



New

Scientific Research

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▷ΔΛΠΔ^c: Nom du projet:Évaluation des bactéries multirésistantes dans la couche de sol active et les régions de pergélisol de l'Extrême-Arctique canadienDescription du projet:L'un des impacts les plus notables du réchauffement de l'Arctique est le dégel du pergélisol, qui pourrait potentiellement réactiver de nombreux micro-organismes dormants qui sont conservés dans les sols du pergélisol pendant des siècles. Certains de ces micro-organismes peuvent être des bactéries pathogènes et/ou résistantes aux antibiotiques (ARA) pouvant entraîner la résurgence de maladies zoonotiques. En outre, les gènes de résistance aux antibiotiques (ARG) peuvent être transportés dans l'environnement arctique par la migration et le mouvement des humains et des oiseaux. Étant donné que les ARG sont maintenant répandus parmi les communautés microbiennes, la question de savoir si la grande diversité des ARG et des ARB dans les réservoirs environnementaux est le résultat d'une influence anthropique est controversée. Ainsi, dans cette proposition, nous avons l'intention d'effectuer une étude complète du sol de la toundra, de la couche active et du pergélisol non seulement pour

évaluer la présence d'ARG et d'ARB potentiels en utilisant une approche dépendante de la culture et indépendante, mais aussi pour délimiter les sources potentielles anthropiques. et/ou les origines anciennes des ARG et des ARB dans la région canadienne de l'Extrême-Arctique. Ainsi, notre projet proposé fournira des données de base sur les ARG et ARB qui pourraient être utilisées pour délimiter les régions de pergélisol à haut risque pour la population locale.

△^bND^c:

Technical Project Proposal Description Rationale: Climate change is predicted to increase the rate and spread of antibiotic resistance among bacterial pathogens (Cavicchioli et al., 2019; Rodríguez-Verdugo et al., 2020). The evolution and spread of antibiotic resistance among pathogenic bacteria are one of the most important challenges in public health today. Permafrost, the most ancient and extreme environmental ecosystem in which microbial life has been reported, is the potential site to study bacteria dated back to the pre-antibiotic era. Antibiotic resistance genes (ARGs) were functionally diverse before the anthropogenic use of antibiotics began, contributing to the evolution of natural reservoirs of resistance genes. Under the ongoing climatic warming scenario, there is a possibility of horizontal transfer of these natural ARGs among other microbes via mobile genetic elements (MGEs) giving rise to the drug-resistance pathogens. Similar to ARGs, virulence factor genes (VFGs) of pathogenic bacteria can also be transferred to other bacteria by phages and plasmids (Wagner and Waldor, 2002). These transmitted genes can disrupt the host immune system, allowing bacterial pathogens to invade and cause infectious diseases (Wang et al., 2021). These drug-resistance pathogens may cause infections that are untreatable with currently available antibiotics (Zhang et al., 2022). ARB was identified in permafrost dated 15–290 ka, with species even more abundant in active layers in older and deeper permafrost (Perron et al., 2015). Subsequently, concerns have been raised about the potential for the exchange of genetic material between antibiotic-resistant permafrost microorganisms and contemporary bacteria to create new antibiotic-resistant strains. The local human settlement (the northerners) near the active permafrost region is at risk of being a potential host of these ancient types of ARGs and ARBs. Besides, these indigenous populations could potentially become a vector for the spread of such ARGs and ARBs. Thus, our proposed project will provide baseline data on the ARGs and ARB which could be utilized to demarcate the high-risk permafrost regions for the local population. In this context, we delineated the following objectives for the proposed project:- Objectives:•Evaluation of Antibiotic-resistant genes (ARGs), virulence-related genes, and antibiotic-resistant bacteria (ARB) in the Canadian high Arctic Soil, and Permafrost regions•Genomics of cryopreserved bacteria from permafrost and comparison with their modern counterparts•To evaluate the presence of resistance genes and analyse antibiotic resistance patterns, thereby allowing to determine the role of anthropogenic pressure in the apparition of antibiotic resistance.This study will provide baseline information on the possible reactivation of ARB in the permafrost, the risks associated with the release of potentially drug-resistant pathogens and antibiotic-resistant genes from permafrost, and the implications for policy and international cooperation in light of the Covid-19 pandemic.Progress to Date: Our works on antibiotic resistance in the Svalbard Arctic on migratory birds; Indicate that migratory birds are one of the potential carriers of Antibiotic resistance in the Svalbard Arctic (Prakash et al., 2022). Our studies on Antibiotic-resistant genes and bacteria from the Tundra, Marine and permafrost samples from the Svalbard Arctic are going on.Methodology: Field methodology includes the collection of samples from the active layer and Permafrost soils using a field core sampler near the CHARs campus. The core samples will be cut aseptically into different layers and stored at -80°C. These samples will be transported back to India (NCPOR-lab) using a cold shipment. In the NCPOR lab, these layers will be used for the isolation, culturing, and screening of various health-significant bacteria (culture-dependent) and for the extraction of DNA and metagenomics studies (culture-independent).Data management: Describe your data management plan, including where and when the data and metadata records will be storedAll data will be made available by the wider community, but with an embargo period (date of collection) to allow publication of the results beforehand. On publication, the data is publically available. Data will be stored at NCPOR, India data center and will be shared on request before publication also. Research outputs: Describe the major research outputs to be generated through the project (academic theses, publications, presentations, reports,

etc.) Major Research output expected from the projects were publications and reports. Publications include • Diversity of multidrug-resistant bacteria and antibiotic-resistant genes from Canadian High Arctic. • Reports on antibiotic-resistant genes and antibiotic-resistant bacteria from Canadian High Arctic.

Inuinnaqtun: Naunaiyainiq micro-organisms-nik qiqumaninganik naunaiyagakhat KanatamiUt Qutiqtumi UkiuqtaqtumiAtauhiq naunaitqiaq akturninga Ukiuqtaqtup uunaqpalianinga auktuqpalianinga nunap qiqumaninganik – atuqtaulaaqtut amihunik microorganism-nik ilipqamayaayut nunap qiqumaninganit. Ilangit hapkua microorganism-guyut aaniarutaulaaqtut ukualu/uvaluniit halumailrut (ARB) pijutaulaaqtut zoonotic-nik aaniarutiniq. Talvalilu, havautinit huuyungnaiqtirutit genes (ARG) agyaqtaunginnariaqaqtut Ukiuqtaqtumut avatianut nuutirnikkut auladjutainnutlu inuit tingmianiklu. Talvanga ARGngit aulaliqtun avatingnun tapkuninga microbial nunalaani, taima anginirmik allatqiinguyut ARGngit ARBngitlu avatiliqinikkut atuqtauffaaqtukharnik taima naunairutiqaqhimayuq talvuuna auladjutikharnik ayungnautigivakhimayainik. Talvuuna, uumani tukhiutimi, piniaqhimajugut naunaijattiaqpiakhimajumik naunaijautikhanik nunap nuna, aullaranginnaqtumik qaliriiktunik, imaalu nunap qiqumaninganik naunaijailimaittut tadjaj PINIARUngnaqhijut ARG unalu ARB aturlutit pitquhikkut-inmikkut imaalu inmikkut atuqtakhainnik kihimi ikiglijuumirlugit piniarungnaqhijut-qanurinningit imaalu/imaaluuniit qaujimattiaqhimajut aullaningit ARGs ukualu ARB Ukiuqtaqtumi avikturnianni. Talvuuna, tukhiqtavut havaaqhangit tuniniaqtun tunngavikharnik naunairutikharnik talvani ARGsnik ARBniklu taima atuqtaugiaqaqtun naunaiyaiyaangat anginirmik ayungnautiqaqtunik nunap qiqumaninga avikturniingit talvani nunalaani inugaingit.* Inuinnaqtun language translation through Automated programme; Not have checked by local language expert

Personnel

Personnel on site: 2

Days on site: 20

Total Person days: 40

Operations Phase: from 2022-11-01 to 2026-10-31

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Six locations inside the polyline with out disturbing activities and envirnment	Drilling	Commissioners	No	The project is planning to take the sample from the 6 locations from the polygon and not have any archeologically and paleontologically important site	No activity in near community area

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$a^b r^c \Delta_{\sigma} \Delta_{\tau} \Delta_{\rho} \Delta_{\delta} \Delta_{\gamma} \Delta_{\alpha}$

Kitikmeot

[illegible][illegible]

Project transportation types

Transportation Type	Distance	Length of Use
Land	Land through Walking	

Project accomodation types

Permanent Camp

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Information is not available				

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There is no expected waste or impact associated with this study. If any unlikely case, waster is generated the proponent will keep in metal containers in approved facility and inaccessible to wild life. Samples will be collected from the field sampling locations with the help of the local community. DNA isolation and bacterial culture isolation were conducted in NCPOR lab India after the transportation of samples.

Additional Information

SECTION A1: Project Info

SECTION A2: Allweather Road

SECTION A3: Winter Road

SECTION B1: Project Info

SECTION B2: Exploration Activity

SECTION B3: Geosciences

SECTION B4: Drilling

SECTION B5: Stripping

SECTION B6: Underground Activity

SECTION B7: Waste Rock

SECTION B8: Stockpiles

SECTION B9: Mine Development

SECTION B10: Geology

SECTION B11: Mine

SECTION B12: Mill

SECTION C1: Pits

SECTION D1: Facility

SECTION D2: Facility Construction

SECTION D3: Facility Operation

SECTION D4: Vessel Use

SECTION E1: Offshore Survey

SECTION E2: Nearshore Survey

SECTION E3: Vessel Use

SECTION F1: Site Cleanup

SECTION G1: Well Authorization

SECTION G2: Onland Exploration

SECTION G3: Offshore Exploration

SECTION G4: Rig

SECTION H1: Vessel Use

SECTION H2: Disposal At Sea

SECTION 11: Municipal Development

[illegible]

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Miscellaneous Project Information

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Cumulative Effects

Impacts

$\mathcal{L}(\mathcal{A}) \subseteq \mathcal{L}(\mathcal{B})$

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1 polyline Six locations inside the polyline with out disturbing activities and envirnment