FROM SENSING TO MAKING SENSE

Preparing For The Next Pandemic: Impact Of Thawing Permafrost For Ancient Pathogens

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By 2100, we may lose 65% of the Arctic's near-surface permafrost, whereby abrupt rates of thaw (~3× the mean global rate) could release ancient radiologicals, chemicals, and microorganisms that have been trapped for hundreds of thousands of years from the deep frozen layers. Recent studies have reported that permafrost biologicals have had devastating effects on wildlife, indigenous populations, and the local flora. As our nation's warfighters are deployed in territories linked to permafrost thaw, it is, thus, critical to actively identify the microbial signatures associated with permafrost sites of varied degrees of thaw and model its dispersion via terrestrial and aerial modalities. The viral and bacterial genomic signatures, particularly through assembled and annotated genomes, suggests its physiological functions, potential relationship to known pathogens, and provides valuable insight as to what current countermeasures could be used in the event of widespread infection. If we are to protect our warfighters from ancient and potentially infectious pathogens, we must actively seek out these biological threats to public health, wildlife, and plant life before they are released.

Herein, our motivated team from Los Alamos National Laboratory and the University of Alaska Fairbanks have initiated efforts to address the potential biological threats from thawing permafrost on two fronts. The first is the viable recovery of potentially novel bacteria for genomic characterization. The second is the dispersion modeling of biological particles. With Alaska permafrost associated soils of varied degrees of thaw, we are utilizing single cell genomics with gel microdroplets to determine if specific growth conditions contribute to enrichment and viable recovery of certain bacteria, as our preliminary genomic survey data suggests. Thus, the recovery of these enriched, yet potentially ancient bacteria, permits genomic characterization via annotated genomes (e.g., antimicrobial resistance genes) and downstream phenotypic studies (e.g., host-pathogen interactions). Our modeling efforts centers on the QUIC-Plume model of dispersion. Currently utilized to model dispersion of radiological particles in an urban setting, QUIC-Plume has been adapted to model aerial dispersion of Bacillus anthracis spores to determine the potentially immediate and long-term threats from these airborne permafrost bioagents. This presentation seeks to report our findings, thus far, and share our future vision to integrate additional novel technologies and genomic approaches to predict microbial infections for developing medical countermeasures.

Altogether, our team is establishing the groundwork for the biosurveillance of ancient biologicals and a predictive modeling of dispersion, thereof, that ultimately supports our deployed warfighters, national security, and public health.