce biochar. Due to its potentially detrimental properties, the application of biochar in soil remediation must first be evaluated on a test plant to infer how the growth process was affected by the impact on soil parameters. The main goal of the current research was to investigate the effects of waste-derived Miscanthus biochars (from contaminated rhizomes (B1) and aboveground biomass (B2)) on soil properties and evaluate the impact of biochar doses and properties on <i>Spinacia oleracea</i> L. growth. It was revealed that incorporation of B1 at a dose of 5% and B2 at doses of 1, 3, and 5% increased soil organic carbon, pH, K (at 3 and 5%), and P2O5 (at 5% B2). Cultivation of <i>S. oleracea</i> reduced organic carbon, soil pH as a function of biochar dosage, and K, P2O5, NH4, and NO3 content in all treatments tested. The highest biomass yield was recorded at 3% B2. The photosynthetic parameters indicated that the doses of 3 and 5% B2 led to dissociation of light-harvesting complexes. Increasing the biochar dose did not necessarily increase yield or improve photosynthetic parameters. <i>S. oleracea</i> adapted to the initial stress by incorporating biochar and managed to establish a balance between nutrients, water supply, and light. It is recommended that the effects of biochar on the development of the target crop be evaluated through preliminary trials before biochar is applied at field scale.	Kononchuk, O.; Pidlisnyuk, V.; Mamirova, A.; Khomenchuk, V.; Herts, A.; Grycová, B.; Klemencová, K.; Leštinský, P.; Shapoval, P. Evaluation of the Impact of Varied Biochars Produced from <i>M. x giganteus</i> Waste and Application Rate on the Soil Properties and Physiological Parameters of <i>Spinacia oleracea</i> L. Environmental Technology & Innovation 2022, 28, 102898, <a href="https://doi.org/10.1016/j.eti.2022.102898">https://doi.org/10.1016/j.eti.2022.102898</a>
40	Phytoremediation of Soil Contaminated by Organochlorine Pesticides and Toxic Trace Elements: Prospects and Limitations of <i>Paulownia tomentosa</i>	<a href="https://doi.org/10.3390/toxics10080465">https://doi.org/10.3390/toxics10080465</a>	<i>Paulownia tomentosa</i> (Thunb.) Steud is a drought-resistant, low-maintenance and fastgrowing energy crop that can withstand a wide range of climatic conditions, provides a high biomass yield (approximately 50 t DM ha <sup>-1</sup> yr <sup>-1</sup> ), and develops successfully in contaminated sites. In Kazakhstan, there are many historically contaminated sites polluted by a mixture of xenobiotics of organic and inorganic origin that need to be revitalised. Pilot-scale research evaluated the potential of <i>P. tomentosa</i> for the phytoremediation of soils historically contaminated with	Mamirova, A.; Baubekova, A.; Pidlisnyuk, V.; Shadenova, E.; Djansugurova, L.; Jurjanz, S. Phytoremediation of Soil Contaminated by Organochlorine Pesticides and Toxic Trace Elements: Prospects and Limitations of <i>Paulownia tomentosa</i> . Toxics

			<p>organochlorine pesticides (OCPs) and toxic trace elements (TTEs) to minimise their impact on the environment. Targeted soils from the obsolete pesticide stockpiles located in three villages of Talgar district, Almaty region, Kazakhstan, i.e., Amangeldy (soil A), Beskainar (soil B), and Kyzylkairat (soil K), were subjected to research. Twenty OCPs and eight TTEs (As, Cr, Co, Ni, Cu, Zn, Cd, and Pb) were detected in the soils. The phytoremediation potential of <i>P. tomentosa</i> was investigated for OCPs whose concentrations in the soils were significantly different (aldrin, endosulfans, endrin aldehyde, HCB, heptachlor, hexabromobenzene, keltan, methoxychlor, and -HCH) and for TTEs (Cu, Zn, and Cd) whose concentrations exceeded maximum permissible concentrations. Bioconcentration (BCF) and translocation (TLF) factors were used as indicators of the phytoremediation process. It was ensured that the uptake and translocation of contaminants by <i>P. tomentosa</i> was highly variable and depended on their properties and concentrations in soil. Besides the ability to bioconcentrate Cr, Ni, and Cu, <i>P. tomentosa</i> demonstrated very encouraging results in the accumulation of endosulfans, keltan, and methoxychlor and the phytoextraction of -HCH (TLFs of 1.9–9.9) and HCB (BCFs of 197–571). The results of the pilot trials support the need to further investigate the potential of <i>P. tomentosa</i> for phytoremediation on a field scale.</p>	<p>2022, 10, 465,  <a href="https://doi.org/10.3390/toxics10080465">https://doi.org/10.3390/toxics10080465</a></p>
41	<p>The Role of Plant Growth Regulators in <i>Miscanthus x giganteus</i> Growth on Trace Elements-Contaminated Soils</p>	<p><a href="https://doi.org/10.3390/agronomy12122999">https://doi.org/10.3390/agronomy12122999</a></p>	<p>Soil contamination with trace elements (TEs) is a pressing problem limiting the cultivation of agricultural crops; however, the non-food energy crop <i>Miscanthus x giganteus</i> (Mxg) can be grown on such soil. The effect of a new plant growth regulator (PGR), Kamethur, and conventional Charkor was studied when Mxg was cultivated in TE-contaminated soils from Všebořice and Chomutov, in the Northern Czech Republic. Kamethur was beneficial for achieving a higher leaves and stem biomass (by 57.1 and 126%, respectively) in the more contaminated Všebořice soil, while Charkor increased only the leaves biomass (49.5%). Analysis of the comprehensive bio-concentration index showed that Charkor decreased stem accumulation of elements essential for plant development (EEs), as well as the potentially toxic (PTEs) elements, by 33.3 and 11.4%, respectively. Kamethur decreased stem accumulation of EEs by 11.4% and</p>	<p>Pidlisnyuk, V.; Mamirova, A.; Newton, R.A.; Stefanovska, T.; Zhukov, O.; Tsygankova, V.; Shapoval, P. The Role of Plant Growth Regulators in <i>Miscanthus x giganteus</i> Growth on Trace Elements-Contaminated Soils. <i>Agronomy</i> 2022, 12, 2999, <a href="https://doi.org/10.3390/agronomy12122999">https://doi.org/10.3390/agronomy12122999</a></p>

			increased the accumulation of PTEs by 23.3%. Statistical evaluation of the current results and literature data illustrated the ability of Charkor to reduce the uptake of PTEs, which is critical for converting clean biomass to bioproducts. Further research should confirm the influence of PGRs on the bioparameters and phytoremediation processes of M $\times$ g at the field plantation level.	
42	<i>Miscanthus x giganteus</i> Phytoremediation of Soil Contaminated with Trace Elements as Influenced by the Presence of Plant Growth-Promoting Bacteria	<a href="https://doi.org/10.3390/agronomy12040771">https://doi.org/10.3390/agronomy12040771</a>	The phytoremediation of industrial crops is becoming popular for the revitalization of land contaminated by trace elements (TEs). This approach combines biomass production with the improvement of soil health. To implement phytoremediation and derive sufficient dry biomass, crop production must be adequately supported by agricultural practices, including the application of bioinoculants. The current study aims to test the influence of several plant growth-promoting bacteria (PGPB), isolated from TEs-contaminated soil—i.e., <i>Stenotrophomonas maltophilia</i> KP-13, <i>Bacillus altitudinis</i> KP-14, and <i>Pseudomonas fluorescens</i> KP-16 and their consortia on the phytoremediation of the industrial crop <i>M. x giganteus</i> cultivated in the same TEs-contaminated soil. Contrary to expectations, the effects of PGPB on the biomass harvest were low. The most significant increase was detected in leaf biomass treated with a consortium of tested PGPBs. More significant effects were detected in the uptake of individual TEs. The phytoparameters of translocation factor, comprehensive bioconcentration index and uptake index were used to characterize the behavior of the TEs; Cr; Mn; Ni; Cu; Zn; Sr; V; and Pb in the presence of isolates. Plants treated with PGPB strains accumulated minimal concentrations of Cu and Pb in their aboveground biomass, while a tendency for Zn accumulation in the leaves and stems, and Sr accumulation in the leaves was observed. The obtained results reveal the combinations of isolates that lead to the minimal uptake of TEs into the stems and the simultaneous increase in DW. This study provides more insight into the leading factors of phytoremediation supported by PGPB and can be helpful when <i>M. x giganteus</i> is grown on TEs-contaminated soils of different origins.	Pidlisnyuk, V., Mamirova, A., Pranaw, K., Stadnik, V., Kuráň, P., Trögl, J., & Shapoval, P. <i>Miscanthus x giganteus</i> Phytoremediation of Soil Contaminated with Trace Elements as Influenced by the Presence of Plant Growth-Promoting Bacteria. <i>Agronomy</i> 2022, 12(4), 771. <a href="https://doi.org/10.3390/agronomy12040771">https://doi.org/10.3390/agronomy12040771</a>
43	The Short-Term Effects of Amendments on Nematode	<a href="https://doi.org/10.3390/agronomy12092063">https://doi.org/10.3390/agronomy12092063</a>	The short-term effects of soil amendments on the structure, diversity and function of a nematode community of <i>Miscanthus x giganteus</i> was investigated. Crop was cultivated on marginal, nutrient-poor land amended with biochar in single and double	Stefanovska, T.; Skwiercz, A.; Pidlisnyuk, V.; Zhukov, O.; Kozacki, D.; Mamirova, A.; Newton, R.A.; Ust'ak, S. The

	<p>Communities and Diversity Patterns under the Cultivation of <i>Miscanthus x giganteus</i> on Marginal Land.</p>		<p>doses (BD1 and BD2), biogas digestate (D), sewage sludge (SS), and hemicellulose waste (HW). Sampling was done after planting, in the middle and end of vegetation; morphology-based approach was used. 28 nematode taxa were identified, including 5 bacterivores genera, 4 fungivores genera, 5 herbivores genera (11 species), 2 omnivores genera, 5 predators genera. The general linear models, correspondence analysis and clustering were applied for evaluation. The total abundance of nematode taxa Filenchus, Dorylaimus, Cephalobus, Panagrolaimus, Aphelenchus, and Ditylenchus was depended on the sampling time and amendments. The incorporation of amendments affected nematode food web and resulted in suppression of plant-parasitic nematodes (PPNs). It was revealed that community structure was more mature for SS, less stable for D and had inconclusive effects for BD1, BD2, and HW. Using amendments ensured pest control benefits which is important given concern that PPNS can inflict crop damage during increased cultivation of M x g. Further research is needed to examine amendments which can minimise PPNS without reducing populations of nitrogen-fixing bacterivores and fungivores.</p>	<p>Short-Term Effects of Amendments on Nematode Communities and Diversity Patterns under the Cultivation of <i>Miscanthus x giganteus</i> on Marginal Land. <i>Agronomy</i> 2022, 12, 2063, <a href="https://doi.org/10.3390/agronomy12092063">https://doi.org/10.3390/agronomy12092063</a></p>
44	<p>Influence of Osmotic, Salt, and Combined Stress on Morphophysiological Parameters of <i>Chenopodium quinoa</i> Photosynthetic Organs</p>	<p><a href="https://doi.org/10.3390/agriculture13010001">https://doi.org/10.3390/agriculture13010001</a></p>	<p><i>Chenopodium quinoa</i> Willd. is an annual facultative halophytic pseudocereal widely studied for its physiology and grain yield owing to its great tolerance to unfavorable growing conditions. However, the morphophysiological and anatomical characteristics of plants' photosynthetic organs under various and combined abiotic stresses during the early stages of development have not been thoroughly studied. Therefore, the current study compared the influence of osmotic, salt, and combined stress at different intensities on the morphology and anatomy of photosynthetic organs in young quinoa plants. The main findings demonstrate that salt stress at an intensity between 100 and 200 mM NaCl is not critical for the growth of young quinoa plants and that the young plants can withstand salt stress at an intensity of 300 mM NaCl. However, it can be concluded that some adaptation mechanisms of the plants were already violated at a salt stress intensity of 200 mM NaCl, while significant changes in the water balance of the plants were observed at an intensity of 300 mM NaCl, possibly caused by damage to the cell structures.</p>	<p>Terletsкая, N. V., Erbay, M., Zorbekova, A. N., Prokofieva, M. Y., Saidova, L. T., &amp; Mamirova, A. Influence of Osmotic, Salt, and Combined Stress on Morphophysiological Parameters of <i>Chenopodium quinoa</i> Photosynthetic Organs. <i>Agriculture</i> 2023, 13(1), Article 1. <a href="https://doi.org/10.3390/agriculture13010001">https://doi.org/10.3390/agriculture13010001</a></p>



45	Rhizosphere Microorganisms: Increasing Phytotechnology Productivity and Efficiency – a Review	<a href="https://doi.org/10.32014/2518-1483_2022_3_34-58">https://doi.org/10.32014/2518-1483_2022_3_34-58</a>	The review contains information on rhizobacteria with plant growth promoting properties (PGPR), on plant mechanisms of bacterial defense against heavy metal pollution and on stimulation of plant growth by nitrogen fixation, phosphorus dissolution, siderophores, phytohormones and ACC deaminase enzyme synthesis. PGPRs are classified according to their functionality, the degree of proximity to the root and the closeness of their association with the plant, and the site of bacterial colonization, and information is provided on the taxonomic affiliation of PGPRs. Issues of phytoremediation of soils contaminated with heavy metals and methods to improve process efficiency using rhizospheric microorganism inoculants are highlighted in the review, as phytoremediation is an economically viable and environmentally friendly technology. The review considers the role of association of endophytic and rhizospheric PGPBs with a plant in enhancing the efficiency of phytoaccumulation and phytostabilisation of soils contaminated with toxic metals and plant productivity.	Nurzhanova, A.; Muratova, A.Yu.; Berzhanova, R.; Pidlisnyuk, V.; Nurmagambetova, A.; Mamirova, A. Rhizosphere Microorganisms: Increasing Phytotechnology Productivity and Efficiency – a Review. Scientific journal «Reports of NAS RK» 2022, 34–58, <a href="https://doi.org/10.32014/2518-1483_2022_3_34-58">https://doi.org/10.32014/2518-1483_2022_3_34-58</a>
46	Сүт сарысуының микробтық қауымдастығының микробиологиялық көрсеткіштері және таксономиялық құрамын зерттеу.	<a href="https://doi.org/10.26577/eb.2022.v92.i3.04">https://doi.org/10.26577/eb.2022.v92.i3.04</a>	Интерес к биоэтанолю значительно вырос в последние десятилетия не только как к растворителю, антифризу или сырью для производства широкого спектра различных органических соединений, но и в некоторой степени как к биотопливу. Биоэтанол имеет следующие преимущества перед бензином: он меньше загрязняет атмосферу, легко разлагается, имеет высокое октановое число и может использоваться для своего производства возобновляемое сырье. Постоянно растущий спрос на биоэтанол требует поиска новых субстратов, более дешевых, чем зерно или картофель. В качестве одного из таких субстратов рекомендуется использовать молочную сыворотку, основным углеводом которой является лактоза. Цель исследования: изучить микробиологические показатели и таксономический состав микробного сообщества молочной сыворотки. В ходе исследования изучены микробиологические показатели и таксономический состав микробного сообщества молочной сыворотки ТОО «Сырзавод «Мерке», ТОО «Амиран» (сыворотка), ТОО «Стелла Альпина» (сырная сыворотка). Из образцов сыворотки выделено 3 штамма	А.А. Жұбанова, Г.Ж. Абдиева, П.С. Уалиева, А.М. Мәлік * Том 92 № 3 (2022): Вестник КазНУ, серия биологическая, С. 36-54. <a href="https://doi.org/10.26577/eb.2022.v92.i3.04">https://doi.org/10.26577/eb.2022.v92.i3.04</a>

			дрожжей и 1 штамм молочнокислых бактерий. В результате предвидовой идентификации культур дрожжей и молочнокислых бактерий штаммы ГБ и ГТ идентифицированы как <i>Kluyveromyces marxianus</i> , штамм M1 - <i>Lactococcus lactis</i> , A1 - <i>Candida inconspicua</i> .	
47	Исследование микробного разнообразие молочной сыворотки и идентификация выделенных чистых культур.	<a href="https://doi.org/10.54596/2309-6977-2022-3-68-80">https://doi.org/10.54596/2309-6977-2022-3-68-80</a>	Для молочной промышленности в XXI веке экологические проблемы приобретают особую актуальность в связи с истощением ресурсов и необходимостью сохранения окружающей среды. Как в отечественной, так и в мировой практике не решена проблема использования молочной сыворотки, обладающей высокой пищевой и биологической ценностью, и в наибольшей степени загрязняющей сточные воды. В последние годы активно и целенаправленно формируется принципиально новое направление промышленной переработки молочной сыворотки - получение производных компонентов, являющихся целевыми продуктами, в частности, спирта. В связи с вышеизложенным важно изучение микробиологических показателей молочной сыворотки и выделение перспективных культур. Цель исследования: изучение микробного разнообразие молочной сыворотки и идентификация выделенных чистых культур. В ходе исследования изучены микробиологические показатели и таксономический состав микробного сообщества молочной сыворотки ТОО «Сырзавод «Мерке», ТОО «Амиран» (сыворотка), ТОО «Стелла Альпина» (сырная сыворотка). Изучены физико-химические и органолептические показатели молочной сыворотки. Из образцов сыворотки выделено 1 штамм дрожжей и 1 штамм молочнокислых бактерий. Изучена морфолого-культуральные свойства выделенных дрожжей и молочнокислых бактерий, в результате штаммы <i>Lactococcus lactis</i> M1, <i>Candida inconspicua</i> A1 были идентифицированы до вида.	Шукурбек М.Ж*, Уалиева П. С., Абдиева Г. Ж., Мәлік А. М., Таңатар А.Е. Вестник СКУ имени М. Козыбаева. № 3 (55). 2022. С. 68-80. <a href="https://doi.org/10.54596/2309-6977-2022-3-68-80">https://doi.org/10.54596/2309-6977-2022-3-68-80</a>
48	Effect of the humic drug "EldORost" on the yeld of potatoes and vegetables /	Book of Abstracts of the Seventh International Conference of the CIS IHSS on humic	Использование экологически безопасных продуктов природного происхождения, а именно гуминовых удобрений, сегодня является мировым трендом, т.к. влияет на рост и развитие растений, на качество сельскохозяйственной продукции и плодородие почвы.	Zhil kibayev O., Aitbayev T., Perminova I., Popov A., Shoinbekova S. Effect of the humic drug "EldORost" on the yeld of potatoes and vegetables



		<p>innovative technologies "Humic substances and technologies for resilience" (HIT-2022), Sailing club "Vodnik", Moscow, November 18–21, 2022. – P.110  <a href="https://doi.org/10.36291/HIT.2022.091">https://doi.org/10.36291/HIT.2022.091</a>  Сборник тезисов: <a href="https://doi.org/10.36291/HIT.2022.091">https://doi.org/10.36291/HIT.2022.091</a></p>	<p>Описано влияние «ЭлдОРоста» ( безбалластный препарат гуминовой природы нового поколения с высокой степенью гумификации). Продукт содержит легкорастворимые физиологически активные соли гуминовых кислот. и фульвокислоты (гуматы и фульваты), комплекс аминокислот, макро- и микроэлементов в форме, доступной для растений.  Действует как фитогормоны: оптимальная концентрация препарата составляет 0,0001%.  «ЭлдОРост» положительно влияет на урожайность картофеля и основных овощных культур, значительно повышая продуктивность их урожая по сравнению с контролем. Варианты полевого опыта, дополнительная урожайность: капуста - 31,3%, огурцы - 30,2%, томаты - 34,7%, свекла столовая - 28,7%, морковь - 33,3% и картофель - 36,8%.</p>	<p>// Book of Abstracts of the Seventh International Conference of the CIS IHSS on humic innovative technologies "Humic substances and technologies for resilience" (HIT-2022), Sailing club "Vodnik", Moscow, November 18–21, 2022. – P.110</p> <p>участие ППС в Международных научных конференциях, сборники которых индексировались в базах данных Thomson Reuters или Scopus; - Scopus</p>
49	Biochar for Improving Soil Biological Properties and Mitigating Salt Stress in Plants on Salt-affected Soils	<a href="https://doi.org/10.1080/00103624.2021.1993884">10.1080/00103624.2021.1993884</a>	<p>Biochar is a solid product obtained by heating of biomass or organic waste in the total or partial absence of oxygen and is applied to improve soil properties, or considered a means of carbon sequestration. Several positive effects of biochar on soil chemical, physical, and biological properties have already been demonstrated. Biochar amendment has also been repeatedly discussed as an effective means to restore saline lands and increase plant tolerance to salt stress. Especially, improved soil cation exchange capacity, water holding capacity, soil nutrient retention, and increased soil enzyme activities and diversity of microbial communities, were reported. However, the underlying mechanisms of such beneficial effects provided by biochar amendment of soils are highly complex. Therefore, more in-depth studies are needed to understand biochar interactions with soil organisms under extreme environments, which will help achieve maximum benefits of biochar under saline soil conditions.</p>	<p>Egamberdieva D., Alaylar B., Kistaubayeva A., Wirth S., Bellingrath-Kimura S.D.</p> <p>Biochar for Improving Soil Biological Properties and Mitigating Salt Stress in Plants on Salt-affected Soils</p> <p>Communications in Soil Science and Plant Analysis, 2022, 53(2), стр. 140–152.</p> <p>DOI:<a href="https://doi.org/10.1080/00103624.2021.1993884">10.1080/00103624.2021.1993884</a></p>
50	The Effect of Non-Thermal Atmospheric Pressure Plasma	<a href="https://doi.org/10.1109/TPS.2022.3145831">10.1109/TPS.2022.3145831</a>	<p>This contribution presents the results of a study of the germination rate and growth parameters of wheat seeds after atmospheric pressure surface coplanar dielectric barrier discharge (DBD) plasma treatment. The germination rate and</p>	<p>Ussenov Y.A., Akildinova A., Kuanbaevich B.A., Kistaubayeva A., Daniyarov T., Ramazanov T.</p>

	Treatment of Wheat Seeds on Germination Parameters and $\alpha$ -Amylase Enzyme Activity		biometric parameters such as the root, shoot length, mass of the seedlings, and the $\alpha$ -amylase enzyme activity were studied at different plasma exposure time. The seed coat surface wettability and morphology were determined by apparent contact angle measurement and scanning electron microscope (SEM) analysis. Seed surface disinfection and the presence of filamentous fungi have also been investigated at different discharge parameters. It is shown that the optimal plasma treatment duration for increasing the growth parameters and enhancing the enzymatic activity is 5-15 s. It was found that the longer plasma exposure requires complete sterilization of the seed surface from pathogens, compared to the optimal treatment time for high germination. Based on the obtained results, the possible mechanisms of the positive effect of plasma treatment on the enhanced germination of wheat seeds are discussed.	The Effect of Non-Thermal Atmospheric Pressure Plasma Treatment of Wheat Seeds on Germination Parameters and $\alpha$ -Amylase Enzyme Activity  IEEE Transactions on Plasma Science, 2022, 50(2), стр. 330–340.  DOI: <a href="https://doi.org/10.1109/TPS.2022.3145831">10.1109/TPS.2022.3145831</a>
51	Advanced “Green” Prebiotic Composite of Bacterial Cellulose/Pullulan Based on Synthetic Biology-Powered Microbial Coculture Strategy	<a href="https://doi.org/10.3390/polym14153224">10.3390/polym14153224</a>	Bacterial cellulose (BC) is a biopolymer produced by different microorganisms, but in biotechnological practice, <i>Komagataeibacter xylinus</i> is used. The micro- and nanofibrillar structure of BC, which forms many different-sized pores, creates prerequisites for the introduction of other polymers into it, including those synthesized by other microorganisms. The study aims to develop a cocultivation system of BC and prebiotic producers to obtain BC-based composite material with prebiotic activity. In this study, pullulan (PUL) was found to stimulate the growth of the probiotic strain <i>Lactobacillus rhamnosus</i> GG better than the other microbial polysaccharides gellan and xanthan. BC/PUL biocomposite with prebiotic properties was obtained by cocultivation of <i>Komagataeibacter xylinus</i> and <i>Aureobasidium pullulans</i> , BC and PUL producers respectively, on molasses medium. The inclusion of PUL in BC is proved gravimetrically by scanning electron microscopy and by Fourier transformed infrared spectroscopy. Cocultivation demonstrated a composite effect on the aggregation and binding of BC fibers, which led to a significant improvement in mechanical properties. The developed approach for “grafting” of prebiotic activity on BC allows preparation of environmentally friendly composites of better quality.	Zhantlessova S., Savitskaya I., Kistaubayeva A., Ignatova L., Talipova A., Pogrebnyak, A., Digel, I.  Advanced “Green” Prebiotic Composite of Bacterial Cellulose/Pullulan Based on Synthetic Biology-Powered Microbial Coculture Strategy  Polymers, 2022, 14(15), 3224  DOI: <a href="https://doi.org/10.3390/polym14153224">10.3390/polym14153224</a>

52	Plant Probiotic Endophytic Pseudomonas flavescens D5 Strain for Protection of Barley Plants from Salt Stress		<p>Soil salinity has become a global issue that is directly related to land degradation and results in many changes in climate, ecosystem services, and biodiversity. The present study focuses on the investigation of beneficial properties of a plant probiotic bacterial strain as an eco-friendly and sustainable approach to promote crop growth in saline soil. The endophytic halotolerant strain <i>Pseudomonas flavescens</i> D5 isolated from common chicory (<i>Cichorium intybus</i> L.) was able to grow on a medium containing 15% NaCl; produced indole-3-acetic acid (45.2 <math>\mu\text{g mL}^{-1}</math>) and polyhydroxyalkanoate (1.72 <math>\text{g L}^{-1}</math>); and had amylolytic, cellulolytic, and proteolytic activities. Polyhydroxyalkanoate had a pronounced antifungal activity against <i>Fusarium graminearum</i>, <i>F. solani</i>, <i>F. oxysporum</i>, and <i>Alternaria alternata</i>. Under salt stress conditions, inoculation with <i>Ps. flavescens</i> D5 increased the shoot biomass of barley plants by 8–30%, root biomass by 7–20%, chlorophyll a by 18–52%, and chlorophyll b by 7–15%. The content of proline decreased by 1.5–1.8 times. An increase in the activity of antioxidant enzymes (catalase, guaiacol peroxidase, and ascorbate peroxidase) was determined. In inoculated plants growing in saline soil, the content of <math>\text{Na}^+</math> ions was lower by up to 54.8% compared to control. This strain is promising for stimulating plant growth and protecting them from diseases and other adverse environmental factors, including salt stress.</p>	<p>Ignatova L., Usmanova, A., Brazhnikova Y., Omirbekova A., Egamberdieva D., Mukasheva T., Kistaubayeva A., Savitskaya I., Karpenyuk T., Goncharova A.</p> <p>Plant Probiotic Endophytic <i>Pseudomonas flavescens</i> D5 Strain for Protection of Barley Plants from Salt Stress</p> <p>Sustainability (Switzerland), 2022, 14(23), 15881</p> <p>DOI: 10.3390/su142315881</p>
53	Advanced “Green” Prebiotic Composite of Bacterial Cellulose/Pullulan Based on Synthetic Biology-Powered Microbial Coculture Strategy	<a href="https://doi.org/10.3390/polym14153224">10.3390/polym14153224</a>	<p>Bacterial cellulose (BC) is a biopolymer produced by different microorganisms, but in biotechnological practice, <i>Komagataeibacter xylinus</i> is used. The micro- and nanofibrillar structure of BC, which forms many different-sized pores, creates prerequisites for the introduction of other polymers into it, including those synthesized by other microorganisms. The study aims to develop a cocultivation system of BC and prebiotic producers to obtain BC-based composite material with prebiotic activity. In this study, pullulan (PUL) was found to stimulate the growth of the probiotic strain <i>Lactobacillus rhamnosus</i> GG better than the other microbial polysaccharides gellan and xanthan. BC/PUL biocomposite with prebiotic properties was obtained by cocultivation of <i>Komagataeibacter xylinus</i> and <i>Aureobasidium pullulans</i>, BC and PUL producers respectively, on molasses medium. The inclusion of PUL in BC is proved gravimetrically by</p>	<p>Zhantlessova S., Savitskaya I., Kistaubayeva A., Ignatova L., Talipova A., Pogrebnyak, A., Digel, I.</p> <p>Advanced “Green” Prebiotic Composite of Bacterial Cellulose/Pullulan Based on Synthetic Biology-Powered Microbial Coculture Strategy</p> <p>Polymers, 2022, 14(15), 3224</p>

			scanning electron microscopy and by Fourier transformed infrared spectroscopy. Cocultivation demonstrated a composite effect on the aggregation and binding of BC fibers, which led to a significant improvement in mechanical properties. The developed approach for “grafting” of prebiotic activity on BC allows preparation of environmentally friendly composites of better quality.	DOI: <a href="https://doi.org/10.3390/polym14153224">10.3390/polym14153224</a>
54	Plant Probiotic Endophytic Pseudomonas flavescens D5 Strain for Protection of Barley Plants from Salt Stress		Soil salinity has become a global issue that is directly related to land degradation and results in many changes in climate, ecosystem services, and biodiversity. The present study focuses on the investigation of beneficial properties of a plant probiotic bacterial strain as an eco-friendly and sustainable approach to promote crop growth in saline soil. The endophytic halotolerant strain Pseudomonas flavescens D5 isolated from common chicory ( <i>Cichorium intybus</i> L.) was able to grow on a medium containing 15% NaCl; produced indole-3-acetic acid (45.2 µg mL <sup>-1</sup> ) and polyhydroxyalkanoate (1.72 g L <sup>-1</sup> ); and had amylolytic, cellulolytic, and proteolytic activities. Polyhydroxyalkanoate had a pronounced antifungal activity against <i>Fusarium graminearum</i> , <i>F. solani</i> , <i>F. oxysporum</i> , and <i>Alternaria alternata</i> . Under salt stress conditions, inoculation with <i>Ps. flavescens</i> D5 increased the shoot biomass of barley plants by 8–30%, root biomass by 7–20%, chlorophyll a by 18–52%, and chlorophyll b by 7–15%. The content of proline decreased by 1.5–1.8 times. An increase in the activity of antioxidant enzymes (catalase, guaiacol peroxidase, and ascorbate peroxidase) was determined. In inoculated plants growing in saline soil, the content of Na <sup>+</sup> ions was lower by up to 54.8% compared to control. This strain is promising for stimulating plant growth and protecting them from diseases and other adverse environmental factors, including salt stress.	Ignatova L., Usmanova, A., Brazhnikova Y., Omirbekova A., Egamberdieva D., Mukasheva T., Kistaubayeva A., Savitskaya I., Karpenyuk T., Goncharova A.  Plant Probiotic Endophytic Pseudomonas flavescens D5 Strain for Protection of Barley Plants from Salt Stress  Sustainability (Switzerland), 2022, 14(23), 15881  DOI: 10.3390/su142315881
55	Advanced “Green” Prebiotic Composite of Bacterial Cellulose/Pullulan Based on Synthetic Biology-Powered Microbial Coculture Strategy	<a href="https://doi.org/10.3390/polym14153224">10.3390/polym14153224</a>	Bacterial cellulose (BC) is a biopolymer produced by different microorganisms, but in biotechnological practice, <i>Komagataeibacter xylinus</i> is used. The micro- and nanofibrillar structure of BC, which forms many different-sized pores, creates prerequisites for the introduction of other polymers into it, including those synthesized by other microorganisms. The study aims to develop a cocultivation system of BC and prebiotic producers to obtain BC-based composite material with prebiotic	Zhantlessova S., Savitskaya I., Kistaubayeva A., Ignatova L., Talipova A., Pogrebnjak, A., Digel, I.  Advanced “Green” Prebiotic Composite of Bacterial Cellulose/Pullulan Based on

			<p>activity. In this study, pullulan (PUL) was found to stimulate the growth of the probiotic strain <i>Lactobacillus rhamnosus</i> GG better than the other microbial polysaccharides gellan and xanthan. BC/PUL biocomposite with prebiotic properties was obtained by cocultivation of <i>Komagataeibacter xylinus</i> and <i>Aureobasidium pullulans</i>, BC and PUL producers respectively, on molasses medium. The inclusion of PUL in BC is proved gravimetrically by scanning electron microscopy and by Fourier transformed infrared spectroscopy. Cocultivation demonstrated a composite effect on the aggregation and binding of BC fibers, which led to a significant improvement in mechanical properties. The developed approach for “grafting” of prebiotic activity on BC allows preparation of environmentally friendly composites of better quality.</p>	<p>Synthetic Biology-Powered Microbial Coculture Strategy</p> <p>Polymers, 2022, 14(15), 3224</p> <p>DOI:<a href="https://doi.org/10.3390/polym14153224">10.3390/polym14153224</a></p>
56	<p>Coding Complete Genome Sequence of the SARS-CoV-2 Virus Strain, Variant B.1.1, Sampled from Kazakhstan</p>	<p>Microbiology Resource Announcements</p> <p>DOI 10.1128/mra.01114-22</p>	<p>This article describes the results of sequencing and analysis of the entire genome of the SARS-CoV-2 virus sampled in Kazakhstan in 2021. The whole-genome sequence of the strain was 29,751 bp. According to the results of phylogenetic analysis (according to the Pangolin COVID-19 database), the SARS-CoV-2/human/KAZ/B1.1/2021 strain studied here was assigned to variant B.1.1.</p>	<p>Microbiology Resource Announcements</p> <p>Burashev Y.;Usserbayev, Bekbolata;Kutumbetov, Lespeka;Abduraimov, Yergalia;Kassenov, Markhabata;Kerimbayev, Aslana;Myrzakhmetova, Balzhana;Melisbek, Aibarysa;Shirinbekov, Meirzhana;Khaidarov, Sakenb;Tulman, Edan R.c</p>
57	<p>Evidence for flock transmission of individual subtypes and strains of avian influenza viruses: A monitoring study of wild birds in Kazakhstan</p>	<p>DOI 10.1016/j.virusres.2022.198898</p>	<p>An active surveillance study of avian influenza viruses (AIVs) in wild birds was carried out in Kazakhstan in 2018–2019. In total, 866 samples were collected from wild birds and analyzed for influenza viruses using molecular and virological tests. Genome segments of Asian, European, and Australian lineages were detected in 25 (4.6%) out of 541 waterfowl samples positive for subtype H3N8, and in two (0.6%) out of 325 H3N8 positive samples from terrestrial birds. No highly pathogenic avian influenza virus (AIV) was detected. The results indicated transmission of closely related strains or identical subtypes of AIVs by a flock-unit of migratory birds or annual cyclical pattern of subtype dominance. The simultaneous circulation of genome segments of the Asian, European and Australian genetic</p>	<p><a href="#">Sultankulova, K.T.</a>, <a href="#">Dzhekebekov, K.K.</a>, <a href="#">Orynbayev, M.B.</a>, ...<a href="#">Zakarya, K.D.</a>, <a href="#">Fereidouni, S.</a> <i>Virus Research</i>, 2022, 320, 198898</p>

			lineages of H3N8 AIVs in wild birds in Kazakhstan indicated the important role of Central Asia as a transmission hub of AI viruses linking the East Asian migratory flyways with European flyways and vice versa	
58	Complete Coding Genome Sequence of an Influenza A/H3N8 Equine Virus Isolated in Kazakhstan in 2007	Microbiology Resource Announcements DOI 10.1128/mra.01147-21	Here, we reported the complete coding sequence of the influenza A/equine/ Otar/3/2007 (H3N8) equine virus, first isolated in Kazakhstan in 2007. The hemagglutinin (HA) sequences of the Kazakhstan isolates appeared to be closely related to viruses isolated in early 2000 in Asia. Phylogenetic analysis characterized the Kazakhstan isolates as a member of the Florida sublineage clade 2 by the HA protein sequence.	Burashev Y.;Orynbayev, Mukhita;Zakarya, Kunsulua;Abduraimov, Yergalia;Kassenov, Markhabat;Strochkov, Vitaliyb;Kozhabergenov, Nurlana;Usserbayev, Bekbolata;Melisbek, Aibarysa;Shirinbekov, Meirzhana;Sypatay, Nuradylb;Sultankulova, Kulyaisan
59	Near-Complete Genome Sequence of a SARS-CoV-2 Variant B.1.1.7 Virus Strain Isolated in Kazakhstan	Microbiology Resource Announcements DOI 10.1128/mra.00619-22	This research describes the genome sequence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) obtained from a patient with symptoms of coronavirus disease 2019 (COVID-19) who was infected in the Republic of Kazakhstan. Strain SARS-CoV-2/ human/KAZ/Britain/2021 consists of 29,815 nucleotides and belongs to lineage B.1.1.7, according to the Pangolin COVID-19 database.	Usserbayev, Bekbolata;Zakarya, Kunsulua;Kutumbetov, Lespeka;Orynbayev, Mukhita;Sultankulova, Kulyaisana;Abduraimov, Yergalia;Myrzakhmetova, Balzhana;Zhugunissov, Kuandyka;Kerimbayev, Aslana;Melisbek, Aibarysa;Shirinbekov, Meirzhana;Khaidarov, Saken Zhunushov, Asankadyrc;Burashev, Yerbol
60	The Prevalence and Genetic Variants of the CCHF Virus Circulating among Ticks in the Southern Regions of Kazakhstan	Pathogens DOI 10.3390/pathogens 11080841	Crimean–Congo hemorrhagic fever (CCHF) disease cases are registered annually in endemic regions of Kazakhstan. To study the prevalence of various Crimean–Congo hemorrhagic fever virus (CCHFV) genotypes, a total of 694 ticks were collected from southern regions of Kazakhstan in 2021. <i>Hyalomma marginatum</i> (n = 323) (46.5%), <i>Hyalomma anatolicum</i> (n = 138) (19.9%), <i>Hyalomma asiaticum</i> (n = 126) (18.2%), <i>Hyalomma scupense</i> (n = 80) (11.5%) and <i>Ixodes ricinus</i> (n = 27) (3.9%) were collected using the standardized flagging technique from	Shynybekova, Gaukhar O. Kozhabergenov, Nurlan S. Mukhami, Nazym N. Mukhami N.N.;Chervyakova, Olga V. Burashev, Yerbol D. Zakarya K.D.; Nakhanov A.K.; Orynbayev, Mukhit B.

			<p>the environment. All the tick samples were analyzed for the presence of CCHFV RNA by RT-PCR. The CCHF-positive samples were found within three Hyalomma asiaticum and one Ixodes ricinus tick sample. For the first time in Kazakhstan, infection of the Ixodes ricinus tick with CCHFV was detected. The results of sequencing and analysis of the S-gene fragment showed that the Asia 1 and Asia 2 CCHF genotypes circulate in the southern regions of Kazakhstan. Viruses isolated in the Zhambyl and Turkestan regions are assigned to the Asia-2 genotype, whereas the virus isolated in the Kyzylorda region to the Asia-1 genotype.</p>	
61	<p>Efficacy and safety of an inactivated whole-virion vaccine against COVID-19, QazCovid-in®, in healthy adults: A multicentre, randomised, single-blind, placebo-controlled phase 3 clinical trial with a 6-month follow-up</p>	<p>eClinicalMedicine DOI 10.1016/j.eclinm.2022.101526</p>	<p>Vaccination remains the primary measure to prevent the spread of the SARS-CoV-2 virus, further necessitating the use of effective licensed vaccines. Methods: From Dec 25, 2020, to July 11, 2021, we conducted a multicenter, randomised, single-blind, placebo-controlled phase 3 efficacy trial of the QazCovid-in® vaccine with a 180-day follow-up period in three clinical centres in Kazakhstan. A total of 3000 eligible participants aged 18 years or older were randomly assigned (4:1) to receive two doses of the vaccine (5 µg each, 21 days apart) or placebo administered intramuscularly. QazCovid-in® is a whole-virion formaldehyde-inactivated anti-COVID-19 vaccine, adjuvanted with aluminium hydroxide. The primary endpoint was the incidence of symptomatic cases of the SARS-CoV-2 infection confirmed by RT-PCR starting from day 14 after the first immunisation. The trial was registered with ClinicalTrials.gov NCT04691908. Findings: The QazCovid-in® vaccine was safe over the 6-month monitoring period after two intramuscular immunisations inducing only local short-lived adverse events. The concomitant diseases of participants did not affect the vaccine safety. Out of 2400 vaccinated participants, 31 were diagnosed with COVID-19; 43 COVID-19 cases were recorded in 600 placebo participants with onset of 14 days after the first dose within the 180-day observation period. Only one severe COVID-19 case was identified in a vaccine recipient with a comorbid chronic heart failure. The protective efficacy of the QazCovid-in® vaccine reached 82.0% (95% CI 71.1–88.5) within the 180-day observation period. Interpretation: Two immunisations with the inactivated QazCovid-in® vaccine</p>	<p>Khairullin B.;Zakarya, Kunsulua;Orynbayev, Mukhita;Abduraimov, Yergalia;Kassenov, Markhabata;Sarsenbayeva, Gulbanua;Sultankulova, Kulyaisana;Chervyakova, Olga;Myrzakhmetova, Balzhana;Nakhanov, Aziza;Nurpeisova, Ainura;Zhugunissov, Kuandyka Assanzhanova, Nurikaa;Nurabayev, Sergazya;Kerimbayev, Aslana;Yershebulov, Zakira;Burashev, Yerbola;Kulmagambetov, Ilyasb;Davlyatshin, Timurc;Sergeeva, Mariad;Buzitskaya, Zhannad;Stukova, Marinad;Kutumbetov, Lespek</p>

			achieved 82.0% (95% CI 71.1–88.5) protective efficacy against COVID-19 within a 180-day follow-up period. Funding: The work was funded by the Science Committee of the Ministry of Education and Science of Kazakhstan within the framework of the Scientific and Technical Program “Development of a vaccine against coronavirus infection COVID-19”. State registration number 0.0927.	
62	Genotoxic and histopathological effects of the Ili River (Kazakhstan) water pollution on the grass carp Ctenopharyngodon idella	doi:10.1080/26395940.2022.2101544	In the present study, genotoxic, histological and hematological effects of water pollution were evaluated in Ctenopharyngodon idella from the Ili river. Water and fish were sampled at three sites. The concentrations of the following heavy metals were measured in the water: Pb, Co, Mg, Cd, Cu, Zn, Fe. Water pollution with metals gradually increased from P1 to P3: in P1, Cu and Fe levels exceeded the maximum permissible concentrations for fish culture, in P2–Pb, Cu, Zn, Fe, and in P3–Pb, Cd, Cu, Zn, Fe. In fish from the Ili river, the highest frequency and severity of DNA damage and liver damage were noted in P3, the lowest in P1. Gill lesions were more pronounced and frequent in fish from P3 compared to grass carp from P2 and P1. Fish from P1 showed a higher frequency of neutrophils and a lower percentage of lymphocytes compared to the control. The results also revealed: genotoxicity measured by comet analysis and liver histology were the most sensitive and showed the magnitude of lesions directly related to the level of water contamination. Gill histology also clearly showed pathological changes caused by pollution, while differential leukocyte count was the least useful indicator, as it showed only minor differences between fish from unpolluted and polluted water. © 2022 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.	Tlenshiyeva A.M., Witeska M. and Shalakhmetova T.M Genotoxic and histopathological effects of the Ili River (Kazakhstan) water pollution on the grass carp Ctenopharyngodon idella // Environmental Pollutants and Bioavailability, 34(1), 297-307. doi:10.1080/26395940.2022.2101544  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85134593092&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85134593092&amp;origin=resultslist&amp;sort=plf-f</a>
63	Waterbird guilds predict environment attributes of saline inland waters at multi-spatial scales	DOI:10.1016/j.scitotenv.2022.158845	Inland saline waters in Central Asia constitute an important part of steppe ecosystems, providing considerable ecological functions and ecosystem services. Here we aim to present a multi-spatial scale analysis of nutrient cycling and transport waterbird guilds, and the environmental attributes of saline-soda aquatic ecosystems in Kazakhstan. The density, biomass, and diversity of waterbird guilds was determined in the case of three nutrient cycling and transport guilds: a) net-importer (IM), b) importer-exporter (IMEX), c) net-exporter (EX), according to the	Boros E., Inelova Z., La'nczos Z., Vegvari Z Waterbird guilds predict environment attributes of saline inland waters at multi-spatial scales // Science of the total Environment, Volume 855, 10 January 2023, 158845. <a href="https://doi.org/10.1016/j.scitotenv.2022.158845">https://doi.org/10.1016/j.scitotenv.2022.158845</a>



			<p>Boros's guild classification method, and for several traditional feeding guilds: carnivorous, herbivorous, invertebrate eater, omnivorous and piscivorous. Our results revealed that waterbird guilds, as predictors represented by the complete waterbird community, are in close relationship with several (N = 12) environmental attributes of inland saline waters through complex trophic linkages of waterbird populations on multi-spatial scales. The density and the biomass of the IM and IMEX guilds are strongly and positively correlated (i) with the productivity metrics of habitats (e.g., CHL, GPP), indicating their trophic position, and (ii) with water depth. We found significant correlations among guild density, biomass, diversity and environmental attributes on multi-spatial scales for IMEX and EX. Our results revealed that IMEX predicts the surrounding environment of aquatic habitats, whereas EX species are substantial environmental predictors of aquatic ecosystems. However, the diversity metric had valid models only with EX. The herbivorous and omnivorous guilds, that feed chiefly on plant materials consist mainly of IMEX and EX duck species, which were positively related to grassland coverage and the shoreline development index. As a methodological result, here we present a novel approach, the guild transport index, which has more robust relationships with environmental attributes than individual guilds, thus it provides a complex evaluation of the nutrient cycling by birds between aquatic and terrestrial environments on multi-spatial scales. © 2022 The Authors</p>	<p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85138464789&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85138464789&amp;origin=resultslist&amp;sort=plf-f</a></p>
64	Assessment of barley crop infestation by leaf and stem phytopathogenic fungi	DOI:10.1080/03235408.2022.2081761	<p>The study aims at selecting ecological approaches to protect barley from phytopathogenic fungi <i>B. sorokiniana</i>, <i>D. graminea</i> and <i>D. Teres</i>. Studies on barley revealed necrotic lesions 0.6–1.4 cm long with a dark brown or greyish centre on stems and a light brown or reddish outer zone on young leaves caused by <i>B. sorokiniana</i> isolates. Symptoms caused by <i>D. teres</i> ranged from necrotic spots to small spots up to 5.5–6 mm in size, but the number of lesions and degree of chlorosis was clearly more expressed on barley leaves than the stem. The detached <i>D. graminea</i> leaf analysis revealed large reddish-brown lesions spreading from the inoculation site to the top and lower part of the barley leaf segments. The practical value of the results obtained is the possibility of using them on agricultural land for</p>	<p>Sardar, A., Sarbaev, A., Tileubayeva, Z., Aytzhanova, M., &amp; Galymbek, K. K.E Assessment of barley crop infestation by leaf and stem phytopathogenic fungi // Archives of Phytopathology and Plant Protection, 55(9), 1102-1116. doi:10.1080/03235408.2022.2081761</p>

			growing cereals in order to minimise the damage caused by plant pathogenic fungi. © 2022 Informa UK Limited, trading as Taylor & Francis Group.	<a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85131574383&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85131574383&amp;origin=resultslist&amp;sort=plf-f</a>
65	Chemical Composition of Flower Volatiles and Seeds Fatty Acids of <i>Rosa iliensis</i> Chrshan, an Endemic Species from Kazakhstan	DOI:10.25135/rnp.271.2105.2083	-linolenic (26.5-28.1%), and oleic (12.0-16.1%) acids were detected as the major constituents. The present study shows that <i>R. iliensis</i> species is rich source of valuable volatiles and fatty acids. $\alpha$ -gurjunene (12.8%), while flowers of P-III (lower reaches of the Ili River) contained any sesquiterpenes. Seven fatty acids were determined in the seeds and unsaturated acids were found to be dominant for studied populations. Linoleic (43.0-51.0%), $\alpha$ -elemene (8.8%), the flowers of P-II (upper reaches of the Ili River) were rich in gAbstract: In the present work, the flower volatiles and seed fatty acids compositions of three populations (P-I, P-II, P-III) of <i>Rosa iliensis</i> were investigated for the first time. <i>R. iliensis</i> is a rare, endangered, narrow-endemic species growing in floodplains of the Ili and Sharyn rivers of Almaty region. The flower volatiles have been investigated with the tandem of MSD-SPME and GC-MS/FID techniques. The seed lipids were extracted from the ripe fruits with microextraction technique. The flower volatiles of <i>R. iliensis</i> three populations were characterized by the abundance of oxygenated monoterpenes with benzaldehyde (13.3-38.7 %) and citronellol (2.6-8.8 %) as the major constituents. There were detected significant differences in floral scents between the populations. The flowers of P-I (from Sharyn River) contain sesquiterpene. © 2021 ACG Publications.	Özek, G., Chidibayeva, A., Ametov, A., Nurmahanova, A., Özek, T. Chemical Composition of Flower Volatiles and Seeds Fatty Acids of <i>Rosa iliensis</i> Chrshan, an Endemic Species from Kazakhstan // Records of Natural Products, 16(3), 225-235. Doi:10.25135/rnp.271.2105.2083  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85122918885&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85122918885&amp;origin=resultslist&amp;sort=plf-f</a>
66	Isolation, identification, and characterization of pathogenic <i>Aeromonas hydrophila</i> from	DOI:10.1016/j.aqrep.2022.101293	The Siberian sturgeon ( <i>Acipenser baerii</i> ) is a long-lived and late-maturing fish; its natural populations are considered endangered and listed in the first class of protected animals in Kazakhstan. To date, attempts have been made to increase the number of sturgeons through artificial reproduction in aquaculture and a release of the resultant juveniles into the Ural River, which flows into the Caspian Sea. This species faces an increased risk of	Bakiyev, Serika, b;Smekenov, Izata, b;Zharkova, Irinac;Kobegenova, Saidinac;Sergaliyev, Nurland;Absatirov, Gaisae;Bissenbaev, Amangeldy

	critically endangered Acipenser baerii		<p>Aeromonas infections. <i>Aeromonas hydrophila</i> is the most important sturgeon pathogen in Kazakhstan, but studies on <i>A. hydrophila</i> infection in Kazakhstan are still inconclusive. In the present work, our purpose was to isolate and characterize dominant bacteria in diseased <i>A. baerii</i>. This isolate, tentatively named AB005, was identified as <i>A. hydrophila</i> in an analysis of its morphological, physiological, and biochemical features and 16S ribosomal-RNA and <i>gyrB</i> gene sequences. A pathogenicity test was carried out for the isolate on healthy <i>Oreochromis niloticus</i> and <i>Acipenser ruthenus</i> via intraperitoneal injection along the caudal peduncle of the fish. Half-lethal doses (LD50) of isolate AB005 for <i>O. niloticus</i> and <i>A. ruthenus</i> were determined: <math>8.37 \times 10^5</math> and <math>2.89 \times 10^6</math> colony-forming units per milliliter, respectively. Virulence gene profiling revealed the presence of seven virulence genes related to pathogenicity (acyltransferase, phospholipase A, serine protease, heat-stable cytotoxic enterotoxin, nuclease, and aerolysins A and B) in this <i>A. hydrophila</i> isolate. Drug sensitivity testing showed that the isolate is sensitive to quinolones, aminoglycosides, nitrofurans, amphenicols, and tetracyclines. The present findings will lay the foundation for future research on this pathogen in Siberian-sturgeon aquaculture. © 2022 The Authors</p>	<p>Isolation, identification, and characterization of pathogenic <i>Aeromonas hydrophila</i> from critically endangered <i>Acipenser baerii</i>// <i>Aquaculture Reports</i>, 26 doi:10.1016/j.aqrep.2022.101293</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85135933960&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85135933960&amp;origin=resultlist&amp;sort=plf-f</a></p>
67	Rice Plants ( <i>Oryza sativa</i> L.) under Cd Stress in Fe Deficiency Conditions	DOI:10.1155/2022/7425085	<p>Due to the environment pollution by cadmium (Cd) near industrial metallurgic factories and the widespread use of phosphorus fertilizers, the problem of toxic Cd effect on plants is well discussed by many authors, but the phytotoxicity of Cd under iron (Fe) deficiency stress has not been sufficiently studied. The aim of the work was to study comprehensively the effect of Cd under Fe deficiency conditions on physiological, biochemical, and anatomical parameters of rice varieties, to identify varietal differences in plant response to the effect of double stress. Relative resistance and sensitivity to the joint effect of Cd and Fe deficiency stress rice varieties have been identified. Double stress decreased a linear growth and biomass accumulation of roots and shoots (by 36-50% and 33-46% and 32-56% and 32-48%, accordingly), content of photosynthetic pigments (Chla, Chlb, and carotenoids by 36-51%, 32-47%, and 64-78%, accordingly), and relative water content (by 18-26%). Proline content increased by 28-103% in all rice varieties, but to</p>	<p>Saule D. Atabayeva , Aqilan B. Rakhymgozhina , Akmaral S. Nurmahanova , Saule S. Kenzhebayeva , Bakdaulet N. Usenbekov , Ravilya A. Alybayeva , Saltanat Sh. Asrandina , Bekzat M. Tynybekov, and Aigul K. Amirova A.K. Rice Plants (<i>Oryza sativa</i> L.) under Cd Stress in Fe Deficiency Conditions // <i>BioMed Research International</i>, 2022 doi:10.1155/2022/7425085</p>

			<p>a lesser extent in sensitive varieties. The thickness of the lower and upper epidermis and the diameter of vascular bundles of leaves decreased by 18-50%, 46-60%, and 13-48%, accordingly. The thickness of the root endodermis and exodermis and diameter of the central cylinder mainly decreased. The thickness of the exodermis increased slightly by 7%, and the diameter of the central cylinder remained at the control level in resistant Madina variety while in sensitive Chapsari variety, these indicators decreased significantly by 50 and 45%, accordingly. Thus, the aggravation of adverse effect of Cd under Fe deficiency conditions and the varietal specificity of plants' response to double stress were shown. It creates the need for further study of these rice varieties using Fe to identify mechanisms for reducing the toxic effect of Cd on plants as well as the study of Fe and Cd transporter genes at the molecular level. © 2022 Saule D. Atabayeva et al.</p>	
68	Recent advances in the therapeutic potential of emodin for human health	DOI:10.1016/j.biopha.2022.113555	<p>Emodin (1,3,8-trihydroxy-6-methylanthraquinone) is a bioactive compound, a natural anthraquinone aglycone, present mainly in herbaceous species of the families Fabaceae, Polygonaceae and Rhamnaceae, with a physiological role in protection against abiotic stress in vegetative tissues. Emodin is mainly used in traditional Chinese medicine to treat sore throats, carbuncles, sores, blood stasis, and damp-heat jaundice. Pharmacological research in the last decade has revealed other potential therapeutic applications such as anticancer, neuroprotective, antidiabetic, antioxidant and anti-inflammatory. The present study aimed to summarize recent studies on bioavailability, preclinical pharmacological effects with evidence of molecular mechanisms, clinical trials and clinical pitfalls, respectively the therapeutic limitations of emodin. For this purpose, extensive searches were performed using the PubMed/Medline, Scopus, Google scholar, TRIP database, Springer link, Wiley and SciFinder databases as a search engines. The in vitro and in vivo studies included in this updated review highlighted the signaling pathways and molecular mechanisms of emodin. Because its bioavailability is low, there are limitations in clinical therapeutic use. In conclusion, for an increase in pharmacotherapeutic efficacy, future studies with carrier</p>	<p>Sharifi-Rad, J., Herrera-Bravo, J., Kamiloglu, S., Petroni, K., Mishra, A.P., Monserrat-Mesquida, M., Sureda, A., Martorell, M., Aidarbekovna, D.S., Yessimsiitova, Zura Ydyrys, A., Hano, C., Calina, D., Cho, W.C. Recent advances in the therapeutic potential of emodin for human health // Biomedicine and Pharmacotherapy, 154 doi:10.1016/j.biopha.2022.113555</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85136463320&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85136463320&amp;origin=resultlist&amp;sort=plf-f</a></p>

			molecules to the target, thus opening up new therapeutic perspectives. © 2022 The Authors	
69	Artemisia spp.: An Update on Its Chemical Compositio, Pharmacological and Toxicological Profiles	DOI:10.1155/2022/5628601	Artemisia plants are traditional and ethnopharmacologically used to treat several diseases and in addition in food, spices, and beverages. The genus is widely distributed in all continents except the Antarctica, and traditional medicine has been used as antimalarial, antioxidant, anticancer, antinociceptive, anti-inflammatory, and antiviral agents. This review is aimed at systematizing scientific data on the geographical distribution, chemical composition, and pharmacological and toxicological profiles of the Artemisia genus. Data from the literature on Artemisia plants were taken using electronic databases such as PubMed/MEDLINE, Scopus, and Web of Science. Selected papers for this updated study included data about phytochemicals, preclinical pharmacological experimental studies with molecular mechanisms included, clinical studies, and toxicological and safety data. In addition, ancient texts and books were consulted. The essential oils and phytochemicals of the Artemisia genus have reported important biological activities, among them the artemisinin, a sesquiterpene lactone, with antimalarial activity. Artemisia absinthium L. is one of the most famous Artemisia spp. due to its use in the production of the absinthe drink which is restricted in most countries because of neurotoxicity. The analyzed studies confirmed that Artemisia plants have many traditional and pharmacological applications. However, scientific data are limited to clinical and toxicological research. Therefore, further research is needed on these aspects to understand the full therapeutic potential and molecular pharmacological mechanisms of this medicinal species. © 2022 Javad Sharifi-Rad et al.	Javad Sharifi-Rad, Jesús Herrera-Bravo, Prabhakar Semwal, Sakshi Painuli, Himani Badoni, Shahira M. Ezzat, Mai M. Farid, Rana M. Merghany, Nora M. Aborehab, Mohamed A. Salem, Surjit Sen, Krishnendu Acharya, Natallia Lapava, Miquel Martorell, Bekzat Tynybekov, Daniela Calina, William C. Artemisia spp.: An Update on Its Chemical Compositio, Pharmacological and Toxicological Profiles// Oxidative Medicine and Cellular Longevity, 2022 doi:10.1155/2022/5628601  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85137853383&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85137853383&amp;origin=resultslist&amp;sort=plf-f</a>
70	Accumulation of Secondary Metabolites of Rhodiola semenovii Boriss. In Situ in the Dynamics of Growth and Development	DOI:10.3390/meta-bo12070622	Rhodiola semenovii Boriss. (Regel and Herder) might be a promising replacement for the well-known but endangered Rhodiola rosea L. In this research, the metabolic profile of R. semenovii, including drug-active and stress-resistant components, was studied in the context of source–sink interactions in situ in the dynamics of growth and development. Gas chromatography with mass spectrometric detection and liquid chromatography methods were used. The data obtained allow for assumptions to be made about which secondary	Terletsкая, N.V.; Graždannikov, A.E.; Seitimova, G.A.; Meduntseva, N.D.; Kudrina, N.O. Accumulation of Secondary Metabolites of Rhodiola semenovii Boriss. In Situ in the Dynamics of Growth and Development // Metabolites,

			<p>metabolites determine the level of stress resistance in <i>R. semenovii</i> at different stages of ontogeny in situ. For the first time, an expansion in the content of salidroside in the above-ground organs, with its maximum value during the period of seed maturation, and a significant decrease in its content in the root were revealed in the dynamics of vegetation. These results allow us to recommend collecting the ground component of <i>R. semenovii</i> for pharmaceutical purposes throughout the seed development stage without damaging the root system. © 2022 by the authors. Licensee MDPI, Basel, Switzerland.</p>	<p>12(7) doi:10.3390/metabo12070622</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85134064639&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85134064639&amp;origin=resultslist&amp;sort=plf-f</a></p>
71	<p>Genome-Wide Association Study of Leaf Rust and Stem Rust Seedling and Adult Resistances in Tetraploid Wheat Accessions Harvested in Kazakhstan</p>	<p>DOI:10.3390/plants11151904</p>	<p>Leaf rust (LR) and stem rust (SR) are diseases increasingly impacting wheat production worldwide. Fungal pathogens producing rust diseases in wheat may cause yield losses of up to 50–60%. One of the most effective methods for preventing such losses is the development of resistant cultivars with high yield potential. This goal can be achieved through complex breeding studies, including the identification of key genetic factors controlling rust disease resistance. The objective of this study was to identify sources of tetraploid wheat resistance to LR and SR races, both at the seedling growth stage in the greenhouse and at the adult plant stage in field experiments, under the conditions of the North Kazakhstan region. A panel consisting of 193 tetraploid wheat accessions was used in a genome-wide association study (GWAS) for the identification of quantitative trait loci (QTLs) associated with LR and SR resistance, using 16,425 polymorphic single-nucleotide polymorphism (SNP) markers in the seedling and adult stages of plant development. The investigated panel consisted of seven tetraploid subspecies (<i>Triticum turgidum</i> ssp. <i>durum</i>, ssp. <i>turanicum</i>, ssp. <i>turgidum</i>, ssp. <i>polonicum</i>, ssp. <i>carthlicum</i>, ssp. <i>dicoccum</i>, and ssp. <i>dicoccoides</i>). The GWAS, based on the phenotypic evaluation of the tetraploid collection's reaction to the two rust species at the seedling (in the greenhouse) and adult (in the field) stages, revealed 38 QTLs (<math>p &lt; 0.001</math>), comprising 17 for LR resistance and 21 for SR resistance. Ten QTLs were associated with the reaction to LR at the seedling stage, while six QTLs were at the adult plant stage and one QTL</p>	<p>Genievskaya, Y.; Pecchioni, N.; Laidò, G.; Anuarbek, S.; Rsaliyev, A.; Chudinov, V.; Zatybekov, A.; Turuspekov, Y.; Abugalieva, Saule Genome-Wide Association Study of Leaf Rust and Stem Rust Seedling and Adult Resistances in Tetraploid Wheat Accessions Harvested in Kazakhstan // <i>Plants</i>, 11(15) doi:10.3390/plants11151904</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85136983036&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85136983036&amp;origin=resultslist&amp;sort=plf-f</a></p>

			was at both the seedling and adult stages. Eleven QTLs were associated with SR response at the seedling stage, while nine QTLs were at the adult plant stage and one QTL was at both the seedling and adult stages. A comparison of these results with previous LR and SR studies indicated that 11 of the 38 QTLs are presumably novel loci. The QTLs identified in this work can potentially be used for marker-assisted selection of tetraploid and hexaploid wheat for the breeding of new LR- and SR-resistant cultivars. © 2022 by the authors.	
72	The effects of thymoquinone on pancreatic cancer: Evidence from preclinical studies	DOI:10.1016/j.biopha.2022.113364	Thymoquinone (TQ) is a secondary metabolite found in abundance in very few plant species including <i>Nigella sativa</i> L., <i>Monarda fistulosa</i> L., <i>Thymus vulgaris</i> L. and <i>Satureja montana</i> L. Preclinical pharmacological studies have shown that TQ has many biological activities, such as anti-inflammatory, antioxidant and anticancer. Both in vivo and in vitro experiments have shown that TQ acts as an antitumor agent by altering cell cycle progression, inhibiting cell proliferation, stimulating apoptosis, inhibiting angiogenesis, reducing metastasis and affecting autophagy. In this comprehensive study, the evidence on the pharmacological potential of TQ on pancreatic cancer is reviewed. The positive results of preclinical studies support the view that TQ can be considered as an additional therapeutic agent against pancreatic cancer. The possibilities of success for this compound in human medicine should be further explored through clinical trials. © 2022 The Authors	Butnariu, M., Quispe, C., Herrera-Bravo, J., Helon, P., Kukula-Koch, W., López, V., Les, F., Vergara, C.V., Alarcón-Zapata, P., Alarcón-Zapata, B., Martorell, M., Pentea, M., Dragunescu, A.A., Samfira, I., Yessimsiitova, ZuraDaştan, S.D., Castillo, C.M.S., Roberts, T.H., Sharifi-Rad, J., Koch, W., Cho, W.C. The effects of thymoquinone on pancreatic cancer: Evidence from preclinical studies// <i>Biomedicine and Pharmacotherapy</i> , 153 doi:10.1016/j.biopha.2022.113364  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85133922047&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85133922047&amp;origin=resultslist&amp;sort=plf-f</a>
73	The complete chloroplast genome sequencing data of	DOI:10.1016/j.dib.2022.108644	The genus <i>Juniperus</i> L. (Cupressaceae Bartl.) is consisting of about 75 species that are divided into sections <i>Caryocedrus</i> Endlicher, <i>Sabina</i> (Miller) Spach, and <i>Juniperus</i> (syn: sect.	Almerekova, S., Yermagambetova, M., Abugaliev, S (Abugaliev,

	<p>Juniperus sabina L. (Cupressaceae Bartl.) from Kazakhstan</p>		<p>Oxycedrus Spach). Juniperus sabina L. from section Sabina is an important shrub for the maintenance of the ecosystem in mountainous regions and a source of medicinal compounds. The species is monoecious, rarely dioecious, and distributed in Europe, Central Asia, China, and Mongolia. The goal of the present study was to sequence and reconstruct the complete chloroplast genome of J. sabina. De novo chloroplast (cp) genome assembly for J. sabina was conducted using Illumina paired-end reads. The assembled cp genome size is 127,646 bp in length and has a typical circular DNA molecule. The genome encodes 118 genes, including 82 protein-coding genes, 32 tRNA genes, and 4 rRNA genes, the overall GC content is 34,36%. The complete cp genome nucleotide sequence of J. sabina was deposited to the NCBI (National Center for Biotechnology Information) under accession number OL467323. The raw data in fastq format was deposited to the NCBI sequence read archive under accession number SRR21515769. © 2022 The Authors</p>	<p>Saule); Turuspekov, Y The complete chloroplast genome sequencing data of Juniperus sabina L. (Cupressaceae Bartl.) from Kazakhstan Data in Brief, 45 doi:10.1016/j.dib.2022.108644</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85139592076&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85139592076&amp;origin=resultlist&amp;sort=plf-f</a></p>
74	<p>Callus induction with 6-BAP and IBA as a way to preserve Prunus ledebouriana (Rosaceae), and endemic plant of Altai and Tarbagatai, East Kazakhstan</p>	<p>DOI:10.13057/biodiv/d230645</p>	<p>Orazov A, Myrzagaliyeva A, Mukhitdinov N, Tustubayeva S. 2022. Callus induction with 6-BAP and IBA as a way to preserve Prunus ledebouriana (Rosaceae), and endemic plant of Altai and Tarbagatai, East Kazakhstan. Biodiversitas 23: 3178-3184. This article presents the results of the study of in vitro conditions for the cultivation and induction of callus tissues of a rare plant species Prunus ledebouriana (Schlecht.) Y.Y.Yao (Ledebour's almond), endemic plant to East Kazakhstan. For the first time, protocol and optimal composition of Murashige &amp; Skoog (MS) were developed for obtaining calendemiclus tissues. The main indicator of successful introduction was the frequency of callus tissue formation in vitro. Two types of explants were used: the whole embryos and embryos with a removed root part. The removal of the root part inhibited the organogenesis of the embryonic root and the first shoot, which allowed the accumulation of nutrients for the growth of the callus mass and increased the frequency by 7.79±0.46%. Various exogenous phytohormones such as Kinetin, 6-BAP, GA, IBA were added to the MS culture medium. A decrease in Kinetin concentrations of 0.04 mg/L resulted in lower intensity, but a higher frequency of formation (72.00±5.66%) and mass gain. The average</p>	<p>Orazov, A., Myrzagaliyeva, A., Mukhitdinov, N., &amp; Tustubayeva, S. Callus induction with 6-BAP and IBA as a way to preserve Prunus ledebouriana (Rosaceae), and endemic plant of Altai and Tarbagatai, East Kazakhstan // Biodiversitas, 23(6), 3178-3184. doi:10.13057/biodiv/d230645</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85134401387&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85134401387&amp;origin=resultlist&amp;sort=plf-f</a></p>



			<p>concentration up to 0.5 mg/L of exogenous phytohormones, such as GA and 6-BAP, resulted in frequency from 65.38±5.44% to 72.00±5.66%, the concentration of IBA up to 1 mg/L increased the frequency from 46.00±2.83 to 72.00±5.66%. The protocol for obtaining callus from an embryonic explant and the composition of the optimal nutrient medium for the induction of callusogenesis made it possible to obtain <i>P. ledebouriana</i> meristem tissues for further use in the development of callus cryopreservation technology. © 2022, Society for Indonesian Biodiversity. All rights reserved.</p>	
75	Genetic Variation in Populations of <i>Picea schrenkiana</i> Fisch. et C.A. Mey. Based on Simple Sequence Repeat Markers	DOI:10.3103/S0096392522020134	<p>Abstract: <i>Picea schrenkiana</i> is a tree species native to the Tian Shan Mountains of Central Asia in Western China, Kazakhstan, Kyrgyzstan. <i>P. schrenkiana</i> is one of the major forest species in the region with a gradually decreasing area due to anthropogenic factors and natural disasters. The goal of the present study was to assess the level of genetic diversity in five populations of <i>P. schrenkiana</i> collected in the Tian Shan mountains of Kazakhstan. Nineteen simple sequence repeat (SSR) markers were selected for the evaluation of the genetic diversity in populations of <i>P. schrenkiana</i> with typical upright and prostrate forms collected in the Tian Shan mountains in Kazakhstan. The analysis of <i>P. schrenkiana</i> samples allowed the identification of twelve polymorphic out of nineteen SSR markers, with six of them having Polymorphism Information Content (PIC) index values of 0.5 or higher. The average Nei's genetic diversity index of the overall populations was 0.54 and comparable with results from studies of other <i>Picea</i> species. The total genetic variation in the species was partitioned as 86% within and 14% between populations. The Principal Coordinate Analysis plot suggested that twelve SSR markers effectively separated populations with typical upright and prostrate forms of <i>P. schrenkiana</i>. The estimated gene flow index (Nm) among populations based on all alleles was 3.05, confirming a high outbreeding rate within the species. Nevertheless, the application of SSR markers separated populations with typical upright and prostrate forms of <i>P. schrenkiana</i>. The results suggest that the maintenance of the genetic variation within <i>P. schrenkiana</i> can be successfully achieved through an in situ conservation strategy. © 2022, Allerton Press, Inc.</p>	<p>Yermagambetova, M. M., Almerkova, S. S., Krekova, Y., Turuspekov, Y. K. Abugalieva S.I. Genetic Variation in Populations of <i>Picea schrenkiana</i> Fisch. et C.A. Mey. Based on Simple Sequence Repeat Markers // Moscow University Biological Sciences Bulletin, 77(2), 76-83. doi:10.3103/S0096392522020134</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85137563437&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85137563437&amp;origin=resultlist&amp;sort=plf-f</a></p>

76	The Changing Dynamics of Kazakhstan's Fisheries Sector: From the Early Soviet Era to the Twenty-First Century	DOI:10.3390/w14091409	Kazakhstan, a former Soviet republic that is now independent, lies near the center of arid Eurasia. Its sparse hydrographic network includes a small number of large rivers, lakes, and reservoirs, many ponds and smaller streams, as well as littoral zones bordering the Caspian Sea and the Aral Sea. A diverse fisheries sector, initially based on wild fish capture and later including aquaculture, developed in these waters during the Soviet era, when animal agriculture was unable to meet the protein needs of Soviet citizens. The sector, which was originally centered on the Volga–Caspian basin, was tightly managed by Moscow and benefitted from coordinated investments in research, infrastructure, and human resources, as well as policies to increase the consumption of fish products. Independence in 1991 administered a political and economic shock that disrupted these relationships. Kazakhstan's wild fish harvests plummeted by more than two-thirds, and aquaculture collapsed to just 3% of its previous level. Per capita consumption of fish products also declined, as did processing capacity. Favorable recent policies to define fishing rights, incentivize investments, prevent illegal fishing, and make stocking more effective have helped to reverse these trends and stabilize the sector. Continued recovery will require additional steps to manage water resources sustainably, prioritize the use of water for fish habitats, and minimize the effects of climate change. This comprehensive assessment of Kazakhstan's fisheries sector over the past century provides the basis to understand how long-term dynamic interactions of the environment with the political economy influence fisheries in Eurasia's largest country. © 2022 by the authors. Licensee MDPI, Basel, Switzerland.	Graham, N.A., Pueppke, S.G., Nurtazin, S., Konysbayev, Talgarbay, Gibadulin, F., Sailauov, M The Changing Dynamics of Kazakhstan's Fisheries Sector: From the Early Soviet Era to the Twenty-First Century // Water (Switzerland), 14(9) doi:10.3390/w14091409  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85129836916&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85129836916&amp;origin=resultlist&amp;sort=plf-f</a>
77	Identification of SNP Markers Associated with Grain Quality Traits in a Barley Collection ( <i>Hordeum vulgare</i> L.)	DOI:10.3390/agronomy12102431	Barley ( <i>Hordeum vulgare</i> L.) is a cereal crop traditionally used in animal feed, malting, and food production. In this study, a collection of barley was analyzed according to key grain quality traits, including protein content (GPC), starch content (GSC), extractivity (EX), and grain test weight per liter (TWL). A genome-wide association study (GWAS) was conducted to identify the quantitative trait loci (QTLs) associated with GPC,	Genievskaya, Y.; Almerikova, S.; Chudinov, V.; Blake, T.; Abugalieva, A.; Turuspekov, Y. Identification of SNP Markers Associated with Grain Quality Traits in a Barley Collection ( <i>Hordeum vulgare</i> L.)

	Harvested in Kazakhstan		<p>GSC, EX, and TWL using a collection of 658 barley accessions from the USA and Kazakhstan. The collection was grown at three breeding organizations in Kazakhstan in 2010 and 2011 and genotyped using the 9K SNP Illumina chip. As a result, 18 marker-trait associations (MTAs) for GPC, 19 MTAs for GSC, 12 MTAs for EX, and 27 MTAs for TWL were detected, resulting in 30 identified QTLs. It was shown that the genetic locations of 25 of these 30 QTLs were in similar positions to the QTLs and genes previously reported in the scientific literature, suggesting that the 5 remaining QTLs are novel putative genetic factors for the studied grain quality traits. Five of the most significant SNP markers (<math>p &lt; 2.6 \times 10^{-5}</math>) for the studied quality traits identified in the GWAS were used for the development of reliable and informative competitive allele-specific PCR (KASP) genotyping assays. The effectiveness of two assays (ipbb_hv_6 and ipbb_hv_128) was confirmed via validation in a separate collection of barley breeding lines grown in large field plots in northern Kazakhstan. Therefore, these KASP assays can be efficiently used in a marker-assisted selection of grain quality traits in barley breeding. © 2022 by the authors.</p>	<p>Harvested in Kazakhstan // Agronomy, 12(10) doi:10.3390/agronomy12102431</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85140439636&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85140439636&amp;origin=resultlist&amp;sort=plf-f</a></p>
78	Sesquiterpenoid lactones as potential anti-cancer agents: an update on molecular mechanisms and recent studies	DOI:10.1186/s12935-022-02721-9	<p>Plants-based natural compounds are well-identified and recognized chemoprotective agents that can be used for primary and secondary cancer prevention, as they have proven efficacy and fewer side effects. In today's scenario, when cancer cases rapidly increase in developed and developing countries, the anti-cancerous plant-based compounds become highly imperative. Among others, the Asteraceae (Compositae) family's plants are rich in sesquiterpenoid lactones, a subclass of terpenoids with wide structural diversity, and offer unique anti-cancerous effects. These plants are utilized in folk medicine against numerous diseases worldwide. However, these plants are now a part of the modern medical system, with their sesquiterpenoid lactones researched extensively to find more effective and efficient cancer drug regimens. Given the evolving importance of sesquiterpenoid lactones for cancer research, this review comprehensively covers different domains in a spectrum of sesquiterpenoid lactones viz (i) Guaianolides (ii) Pseudoguaianolide (iii) Eudesmanolide (iv) Melampodin A and (v) Germacrene, from important plants such as Cynara</p>	<p>Praveen Dhyani, Priyanka Sati, Eshita Sharma, Dharam Chand Attri, Amit Bahukhandi, Bekzat Tynybekov, Agnieszka Szopa, Javad Sharifi Rad, Daniela Calina, Hafiz A. R. Suleria, William C. Cho Sesquiterpenoid lactones as potential anti-cancer agents: an update on molecular mechanisms and recent studies // Cancer Cell International, 22(1) doi:10.1186/s12935-022-02721-9</p>

			scolymus (globe artichoke), Arnica montana (wolf weeds), Spilanthes acmella, Taraxacum officinale, Melampodium, Solidago spp. The review, therefore, envisages being a helpful resource for the growth of plant-based anti-cancerous drug development. © 2022, The Author(s).	<a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85139467963&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85139467963&amp;origin=resultslist&amp;sort=plf-f</a>
79	Feasibility of waste-free use of microalgae in aquaculture	DOI:10.1007/s10811-022-02787-y	Following the circular bioeconomy approach, this study shows the possibility of effective microalgal bioremediation of aquaculture wastewater integrated with the production of protein-rich biomass, which can be used as a feed additive. Screening was carried out among strains of <i>Chlorella vulgaris</i> BB-2, <i>Parachlorella kessleri</i> Bh-2 and <i>Chlamydomonas reinhardtii</i> C-124 with the aim of selecting the strain which is characterized by high indicators of growth in the fish farms wastewaters. Among these three strains, <i>C. vulgaris</i> BB-2 was selected due to its increased growth rate in aquaculture wastewater with ammonia, nitrite, and nitrate and phosphate removal. In addition, in the water when cultivating microalgae in it the coliform index and total microbial number decreased to 5 and $1.8 \times 10^3$ colony-forming unit $\text{cm}^{-3}$ . Large-scale microalgae cultivation utilizing aquaculture wastewater gave biomass production of $43.5 \text{ mg L}^{-1} \text{ day}^{-1}$ . The biochemical composition analysis of the aquaculture wastewater phycoremediation-derived biomass of <i>C. vulgaris</i> BB-2 revealed that the content of $57.0 \pm 1.2\%$ protein, $16 \pm 1.2\%$ lipid, and $11.4 \pm 1.4\%$ carbohydrate. The obtained data indicate that the lipid extract of microalgae <i>C. vulgaris</i> BB-2 contained saturated 30.7% and polyunsaturated fatty acids 69.3%. The main fraction of amino acids consisted of glutamic acid, lysine, aspartic acid and leucine. The utilization of 25% microalgal biomass as a feed additive in the diet of fish has shown a positive effect on the morpho-physiological and biochemical growth parameters and intestinal microflora of Nile tilapia ( <i>Oreochromis niloticus</i> ). Graphical abstract: [Figure not available: see fulltext.] © 2022, The Author(s), under exclusive licence to Springer Nature B.V.	Nurziya R. Akmukhanova, Assemgul K. Sadvakasova, Makpal M. Torekhanova, Meruyert O. Bauenova, Bolatkhan K. Zayadan, Saule M. Shalgimbayeva, Kenzhegul Bolatkhan, Saleh Alwasel, Yoong Kit Leong, Jo Shu Chang, Suleyman I. Allakhverdiev Feasibility of waste-free use of microalgae in aquaculture // Journal of Applied Phycology, 34(5), 2297-2313. doi:10.1007/s10811-022-02787-y  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85132988406&amp;origin=resultslist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85132988406&amp;origin=resultslist&amp;sort=plf-f</a>
80	Antihypothyroid Effect of Solidoside	DOI:10.3390/molecules27217487	In terms of prevalence, thyroid pathology, associated both with a violation of the gland function and changes in its structure, occupies one of the main places in clinical endocrinology. The	Korbozova, N.K.; Kudrina, N.O.; Zhukova, N.A.; Grazhdannikov, A.E.; Blavachinskaya, I.V.;

			<p>problem of developing low-toxic and highly effective herbal preparations for the correction of thyroid hypofunction and its complications is urgent. Salidroside is a glucoside of tyrosol, found mostly in the roots of <i>Rhodiola</i> spp., and has various positive biological activities. The purpose of this study was to study the antihypothyroid potential of salidroside-containing extract from <i>R. semenovii</i> roots, which was evaluated on a mercazolyl hypothyroidism model. We showed that extract containing salidroside is a safe and effective means of hypothyroidism correction, significantly reducing (<math>p \leq 0.001</math>) the level of thyroid-stimulating hormone and increasing the level of thyroid hormones. The combined use of <i>R. semenovii</i> extract with potassium iodide enhances the therapeutic effect of the extract by 1.3-times. © 2022 by the authors.</p>	<p>Seitimova, G.A.; Kulmanov, T.E.; Tolstikova, T.G Antihypothyroid Effect of Salidroside // <i>Molecules</i> Открытый доступ Том 27, Выпуск 21 November 2022 Номер статьи 7487 DOI: 10.3390/molecules27217487</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85141797322&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85141797322&amp;origin=resultlist&amp;sort=plf-f</a></p>
81	Microalgae Indicators of Charophyte Habitats of South and Southeast Kazakhstan.	DOI:10.3390/d14070530	<p>Charophyte algae is a very sensitive group of organisms occupying Kazakhstan waterbodies. They are distributed throughout the country; however, not enough studies have been conducted, especially in the southern region. Research carried out in 2019–2022 identified 33 habitats of charophyte algae in the south and southeastern regions of Kazakhstan, including 15 new to Kazakhstan. Bioindicators and the statistical analysis of 223 species of nine phyla of microalgae associated with charophytes revealed that the main factors influencing the distribution of algal diversity may be habitat altitude and hydrology. The habitat altitude of about 700 m above sea level was shown to be the boundary between the different diversity distributions. The application of bioindicator methods can expand our knowledge on the ecology of the charophyte species in Kazakhstan. The study of algal diversity in charophyte habitats can serve as a tool for tracking climate change under potential future climate warming. © 2022 by the authors. Licensee MDPI, Basel, Switzerland.</p>	<p>Sametova, E.; Jumakhanova, G.; Nurashov, S.; Barinova, S.; Jiyenbekov, A.; Smith, T. Microalgae Indicators of Charophyte Habitats of South and Southeast Kazakhstan. // <i>Diversity</i>, 14(7) doi:10.3390/d14070530</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85133539348&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85133539348&amp;origin=resultlist&amp;sort=plf-f</a></p>
82	Structural Characteristics of <i>Rosa iliensis</i>	DOI:10.12911/22998993/143943	<p>The article provides brief geobotanical characteristics of plant communities of three populations of <i>R. iliensis</i> Chrshan. found in the floodplains of the Ili and Sharyn rivers, as well as presents</p>	<p>Assel Childibayeva, Abibulla Ametov, Natalia Vladimirovna Kurbatova, Aigul Akhmetova,</p>

	Chrshan. under Conditions of the Floodplains of the Rivers Ili and Sharyn		the morpho-anatomical structure of vegetative organs (stem and leaf) of the species under study. <i>R. iliensis</i> Chrshan. is undoubtedly a rare, endangered species of the flora of Kazakhstan. Its distribution area is shrinking from year to year as a result of the anthropogenic pressure on the environment. The biometric indicators of vegetative organs in the samples collected from populations 1 and 2 were approximately the same. The indicators of the samples collected from population 3 differed substantially. This is a completely natural process, since there are substantial differences in the climatic conditions of the upper and lower parts of the basin where the Ili River flows: a sharp increase in temperature and a decrease in precipitation from high to low hypsometric levels of the basin. Moreover, there is a gradual aridization of the territory from east to west. Naturally, this entails a change in both soil and vegetation cover as well as leaves its mark on the morpho-anatomical structure of vegetative organs. With this in mind, the authors recommend continuous monitoring of the state of the populations at the three sites where <i>R. iliensis</i> Chrshan. was found. © 2022. Journal of Ecological Engineering. All Rights Reserved	Bekzat Makulbayevich Tynybekov, Gulzhanat Amangeldykyzy Mukanova. Structural Characteristics of <i>Rosa Iliensis</i> Chrshan. under Conditions of the Floodplains of the Rivers Ili and Sharyn // Journal of Ecological Engineering, 23(1), 296-304. <a href="https://doi.org/10.12911/22998993/143943">https://doi.org/10.12911/22998993/143943</a>  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85122232847&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85122232847&amp;origin=resultlist&amp;sort=plf-f</a>
83	Exotic Fish Species in the Balkhash Lake Basin (Kazakhstan)	DOI:10.1134/S1995082922010084	Abstract: An exotic species, channel catfish <i>Ictalurus punctatus</i> , has been recorded in the ichthyofauna of the Republic of Kazakhstan for the first time. The specimens were caught in the Ili River upstream of the Kapchagai Reservoir in October 2020. Based on repeated findings of Nile tilapia <i>Oreochromis niloticus</i> and its hatchlings in the Borokhudzir River (a tributary of the Ili River), it has been concluded that a self-reproducing population of this species has appeared here. The possibility of naturalization of channel catfish in the Balkhash basin, which poses a threat to the remains of the native Ili ichthyofauna, is discussed. © 2022, Pleiades Publishing, Ltd.	Mamilov, N.Sh.; Konysbaev T.G.; Belyaev A.I.; Vasil'eva E.D. Exotic Fish Species in the Balkhash Lake Basin (Kazakhstan) // Inland Water Biology, 15(1), 84-87. doi:10.1134/S1995082922010084 <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85127221079&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85127221079&amp;origin=resultlist&amp;sort=plf-f</a>
84	Identification of quantitative trait loci for leaf rust and stem	DOI:10.3390/plants11010074	In recent years, leaf rust (LR) and stem rust (SR) have become a serious threat to bread wheat production in Kazakhstan. Most local cultivars are susceptible to these rusts, which has affected	Zatybekov, A., Genievskaya, Yuliyaa, b

	<p>rust seedling resistance in bread wheat using a genome-wide association study</p>		<p>their yield and quality. The development of new cultivars with high productivity and LR and SR disease resistance, including using marker-assisted selection, is becoming an important priority in local breeding projects. Therefore, the search for key genetic factors controlling resistance in all plant stages, including the seedling stage, is of great significance. In this work, we applied a genome-wide association study (GWAS) approach using 212 local bread wheat accessions that were phenotyped for resistance to specific races of <i>Puccinia triticina</i> Eriks. (Pt) and <i>Puccinia graminis</i> f. sp. <i>tritici</i> (Pgt) at the seedling stages. The collection was genotyped using a 20 K Illumina iSelect SNP assay, and 11,150 polymorphic SNP markers were selected for the association mapping. Using a mixed linear model, we identified 11 quantitative trait loci (QTLs) for five out of six specific races of Pt and Pgt. The comparison of the results from this GWAS with those from previously published work showed that nine out of eleven QTLs for LR and SR resistance had been previously reported in a GWAS study at the adult plant stages of wheat growth. Therefore, it was assumed that these nine common identified QTLs were effective for all-stage resistance to LR and SR, and the two other QTLs appear to be novel QTLs. In addition, five out of these nine QTLs that had been identified earlier were found to be associated with yield components, suggesting that they may directly influence the field performance of bread wheat. The identified QTLs, including novel QTLs found in this study, may play an essential role in the breeding process for improving wheat resistance to LR and SR. © 2021 by the authors. Licensee MDPI, Basel, Switzerland.</p>	<p>Rsaliyev, Aralbekc  Send mail to Rsaliyev A.;Maulenbay, Akerkec  .;Yskakova, Gulbaharc  G.;Savin, Timurd  .;Turuspekov, Yerlana,  Y.;Abugalieva, Saulea,  Identification of quantitative trait loci for leaf rust and stem rust seedling resistance in bread wheat using a genome-wide association study // <i>Plants</i>, 11(1)  doi:10.3390/plants11010074    <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85121687724&amp;origin=resultslst&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85121687724&amp;origin=resultslst&amp;sort=plf-f</a></p>
85	<p>New data on diversity and distribution of fish in shallow waters in western Lake Balkhash (Kazakhstan)</p>	<p>DOI:10.1111/jai.14294</p>	<p>Lake Balkhash is one of the largest lakes of Asia and belongs to the Republic of Kazakhstan. The lake has suffered from alien fish introduction, water pollution and overfishing during last decades. The goal of this study was to investigate contemporary fish diversity in shallow waters in western part of the Lake Balkhash. Fish samples were collected there 2018 and 2019. The data obtained showed changes in fish species diversity and significant decrease in the proportion of juvenile commercial fish in shallow sites of western part of the lake. The distribution of species seems random and needs further study to elucidate key factors. Thus, our data indicated deterioration of shallow waters</p>	<p>Mamilov N., Shalakhmetova T., Konysbayev T., Sutuyeva L., Abdullayeva B. New data on diversity and distribution of fish in shallow waters in western Lake Balkhash (Kazakhstan) // <i>Journal of Applied Ichthyology</i>, 38(2), 241-246.  Doi:10.1111/jai.14294  <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-">https://www.scopus.com/record/display.uri?eid=2-s2.0-</a></p>

			in the western Balkhash as “nursery” for commercial fish species. © 2022 Wiley-VCH GmbH	85122753584&origin=resultslst &sort=plf-f
86	Past, Current and Future of Fish Diversity in the Alakol Lakes (Central Asia: Kazakhstan)	DOI:10.3390/d14010011	The aboriginal ichthyofauna of the Balkhash basin consists mainly of endemic fish species. By the end of the last century, indigenous fish species were driven out of Lake Balkhash and the Alakol Lakes remain the largest refuges of aboriginal fish fauna. Knowledge of regularities of the modern distribution of the indigenous fishes is crucial for biodiversity conservation as well as restoring aquatic ecosystems. The modern diversity of fish species was investigated there in this study. Significant changes for the indigenous and some alien fish distributions were revealed in contrast with earlier known data. Canonical correspondence analysis (CCA) was used to study the relationships between habitat characteristics and species abundance. Water mineralization and maximal observed water temperatures were estimated as the main environmental variables in fish distribution at the local scale. Habitat change leads to fish fauna homogenization as a result of rare species extinction and alien penetration. Growing human population and poor water management make the future of the indigenous fishes unpredictable. © 2021 by the authors. Licensee MDPI, Basel, Switzerland.	Sharakhmetov S., Amirbekova F., Bekkozhayeva D., Sapargaliyeva N., Kegenova G., Tanybayeva A., Abilkasimov K. Past, Current and Future of Fish Diversity in the Alakol Lakes (Central Asia: Kazakhstan) // Diversity, 14(1) doi:10.3390/d14010011 <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85121871691&amp;origin=resultslst &amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85121871691&amp;origin=resultslst &amp;sort=plf-f</a>
87	Phytochemical study of <i>Crambe tatarica</i> Sebeok, a promising source of medicinal plant extracts	DOI:10.30848/PJB2022-2(38)	The article presents the results of a phytochemical study of <i>Crambe tatarica</i> Sebeok, a promising plant of the family Brassicaceae growing in Western Kazakhstan. The results of qualitative and quantitative analyses confirmed that the aboveground parts of <i>C. tatarica</i> are richer in alkaloids, carotenoids, monosaccharides (glucose, galactose, rhamnose, mannose, xylose, arabinose, and rutinose) and phospholipids than the root system. In the roots of <i>C. tatarica</i> , a higher content of tannins has been recorded (2,3-O-hexaoxidifenoyl-4,6-O-sanguisorbil-D-glucose, 2,3-di-O-galloyl-D-glucose, 1,2,4-tri-O-galloyl-β-D-glucose), coumarins (4,5-dioxycoumarin, 7-hydroxycoumarin, scopoletin), polysaccharides, triterpenoids, phenolic and hydroxycinnamic acids (gallic, caffeic, ferulic, lilac, gentisic, vanillic, o-cumaric) and flavonoids (kaempferol, quercetin, gossipetin, myricetin, (+)-catechin, 3-O α-L-rhamnopyranoside kaempferol). Regardless of the place of growth, the Kazakh species <i>C. tatarica</i> contains alkaloids,	Turalin B., Kurbatova N., Inelova Z., Kurmanbayeva M., Abidkulova K. Phytochemical study of <i>Crambe tatarica</i> Sebeok, a promising source of medicinal plant extracts // Pakistan Journal of Botany, 54(2), 653-666. doi:10.30848/PJB2022-2(38) <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85128173057&amp;origin=resultslst &amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85128173057&amp;origin=resultslst &amp;sort=plf-f</a>



			<p>tannins of the hydrolyzable type, carotenoids, coumarins, polysaccharides, triterpenoids, phenolic acids, flavonoids and phospholipids. We studied antibacterial and fungicidal activity of the aqueous, alcohol and acetone extracts of the aboveground parts and roots of <i>C. tatarica</i>. We found that certain concentrations of these extracts had both bactericidal and fungicidal activity. The highest activity of the tested samples of acetone extracts was shown against the test strain <i>S. aureus</i> ATCC 6538-P. Thus, acetone extracts of the aboveground parts and roots of <i>C. tatarica</i> were active against staphylococcus at a concentration of 0.78 mg / ml, where 0.9% saline was used as a solvent. When dissolved in 96% ethanol, acetone extracts also showed increased activity against the museum test strain of <i>S. aureus</i> ATCC 6538-P. Extracts from the aboveground parts and roots of <i>C. tatarica</i> had fungicidal activity against <i>Candida albicans</i> ATCC 10231 at concentrations of 0.78 mg / ml 12.5 mg / ml, respectively (96% ethanol was used as a solvent). © 2022, Pakistan Botanical Society. All rights reserved.</p>	
88	<p>The Reactions of Photosynthetic Capacity and Plant Metabolites of <i>Sedum hybridum</i> L. in Response to Mild and Moderate Abiotic Stresses</p>	<p>DOI:10.3390/plants10061196</p>	<p>Plants of the Crassulaceae family are natural accumulators of many medicinal secondary metabolites (SM). This article describes the study of morphophysiological, anatomic and phytochemical responses of immature plants of <i>Rhodiola semenovii</i> under water deficit and (or) cold-stress conditions. Changes in biomass production due to water content in plant tissues such as a decrease in water deficit and an increase in cold stress were revealed. A significant decrease in the efficiency of the photosynthetic apparatus under stress conditions was noted, based on the parameters quantum efficiency of Photosystem II and electron transport rate and energy dissipated in Photosystem II. The greatest decrease in efficiency was pointed out in conditions of water shortage. The anatomical modulations of root and shoot of <i>R. semenovii</i> under stress conditions were found. For the first time, a detailed study of the chemical composition of the ethanol extract of root and shoot of <i>R. semenovii</i> under stress was carried out using gas chromatography–mass spectrometry. The qualitative and quantitative composition of SM associated with acclimation to the effects of abiotic stresses was determined. Both nonspecific and specific phytochemical changes caused by the action of</p>	<p>Nina V. Terletsкая., Gulnaz A. Seitimova ., Nataliya O. Kudrina Nataliya., D. Meduntseva., Kazhybek Ashimuly The Reactions of Photosynthetic Capacity and Plant Metabolites of <i>Sedum hybridum</i> L. in Response to Mild and Moderate Abiotic Stresses // <i>Plants</i>, 10(6) doi:10.3390/plants10061196 <a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85107566560&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85107566560&amp;origin=resultlist&amp;sort=plf-f</a></p>

			<p>water deficiency and cold treatment were identified. It has been shown that the antioxidant system in plant tissues is complex, multicomponent, depending on a number of natural and climatic factors. Further research should be focused on the use of abiotic stressors for the targeted synthesis of bioactive SMs valuable for pharmaceutical use. © 2021 by the author. Licensee MDPI, Basel, Switzerland.</p>	
89	<p>Introduced, Mixed, and Peripheral: Conservation of Mitochondrial-DNA Lineages in the Wild Boar (<i>Sus scrofa</i> L.) Population in the Urals</p>	<p>DOI:10.3390/d14110916</p>	<p>Translocations and introductions are important events that allow organisms to overcome natural barriers. The genetic background of colonization success and genetic consequences of the establishment of populations in new environments are of great interest for predicting species' colonization success. The wild boar has been introduced into many parts of the world. We analyzed sequences of the mitochondrial-DNA control region in the wild boars introduced into the Ural region and compared them with sequences from founder populations (from Europe, the Caucasus, Central Asia, and the Far East). We found that the introduced population has high genetic diversity. Haplotypes from all the major phylogenetic clades were detected in the analyzed group of the animals from the Urals. In this group, no haplotypes identical to Far Eastern sequences were detectable despite a large number of founders from that region. The contribution of lineages originating from Eastern Europe was greater than expected from the proportions (%) of European and Asian animals in the founder populations. This is the first study on the genetic diversity and structure of a wild boar population of mixed origin at the northern periphery of this species' geographical range. © 2022 by the authors.</p>	<p>Markov, N.I. (Markov, Nikolay); Ranyuk, M.N. (Ranyuk, Maryana N.); Babaev, E.A. (Babaev, Elmar A.); Seryodkin, I.V. (Seryodkin, Ivan, V.); Senchik, A.V. (Senchik, Alexander, V.); Bykova, E.A. (Bykova, Elena A.); Esipov, AV (Esipov, Alexander, V); Nurtazin, ST (Nurtazin, Sabir T.); Pavlova, OS (Pavlova, Olga S.) Introduced, Mixed, and Peripheral: Conservation of Mitochondrial-DNA Lineages in the Wild Boar (<i>Sus scrofa</i> L.) Population in the Urals // <i>Diversity</i> Открытый доступ Том 14, Выпуск 11 November 2022 Номер статьи 916 DOI:10.3390/d14110916</p> <p><a href="https://www.scopus.com/record/display.uri?eid=2-s2.0-85141765073&amp;origin=resultlist&amp;sort=plf-f">https://www.scopus.com/record/display.uri?eid=2-s2.0-85141765073&amp;origin=resultlist&amp;sort=plf-f</a></p>