Microbiomes of natural and abandoned agricultural soils of the Central part of Yamal region

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Abstract. Soil cover of the northern most regions of Eurasia are considered as underestimated in terms of their possible role in expansions of current agriculture to the cryolithozone. In this context, abandoned agricultural soils of Yamal region were investigated in terms of morphology, chemistry and taxonomy microbiome compositions and compared in these terms with mature tundra and taiga soils of pristine environments. The level of soil fertility was low in all cases – former agricultural soils and pristine ones. The level of microorganism’s biodiversity was higher in soils of agricultural lands. This fact indicates that the agricultural soil treatment in polar terrestrial ecosystem results in increasing of soil microbial biodiversity due to diversification of ecological niches. Also the is an essential lack of nitrogen sources in all permafrost affected soils studied.

1. Introduction

Currently, from 30 to 40 million hectares of arable land are removed from agricultural use in Russia and are not used. They are converted to abandoned land and transformed by natural and anthropogenic processes of soil formation, soil degradation and degradation, aorestation, waterlogging etc [1]. In recent decades, cryolithozone has been significantly altered by humans, resulting in noticeable changes in soil cover patterns, which have a consistent impact on ecosystem resilience.

Many northern regional governments see the increasingly favourable growing environment as an opportunity to manage agricultural expansion [2]. For example, Siberia is currently less than 50% of its estimated food production potential, including restoration of previously abandoned land, and is described by some authors as a hidden food basket [3]. Despite extreme climatic conditions, existence of cold weather and a permafrost conditions of soils within 8-10 months in a year, the focal nature of industrial and economic development of the territory, the Yamalo-Nenets Autonomous Okrug (YNAO) has sufficient opportunities for providing the population with the main crops cultivated on Far North (vegetables, barley, long-term herbs).

An important factor in the development of agricultural production in the Yamalo-Nenets Autonomous Okrug is an increase in the efficiency of the use of agropotential natural and effective fertility of arable and abandoned soils in accordance with their ecological-genetic status, granulometric composition, taking into account hydrothermal climatic indicators (precipitation, vegetation period duration, rainfall, regional features of their pedogenesis and metabolism).
For residents of the Arctic, where short summers and very severe, long winters with polar nights, fresh vegetable crops are extremely necessary, given their high vitamin content and the presence of other biologically active substances. When transporting vegetables from other regions, some valuable properties are lost. Therefore, the resumption of active cultivation of crops in the territory of the Yamalo-Nenets Autonomous Okrug is even more updated. A study of the microbiome of soils located in the agro-landscapes of the Yamalo-Nenets Autonomous Okrug has not previously been carried out. Therefore, this study is aimed at studying abandoned agricultural land, as well as the soils of current agricultural fields, which will be investigated from the point of view of microbiology.

The use of a metagenomic approach in the study of soil genesis was published in previous work [4]. Since soil formation largely depends on the physiological and metabolic activity of the soil microbiota, its study is important for understanding the general mechanisms of soil education processes [5]. In view of the above, the purpose of the present study was to study the microbiome of abandoned agrosols and natural tundra and taiga soils of the central part of the Yamal region.

2. Materials and methods

Natural soils and soils of abandoned fallow lands in the central part of the Yamal region (North of Western Siberia, Russia) have been studied. Agrogenic soils were studied within the city of Salekhard (Agrozem in the field of the Yamal agricultural station, designation - field) and the village of Yamgort of the Shuryksarsky district of the Yamal-Nenets Autonomous Okrug (Agrozem, vegetable garden, annual fallow land, designation - garden). Natural background soils have been studied near the city of Salekhard (Cryozem, tundra, designation - tundra) and in the vicinity of the previously designated village of Yamgort (Cryogenic Podzol, designation - taiga) (Figure 1).

![Figure 1](image_url)  
Figure 1. Examples of soils, studies.

The studied soils are acidic (pH less than 4.5), low-humus (carbon content of organic compounds less than 2%), characterized by poor enrichment with nitrogen and low content of nutrients. This is typical of most soils in the Yamal region [6].
Metagenomic studies. DNA isolation. DNA was isolated by the MN NucleoSpin Kit (MN, Germany). Precellus 24 homogenizer (Bertin, USA) was used as a disruptive mechanical action. The quality of the resulting preparation was tested electrophoretically (1% agarose gel, Bio-Rad, USA) and by PCR (Bio-Rad T100 Thermal Cycler). DNA sequencing. Sequencing of DNA carried out by means of the system of sequencing of Illumina MiSEQ (USA) with primers of F515 (GTGCGACAGCMGCCGCGTAA) and R806 (GGACTACVSSGSGCATCTTAAT) for variable V4 area of a 16s rDNA gene [7], according to manufacturer's guidance. Bioinformatic data processing. Sequencing was performed in Trimmomatic [8]. Forward and reverse readings were combined using fastq-join expression analysis software [9]. The open source tool VSEARCH [10] was used to search for and filter chimeric sequences. Operational taxonomic units (OTUs) were determined using the SILVA database-based precision reference method [11, 12]. OTUs classified as chloroplasts/mitochondria were removed. Alpha and beta diversity analysis was also performed using the QIIME package [13] and the mantel test from the QIIME package with 999 permutations. Real-time PCR. For quantitative PCR, primers were used against three groups of microorganisms: bacteria - EUB338 (ACTCCGGGAGGCAGCAG) and EUB518 (ATTACCGCGGGCCTGCTGG); archej - ARC915f (AGGAATTGGGGGAGCAC) and ARC1059r (GCCATGCACCWCCTCTCT); gribov - ITS1f (TCCGTAGGTGAACCTGCGG) and 5.8S (CGCTGCGTTCTTCATCG). For preparation of reactionary mix used the qPCRmix-HS SYBR Kit set (Eurogen, Russia) according to instructions of the producer. A series of ten-fold dilutions of fragments of 16S (E. Coli and H. Pilori) and ITS1 (S. cerevisiae) were used as standards. For the PCR, the thermocycler CFX96 (BioRad, Germany) was used with the cycle parameters: 95 ° C for 3 minutes, 40 cycles at 95 ° C for 20 seconds, 50 ° C for 20 seconds, 72 ° C for 20 seconds. For beta diversity, the Unifrac weighted metric (as part of the QIIME package) was used to calculate the degree of inconsistency (distance) between bacterial communities for comparison. The results were presented in the PCoA analysis using "Emperor" implemented in QIIME. All estimates were measured for normalized data (normalization was performed to the smallest number of sequences present in the sample).

3. Results and discussion

The taxonomic composition of the studied soils is generally characteristic of cryolithozone soils and is represented by the following dominant phyla: Acidobateria, Alphaproteobacteria, Gammaproteobacteria, Actinobacteria, Chloroflexi, Planctomycetota, Bacteroidota, VV These phylum are quite characteristic of the soils of this region [6, 14] and different form the microbiome of other natural zones [4, 15-17]. The background (mature) soil of the tundra is characterized by an increase in the autotrophic anaerobic component of the microbiome (Chloroflexi). The abandoned soil were characterized by the absence of an archaeal nitrogen reducing component (Nitrosopheracea) and a high proportion of nitrogen fixing microorganisms (Bradyrhizobium, Alphaproteobacteria), which indicates that even in the case of agroecosystems there is a high shortage of available nitrogen in the soil. Also, at all points studied, there is a high proportion of representatives of the fila Acitobacteriota, characteristic rather of the natural habitats of the arid zones. Unlike the soils of the arid zones, or for agrogenic soils in this dataset, the proportion of representatives of the Actinobacteria phylum is low. This also indicates the specificity of cryolithozone agroecosystems. This should be taken into account by decision makers because the permafrost underlayed soils represents about 60 % of whole Russian territory.
For alpha diversity indices (Figure 2) a significant increase was shown for agroecosystems (to a greater extent for the garden of Yamgorod village, to a lesser extent for the experimental station) compared with the control soil of taiga and tundra. These results are generally uncharacteristic of agroecosystems studies - usually natural soils show greater microbiome diversity [15-17]. In turn, the intra-group variance of beta diversity was shown to be inversely correlated with microbiome richness (Pearson correlation -0.65, p-value < 0.001). Apparently, the adaptation of the microbiome for cryolithozone agroecosystems has a different (in this case, rather reverse) dynamics than for temperate soils. Thus, quantitative and qualitative characterization of the differentiation of the cryolithozone soil microbiome during their agrogenic development was carried out for selected soils of Yamal region. These experience should be expanded to other regions of the Yamal region. This should be useful for better understanding the microbial drivers of soil formation and soil fertility in current climatic conditions.

4. Conclusions
During agrogenic development, a significant transformation of the taxonomic composition of soil microbiomes occurs. In agrogenic soils, there is an increase in the diversity of microorganisms. This is due to the emergence of more ecological niches than are available in natural soils.

Arctic soils are a unique object for studying the parameters of microbial diversity in agrogenesis. Further studies will identify key microbial drivers of soil fertility, which is especially important in the context of the return of agricultural production to cryolithozone.

The return of fallow agricultural soils to modern agriculture in permafrost conditions leads to the inhabitations of these soils by new types of microorganisms.
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References
[1] Lyuri D I, Karelin D V, Kudikov A V and Goryachkin S V 2013 Eurasian Soil Science vol 46 (9) p 93547
[2] Hohle E E, Lyssandtræ F, Orlund K, Næss Killingland R K, Mortensen P, Kvam R S and et al 2016 Agriculture and climate change: Working group report (Norway)
[3] Swinnen J, Burkitbayeva S, Schierhorn F, Prishchepev A V and Müller D 2017 Global Food Security vol 14 p 3853
[4] Abakumov E, Zverev A, Kichko A, Kimeklis A and Andronov E 2021 Open Agriculture vol 6 (1) p 5766
[5] Šourková M, Frouz J, Fettweis U, Bens O, Hüttl R F and Šantrůčková H 2005 Geoderma vol 129 (1) p 7380
[6] Alekseev I, Zverev A and Abakumov E 2021 Polar Research vol 40
[7] Caporaso J G, Lauber C L, Walters W A, Berg-Lyons D, Lozupone C A, Turnbaugh P J, Fierer N and Knight R 2011 Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample (Proc Natl Acad Sci U S A vol 108 (Suppl)) pp 4516–4522 DOI: https://doi.org/10.1073/pnas.1000080107
[8] Bolger A M, Lohse M and Usadel B 2014 Bioinformatics vol 170
[9] Aronesty A 2013 TOBioiJ vol 7 pp 1–8
[10] Rognes T, Flouri T, Nichols B, Quince C and Mahe F 2016 PeerJ vol 4 p 2584
[11] Quast C, Pruesse E, Yilmaz P, Gerken J, Schweer T, Yarza P, Peplies J and Glöckner F O 2013 Acids Res vol 41 (D1) pp D590–D596
[12] Yilmaz P, Parfrey L W, Yarza P, Gerken J, Pruesse E, Quast C, Schweer T, Peplies J, Ludwig W and Glöckner F O 2014 Acids Res vol 42 pp D643–D648
[13] Caporaso J G, Kuczynski J, Stombaugh J, Bittinger K, Bushman F D, Costello E K, Fierer N, Peña A G, Goodrich J K, Gordon J I, Huttley G A, Kelley S T, Knights D, Koenig J E, Ley R E, Lozupone C A, McDonald D, Muegge B D, Pirrung M, Reeder J, Sevinsky J R, Turnbaugh P J, Walters W A, Widmann J, Yatsunenko T, Zaneveld J and Knight R 2010 PMID 20383131
[14] Abakumov E, Zverev A, Morgun E and Alekseev I 2020 Open Agriculture vol 5 (1) p 335441
[15] Chernov T I, Ledebova M P, Tkhatakhova A K and Kudovaya O V 2017 Eurasian Soil Science vol 50 (1) p 649
[16] Semenov M V, Chernov T I, Tkhatakhova A K, Zhelezova A D, Ivanova E A, Kolganova T V and et al 2018 Applied Soil Ecology vol 127 p 818
[17] Abakumov E, Zverev A, Suleymanov A and Suleymanov R 2020 Open Agriculture vol 5 (1) p 52938