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**Центр коллективного пользования «Инструментальные методы в экологии»**

**Перечень публикаций, подготовленных по результатам работ, выполненных с использованием научного оборудования ЦКП за 2021 год**

№ п/п	Вид публикации	Наименование публикации	DOI публикации	Автор(ы)	Издание, номер, год	ISSN / ISBN издания	Индексация издания	Краткое описание научных результатов, полученных на оборудовании ЦКП	Наличие в публикации ссылки на ЦКП	Страница , содержащая ссылку на ЦКП
1	2	3	4	5	6	7	8	9	10	11
1.	научная статья	A New Shrimp Genus (Crustacea: Decapoda) from the Deep Atlantic and an Unusual Cleaning Mechanism of Pelagic Decapods	<a href="https://doi.org/10.3390/d13110536">https://doi.org/10.3390/d13110536</a>	Vereshchaka A., Kulagin D.N., Lunina A.A.	Diversity, 13(11), 2021	1424-2818	БАК; РИНЦ; Web of Science; Scopus	The deep sea is the largest biome on Earth and hosts the majority of as yet undescribed species; description of these may trigger a new mindset about evolution and function of characters. We describe and diagnose a new genus and species <i>Sclerodora crosnieri</i> sp. nov. belonging to the superfamily Oplophoroidea. We examined and coded 81 characters for morphological analyses and used four gene markers for molecular analyses involving the new taxon and representatives of all other genera of Oplophoroidea. Retrieved morphological and molecular trees were similar and suggested that the new genus is a sister group to <i>Hymenodora</i> and both form a clade sister to the rest of Acanthephyridae. We provide an amended key to all genera of Oplophoroidea. We found an unusual chelate structure on the dactyl of the fifth pereopod, tested and confirmed a hypothesis that this structure is common for the whole family Acanthephyridae. We suggest that this derived structure is linked to an active cleaning of branchia-a function associated with chelipeds in some other carid shrimps. Convergent chelate structures are likely efficient for cleaning branchia, whichever appendage is adapted for these functions. In Oplophoridae (sister to Acanthephyridae), cleaning function is carried out by well-developed epipods.	Да (если в тексте публикации указано название ЦКП или УНУ)	6

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1	2	3	4	5	6	7	8	9	10	11
2.	научная статья	A new species of Flavalona Sinev & Dumont, 2016 (Crustacea: Branchiopoda) from Bale Mountains, Ethiopia	<a href="https://doi.org/10.11646/zootaxa.4948.1.6">https://doi.org/10.11646/zootaxa.4948.1.6</a>	Neretina A.N., Sinev A.Y.	Zootaxa, 4948, 2021	1175-5326	BAK; Ринц; Web of Science; Scopus	Here we describe a new species of Flavalona Sinev & Dumont, 2016 (Cladocera: Chydoridae) based on material from Bale Mountains, Ethiopia. <i>F. darkovi</i> sp. nov. clearly differs from other species of Flavalona known to date by fine ornamentation of valves, proportions of head pores, proximal exopod spine and seta on the middle exopod segment of antenna II. This species may be considered as endemic taxon of high mountain water bodies of Bale Mountains at an altitude of about 4000 m.a.s.l. Investigated species of the genus Flavalona in Africa demonstrate strong local mountain endemism accompanied by morphological differences between closest taxa, but the real diversity of this group in Africa is underestimated yet, and further studies are urgently need. Since the high mountain water ecosystems in Africa are especially vulnerable to increasing anthropogenic impact and global climate warming, it is necessary to speed up the studies of high mountain invertebrates and develop special measures for protection of such ecosystems.	Да (если в тексте публикации указано название ЦКП или УНУ)	121
3.	научная статья	A new species of the genus <i>Lucasioides</i> Kwon, 1993 (Isopoda, Oniscidea, Agnaridae) from Siberia, Russia	<a href="https://doi.org/10.11646/zootaxa.4903.1.9">https://doi.org/10.11646/zootaxa.4903.1.9</a>	Gongalsky K.B., Nefediev P.S., Turbanov I.S.	Zootaxa, 4903, 2021	1175-5326	BAK; Ринц; Web of Science; Scopus	A new species of the family Agnaridae, <i>Lucasioides altaicus</i> sp. nov., is described from the Altai Mountains, southwestern Siberia, based both on morphological characters and molecular data. This species is the first record of <i>Lucasioides</i> from Russia, whose location is the northernmost habitat of terrestrial isopods in indigenous habitats presently known to Eurasia. The diagnostic characters of the new species and a preliminary phylogenetic analysis within Agnaridae are provided.	Да (если в тексте публикации указано название ЦКП или УНУ)	149

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4.	научная статья	A Review of Recently Discovered Remains of the Pleistocene Branchiopods (Anostraca, Notostraca) from NE Siberia and Arctic Canada	<a href="https://doi.org/10.3390/w13030280">https://doi.org/10.3390/w13030280</a>	Rogers D.Ch., Zharov A.A., Neretina A.N., Kuzmina S.A., Kotov A.A.	Water, 13, 2021	2073-4441	BAK; Ринц; Web of Science; Scopus	In this study, we examine, identify, and discuss fossil remains of large branchiopod crustaceans collected from six sites across the Beringian region (north- eastern Asia and north-western North America). Eggs and mandibles from Anostraca and Notostraca, as well as a notostracan telson fragment and a possible notostracan second maxilla, were collected from both paleosediment samples and also from large mammal hair. The remains of large branchiopods and other species that are limited to seasonally astatic aquatic habitats (temporary wetlands) could be useful indicator organisms of paleoecological conditions. Different recent large branchiopod species have very different ecological preferences, with each species limited to specific geochemical component tolerance ranges regarding various salinity, cation, and gypsum concentrations. Our purpose is to bring the potential usefulness of these common fossil organisms to the attention of paleoecologists.	Да (если в тексте публикации указано название ЦКП или УНУ)	11

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5.	научная статья	Accumulation of polychlorinated biphenyls (PCB) associated with bottom sediments in larvae of Chironomus riparius Meigen	<a href="https://doi.org/10.1016/j.limno.2021.125912">https://doi.org/10.1016/j.limno.2021.125912</a>	Chuiko G.M., Tomilina I.I., Brofsky E.F., et al.	Limnologica, 90, 2021	00759511	BAK; Ринц; Web of Science; Scopus	Patterns of bioaccumulation of polychlorinated biphenyls (PCBs) by chironomid larvae ( <i>Chironomus riparius</i> Meigen) were studied under laboratory conditions. Larvae were maintained for 20 days, separately in two batches of natural bottom sediments sampled from Rybinsk Reservoir (Russia), each differing in PCB content (425.6 µg / kg or 24.8 µg / kg dry weight, respectively). The study revealed that chironomid larvae accumulated PCBs at levels comparable to the PCB content measured in sediments from each exposure. The bioaccumulation coefficient (1.11 and 1.59, respectively, as per dry weight for compared sediment batches) depended directly on the sum PCB content in sediments. At high sediment PCB content, the ratios of homologous groups of PCBs in larvae and sediment were identical and corresponded to the Aroclor 1254 congeners profile; at lower PCB content, pronounced differences were revealed. In larvae, the ratios of 3, 4, 5, and 6CB homologues were evenly distributed at levels of 20–34 %, while the 4CB homologues prevailed (47 %) in sediments. The content of the latter compounds in larvae was lower than in sediments, and higher for the other homologous groups. The study indicates selective bioaccumulation of various homologous groups of PCBs under conditions of low sediment PCB content.	Нет	0

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6.	научная статья	Across the benthic and pelagic realms: a species-level phylogeny of Benthesicymidae (Crustacea : Decapoda)	<a href="https://doi.org/10.1071/IS21004">https://doi.org/10.1071/IS21004</a>	Vereshchaka A.L., Kulagin D.N., Lunina A.A.	Invertebrate Systematics, 35, 2021	1445-5226	БАК; Ринц; Web of Science; Scopus	Benthesicymidae is a monophyletic group of Decapoda adapted to a life on the sea-floor, in the near-bottom layer, in the bathy- and in the mesopelagic, within an impressive depth range from a few hundred metres (Gennadas) to several thousand metres (Benthesicymus). Higher taxa are known to conquer all main oceanic biotopes such as the benthic, benthopelagic, and pelagic and a wide depth range but few family-level groups have clades evolved within all these oceanic realms. Therefore, the global fauna of Benthesicymidae provides a rare opportunity for an insight into phylogenetic processes favouring colonisation of all principal oceanic biotopes. The first comprehensive phylogenetic study of Benthesicymidae (all 37 valid species) is based on six molecular markers and 105 morphological characters (including 72 female and male copulatory characters). Analyses resulted in trees with similar topology and the same set of robust clades. Molecular methods based on 167 sequences (84 new) provided better resolution of deeper nodes and generally higher support of the clades, while morphological methods allowed analyses of all valid species of the global fauna. Phylogenetic analyses support the monophyly and robustness of all currently known genera except Gennadas, which was split into Gennadas Bate, 1881, Amalopenaeus Smith, 1882, and Notogennema gen. nov. We also retrieved two major clades for which we erected two new subfamilies: Benthesicyminae subfam. nov. (presumably benthic, genera Altelatipes, Bathicaris, Benthesicymus, and Benthonectes) and Gennadinae subfam. nov. (presumably pelagic, genera Amalopenaeus, Bentheogenennema, Benthoecetes, Boreogenennema, Gennadas, Maorrancaris, and Notogenennema gen. nov.). We revealed two groups of morphological characters, that are interlinked evolutionarily: (1) petasma and thelycum; (2) body, mouthparts, and pereopods. Morphological traits within benthic and pelagic clades are different, a model explaining the differences is proposed. Along with previous studies, our results confirm the idea that the elaboration of the copulatory structures is a key to successful colonisation of the pelagic realm. These results extend our knowledge about evolution in the largest habitual biotope of our planet and phylogenetic processes favouring colonisation of all principal oceanic biotopes.	Да (если в тексте публикации указано название ЦКП или УНУ)	778

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7.	научная статья	Bosminopsis deitersi (Crustacea: Cladocera) as an ancient species group: a revision	10.7717/pe erj.11310	Garibian P.G., Karabanov D.P., Neretina A.N., Taylor D.J., Kotov A.A.	PeerJ, PeerJ 9:e11310, 2021	21678359	BAK; Ринц; Web of Science; Scopus	Water fleas (Crustacea: Cladocera) of the Family Bosminidae have been studied since the founding of paleolimnology and freshwater ecology. However, one species, <i>Bosminopsis deitersi</i> , stands out for its exceptional multicontinental range and broad ecological requirements. Here we use an integrated morphological and multilocus genetic approach to address the species problem in <i>B. deitersi</i> . We analyzed 32 populations of <i>B. deitersi</i> s. lat. Two nuclear and two mitochondrial loci were used to carry out the bGMYC, mPTP and STACEY algorithms for species delimitation. Detailed morphological study was also carried out across continents. The evidence indicated a widely distributed cryptic species in the Old World ( <i>Bosminopsis zernowi</i> ) that is genetically divergent from <i>B. deitersi</i> s.str. We revised the taxonomy and redescribed the species in this complex. Our sampling indicated that <i>B. zernowi</i> had weak genetic differentiation across its range. A molecular clock and biogeographic analysis with fossil calibrations suggested a Mesozoic origin for the <i>Bosminopsis deitersi</i> group. Our evidence rejects the single species hypothesis for <i>B. deitersi</i> and is consistent with an ancient species group (potentially Mesozoic) that shows marked morphological conservation. The family Bosminidae, then, has examples of both rapid morphological evolution (Holocene <i>Bosmina</i> ), and morphological stasis ( <i>Bosminopsis</i> ).	Да (если в тексте публикации указано название ЦКП или УНУ)	34

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1	2	3	4	5	6	7	8	9	10	11
8.	научная статья	Ceriodaphnia smirnovi (Crustacea: Cladocera), a new species from the Mediterranean Region, and a phylogenetic analysis of the commonest species	<a href="https://doi.org/10.11646/zootaxa.4974.1.1">https://doi.org/10.11646/zootaxa.4974.1.1</a>	Alonso M., Neretina A., Ventura M.	Zootaxa, 4974, 2021	1175-5326	BAK; Ринц; Web of Science; Scopus	Species of the genus Ceriodaphnia Dana, 1853 (Crustacea: Cladocera: Daphniidae) are present in the plankton of many freshwater bodies all around the World. However, the taxonomy of the genus is still poorly developed. Most species have been described in the nineteenth century and data on their morphology and distribution should be revised according to current standards. Currently, due to lack of reliable morphological and genetic data, almost all nominal species of Ceriodaphnia are considered as species groups rather than separate biological species, complicating the detection and description of new species of the genus. Here, we redescribe the morphology of Ceriodaphnia quadrangula (O.F. Müller, 1785) based on material close to the type locality in Denmark, and describe a new species of Ceriodaphnia from the Mediterranean region. Also, we provide a phylogenetic analysis using existing and novel sequences of mitochondrial DNA of the commonest species of the genus. Ceriodaphnia smirnovi sp. nov. can be easily distinguished from C. quadrangula via presence of the head pore and the structure of the second thoracic limb, the postabdomen and the ephippium. From other species of Ceriodaphnia known to date C. smirnovi sp. nov. can also be separated on ephippium structure and some other fine morphological features. Although distribution range of C. smirnovi sp. nov. must be clarified in the future based on analysis of more sampling points, most likely, it is restricted to the Mediterranean region. The phylogenetic analyses showed high divergence among 16 different clades (mean clade separation of $13\pm2.3\%$ (mean $\pm$ SD) and $20.7\pm2.1\%$ for 16S and COI respectively). These clades belonged to 11 described species and 5 undescribed. The high intraspecific variability of some species indicates the possible existence of more undescribed species within present species groups.	Да (если в тексте публикации указано название ЦКП или УНУ)	43

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1	2	3	4	5	6	7	8	9	10	11
9.	научная статья	Connected across the ocean: taxonomy and biogeography of deep-water Nudibranchia from the Northwest Pacific reveal trans-Pacific links and two undescribed species	<a href="https://doi.org/10.1007/s13127-021-00526-8">https://doi.org/10.1007/s13127-021-00526-8</a>	Ekimova I., Valdés A., Stananova M., et al.	Organisms Diversity Evolution, 21, 2021	14396092	BAK; Ринц; Web of Science; Scopus	In this paper, we investigate a collection of Northwest Pacific nudibranch molluscs by means of integrative taxonomy, including morphological analyses, molecular data from the cytochrome c oxidase subunit I, 16S rRNA, histone H3, 28S rRNA, 18S rRNA markers, and ecological data. Two new species, <i>Bathydoris antoni</i> sp. nov. and <i>Dendronotus kurilensis</i> sp. nov., are described, and their phylogenetic relationships reconstructed. We also document two potentially new species of the genera <i>Cadlina</i> (Cadlinidae) and <i>Cuthona</i> (Fionidae s.l.). For the first time, we report molecular data for the Northwest Pacific specimens of <i>Colga pacifica</i> (Polyceridae), <i>Dendronotus patricki</i> (Dendronotidae), <i>Ziminella vrijenhoeki</i> (Paracoryphellidae), and <i>Zeusia herculea</i> (Aeolidiidae). Our molecular data supports the existence of biogeographic connections between the shallow water nudibranch fauna and their continental slope counterparts and communities on both sides of the North Pacific with possible ongoing gene exchange between fauna of both regions. We found two general types of deep shelf and bathyal communities inhabited by nudibranchs in the Northwest Pacific, each characterized by a certain type of fauna and a connectivity with different bathymetric and geographic areas.	Да (если в тексте публикации указано название ЦКП или УНУ)	27
10.	научная статья	Contribution to the knowledge of the immature stages of Palaearctic species of the genus <i>Anthonomus Germar</i> (Coleoptera: Curculionidae)	<a href="https://doi.org/10.1164/zootaxa.5032.4.1">https://doi.org/10.1164/zootaxa.5032.4.1</a>	Zabaluev I.A.	Zootaxa, 5032, 2021	1175-5326	BAK; Ринц; Web of Science; Scopus	The mature larvae and pupae of <i>Anthonomus (Anthonomidioides) rubripes</i> Gyllenhal, A. (s. str.) <i>incurvus</i> (Panzer), A. (s. str.) <i>conspersus</i> Desbrochers des Loges, and A. (s. str.) <i>latior</i> Pic, are described for the first time. The immature stages of <i>A. (Anthomorphus) pinivorax</i> Silfverberg, A. (s. str.) <i>pedicularius</i> (Linnaeus) (larva only), A. (s. str.) <i>rubi</i> (Herbst) are redescribed. The previous description of <i>A. (s. str.) pomorum</i> (Linnaeus) is checked and updated with new data. Keys for the identification of species of 9 larvae and 10 pupae of Palaearctic species are presented. Additional information on the biology of some species is provided. <i>Crataegus pinnatifida</i> is established as a host plant for the first time for <i>A. (s. str.) latior</i> .	Да (если в тексте публикации указано название ЦКП или УНУ)	487

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<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>	<b>9</b>	<b>10</b>	<b>11</b>
11.	научная статья	Dioxin Soil Contamination near Former Landfills	10.1134/S1 064229321 080123	Kudryavtseva A.D., Mir- Kadyrova E.Ya., Kalinkevich G.A., Brodskii E.S.	Eurasian Soil Science, 54, 2021	064-2293	BAK; Ринц; Web of Science; Scopus	Dioxin contamination levels and profiles of soils in New Moscow area were studied to identify the potential sources of contamination at a distance of 300 to 1000 m from the former Salar'evo, Shcherbinka, Sosenki, and Malinki landfills. The potential sources are derived using principal component analysis and positive matrix factorization. The total contamination level near the landfills does not significantly differ from those of urban soils in the same area. The congener profiles correspond to a combination of several dioxin contamination sources, including atmospheric deposition, various thermal processes, and spill of polychlorinated biphenyl technical fluids. A higher relative contribution of vehicle exhaust is characteristic of urban soils. As for the soils near former landfills, the congener profiles are more variable as well as, consequently, sources of contamination.	Нет	0

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12.	научная статья	Distribution, habitats, and redescription of the rare mite species <i>Iphidionopsis</i> <i>sculptus</i> Gwiazdowicz, 2004 (Mesostigmata: Ascidae)	<a href="https://doi.org/10.1164/zootaxa.4952.3.2">https://doi.org/10.1164/zootaxa.4952.3.2</a>	Makarova O.L., Marchenko I.I., Lindquist E.E.	Zootaxa, 4952, 2021	1175-5326	BAK; Ринц; Web of Science; Scopus	Iphidionopsis sculptus Gwiazdowicz, 2004, is currently known only from the type locality in eastern Poland and a record in southwestern Finland (Huhta, 2016). Here, we record this species from twelve localities elsewhere (Europe, Siberia, Far East of Russia, Canada) indicating its broadly Holarctic geographical range. Another genus member, <i>Iphidionopsis magnanalis</i> (Ma & Yin, 1999), is known only from China. About half of <i>Iphidionopsis sculptus</i> records are associated with litter of coniferous or mixed forests, but the others, including samples with juveniles (deutonymphs), were found in bracket fungi or under tree bark. The finding of two adult females on a bark beetle, <i>Dryocoetes affaber</i> (Mannerheim) (Coleoptera: Curculionidae: Scolytinae), suggests a phoretic association, though members of the closely related genus <i>Zerconopsis</i> Hull, 1918 as well as of all of the subfamily Arctoseiinae are known only from phoretic dispersal by nematoceran dipterans. The morphology of adults and an immature instar (deutonymph) of <i>I. sculptus</i> is redescribed and newly described, respectively, and illustrated in detail. A subdivision of the subfamily Arctoseiinae Evans, 1963 into three tribes is proposed—Arctoseiini Evans, 1963 (including <i>Arctoseius</i> Thor, 1930 and <i>Iphidozercon</i> Berlese, 1903), Zerconopsini tribe n. ( <i>Zerconopsis</i> Hull, 1918; <i>Xenoseius</i> Lindquist & Evans, 1965; and <i>Iphidionopsis</i> Gwiazdowicz, 2004), and Maxiniini tribe n. ( <i>Maximia</i> Lindquist & Makarova, 2012).	Да (если в тексте публикации указано название ЦКП или УНУ)	463

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13.	научная статья	ESTIMATION OF CARBON DIOXIDE FLUXES ON A RIDGE-HOLLOW BOG COMPLEX USING A HIGH RESOLUTION ORTHOPHOTOPLA N	10.24189/n cr.2021.02 0	Ivanov D.G., Kotlov I.P., Minayeva T.Yu., Kurbatova J.A.	Nature Conservation Research, 6(2), 2021	2500-008X	BAK; Ринц; Web of Science; Scopus	The use of unmanned aerial vehicles for detailed mapping of ecosystems has become increasingly important in recent years. As one of the main terrestrial carbon reserves, peatland ecosystems are of the great interest in obtaining highly detailed orthophotoplans. At the same time, there is a lack of publications devoted to the total carbon dioxide fluxes in each type of bog microforms. This paper presents the results of our study, which aimed to develop methods for mapping peatland microlandscapes and for estimation of integral carbon dioxide fluxes between the peatland surface and the atmosphere. Based on a highly detailed orthophotoplan compiled using unmanned aerial vehicles, we assessed the areas of major microform groups (swamps, hollows, and ridges) in a bog located in the Central Forest State Nature Biosphere Reserve (European Russia). The classification accuracy ranged from 79% to 93%. The areas of ridges, hollows, and swamps were 0.16 km <sup>2</sup> , 0.32 km <sup>2</sup> , and 0.12 km <sup>2</sup> , respectively. To make an integral estimation of carbon dioxide fluxes, we used earlier data on carbon dioxide emissions (ecosystem respiration), uptake (gross ecosystem exchange), and balance (net ecosystem exchange) measured by soil chamber method on representative experimental plots of respective microform types. After recalculating fluxes to areas of microforms, the integral values for different classes in the summer seasons of 2014, 2016 and 2017 were 15–91 kg CO <sub>2</sub> × h <sup>-1</sup> for ecosystem respiration, 21–190 kg CO <sub>2</sub> × h <sup>-1</sup> for gross ecosystem exchange, and from -122 kg CO <sub>2</sub> × h <sup>-1</sup> to 41 kg CO <sub>2</sub> × h <sup>-1</sup> for net ecosystem exchange. The results of the study confirmed that highly detailed orthophotoplans, obtained with the use of unmanned aerial vehicles, make it possible to distinguish the boundaries of such bog microforms as swamps, hollows and ridges with a high accuracy, despite the presence of some errors in the classification. The study of the structural and functional organisation of the bog should be carried out with considering its seasonal and interannual dynamics as well as all microform types.	Да (если в тексте публикации указано название ЦКП или УНУ)	7

№ п/п	Вид публикации	Наименование публикации	DOI публикации	Автор(ы)	Издание, номер, год	ISSN / ISBN издания	Индексация издания	Краткое описание научных результатов, полученных на оборудовании ЦКП	Наличие в публикации ссылки на ЦКП	Страница, содержащая ссылку на ЦКП
1	2	3	4	5	6	7	8	9	10	11
14.	научная статья	Foliar stable isotope ratios of carbon and nitrogen in boreal forest plants exposed to long-term pollution from the nickel-copper smelter at Monchegorsk, Russia	<a href="https://doi.org/10.1007/s11356-022-19261-4">https://doi.org/10.1007/s11356-022-19261-4</a>	Manninen S., Zverev V., Kozlov M.	Environmental Science and Pollution Research, 188, 2021	0944-1344	BAK; Ринц; Web of Science; Scopus	Long-term exposure to primary air pollutants, such as sulphur dioxide (SO <sub>2</sub> ) and nitrogen oxides (NO <sub>x</sub> ), alters the structure and functions of forest ecosystems. Many biochemical and biogeochemical processes discriminate against the heavier isotopes in a mixture; thus, the values of δ <sup>13</sup> C and δ <sup>15</sup> N (i.e. the ratio of stable isotopes <sup>13</sup> C to <sup>12</sup> C and that of <sup>15</sup> N to <sup>14</sup> N, respectively) may give insights into changes in ecosystem processes and identify the immediate drivers of these changes. We studied sources of variation in the δ <sup>13</sup> C and δ <sup>15</sup> N values in the foliage of eight boreal forest C <sub>3</sub> plants at 10 sites located at the distance of 1–40 km from the Monchegorsk nickel-copper smelter in Russia. From 1939–2019, this smelter emitted over 14,000,000 metric tons (t) of SO <sub>2</sub> , 250,000 t of metals, primarily nickel and copper, and 140,000 t of NO <sub>x</sub> . The δ <sup>13</sup> C value in evergreen plants and the δ <sup>15</sup> N value in all plants increased near the smelter independently of the plant mycorrhizal type. We attribute the pollution-related increase in the foliar δ <sup>13</sup> C values of evergreen species mainly to direct effects of SO <sub>2</sub> on stomatal conductance, in combination with pollution-related water stress, which jointly override the potential opposite effect of increasing ambient CO <sub>2</sub> concentration on δ <sup>13</sup> C values. Stomatal uptake of NO <sub>x</sub> and root uptake of <sup>15</sup> N-enriched organic N compounds and NH <sub>4</sub> <sup>+</sup> may explain the increased foliar δ <sup>15</sup> N values and elevated foliar N concentrations, especially in the evergreen trees ( <i>Pinus sylvestris</i> ), close to Monchegorsk, where the soil inorganic N supply is reduced due to the impact of long-term SO <sub>2</sub> and heavy metal emissions on plant biomass. We conclude that, despite the uncertainties in interpreting δ <sup>13</sup> C and δ <sup>15</sup> N responses to pollution, the Monchegorsk smelter has imposed and still imposes a great impact on C and N cycling in the surrounding N-limited subarctic forest ecosystems.	Да (если в тексте публикации указано название ЦКП или УНУ)	5

№ п/п	Вид публикац ии	Наименование публикации	DOI публикац ии	Автор(ы)	Издание, номер, год	ISSN / ISBN издания	Индексация издания	Краткое описание научных результатов, полученных на оборудовании ЦКП	Наличие в публикации ссылки на ЦКП	Страница , содержащ ая ссылку на ЦКП
1	2	3	4	5	6	7	8	9	10	11
15.	научная статья	Food-web modification in the eastern Gulf of Finland after invasion of <i>Marenzelleria arctica</i> (Spionidae, Polychaeta)	10.3897/ne obiota.66.6 3847	Golubkov S., Tiunov A., Golubkov M.	NeoBiota, 66, 2021	1619-0033	BAK; Ринц; Web of Science; Scopus	The paucity of data on non-indigenous marine species is a particular challenge for understanding the ecology of invasions and prioritising conservation and research efforts in marine ecosystems. <i>Marenzelleria</i> spp. are amongst the most successful non-native benthic species in the Baltic Sea during recent decades. We used stable isotope analysis (SIA) to test the hypothesis that the dominance of polychaete worm <i>Marenzelleria arctica</i> in the zoobenthos of the Neva Estuary after its invasion in the late 2000s is related to the position of this species in the benthic food webs. The trend towards a gradual decrease in the biomass of <i>Marenzelleria</i> worms was observed during 2014–2020, probably due to significant negative relationships between the biomass of oligochaetes and polychaetes, both of which, according to SIA, primarily use allochthonous organic carbon for their production. The biomass of benthic crustaceans practically did not change and remained very low. The SIA showed that, in contrast to the native crustacean <i>Monoporeia affinis</i> , polychates are practically not consumed either by the main invertebrate predator <i>Saduria entomon</i> , which preys on <i>M. affinis</i> , oligochaetes and larvae of chironomids or by benthivorous fish that prefer native benthic crustaceans. A hypothetical model for the position and functional role of <i>M. arctica</i> in the bottom food web is presented and discussed. According the model, the invasion of <i>M. arctica</i> has created an offshoot food chain in the Estuary food webs. The former dominant food webs, associated with native crustaceans, are now poorly developed. The lack of top-down control obviously contributes to the significant development of the <i>Marenzelleria</i> food chain, which, unlike native food chains, does not provide energy transfer from autochthonous and allochthonous organic matter to the upper trophic levels. The study showed that an alien species, without displacing native species, can significantly change the structure of food webs, creating blind offshoots of the food chain.	Да (если в тексте публикации указано название ЦКП или УНУ)	80

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1	2	3	4	5	6	7	8	9	10	11
16.	научная статья	Genetic diversity and population structure of the grey wolf ( <i>Canis lupus</i> Linnaeus, 1758) and evidence of wolf × dog hybridisation in the centre of European Russia	<a href="https://doi.org/10.1007/s42991-020-00074-2">https://doi.org/10.1007/s42991-020-00074-2</a>	Korablev M.P., Korablev N.P., Korablev P.N.	Mammalian Biology, 101, 2021	1616-5047	BAK; Ринц; Web of Science; Scopus	Throughout history the human-wolf interaction has not evolved in favour of the wolf, however, wolves have never been endangered in Russia. The wolf ( <i>Canis lupus lupus</i> L., 1758) population in the central part of European Russia is relatively high, where environmental conditions, such as relatively undisturbed habitats, wide forested areas and abundance of natural prey, have always contributed to the long-term survival of the species. The human persecution of wolves has resulted in almost total extinction of the species in many European countries. In Russia, extermination campaigns have led to severe fluctuations in the number of wolves during the second half of the twentieth century, however, since the early 1990s there has been a tendency towards constant growth in the numbers. Previous studies provided preliminary data on population genetics of the wolf population in European Russia and have generally shown homogeneity of the population structure as well as detecting genetic bottleneck. However, the comprehensive study of genetic diversity and population structure during the period following the last severe decline is of great interest. Another important aspect in the study of wolf populations is the assessment of the magnitude of wolf × dog hybridisation, which is a phenomenon of conservation and social significance. We used 101 samples from the wolf population and 32 dogs to examine population structure, genetic diversity and events of interspecific hybridisation in the centre of European Russia, based on analysis of 11 autosomal microsatellites. In the studied region, wolves exhibit a high level of genetic diversity ( $HE = 0.79 \pm 0.03$ , $HO = 0.74 \pm 0.01$ , $NA = 10.00 \pm 5.02$ ) which is superior to that in most European populations. Analysis of temporal samples suggests a slight increase in heterozygosity over time, although in the first period following population decline, the level of genetic diversity is not depleted. We found a lack of spatial structure and a weak pattern of isolation by distance ( $b = -0.007$ , $P < 0.001$ ), which are clear cases of intense gene flow and social organisation of the species. Our preliminary results suggest a relatively low rate of hybridisation in the studied region (around 3%), however, additional studies are needed to provide more reliable conclusions on this topic. This paper is the first attempt at both a detailed study of spatio-temporal population genetics and analysis of hybridisation in the wolves of Central Russia.	Да (если в тексте публикации указано название ЦКП или УНУ)	101
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№ п/п	Вид публикац ии	Наименование публикации	DOI публикац ии	Автор(ы)	Издание, номер, год	ISSN / ISBN издания	Индексация издания	Краткое описание научных результатов, полученных на оборудовании ЦКП	Наличие в публикации ссылки на ЦКП	Страница , содержащ ая ссылку на ЦКП
1	2	3	4	5	6	7	8	9	10	11
17.	научная статья	Geographical distribution of dioxins, cadmium, and mercury concentrations in reindeer liver, kidneys, and muscle in the Russian Far North	<a href="https://doi.org/10.1007/s11356-021-16310-2">https://doi.org/10.1007/s11356-021-16310-2</a>	Makarov D.A., Ovcharenko V.V., Nebera E.A., Kozhushkevich A.I., et al.	Environmental Science and Pollution Research, 29, 2021	1614-7499	BAK; Ринц; Web of Science; Scopus	Reindeer herding is a vitally important agricultural sector in the Russian Far North. It is believed that Northern ecosystems readily accumulate persistent pollutants because of trophic chains and climate features peculiar to the region. Reindeers graze on vast areas, and their seasonal migrations to distances of up to hundreds of kilometers in the North-South direction increase the likelihood of crossing a locally polluted area. Here, we present the results of a large-scale nationwide study of reindeer liver, kidneys, and muscle pollution by dioxins, cadmium, and mercury. Samples were taken in 2015–2020 from 41 locations in 8 reindeer-herding regions of Russia. Dioxins were determined in 383 samples of liver and 13 of muscle, and cadmium and mercury—in 505 samples of liver, 315 of kidneys, and 22 of muscle. Dioxin pollution has shown a clear geographical trend, i.e., liver concentrations of dioxins steadily decrease from the Western to the Eastern parts on the Russian Far North, with the highest concentration of 76.5 pg/g of fat WHO-TEQ. The discovered trend may be explained by the pattern of chemical plants' localization and by the density of reindeer population (as known from the literature sources). The highest concentrations of metals were found in kidneys (7.3 mg/kg of cadmium and 1.1 mg/kg of mercury). The contribution of local sources to cadmium and mercury pollution was found to be less than expected. We also suggest that reindeer liver may serve as a good additional indicator of environmental pollution by dioxins and heavy metals.	Нет	0

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1	2	3	4	5	6	7	8	9	10	11
18.	научная статья	Hair microstructure in some rodent species of Diatomyidae, Ctenodactylidae, and Echimyidae (Ctenohystrica, Rodentia)	<a href="https://doi.org/10.1016/j.jcz.2021.02.006">https://doi.org/10.1016/j.jcz.2021.02.006</a>	Chernova O.F., Zhrebtsova O.V.	Zoologischer Anzeiger, 291, 2021	00445231	BAK; Ринц; Web of Science; Scopus	The pelage differentiation, microstructure and internal architecture of hair and their derivatives were studied for the first time at the level of scanning electron microscopy in the relict species <i>Laonastes aenigmamus</i> and in some other poorly studied representatives of the clade Ctenohystrica (Rodentia): <i>Pectinator spekei</i> , <i>Ctenodactylus gundi</i> , <i>Proechimys guyannensis</i> , <i>Echimys</i> sp., and <i>Thrichomys apereoides</i> . The data obtained are relevant for comparative taxonomic and morpho-functional analysis. Fur differentiation in the studied species is species-specific, but the microstructure of trunk hairs and its quantitative characteristics are mostly specific at the family level. Hair architectonics always shows a tendency toward increasing complexity and functional specialization at such special locations as the facial region, tail, and toes. Hair microstructure of <i>Laonastes</i> is highly unusual and is unknown in other Ctenohystrica and other rodents studied to date, which supports the notion that this species constitutes a phylogenetically distinct group. Microstructure of spines in Echimyidae is similar to that in Cricetidae and Muridae (Myomorpha), which suggests a certain similarity between early stages of formation of spines as protective structures in different evolutionary lineages of the Rodentia.	Да (если в тексте публикации указано название ЦКП или УНУ)	63

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1	2	3	4	5	6	7	8	9	10	11
19.	научная статья	Intra-Body Variations of Stable Isotope Ratios (δ13C, δ15N) and Influence of Storage Methods in Aquatic and Post- Aquatic Stages of the Common Toad, <i>Bufo bufo</i>	<a href="https://doi.org/10.3390/w13182544">https://doi.org/10.3390/w13182544</a>	Reshetnikov A.N., Korobushkin D.I.	Water, 82, 2021	2073-4441	BAK; Ринц; Web of Science; Scopus	Isotopic signatures of carbon and nitrogen are widely used for analysis of the structure of food webs in aquatic ecosystems. The study of animals raises a number of methodological questions, including choice of representative tissues and organs for sampling as well as storage of the studied organisms. Furthermore, the impacts of preservation methods can be tissue-specific, age-specific, and even taxon-specific; thus, studies of these impacts on particular taxa are necessary. We focused on the C and N isotope composition of the common toad ( <i>Bufo bufo</i> ), one of the most widespread European anuran amphibians. We hypothesized that its different tissues and organs may vary in isotopic composition, and ethanol and freezing may have different effects on isotopic values. Our results showed that both "tissue" and "storage method" factors significantly affected the δ13C values of tadpoles and postmetamorphic juveniles, whereas only the "tissue" factor had a significant effect on the δ15N values. The two stages, tadpoles and postmetamorphs, should be analyzed separately despite the brief postmetamorphic period of the juveniles. The skin, legs, muscles, and tail in tadpoles and legs, muscles and heart in juveniles can be used for δ13C and δ15N analysis regardless of the method of storage. The results will serve for the optimization of future study designs in isotopic ecology.	Да (если в тексте публикации указано название ЦКП или УНУ)	3

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1	2	3	4	5	6	7	8	9	10	11
20.	научная статья	Large-scale and fine-grain population structure and genetic diversity of snow leopards ( <i>Panthera uncia</i> Schreber, 1776) from the northern and western parts of the range with an emphasis on the Russian population	<a href="https://doi.org/10.1007/s10592-021-01347-0">https://doi.org/10.1007/s10592-021-01347-0</a>	Korablev M.P., Poyarkov A.D., Karnaughov A.S., Zvychaynaya E.Yu., et al.	Conservation Genetics, 22, 2021	1566-0621	BAK; Ринц; Web of Science; Scopus	The snow leopard ( <i>Panthera uncia</i> Schreber, 1776) population in Russia and Mongolia is situated at the northern edge of the range, where instability of ecological conditions and of prey availability may serve as prerequisites for demographic instability and, consequently, for reducing the genetic diversity. Moreover, this northern area of the species distribution is connected with the western and central parts by only a few small fragments of potential habitats in the Tian-Shan spurs in China and Kazakhstan. Given this structure of the range, the restriction of gene flow between the northern and other regions of snow leopard distribution can be expected. Under these conditions, data on population genetics would be extremely important for assessment of genetic diversity, population structure and gene flow both at regional and large-scale level. To investigate large-scale and fine-grain population structure and levels of genetic diversity we analyzed 108 snow leopards identified from noninvasively collected scat samples from Russia and Mongolia (the northern part of the range) as well as from Kyrgyzstan and Tajikistan (the western part of the range) using panel of eight polymorphic microsatellites. We found low to moderate levels of genetic diversity in the studied populations. Among local habitats, the highest heterozygosity and allelic richness were recorded in Kyrgyzstan ( $He = 0.66 \pm 0.03$ , $Ho = 0.70 \pm 0.04$ , $Ar = 3.17$ ) whereas the lowest diversity was found in a periphery subpopulation in Buryatia Republic of Russia ( $He = 0.41 \pm 0.12$ , $Ho = 0.29 \pm 0.05$ , $Ar = 2.33$ ). In general, snow leopards from the western range exhibit greater genetic diversity ( $He = 0.68 \pm 0.04$ , $Ho = 0.66 \pm 0.03$ , $Ar = 4.95$ ) compared to those from the northern range ( $He = 0.60 \pm 0.06$ , $Ho = 0.49 \pm 0.02$ , $Ar = 4.45$ ). In addition, we have identified signs of fragmentation in the northern habitat, which have led to significant genetic divergence between subpopulations in Russia. Multiple analyses of genetic structure support considerable genetic differentiation between the northern and western range parts, which may testify to subspecies subdivision of snow leopards from these regions. The observed patterns of genetic structure are evidence for delineation of several management units within the studied populations, requiring individual approaches for conservation initiatives, particularly related to translocation projects. The causes for the revealed patterns of genetic structure and levels of genetic diversity are discussed.	Да (если в тексте публикации указано название ЦКП или УНУ)	407
	16.11.2022			Центр коллективного пользования «Инструментальные методы в экологии» (Коллективный проект)						18 из 34

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1	2	3	4	5	6	7	8	9	10	11
21.	научная статья	Molecular phylogeny and revised classification of the Buccinoidea (Neogastropoda)	<a href="https://doi.org/10.1093/zoolinnean/zlab031">https://doi.org/10.1093/zoolinnean/zlab031</a>	Kantor Yu.I., Fedosov A.E., Kosyan A.R., Puillandre N., et al.	Zoological Journal of the Linnean Society, 194, 2021	0024-4082	BAK; Ринц; Web of Science; Scopus	The superfamily Buccinoidea is distributed across the oceans of the world from the Arctic Ocean to the Antarctic and from intertidal to abyssal depths. It encompasses 3351 recent species in 337 genera. The latest taxonomic account recognized eight full families. For the first time, the monophyly of the superfamily and the relationships among the families are tested with molecular data supplemented by anatomical and radula data. Five genetic markers were used: fragments of mitochondrial COI, 16S rRNA, 12S rRNA and nuclear Histone 3 (H3) and 28S rRNA genes (for 225 species of 117 genera). Our analysis recovered Buccinoidea monophyletic in Bayesian analyses. The relationships between the formerly recognized families and subfamilies are drastically revised and a new classification of the superfamily is here proposed, now including 20 taxa of family rank and 23 subfamilies. Five new families (Chauvetiidae, Dolicholatiridae, Eosiphonidae, Prodottiidae and Retimohniidae) and one subfamily of Nassariidae (Tomliniinae) are described. Austrosiphonidae and Tuditidae are resurrected from synonymy and employed in a new taxonomical extension. All but 40 recent genera are reclassified. Our results demonstrate that anatomy is rather uniform within the superfamily. With exceptions, the rather uniform radular morphology alone does not allow the allocation of genera to a particular family without additional molecular data.	Да (если в тексте публикации указано название ЦКП или УНУ)	63

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1	2	3	4	5	6	7	8	9	10	11
22.	научная статья	Novel Extract from Beetle <i>Ulomoides dermestoides</i> : A Study of Composition and Antioxidant Activity	<a href="https://doi.org/10.3390/antiox10071055">https://doi.org/10.3390/antiox10071055</a>	Ushakova N.A., Brodsky E.S., Tikhonova O.V., Dontsov A.E., et al.	Antioxidants, 10, 2021	20763921	BAK; Ринц; Web of Science; Scopus	A biologically active extract from the darkling beetle <i>Ulomoides dermestoides</i> was obtained using the electro-pulse plasma dynamic extraction method. The beetle water extract contained a complex of antioxidant substances such as antioxidant enzymes and nonprotein antioxidants, as well as a complex of heat shock antistress proteins. This determines the rather high antioxidant activity of the aqueous extract of the beetle, i.e., 1 mg of dry matter/mL of the extract has an equivalent antioxidant activity to 0.2 mM Trolox (a water-soluble analog of vitamin E). It was shown that the beetle extract can lead to a 25–30% increase in the average lifespan of nematode <i>Caenorhabditis elegans</i> , under normal conditions, and a 12–17% increase under conditions of oxidative stress (with paraquat), and significantly inhibits the fructosylation reaction of serum albumin. Therefore, the beetle aqueous extract shows promise as a biologically active complex exhibiting antioxidant activity.	Нет	0

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1	2	3	4	5	6	7	8	9	10	11
23.	научная статья	Properties of the Yeast Communities Associated with Termites of a Tropical Monsoon Forest: Cat Tien National Park, Vietnam	10.1134/S0026261721040172	Zueva A.I., Kachalkin A.V., Maksimova I.A., Van Thinh N., Tiunov A.V.	Microbiology, 90 (4), 2021	0026-2617	BAK; Ринц; Web of Science; Scopus	Исследовано дрожжевое население субстратов, связанных с термитниками пяти видов терmitов, распространенных на территории национального парка Кат Тиен (южный Вьетнам): стенок гнезда, грибных садов (при их наличии), кишечника и поверхности тела терmitов, а также листового опада и верхних горизонтов почвы вблизи термитников. Проанализированы морфо-физиологические особенности выделенных из ассоциаций с термитами дрожжей. Выделенные грибы с дрожжевым ростом отнесены к 39 видам, из которых 10 не были описаны на момент проведения исследования. Сообщества дрожжей, формирующиеся на поверхности тел и в кишечнике терmitов, характеризуются низким видовым разнообразием. Для дрожжевых грибов, выделенных из кишечника и с поверхности тел терmitов, характерен относительно широкий спектр морфологических и физиологических свойств (от 24 до 33 показателей из 34 пунктов стандартного описания), среди наиболее общих свойств можно отметить наличие структур мицелиального роста, способность сбраживать глюкозу, потреблять в качестве источника питания растительные гликозиды (салцицин) и простые продукты разрушения древесины (ксилозу и целлобиозу).	Да (если в тексте публикации указано название ЦКП или УНУ)	490

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1	2	3	4	5	6	7	8	9	10	11
24.	научная статья	Rare, deep-water and similar: revision of Sibogasyrinx (Conoidea: Cochlespiridae)	<a href="https://doi.org/10.5852/ejt.2021.773.1509">https://doi.org/10.5852/ejt.2021.773.1509</a>	Kantor Yu.I., Puillandre N.	European Journal of Taxonomy, 773, 2021	2118-9773	BAK; Ринц; Web of Science; Scopus	The genus Sibogasyrinx has to date included only four species of rare deep-water Conoidea, each known from few specimens. In shell characters it strongly resembles three distantly-related genera, two of which, Comitas and Leucosyrinx, belong to a different family, the Pseudomelatomidae. A molecular phylogenetic analysis of a large amount of material of Conoidea has revealed the existence of much additional undescribed diversity within Sibogasyrinx from the central Indo-Pacific and temperate Northern Pacific. Based on partial sequences of the mitochondrial cox1 gene and morphological characters of 54 specimens, 10 species hypotheses are proposed, of which six are described as new species: <i>S. subula</i> sp. nov., <i>S. lolae</i> sp. nov., <i>S. maximei</i> sp. nov., <i>S. clausura</i> sp. nov., <i>S. pagodiformis</i> sp. nov. and <i>S. elbakyanae</i> Kantor, Puillandre & Bouchet sp. nov. One of the previously described species was absent in our material. Most of the new species are very similar and are compared to Leucosyrinx spp. Species of Sibogasyrinx are unique among Conoidea on account of the high intrageneric variability in radular morphology. Three distinct radula types are found within Sibogasyrinx, two of which are confined to highly supported subclades.	Да (если в тексте публикации указано название ЦКП или УНУ)	58

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1	2	3	4	5	6	7	8	9	10	11
25.	научная статья	Spruce girdling decreases abundance of fungivorous soil nematodes in a boreal forest	<a href="https://doi.org/10.1016/j.soilbio.2021.108184">https://doi.org/10.1016/j.soilbio.2021.108184</a>	Kudrin A.A., Zuev A.G., Taskaeva A.A., Konakova T.N., et al.	Soil Biology and Biochemistry, 155, 2021	0038-0717	BAK; Ринц; Web of Science; Scopus	The relative importance of belowground and aboveground energy inputs for the decomposer communities in soil remains largely unknown. In particular, no research has been done on the significance of root-derived resources for nematode communities in boreal forests. In two spruce stands in the taiga zone, we set up a field experiment in which girdling of spruce trees and clipping of dwarf shrubs was performed. Root-derived resources were hypothesized to be highly important; accordingly, we expected to observe a suppression of the nematode community after experimental manipulations. To obtain information on the nature of changes in the soil food web, nematode community structure indices were applied. In partial confirmation of our hypothesis, spruce girdling decreased mycorrhizal hyphae biomass as assessed via in-growth mesh bags, as well as the abundance of fungivorous nematodes, mostly of the Aphelenchoides and Filenchus genera. The enrichment index (EI) value decreased, indicating reduction of organic matter inputs into the soil food web, whereas nematode channel ratio (NCR) index value increased, indicating a shift towards domination of the bacterial energy channel. Total nematode abundance, genera richness, and abundance of herbivores, omnivores, and predators did not change in response to spruce girdling. Clipping of dwarf shrubs decreased fungal and bacterial PLFA biomarkers, but did not affect nematode communities. Thus, the resources channeled in soil by the roots of canopy trees are of different relative importance for nematodes having different trophic habits. Fungivorous nematodes are at least partly dependent on root-derived resources, suggesting feeding on ectomycorrhizal mycelium. Rhizodeposits of understory vegetation are likely of low importance for nematodes.	Да (если в тексте публикации указано название ЦКП или УНУ)	3

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1	2	3	4	5	6	7	8	9	10	11
26.	научная статья	The FLUXNET2015 dataset and the ONEFlux processing pipeline for eddy covariance data	<a href="https://doi.org/10.1038/s41597-020-0534-3">https://doi.org/10.1038/s41597-020-0534-3</a>	Pastorello G., et al.	Scientific data, 8:72, 2021	2052-4463	BAK; Ринц; Web of Science; Scopus	The FLUXNET2015 dataset provides ecosystem-scale data on CO <sub>2</sub> , water, and energy exchange between the biosphere and the atmosphere, and other meteorological and biological measurements, from 212 sites around the globe (over 1500 site-years, up to and including year 2014). These sites, independently managed and operated, voluntarily contributed their data to create global datasets. Data were quality controlled and processed using uniform methods, to improve consistency and intercomparability across sites. The dataset is already being used in a number of applications, including ecophysiology studies, remote sensing studies, and development of ecosystem and Earth system models. FLUXNET2015 includes derived-data products, such as gap-filled time series, ecosystem respiration and photosynthetic uptake estimates, estimation of uncertainties, and metadata about the measurements, presented for the first time in this paper. In addition, 206 of these sites are for the first time distributed under a Creative Commons (CC-BY 4.0) license. This paper details this enhanced dataset and the processing methods, now made available as open-source codes, making the dataset more accessible, transparent, and reproducible.	Нет	0
27.	научная статья	The re-description of <i>Synoeasnema hirsutum</i> Timm, 1959 ( <i>Synoeasneminae</i> , <i>Ungellidae</i> , <i>Drilonematoidea</i> ) from a pheretimoid earthworm in Vietnam with the analysis of its phylogenetic relationships	10.3897/zootkeys.107675932	Ivanova E.S., Efeykin B.D., Spiridonov S.E.	ZooKeys, 1076, 2021	1313-2989	BAK; Ринц; Web of Science; Scopus	<i>Synoeasnema hirsutum</i> Timm, 1959 ( <i>Ungellidae</i> , <i>Drilonematoidea</i> ), found in the body cavity of the pheretimoid earthworm at the border of Laos and Vietnam, was re-described and illustrated. The mitochondrial genome of <i>S. hirsutum</i> obtained with Illumina HiSeq sequencing is the first annotated mitochondrial genome as a representative of the superfamily <i>Drilonematoidea</i> . The phylogeny inferred from the analysis of 12 mitochondrial genes has shown some similarity of <i>S. hirsutum</i> with a cephalobid <i>Acroboloides varius</i> .	Да (если в тексте публикации указано название ЦКП или УНУ)	138

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1	2	3	4	5	6	7	8	9	10	11
28.	научная статья	Trophic positions and niche segregation of two anuran species in the ecosystem of a forest lake	10.1007/s1 0750-021-0 4674-y	Reshetnikov A.N., Korobushkin D.I., Gongalsky K.B., et al.	Hydrobiologia, 848, 2021	00188158	BAK; РИНЦ; Web of Science; Scopus	Different species of amphibians often breed in the same water bodies and their diets overlap. Theoretically, this might lead to a competitive elimination of either one but there are multispecies temporal larval communities persisting over the years. We hypothesized that larvae of two common European anuran species segregate their trophic niches despite their omnivorous habits and possible similarity of trophic levels. We assessed interspecific differences in food assimilation at larval and postmetamorphic stages of two anurans in an ecosystem of forest lake and an adjacent terrestrial ecosystem using a stable isotope approach. Trophic level of tadpoles of both species corresponded to those of some benthic invertebrate predators. Trophic positions of postmetamorphic juveniles corresponded to those of terrestrial invertebrate predators. The unpredictable decrease of $\delta^{15}\text{N}$ values in anuran tissues during the transition from aquatic to terrestrial habitats corresponded to the differences between aquatic and terrestrial isotopic baselines whereas dynamics of normalized $\delta^{15}\text{N}$ confirmed an increase in their trophic level. Finally, we detected a strong segregation of trophic niches of the two species at both larval and postmetamorphic stages. The described niche separation provides an important prerequisite for decreasing possible intraspecific competition and promoting long-term co-existence of these syntopic anurans.	Да (если в тексте публикации указано название ЦКП или УНУ)	4812

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1	2	3	4	5	6	7	8	9	10	11
29.	научная статья	Trophic-based diversification in benthivorous charrs ( <i>Salvelinus</i> ) dwelling littoral zones of Northern lakes	<a href="https://doi.org/10.1007/s10750-021-04628-4">https://doi.org/10.1007/s10750-021-04628-4</a>	Markevich G.N., Esin E.N., Medvedev D.A., Busarova O.Yu., Tiunov A.V.	Hydrobiologia, 265, 2021	00188158	BAK; Ринц; Web of Science; Scopus	Charrs of the genus <i>Salvelinus</i> form distinct trophic morphs living in sympatry in numerous postglacial lakes. Here we demonstrate that charrs can diversify into amphipod foraging specialists and sedentary macrobenthos consumers in the shallow-water ecosystems. This pattern was revealed in three out of six lakes under exploration supported by differences in stomach content, trophic-transmitted parasite, and stable isotope ratio analyzes. The body shape and growth rate comparison indicates that this kind of trophic-based diversification emerges at a juvenile stage and is maintained throughout the whole life. The restriction in gene flow found between the morphs allows to propose the possibility for the heritable-based specialization to evolve. We found that those diversification phenomena are possible only in the lakes situated in vicinity of the ocean coastline, while no evidence of this split was found for inland mountain lakes. We suggest that the trophic-based diversification in the littoral ecosystems is accounted for the heterogeneity in the ecological conditions and food resources' distribution linked to coastal wind action. This phenomenon was previously reported for the charr in Lake Fjellfrosvatn, Scandinavia, so it seems to be some universal yet poorly described kind of disruptive selection pressure for northern latitude fishes.	Да (если в тексте публикации указано название ЦКП или УНУ)	4117

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1	2	3	4	5	6	7	8	9	10	11
30.	научная статья	Unexpected mitochondrial lineage diversity within the genus <i>Alonella</i> Sars, 1862 (Crustacea: Cladocera) across the Northern Hemisphere	10.7717/peerj.10804	Neretina A.N., Karabanov D.P., Sacherova V., Kotov A.A.	PeerJ, peerj.10804, 2021	21678359	BAK; Ринц; Web of Science; Scopus	Representatives of the genus <i>Alonella</i> Sars (Crustacea: Cladocera: Chydorinae) belong to the smallest known water fleas. Although species of <i>Alonella</i> are widely distributed and often abundant in acidic and mountain water bodies, their diversity is poorly studied. Morphological and genetic approaches have been complicated by the minute size of these microcrustaceans. As a result, taxonomists have avoided revising these species. Here, we present genetic data on <i>Alonella</i> species diversity across the Northern Hemisphere with particular attention to the <i>A. excisa</i> species complex. We analyzed 82 16S rRNA sequences (all newly obtained), and 78 COI sequences (39 were newly obtained). The results revealed at least twelve divergent phylogenetic lineages, possible cryptic species, of <i>Alonella</i> , with different distribution patterns. As expected, the potential species diversity of this genus is significantly higher than traditionally accepted. The <i>A. excisa</i> complex is represented by nine divergent clades in the Northern Hemisphere, some of them have relatively broad distribution ranges and others are more locally distributed. Our results provide a genetic background for subsequent morphological analyses, formal descriptions of <i>Alonella</i> species and detailed phylogeographical studies.	Да (если в тексте публикации указано название ЦКП или УНУ)	17

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1	2	3	4	5	6	7	8	9	10	11
31.	научная статья	Vocal phenotype of male rutting roars and genetic markers delineate East European red deer ( <i>Cervus elaphus</i> ) from Central and West European populations	<a href="https://doi.org/10.1007/s00114-021-01742-0">https://doi.org/10.1007/s00114-021-01742-0</a>	Golosova O.S., Kholodova M.V., Volodin I.A., Volodina E.V., et al.	The Science of Nature, 108, 2021	0028-1042	BAK; Ринц; Web of Science; Scopus	century from Germany to the Voronezh region of the European part of Southern Russia and then developed without further introductions. We characterize for the first time the vocal phenotype of the Voronezh red deer male rutting calls in comparison with similar data on the Pannonian (native Central European) and Iberian (native West European) red deer obtained by the authors during preceding studies. In addition, we provide for the first time the genetic data on Pannonian red deer. In Voronezh stags, the number of roars per bout ( $2.85 \pm 1.79$ ) was lower than in Pannonian ( $3.18 \pm 2.17$ ) but higher than in Iberian ( $2.11 \pm 1.71$ ) stags. In Voronezh stags, the duration of main (the longest within bouts) roars was longer ( $2.46 \pm 1.14$ s) than in Pannonian ( $1.13 \pm 0.50$ s) or Iberian ( $1.90 \pm 0.50$ s) stags. The maximum fundamental frequency of main roars was similar between Voronezh ( $175 \pm 60$ Hz) and Pannonian ( $168 \pm 61$ Hz) but higher in Iberian stags ( $223 \pm 35$ Hz). Mitochondrial cytochrome b gene analysis of red deer from the three study populations partially supports the bioacoustical data, of closer similarity between Voronezh and Pannonian populations. In contrast, microsatellite DNA analysis delineates Voronezh red deer from either Pannonian or Iberian red deer. We discuss that population bottlenecking might affect the acoustics of the rutting roars, in addition to genotype.	Да (если в тексте публикации указано название ЦКП или УНУ)	5

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1	2	3	4	5	6	7	8	9	10	11
32.	монография	ВНУТРИПОПУЛЯЦИОННАЯ ИЗМЕНЧИВОСТЬ И ЭКОЛОГИЯ ПСОВЫХ		Кораблёв Н.П., Кораблёв М.П., Кораблёв П.Н.	ФГБУ «Центрально-Лесной государственный заповедник», ИПЭЭ РАН, 0, 2021	978-5-6046 357-9-7	не индексируется	В книге представлены результаты изучения внутрипопуляционной изменчивости трех широко распространенных видов хищных млекопитающих: лисицы <i>Vulpes vulpes</i> , енотовидной собаки <i>Nyctereutes procyonoides</i> и волка <i>Canis lupus</i> . В основу положены материалы, полученные в ходе многолетнего изучения краинологических коллекций, собранных авторами в Центрально-Лесном заповеднике и находящихся в отечественных и зарубежных музеевых фондах. Рассматриваются факторы и формы проявления внутрипопуляционного краинометрического, эпигенетического и молекулярно-генетического разнообразия симпатрических видов млекопитающих в ограниченном географическом пространстве в интервале 60-летнего периода. В рамках анализа различных форм полиморфизма для каждого из трех видов определены масштабы внутрипопуляционной изменчивости, особенности проявления этого феномена, обсуждаются возможные механизмы влияния отдельных факторов. Впервые представлены результаты детального пространственно-временного анализа молекулярно-генетической изменчивости волка и гибридизации его с собаками в Центральной России	Да (если в тексте публикации указано название ЦКП или УНУ)	8
33.	тезисы	ДИАТОМОВЫЕ ВОДОРОСЛИ ОСТРОВА УНАЛАШКА (АЛЕУТСКИЕ ОСТРОВА, США)		Неплюхина А.А., Гололобова М.А.	Диатомовые водоросли: морфология, биология, систематика, флористика, экология, палеогеография, биостратиграфия: материалы XVII Междунар. науч. конф. (Минск, 23-28 авг. 2021 г.), 0, 2021	978-985-59 6-942-7	не индексируется	В работе впервые проанализировано разнообразие современных диатомовых водорослей с острова Уналашка, проведено сравнение полученного списка видов со списками видов для двух других островов Алеутской гряды и материковой Аляски.	Да (если в тексте публикации указано название ЦКП или УНУ)	62

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1	2	3	4	5	6	7	8	9	10	11
34.	научная статья	К ВОПРОСУ О ВРЕМЕНИ И СРЕДЕ ОБИТАНИЯ STEPHANORHINUS KIRCHBERGENSIS JÄGER 1839 (MAMMALIA, RHINOCERATIDAE) НА АЛТАЕ И СЕВЕРО-ВОСТОКЕ РОССИИ	10.31857/S 004451342 1050068	Кириллова И.В., Вершинина А.О., Зазовская Э.П., Занина О.Г., и др.	ЗООЛОГИЧЕСКИЙ ЖУРНАЛ, 100, 2021	0044-5134	BAK; Ринц; Web of Science; Scopus	Остатки хорошо изученного в Западной Европе вымершего носорога Мерка ( <i>Stephanorhinus kirchbergensis</i> (Jäger 1839)) на территории России редки. Однако, благодаря работам ряда исследователей, география находок и реконструированный ареал вида значительно расширены. Временем оптимального существования носорога Мерка в Якутии сейчас признается средний плейстоцен; наиболее поздние находки, датируемые началом позднего плейстоцена, известны с юго-востока Западной Сибири. Мы приводим новые данные. Две впервые сделанные радиоуглеродные датировки по корню зуба и костной ткани ранее не изученной нижней челюсти носорога Мерка с Алтая (AltR) совпадают на значении около 40 тыс. лет, что соответствует каргинскому времени (МИС 3), и являются самыми молодыми для вида на территории России. Спорово-пыльцевой спектр из грунта, заполнившего канал кости, характеризует растительные сообщества открытых ландшафтов с лесными участками на плакоре или в пойме и отражает либо локальные особенности среди, либо сообщества холодного этапа внутри каргинского интерстадиала. Время жизни носорога Мерка с реки Чондон (ChR), череп которого найден на крайнем северо-востоке Якутии, предыдущие исследователи определяли в двух предполагаемых неперекрывающихся диапазонах: 45–70 тыс. лет и начало среднего плейстоцена. По нашему мнению, он мог обитать во время последнего – казанцевского – межледникового (МИС 5е) и позже. Обе находки, AltR и ChR, расширяют временной диапазон существования вида. Генетический анализ подтверждает идентификацию AltR по морфологии. Филогения ныне существующих и вымерших носорогов определяет носорога Мерка сестринским видом шерстистому носорогу.	Да (если в тексте публикации указано название ЦКП или УНУ)	559

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35.	научная статья	МИКСОТРОФНЫЕ АЛЬПИЙСКИЕ РАСТЕНИЯ ИЗ СЕМЕЙСТВА GENTIANACEAE?	10.1134/S207908642105008X	Онипченко В.Г., Лавренов Н.Г., Тиунов А.В., Макаров М.И., и др.	ЖУРНАЛ ОБЩЕЙ БИОЛОГИИ / BIOLOGY BULLETIN REVIEWS, 11, 2021	2079-0864	ВАК; РИНЦ; Scopus	Считается, что частично миксогетеротрофные (миксотрофные) растения более обычны в филогенетических линиях, которые включают полностью миксогетеротрофные растения. Сем. Gentianaceae – одна из таких групп. Миксотрофия мало изучена у альпийских растений по сравнению с тропическими и умеренными лесами. Проверена гипотеза о том, что альпийские виды из сем. Gentianaceae с зелеными листьями могут быть частично миксогетеротрофны. Листья девяти пар видов (альпийские растения из сем. Gentianaceae и эталонное растение из другого семейства с арбузуллярной микоризой, растущее поблизости) были собраны в горах Тибета (Сычуань, Китай) и Кавказа (Карачаево-Черкесская Республика, Россия). В полностью развитых листьях было определено естественное содержание стабильных изотопов ( $^{13}\text{C}$ , $^{15}\text{N}$ ). В каждом случае листья растений из сем. Gentianaceae были обогащены $^{15}\text{N}$ сильнее, чем листья других растений, которые служили для сравнения. За исключением двух видов из секции Pneumonanthe (Gentiana asclepiadea и G. septemfida), изученные растения из сем. Gentianaceae не показали значимого обогащения $^{13}\text{C}$ . Мы предполагаем, что относительное обогащение листьев $^{15}\text{N}$ может считаться указанием на частичную миксогетеротрофию у альпийских видов Gentianaceae.	Да (если в тексте публикации указано название ЦКП или УНУ)	431

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1	2	3	4	5	6	7	8	9	10	11
36.	научная статья	СИМБИОТИЧЕСКАЯ АЗОТФИКСАЦИЯ БОБОВЫМИ РАСТЕНИЯМИ АЛЬПИЙСКИХ ЭКОСИСТЕМ: ВЕГЕТАЦИОННЫЙ ЭКСПЕРИМЕНТ	10.1134/S1067413621010094	Макаров М.И., Онипченко В.Г., Малышева Т.И., Зуев А.Г., Тиунова А.В,	Экология / Russian Journal of Ecology, 52, 2021	1067-4136	BAK; Ринц; Web of Science; Scopus	Анализ естественного изотопного состава азота бобовых растений не всегда позволяет рассчитать интенсивность симбиотической фиксации ими атмосферного азота и требует совершенствования. Пять типичных для альпийского пояса Тебердинского заповедника видов бобовых растений ( <i>Anthyllis vulneraria</i> , <i>Astragalus levieri</i> , <i>Hedysarum caucasicum</i> , <i>Oxytropis kubanensis</i> , <i>Trifolium polypodium</i> ) выращивали из семян в условиях лабораторного вегетационного эксперимента. Показано, что формирование клубеньков на корнях происходит на ранних стадиях их развития; <i>Trifolium polypodium</i> , не образующий клубеньки в условиях высокогорий, не формирует их и при вегетации в лаборатории. Естественная концентрация $^{15}\text{N}$ в листьях бобовых растений альпийских экосистем позволяет рассчитать вклад атмосферного $\text{N}_2$ в азотное питание уже в первый год их развития, тогда как изотопный состав азота в корнях не дает такой возможности. При расчете интенсивности фиксации атмосферного азота следует принимать во внимание фракционирование изотопов между симбиотическими бактериями (клубеньками) и растением-хозяином, без учета которого доля фиксированного азота в питании растений может быть занижена.	Да (если в тексте публикации указано название ЦКП или УНУ)	13

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37.	научная статья	СОВРЕМЕННОЕ СОСТОЯНИЕ ИДЕНТИФИКАЦИИ ОННОЙ ПТИЛОЛОГИИ В РОССИИ	10.31857/S 004213242 1060089	Силаева О.Л. , Чернова О.Ф.	УСПЕХИ СОВРЕМЕННОЙ БИОЛОГИИ, 141, 2021	0042-1324	ВАК; Ринц	Статья обзорного характера посвящена актуальным прикладным вопросам идентификационной птилологии – раздела науки о первом покрове птиц, занимающейся проблемой идентификации птиц по целым перьям и их микроскопическим остаткам. Идентификационная птилология развивается в тесном взаимодействии с авиационной орнитологией1. Статья содержит анализ данных зарубежной и отечественной литературы по вопросам влияния идентификационной птилологии на авиационную орнитологию, а также развития прикладных, организационных и стратегических вопросов последней. Приведены конкретные примеры таксономической идентификации перьев по микро- и макроструктуре, определена роль некоторых признаков макро- и макро- структуры пера для экспертизы и филогенетических построений. Разработана система диагностических признаков одиночного пера, описано несколько новых элементов пера и дополнены сведения по известным перьевым структурам. С помощью математических методов (кластеризация по морфометрическим данным макро- и макро- структурных компартаментов пера) определены филогенетические связи между таксонами высшего и среднего ранга. Определена роль коллекций и определятелей птиц по макро- и макро- структуре пера для идентификационных исследований перьевого материала. Рассмотрены прикладные и научные пути решения проблем аэродромной экологии, а именно защиты воздушных судов от биоповреждений, вызываемых птицами. Отмечена необходимость идентификации видов – участников столкновений с воздушными судами. Начат проект по физико-географическому и климатическому районированию. Цель проекта – определить наиболее опасные для полетов авиации виды птиц в районах и на территориях аэропортов в разные сезоны года. Созданы комплексные системы видового определения птицы по перьевым остаткам для авиационной орнитологии, куда входит анализ структуры перьевого материала, эколого-географический и молекулярно-генетический анализы; совокупность методов позволяет обрабатывать большие массивы данных исключительно по структуре групп перьев, одиночного пера или фрагментов.	Да (если в тексте публикации указано название ЦКП или УНУ)	608
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38.	научная статья	ЦИАНОБАКТЕРИИ КАК ИСТОЧНИК ПИТАНИЯ БЕСПОЗВОНОЧНЫХ: РЕЗУЛЬТАТЫ МОДЕЛЬНОГО ЭКСПЕРИМЕНТА	10.31857/S0367059721030033	Березина Н.А., Тиунова А.В., Цуриков С.М., Курбатова С.А., Корнева Л.Г., Макарова О.С., Быкова С.Н.	Экология / Russian Journal of Ecology, 52, 2021	1067-4136	BAK; Ринц; Web of Science; Scopus	Массовое развитие цианобактерий в водоемах считается одной из глобальных экологических проблем. До сих пор роль этих прокариот в трофической сети водоемов не ясна. Нами было выполнено экспериментальное исследование трофических связей беспозвоночных в период массового развития цианобактерий <i>Aphanizomenon flos-aquae</i> . Ключевые звенья трофической сети: планктон, микроперифитон, детрит и бентосные беспозвоночные, были собраны для изотопного анализа углерода ( $\delta^{13}\text{C}$ ) и азота ( $\delta^{15}\text{N}$ ) после 20-суточного экспонирования мезокосмов, имитирующих условия прибрежного биотопа Рыбинского водохранилища при отсутствии цианобактерий (вариант I) и их высоком обилии (вариант II). Выявлены статистически значимые различия величин $\delta^{15}\text{N}$ ракообразных <i>Cladocera</i> , <i>Sorepoda</i> , <i>Asellus aquaticus</i> и <i>Gmelinoides fasciatus</i> и личинок поденок между вариантами: в присутствии цианобактерий эти величины были на 1-4 % ниже, чем при их отсутствии. Индуцированные цианобактериями сдвиги в величине $\delta^{15}\text{N}$ консументов свидетельствуют об ассимиляции диазотрофного азота и включении питательных веществ цианобактерий в пищевые цепи.	Да (если в тексте публикации указано название ЦКП или УНУ)	236

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