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DEGRADATION, REHABILITATION, AND CONSERVATION OF SOILS

Secondary Successions of Biota in Oil-Polluted Peat Soil upon Different Biological Remediation Methods

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Abstract—The effects of different bioremediation methods on restoration of the oil-polluted peat soil (Histosol) in the northernmost taiga subzone of European Russia was studied. The population dynamics of microorganisms belonging to different trophic groups (hydrocarbon-oxidizing, ammonifying, nitrifying, and oligonitrophilic) were analyzed together with data on the soil enzyme (catalase and dehydrogenase) activities, population densities of soil microfauna groups, their structures, and states of phytocenoses during a seven-year-long succession. The remediation with biopreparations Roder composed of oil-oxidizing microorganisms—Roder with *Rhodococcus rubber* and *R. erythropolis* and Universal with *Rhodotorula glutinis* and *Rhodococcus* sp.—was more efficient than the agrochemical and technical remediation. It was concluded that the biopreparations activate microbiological oil destruction, thereby accelerating restoration succession of phytocenosis and zoocenosis. The succession of dominant microfauna groups was observed: the dipteran larvae and Mesostigmata mites predominant at the early stages were replaced by collembolans at later stages. The pioneer oribatid mite species were *Tectocepheus velatus, Oppiella nova, Liochthonius sellnicki, Oribatula tibialis*, and *Eupelops* sp.

Keywords: soil biota, microorganisms, microarthropods, oil pollution, peat soil (Histosol), bioremediation

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INTRODUCTION

The study of the patterns of secondary successions of the soil communities damaged by anthropogenic activities and determination of the set of abiotic and biotic parameters that mark certain stages in remediation are most important for diagnosing the soil state and estimating the efficiency of applied remediation methods. Many researchers focus on clarification of the ecological mechanisms underlying the primary and secondary successions of various geneses, as well as the relationships and interdependences of individual components in the remediating ecosystems [1, 13, 27, 35, 36, 38, 39, 43]. The integrated studies of restoration successions in oil-polluted soil communities are few in number [3, 4]. They are of special importance for the regions of commercial oil production in the extreme North, where emergency oil spills pollute natural ecosystems. The goal of this work was to study the patterns of secondary successions of biota in oil-polluted peat soil (Histosol) upon application of different bioremediation methods with the use of agrochemicals and oil-oxidizing biopreparations; to assess a coupled character of secondary successions of the microbial cenosis, phytocenosis, and zoocenosis; and to determine feasibility of estimating the efficiency of bioremediation methods on the basis of characteristics of the soil biota.

MATERIALS AND METHODS

The secondary successions of soil biota were studied in the Usinsk district of the Komi Republic. The examined area is located in the lower and middle reaches of the Kolva River, in the Usinsk–Kolva spruce forest–tundra geobotanical area within the forest-tundra and northernmost taiga subzones of the Pechora–Ural subprovince [33]. This area is characterized by cold moderately continental climate. The mean annual temperature is 4°C; the mean January temperature is –18 to –20°C, and the mean July temperature is +14°C. Snow cover lies for 210 days per year from the end of October to the early June [5]. The major part of the area belongs to the Pechora–Usinsk district of the bog-podzolic, gley-podzolic, tundra bog, and peat bog soils (Histosols) [4]. The peat is strongly acid through the entire profile (pH_{water} 3.7–4.3).

The samples were taken from experimental site 20 (Vozeiskoe oil field; 66°37′40″ N, 57°07′56″ E) within the Lukoil–Usinskneftegaz Venture area. Peat soils are developed in this area. An oil spill took place in 1996; the peat deposit was soaked with oil to a depth of

1.0–1.5 m. The experiment on assessing the efficiency of different bioremediation methods was commenced in June 2002. Technical remediation, including drainage of the plot, removal of oil from the surface, and rotary cultivation to a depth of 30–40 cm preceded the experiment [23]. The soil water content after drainage was 65 to 88%; pH of salt extract, 4.20–4.80; pH of water extract, 4.35–5.66; and oil concentration varied from 250 to 450 mg/g [23].

This paper describes the results of integrated monitoring of four experimental plots over seven years of remediation (2002–2009). The soil of plot 9 was limed, treated with mineral fertilizers and the Roder biopreparation (designed at the Chemical Faculty of Moscow State University), and seeded with the perennial grasses (reed canary grass (*Phalaroides arundinacea*) and timothy grass (*Phleum pratense*)). The soil of plot 6 was treated with mineral fertilizers, lignin sorbents, and the Universal biopreparation (designed at the Institute of Biology of the Komi Science Center, Ural Branch of the Russian Academy of Sciences) and seeded with perennial tufted hair grass (*Deschampsia cespitosa*). On plot 7 (agrostimulation), the soil was limed, treated with mineral fertilizers, and seeded with a mixture of perennial grasses and oats (*Avena sativa*). The Universal biopreparation contains the oil-oxidizing yeast *Rhodotorula glutinis* (strains U5-Us 26 and 55-1-R) and *Rhodococcus* sp. bacteria (strains U7-28 (K-2 7), R-72-00 (K-2 6-2), and 34-1 (28-99/2)). The Roder biopreparation consists of the oil destructing bacterial strains *Rhodococcus rubber* AC-1513 D and *R. erythropolis* AC-1514 D. The Universal biopreparation was used in a dried form (titer, 10^{10} cells/g) and the Roder biopreparation was used as a water solution (1 kg/1000 L water) of stabilized concentrated bacterial suspension (titer, 10^{11-12} cells/mL). ANP (ammonium nitrate phosphate) fertilizer at a rate of 350 kg/ha was applied on all the plots [23].

Only technical reclamation was used on plot 2 (no biopreparations or fertilizers); this plot was used as a control for the plots subjected to bioremediation [23]. The background plant community was a willow–dwarf birch sedge–horsetail bog with a peat soil (water content of 80–89%, pH_{KCl} 4.55, and pH_{water} 4.88). The main plant species were the swamp willow (*Salix myrtilloides*), downy willow (*S. lapponum*), dwarf birch (*Betula nana*), water horsetail (*Equisetum fluviatile*), bogbean (*Menyanthes trifoliata*), purple marshlocks (*Comarum palustre*), bog rosemary (*Andromeda polifolia*), common cotton grass (*Eriophorum polystachion*), tussock cotton grass (*E. vaginatum*), and Lapland reedgrass (*Calamagrostis lapponica*). The native plant community (before the oil spill) on the oil-polluted plots was identical to this background community. Before bioremediation, no plants grew on the experimental plots.

Microbiological sampling and initial specimen processing (in triplicate) followed the protocol by Zvyagintsev et al. [9]. The samples of microfauna were taken in August 2006 and 2009 according to routine protocols [18] in 12 replicates for each series; in total, 264 specimens with a size of 5 × 5 cm and a depth of 10 cm were collected. The intensity of oil destruction was assessed according to the contents of total petroleum hydrocarbons (TPH) in the soil [21] and the structure of the alkane fraction. Qualitative composition of the C_{14} alkane homologous series of the C_{35} extract was determined by chromato-mass spectrometry, as was their concentration (mg/g), portion in the structure of alkane fraction, and the ratio of petrogenic (C_{14}–C_{18}) to biogenic (C_{19}–C_{35}) *n*-alkanes [22]. The composition of acyclic hydrocarbons reflects the contribution of biogenic factors to the hydrocarbon pool formed in soils [2, 22]. The plant species composition and the total projective cover (TPC) of the grass layer were taken into account when characterizing phytocenoses. The soil biological activity was assessed according to the population dynamics of microorganisms belonging to different trophic groups [11, 19, 24] earlier detected as priority representatives for the evaluation of the remediation intensity in oil-polluted northern soils [29] and according to the redox enzyme (catalase and dehydrogenase) activities [30, 31]. These enzymes belong to the indicator enzymes; along with the abundances of major groups constituting the soil microbiota, their activities reflect the intensity of soil self-purification from oil [10, 32]. The specific features in the dynamics of the soil microfauna composition and structure were characterized according to the population density (individuals/m^2) and relative abundance (%) of the taxa [18]. The Microsoft Excel for Windows XP and Statistica 6.0 software products were used for statistical data processing. The Mann–Whitney test at $P < 0.05$ (the PAST program [37]) was used for assessing statistical significance of the differences in population densities of microarthropods.

RESULTS

The plant communities with a dominance of the seeded grass species developed four years after the beginning of remediation (2006) on the experimental plots. In particular, plot 9 was overgrown with grasses (TPC, 70–80%) with a prevalence of timothy grass (*Phleum pratense*) and reed canary grass (*Phalaroides arundinacea*). Plot 6 was overgrown with a tufted hair grass–forb community (TPC, 90–95%) with a prevalence of the tufted hair grass (*Deschampsia cespitosa*) (TPC, 60–70%). Plot 7 was overgrown with grasses and forbs (TPC, 30–40%) with patches displaying a high projective cover (up to 70%) of the timothy grass (*P. pratense*). In 2009 (after seven years of the experiment), the seeded grass species retained their dominant position in the phytocenoses and the TPC values did not significantly change. A mosaic pattern of the vegetation cover was preserved; depending on the degree of vegetation development, the secondary succession stages were referred to as (a) plantless barrens,

Table 1. Dynamics of the soil enzyme activities on the experimental plots and the contents of residual TPH in the soil

Experimental plot	2002		2003	2004	2006	2009
	1	*2*				
Dehydrogenase activity, mg formazan/g						
Control	0.26 ± 0.1	0.25 ± 0.1	0.34 ± 0.1	0.45 ± 0.2	0.60 ± 0.2	1.24 ± 0.4
Universal and lignin sorbent	0.25 ± 0.1	2.34 ± 0.1	4.70 ± 0.1	3.54 ± 1.0	1.39 ± 0.5	1.93 ± 0.7
Roder	0.25 ± 0.1	2.45 ± 1.0	4.12 ± 1.0	3.01 ± 1.0	1.38 ± 0.5	0.98 ± 0.7
Agrostimulation	0.15 ± 0.1	1.56 ± 0.5	2.55 ± 0.1	2.56 ± 1.0	1.37 ± 0.5	1.61 ± 0.5
Background soil	0.21 ± 0.1	Not det.			0.21 ± 0.1	0.28 ± 0.1
Catalase activity, mL 0.1 M $KMnO_4$/g						
Control	2.19 ± 0.5	1.28 ± 0.4	1.95 ± 0.1	1.02 ± 0.1	1.0 ± 0.3	1.06 ± 0.3
Universal and lignin sorbent	2.16 ± 0.5	2.95 ± 1.0	3.96 ± 0.2	5.04 ± 0.3	3.91 ± 1.0	1.34 ± 0.4
Roder	2.10 ± 0.5	3.10 ± 0.1	4.02 ± 1.2	6.11 ± 2.0	4.82 ± 1.6	1.26 ± 0.4
Agrostimulation	2.35 ± 0.5	1.05 ± 0.1	1.23 ± 0.6	2.45 ± 0.8	4.51 ± 1.5	1.04 ± 0.3
Background soil	2.30 ± 0.5	Not det.			2.30 ± 0.7	1.54 ± 0.5
TPH, mg/g						
Control	87.0 ± 30.0	85.0 ± 30.0	85.0 ± 30.0	83.0 ± 27.0	80.0 ± 26.0	78.0 ± 25.0
Universal and lignin sorbent	420.0 ± 130.0	380.0 ± 125.0	210.0 ± 70.0	130.0 ± 35.0	120.0 ± 33.0	65.0 ± 20.0
Roder	465.0 ± 155.0	450.0 ± 150.0	280.0 ± 90.0	230.0 ± 60.0	210.0 ± 70.0	110.0 ± 40.0
Agrostimulation	315.0 ± 110.0	310.0 ± 110.0	275.0 ± 90.0	250.0 ± 65.0	243.0 ± 80.0	210.0 ± 70.0
Background soil	0.41 ± 0.11	0.40 ± 0.10	0.36 ± 0.09	0.41 ± 0.10	0.43 ± 0.12	0.41 ± 0.11

(*1*) Beginning of the experiment and (*2*) 60 days of the experiment.

(b) low (30–40%) projective cover (LPC), and (c) high (>70–80%) projective cover (HPC) stages.

On the plots treated with biopreparations, the soil biological activity drastically increased immediately after commencement of the experiment. Abundances of the microorganisms belonging to different trophic groups and the activities of the soil enzymes both significantly increased (Table 1, Fig. 1). The counts of hydrocarbon-oxidizing microorganisms increased for three years on the plot treated with the Universal biopreparation and for five years on the plot treated with the Roder biopreparation. They tended to decrease after four and seven years, respectively. The maximum counts of ammonifying bacteria were recorded a year after the beginning of the experiment and began to decrease in two years. A considerable increase in the abundance of nitrifying bacteria was recorded 60 days after the beginning of the experiment. Their counts continued to grow during the first three years and started to decrease after four years of remediation. The counts of oligonitrophilic organisms changed in a similar manner; moreover, they remained considerably higher as compared with the initial and background abundances both after four and seven years of bioremediation. The plot treated with agrochemicals (without biopreparations) displayed a slow increase in the abundances of microorganisms belonging to different trophic groups during seven years of our observations.

The remediation induced an increase in the redox enzyme (catalase and dehydrogenase) activities. The catalase activity began to decrease after four years in the soil treated with biopreparations and only after seven years in the soil subjected to the agrochemical reclamation (Table 1). The dehydrogenase activity began to decrease after two years of the experiment on the plots with biopreparations and after four years in the variants with agrostimulation. As for the plot with technical remediation, the TPH contents there decreased insignificantly in seven years of the experiment. The maximum decrease in the concentrations of TPH was recorded in the soil treated with biopreparations.

The abundance, composition, and structure of soil invertebrate populations changed in the course of the secondary succession, following a certain pattern (Tables 2 and 3). Four years after the remediation (2006), the early stage of the succession (plantless stage) was characterized by low density of the animal population. In the structure of microfauna, dipterans at their larval stage (in some samples, they were the only faunal component) and mesostigmatic mites predominated. The variants without plants were similar to the control plot at the first stages of the succession in the structure and population density of their microarthropod community. At the subsequent succession stages of the plant community (LPC), the diversity of microarthropods increased in both the number of taxa

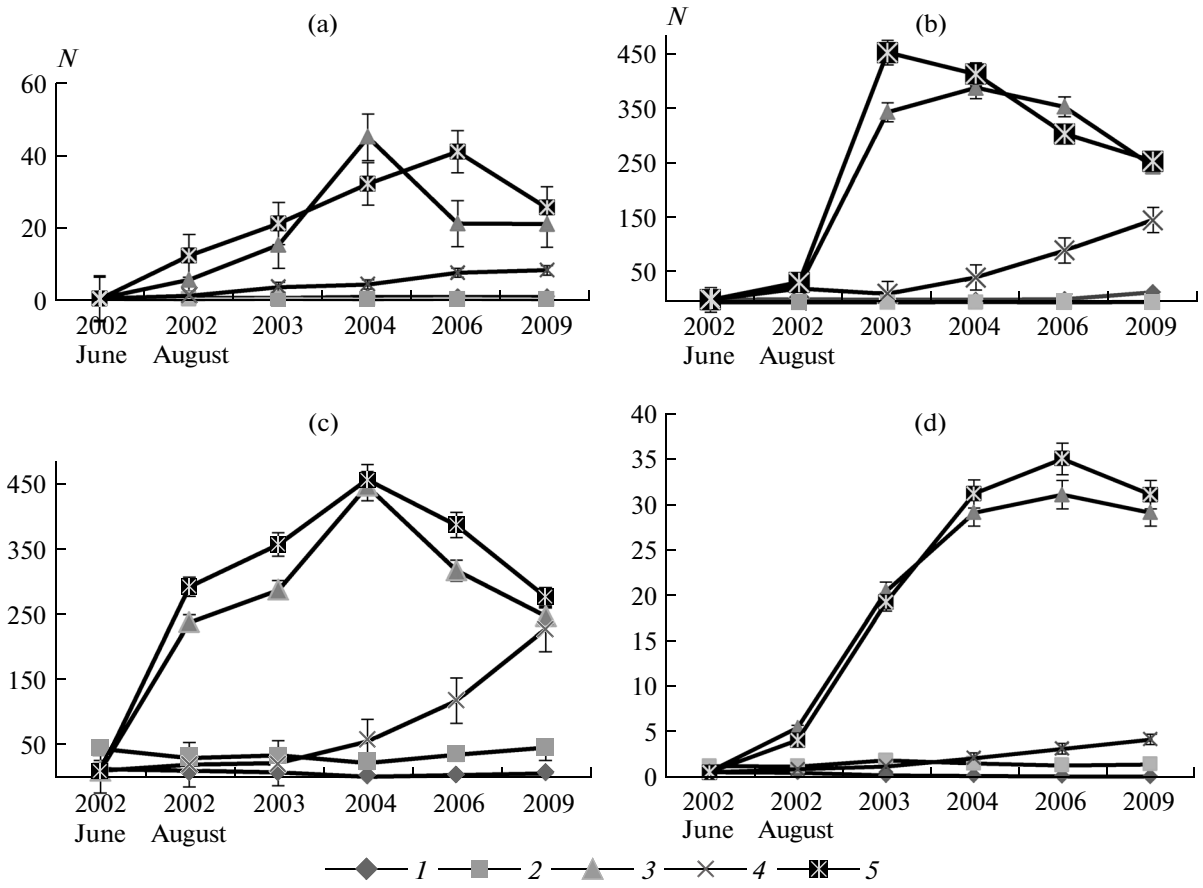

Fig. 1. Population dynamics of (a) hydrocarbon-oxidizing, (b) ammonifying, (c) nitrifying, and (d) oligonitrophilic groups of microflora (*N,* million cells/g) counted in July of 2003–2009: (*1*) control plot, (*2*) background plot, (*3*) plot 6 (Universal and lignin sorbent), (*4*) plot 7 (agrochemicals), and (*5*) plot 9 (Roder).

and their population densities. Mites (Mesostigmata, Prostigmata, and Acaridae) were the most abundant groups; dipterans remained among the dominants with the highest relative abundance on plot 7 (with agrostimulation). At later stages (phytocenoses with HPC), the maximum population densities for invertebrates were recorded. The mesostigmatic and acaridan mites were the most abundant on all the plots; dipterans appeared on plot 7; and collembolans appeared within the dominant species on 9 (treated with the Roder biopreparation). In 2009 (seven years after the beginning of the experiment), the population density of microfauna increased on the plots treated with biopreparations, namely, on plot 6 (with both LPC and HPC variants) and on plot 9 (with LPC). At the same time, a decrease in the population density was recorded for the HPC variants on plots 9 and 7. The trends for a decrease in the population densities of dipterans and mesostigmatic mites in the bioremediated soil and, on the contrary, an increase in the collembolan population density with time were observed. The dipteran population densities during individual observation stages in the HPC variants on plots 7 and 9, LPC variants on plots 6 and 7, and in the control (technical remediation) variant differed in a statistically significant manner, as did the mesostigmatic mite populations for the HPC variant on all the bioremediated plots and the control. The collembolan population density increased in the soil with vegetation cover, namely, in HPC and LPC variants on plots 6 and 7 and LPC variant on plot 9.

DISCUSSION

Heavy pollution with oil inhibits the soil biological activity, causes a decrease in the population and taxonomic diversity of microorganisms, and changes the structure of bacterial communities [14, 20]. Our results have demonstrated that the restoration of biota in the remediated soil commences from an increase in the microbial populations belonging to different trophic groups (hydrocarbon-oxidizing, ammonifying, nitrifying, and oligonitrophilic) and in the soil enzyme activities. The biological purification of the oil-polluted soil takes place during the period of the high activity of the soil microbial cenosis [14, 15]. In the course of the succession, the role of biogenic factors in oil utilization increased; namely, the grasses

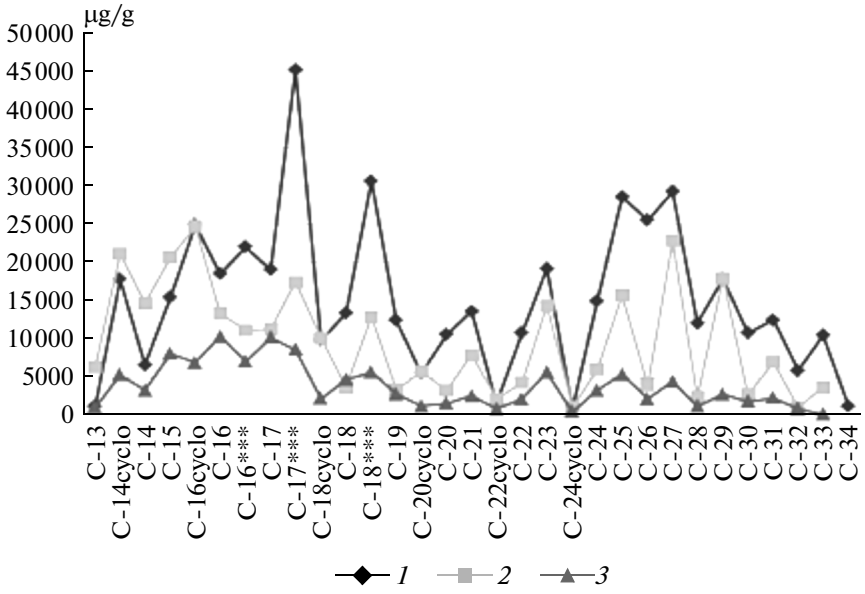

Fig. 2. Structure of the alkane fraction of residual oil in the soils of plot 6 (*1*—plantless and *2*—high projective cover of grasses) and control (*3*—2006).

became more important contributors to these processes with the development of phytocenosis. This is proved by changes in the structure of the *n*-alkane fraction, namely, an increase in the portion of biogenic *n*-alkanes and a decrease in the portion of petrogenic alkanes at later stages of the succession (Fig. 2).

Artem'eva [3] showed a correlation of the succession of invertebrates in the oil-polluted chernozem and soddy-podzolic soils with the successions of the microbial cenosis and phytocenosis. It was demonstrated that the first stage of remediation is a microbiological stage. The role of microorganisms (chromogenic coryneform and psychrophilic bacteria and some other groups) in preparing the substrate for colonization by invertebrates and plants was also shown for cinder and ash fields formed after volcanic eruptions [27]. As is known, microorganisms not only change the habitat for the soil invertebrates but are also involved in trophic interactions with them [7, 12, 28].

Heavy soil pollution with oil and subsequent mechanical disturbance of the soil in the course of reclamation killed invertebrates; thus, we believe that the regeneration of zoocenosis in this case followed the primary succession pattern. As has been shown, invertebrates started to colonize the soil before any plants appeared there, at the plantless succession stage of the phytocenosis. In this process, the dipteran larvae and predatory (mesostigmatic) mites played the leading role. Along with these taxa, collembolans as well as acaridan, prostigmatic, and oribatid mites were pioneer microarthropods. Collembolans and oribatid mites were repeatedly observed to be pioneer taxa in successions of the soil fauna, in particular, in colonizing postglacial substrates [35, 36], stone quarry refuses [25], and oil-polluted soils [3, 4].

Our results demonstrate that any of the experimental plots seven years after the remediation still did not reach the level of the background plant community in the structure of their microarthropod population. The background plot retained considerable stability in the population structure of microfauna during that period: the oribatid mites were dominants and the share of collembolans, mesostigmatic mites, and dipterans did not exceed 15% each (Table 3). On the experimental remediated plots, the replacement of the prevalent taxa was observed over time. As a rule, the most abundant taxa four years after the remediation were dipterans and mites (mesostigmatic, acaridan, and prostigmatic); however, collembolans entered the group of dominants after seven years of the experiment. As has been shown, the oribatid mites colonized the remediated soil more slowly than representatives of the other taxa. After four years, oribatids were detectable only in one sample (the HPC variant of plot 7). After seven years, these mites were present in several groups (HPC variants of plots 6 and 9 and LPC variant of plot 9) but displayed a relatively low population density. These results agree with the earlier proposed secondary succession pattern for the soil microfauna. We consider three secondary succession stages in the restoration of microfauna after oil pollution. Each stage is characterized by the presence and high relative abundance of a certain group of microarthropods. At the first stage, the major group is represented by dipterans at their larval stage and by mesostigmatic mites. Collembolans are the indicators of the second stage; their portion is not high at the beginning of this stage and reaches the

Table 2. Dynamics of the population density (N, individuals/m^2) and the relative abundance (p, %) of soil microfauna on the experimental plots

Taxon	Plantless				Low projective cover of plants				High projective cover of cereals			
	2006		2009		2006		2009		2006		2009	
	N	p	N	p	N	p	N	p	N	p	N	p
Experimental plot 6												
Mesostigmata	4933 ± 1106[a]	51.7	450 ± 297[b]	17.6	6550 ± 2155[a]	47.1	4550 ± 618[a]	13.2	9388 ± 2756[a]	51.3	1466 ± 510[b]	2.5
Prostigmata	267 ± 198[a]	2.8	550 ± 447[a]	21.6	2700 ± 766[a]	19.4	17100 ± 5915[b]	49.8	965 ± 516	5.3	–	–
Trombidiidae	–	–	–	–	2150 ± 717	15.5	–	–	–	–	–	–
Acaridae:												
adulti	–	–	800 ± 165	31.4	–	–	1550 ± 674	4.5	6706 ± 3619[a]	36.6	24467 ± 5168[a]	42.1
deutonymph	–	–	300 ± 550	11.7	–	–	150 ± 150	0.4	–	–	28000 ± 9054	48.2
Oribatida	–	–	–	–	–	–	–	–	–	–	33 ± 33	0.1
Collembola	3133 ± 1114[a]	32.9	350 ± 244[a]	13.7	600 ± 169[a]	4.3	9550 ± 2698[b]	27.8	212 ± 925[a]	1.1	3533 ± 1502[b]	6.1
Diptera larvae	1000 ± 409[a]	10.5	100 ± 65[a]	3.9	1700 ± 439[a]	12.2	350 ± 140[b]	1.0	565 ± 154[a]	3.1	567 ± 194[a]	0.9
Coleoptera:												
imago	133 ± 133	1.4	–	–	50 ± 50[a]	0.4	100 ± 100[a]	0.3	141 ± 68[a]	0.8	36 ± 35[a]	0.1
larvae	67 ± 67	0.7	–	–	150 ± 105[a]	1.1	400 ± 239[a]	1.2	47 ± 47	0.3	–	–
Hymenoptera:												
imago	–	–	–	–	–	–	50 ± 50	0.1	–	–	–	–
larvae	–	–	–	–	–	–	50 ± 50	0.1	–	–	–	–
Psocoptera	–	–	–	–	–	–	550 ± 261	1.6	282 ± 145	1.5	–	–
Total	9533 ± 879[a]	100	2914 ± 926[b]	100	13900 ± 2864[a]	100	34400 ± 4424[b]	100	18306 ± 5946[a]	100	58100 ± 13377[b]	100
Experimental plot 9												
Mesostigmata	–	–	8400 ± 2503	49.8	1800 ± 476[a]	7.2	967 ± 233[a]	0.9	57520 ± 47503[a]	37.7	2800 ± 1007[b]	4.3
Prostigmata	–	–	1000 ± 581	5.9	15800 ± 6368[a]	63.2	17333 ± 573[a]	1.6	9920 ± 4814[a]	6.5	5960 ± 1478[a]	9.1
Acaridae:												
adulti	–	–	2350 ± 870	14.0	3700 ± 2138[a]	14.8	23333 ± 971[a]	2.0	–	–	2800 ± 683	4.3
deutonymph	–	–	–	–	–	–	4567 ± 1261	3.9	1960 ± 541[a]	1.3	1600 ± 1222[a]	2.4
Oribatida	–	–	–	–	–	–	200 ± 104	0.2	–	–	160 ± 107	0.2
Aranei	–	–	–	–	–	–	–	–	40 ± 40	0.1	–	–
Collembola	–	–	3200 ± 637	18.9	–	–	94667 ± 28096	89.8	76400 ± 14504[a]	50.1	49240 ± 29663[a]	75.2
Diptera:												
imago	520 ± 320[a]	71.4	650 ± 168[a]	3.9	1000 ± 346[a]	4.0	300 ± 87[a]	0.3	2120 ± 327	1.4	–	–
larvae	200 ± 200[a]	28.6	700 ± 290[a]	4.2	2600 ± 1361[a]	10.4	1133 ± 525[a]	1.1	4240 ± 1005[a]	2.8	1800 ± 439[b]	2.8

Table 2. (Contd.)

Taxon	Plantless				Low projective cover of plants				High projective cover of cereals			
	2006		2009		2006		2009		2006		2009	
	N	*p*	*N*	*p*	*N*	*p*	*N*	*p*	*N*	*p*	*N*	*p*
Coleoptera:												
imago	–	–	150 ± 73	0.9	–	–	–	–	200 ± 67[a]	0.1	200 ± 89[a]	0.3
larvae	–	–	200 ± 151	1.2	100 ± 100[a]	0.4	133 ± 102[a]	0.1	–	–	240 ± 107	0.3
Hymenoptera larvae	–	–	–	–	–	–	–	–	–	–	40 ± 40	0.1
Psocoptera	–	–	200 ± 106	1.2	–	–	200 ± 92	0.1	–	–	600 ± 209	1.0
Total	720 ± 450[a]	100	16850 ± 3431[b]	100	25000 ± 8631[a]	100	106233 ± 30538[a]	100	152400 ± 56335[a]	100	65440 ± 31661[b]	100
Experimental plot 7												
Mesostigmata	600 ± 258[a]	11.8	4160 ± 1130[b]	41.6	15438 ± 534	12.4	–	–	7820 ± 1872[a]	35.5	80.0 ± 53.3[b]	2.2
Prostigmata	–	–	240 ± 160	2.4	2114 ± 1180[a]	17.1	436 ± 166[a]	9.5	2300 ± 91	10.4	–	–
Acaridae: adulti	–	–	1920 ± 950	19.2	6057 ± 1284[a]	48.8	2545 ± 2037[b]	56.5	5440 ± 1372	24.7	–	–
deutonymph	–	–	–	–	–	–	109 ± 56	2.4	2760 ± 1184[a]	12.5	120 ± 120[b]	3.3
Oribatida	–	–	–	–	–	–	–	–	80.0 ± 46.8	0.4	–	–
Aranei	100 ± 100	1.9	–	–	–	–	–	–	–	–	–	–
Collembola	–	–	720 ± 621	7.2	57 ± 57[a]	0.5	1164 ± 648[b]	25.4	–	–	2400 ± 880	65.2
Diptera larvae	4400 ± 1120[a]	86.3	2640 ± 688[a]	26.4	2571 ± 616[a]	20.7	109 ± 56[b]	2.4	3520 ± 819[a]	16.0	680 ± 179[b]	18.4
Coleoptera:												
imago	–	–	–	–	57 ± 57	0.5	–	–	120 ± 59	0.5	40 ± 40	–
larvae	–	–	–	–	–	–	109 ± 56	2.4	–	–	–	1.1
Psocoptera	–	–	320 ± 233	3.2	–	–	109 ± 56	2.4	–	–	360 ± 163	9.8
Total	5100 ± 1340[a]	100	10000 ± 1448[a]	100	12400 ± 2823[a]	100	4582 ± 2240[b]	100	22040 ± 3009[a]	100	3680 ± 772[b]	100

Note: Here and in Table 3, 1 letters [a] and [b] indicate statistically significant differences between population densities in pairwise comparisons at each succession stage of the phytocenosis in different years.

Table 3. Dynamics of the population density (N, individuals/m^2) and relative abundance (p, %) of soil microfauna on the control plot and in the background plant community

Taxon	Control plot				Background community			
	2006		2009		2006		2009	
	N	p	N	p	N	p	N	p
Mesostigmata	36295 ± 696[a]	67.2	1867 ± 804[b]	71.8	4300 ± 1799[a]	6.7	3667 ± 648[a]	6.2
Prostigmata	200 ± 109	3.7	–	–	–	–	1867 ± 642	3.1
Acaridae adulti	–	–	–	–	5600 ± 1488[a]	8.6	1267 ± 240[b]	2.1
Oribatida	–	–	133 ± 57	5.1	43300 ± 7184[a]	66.8	35600 ± 86648[a]	59.8
Collembola	114 ± 65[a]	2.1	233 ± 233[a]	8.9	4400 ± 1131[a]	6.8	8733 ± 2100[a]	14.7
Diptera larvae	1429 ± 345[a]	26.5	100 ± 72[b]	3.8	6400 ± 3007[a]	9.9	7867 ± 1638[a]	13.2
Coleoptera:								
imago	296 ± 29	0.5	–	–	100 ± 100	0.1	–	–
larvae	–	–	100 ± 72	3.8	600 ± 600[a]	1.0	133 ± 84[a]	0.2
Hymenoptera:								
imago	–	–	33 ± 33	1.3	100 ± 100[a]	0.1	67 ± 67[a]	0.1
Psocoptera	–	–	133 ± 103	5.1	–	–	67 ± 67	0.1
Lumbricidae	–	–	–	–	–	–	267 ± 198	0.5
Total	5400 ± 641[a]	100	3467 ± 926[b]	100	64800 ± 5025[a]	100	59533 ± 10118[a]	100

dominant position closer to its end. The appearance of oribatid mites and a gradual increase in their abundance characterize the third stage [16, 17]. At the early succession stages of the phytocenosis, the microfauna in plantless samples on plots 9 and 7 (2006) can be regarded as the beginning of the first succession stage of the zoocenosis because invertebrates were represented by either exclusively dipterans (plot 9) or a small number of taxa with a prevalence of dipterans and mesostigmatic mites (plot 7 and the control). The microfauna determined in the LPC and HPC variants on plots 6 and 7 in 2006 was in the state typical of the end of the first stage of the succession: the microarthropod population was more diverse and the core of dominants contained prostigmatic and acaridan mites along with the dipterans and mesostigmatic mites. The variants with collembolans among the dominant taxa corresponded to the second stage in the zoocenosis succession (LPC variants on plots 6 and 7 in 2009). The groupings containing oribatids in their population structure in the LPC and HPC variants on plot 9 and HPC variant on plot 6 in 2009 can be regarded as the beginning of the third succession stage. This suggests that the diversity of microfauna in the remediated plots was associated with the degree of development of the phytocenosis. In the course of the phytocenosis development, the structure of invertebrate groupings became more complex and the abundances of collembolans and oribatid mites indicative of the later stages in the succession of the zoocenosis increased. The dependence of the spatial distribution and abundance of soil invertebrates on the composition and development of vegetation was shown both for the succession stages [3, 27] and mature communities [34].

The following oribatid mite species were pioneering: *Liochthonius sellnicki* Thor, 1930 (family Brachychthoniidae), *Oppiella nova* Oudemans, 1902 (Oppiidae), *Tectocepheus velatus* Michael, 1880 (Tectocepheidae), *Oribatula tibialis* Nicolet, 1855 (Oribatulidae), and *Eupelops* sp. (Phenopelopidae). The fact that the species *Tectocepheus velatus, Oppiella nova*, and *Oribatula tibialis* commenced colonizing of the oil-polluted soil is explainable by their eurytopicity. It is known that these species are met in a wide range of both intact and anthropogenically disturbed natural communities. It is evident that parthenogenesis—a characteristic of Brachychthoniidae and Oppiidae species regarded as a specific adaptive feature of these mites [8, 26, 27, 40]—is among the major factors allowing them to successfully colonize remediated soils. The species belonging to the families Brachychthoniidae and Oppiidae, as well as the species *Tecto-*

cepheus velatus, have been frequently observed among the pioneer species in successions of oribatid mites on new substrates of both natural and anthropogenic origins [25, 27, 36, 41, 42]. As has been repeatedly noticed, the population structure of oribatids becomes more complex, and their diversity and abundance increase in the course of the succession [1, 13, 25, 44].

The dependence of the rate of remediation of soil biotic communities on the applied remediation methods was shown. The oil was destructed more intensively on the plots treated with biopreparations (Roder and Universal) as compared with the plots reclaimed by agrochemical methods and mechanical soil cultivation. This can be judged from data on the duration of the period of the intensified soil biological activity and the state of phytocenoses and zoocenoses. This period continued for three to four years on the plots treated with biopreparations; it was followed by a gradual decrease in the microbial counts and soil enzyme activities to the background levels. The population density of invertebrates was the highest there during the entire observation period, and the zoocenosis after seven years of remediation was at the later (third) succession stage as indicated by the presence of oribatids. As for the soil with agrochemical remediation, the period of the microbiological oil destruction was longer (five to seven years), and the oil content in the soil decreased insignificantly. The phytocenosis developed slower, so that the TPC was considerably lower relative to the plots treated with the Roder and Universal biopreparations. The development of the zoocenosis was delayed as compared with the plots treated with the biopreparations. During the entire observation period, the population density of invertebrates there was lower; the portion of dipterans (marking early stages of regeneration of the zoocenosis) remained rather high at all the succession stages of phytocenosis, whereas on the plots treated with biopreparations (6 and 9) it decreased in the course of the succession. On the plot with technical reclamation alone, an increase in the soil biological activity was observed only in year seven of the experiment. Moreover, the oil content in the soil almost did not change over seven years, and the grass cover was still absent after four years; the LPC stage was observed after seven years, and the zoocenosis remained at the early succession stages.

These results allow us to infer that the use of biopreparations for remediation activates the microbiological oil destruction by oil-oxidizing microflora contained in these biopreparations, thereby accelerating the secondary successions of phytocenosis and zoocenosis. Agrochemical remediation stimulates the biological purification of the soil from oil by natural microflora. After technical manipulations with the soil, the self-restoration of vegetation proceeds upon low activity of the natural soil microflora. The bioremediation of peat soil using the microbial preparations Roder and Universal is more efficient as compared with the agrochemical and technical remediation variants.

CONCLUSIONS

Our studies have clarified some patterns in the secondary succession of the biota after bioremediation of the oil-polluted peat soil in the northernmost taiga subzone. The restoration began with an increase in the abundances of microorganisms belonging to different trophic groups (hydrocarbon-oxidizing, ammonifying, nitrifying, and oligonitrophilic) and in the soil enzyme activities. The activation of the microbiological destruction of oil and the involvement of grasses in utilization of oil products at later stages of the phytocenosis succession led to a decrease in the content of oil and its products in the soil. On the bioremediated plots, the plant communities consisting of seeded grass species as the major component were formed.

The invertebrates started to colonize the soil even before plants, during the plantless stage of the hytocenosis succession. Dipterans (at the larval stage); collembolans; and mesostigmatic, acaridan, prostigmatic, and oribatid mites were the pioneer groups of microarthropods. With the development of the phytocenosis and a decrease in the TPH content in the soil, the population density of invertebrate groupings increased, their structure became more complex, and dominant groups of microfauna changed. At the initial stages, dipteran larvae and mesostigmatic (predatory) mites were the key players in the invertebrate groupings. At the subsequent stages, the collembolans and oribatid mites became more abundant. *Tectocepheus velatus, Oppiella nova, Liochthonius sellnicki, Oribatula tibialis*, and *Eupelops sp.* were the pioneer oribatid species.

The analysis of the soil biota characteristics—abundances of microorganisms belonging to individual trophic groups, soil enzyme activities, duration of the period with increased biological activity, and the state of zoocenoses and phytocenoses—attests to the dependence of the intensity of remediation on the applied methods. The remediation of peat soil with the Roder and Universal biopreparations proves to be more efficient than remediation with agrochemical methods and technical cultivation of the soil.

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