

The Impact of Global Warming on Permafrost-locked Pathogens: A Systematic Review

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BACKGROUND

- A systematic literature review was performed to investigate the relationship between global warming and emerging & re-emerging infectious diseases in the permafrost.

METHODS

- A search of published studies on the effects of global warming on emerging and re-emerging infectious pathogens frozen in the permafrost was undertaken by probing PubMed for articles that met predetermined inclusion criteria.

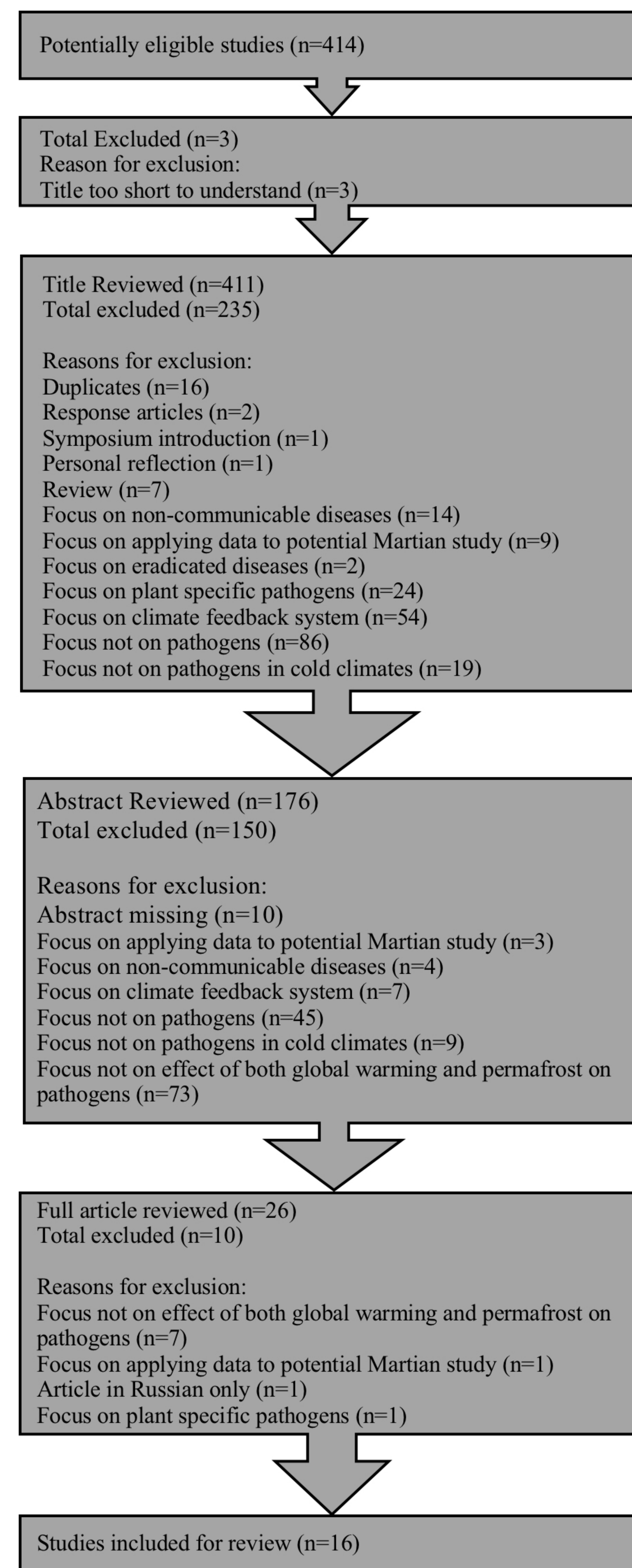


Table 1. Characteristics of included studies

Author, publication date, [citation no.]	Location	Study design
Coolen, 2000, [1]	Alaska	Test-tube Lab Research
Deng, 2015, [2]	Alaska	Test-tube Lab Research
Frank-Fahle, 2014, [3]	Canada	Test-tube Lab Research
Hansen, 2007, [4]	Norway	Test-tube Lab Research
Kashuba, 2017, [5]	Siberia	Test-tube Lab Research
La Ferla, 2017, [6]	Antarctica	Test-tube Lab Research
Laaksonen, 2010, [7]	Finland	Meta-Analysis
Legendre, 2014, [8]	Siberia	Test-tube Lab Research
Legendre, 2015, [9]	Siberia	Test-tube Lab Research
Park, 2017, [10]	Svalbard	Test-tube Lab Research
Revich, 2011, [11]	Russia	Meta-Analysis
Revich, 2012, [12]	Russia	Meta-Analysis
Rivkina, 2000, [13]	Siberia	Test-tube Lab Research
Tuorto, 2013, [14]	Alaska	Test-tube Lab Research
Zhang, 2013, [15]	Siberia	Test-tube Lab Research
Zhang, 2007, [16]	China	Test-tube Lab Research

Table 2. Summary of Findings

Author, publication date, citation no.	Testing method	Identified Pathogens	Other findings
Coolen, 2000, [1]	16S rRNA and radiocarbon dating	Archaea, Eukaryotes, Bacteria from: phylum Bacteroidetes, Firmicutes, Gemmatimonadetes, subphylum Acidobacteria, class BetaProteobacteria, AlphaProteobacteria	dated 3710 ± 35 years BP at 126 ± 2 cm
Deng, 2015, [2]	16S rRNA and 806R	Bacteria from genus Actinoplanes, Micromonospora, Mycobacterium, Rhodococcus	
Frank-Fahle, 2014, [3]	16S rRNA	Bacteria from genus Methanobacterium, Methanosarcina, phylum Bacteroidetes, Firmicutes, subphylum Acidobacteria, class Deltaproteobacteria, Betaproteobacteria, Alphaproteobacteria, Gammaproteobacteria	
Hansen, 2007, [4]	Oxic and Anoxic cultivation and isolation techniques with culture-independent methods	Bacteria from genus Clostridia, phylum Bacteroidetes, Planctomycetacia, Spirochaetes, Sphingobacteria, subphylum Acidobacteria, class Thermomicrobia, Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, Deltaproteobacteria, Flavobacteria Mollicutes	Bacteria from the phylum: Verrucomicrobiae, (candidate division only known by sequence) and Unclassified Bacteria
Kashuba, 2017, [5]	16S rRNA	Bacteria from phylum Actinobacteria, Bacteroidetes, Firmicutes, subphylum, class Gammaproteobacteria, Alphaproteobacteria, order Actinomycetales	Antibiotic resistance and virulence genes, metabolic activity
La Ferla, 2017, [6]	FACSCalibur flow cytometer, viability of prokaryotic cells: Molecular Probes Live/Dead Bac Light Bacterial Viability Kit, for respiring cells: Bac Light Redox Sensor CTC Vitality Kit	Prokaryotic cells	Depth levels less than 550 cm
Laaksonen, 2010, [7]	Possibility of <i>Setaria tundra</i> , filarioid nematode, outbreak through generalized linear modeling	N/A	Outbreak would be associated with a new strain and a delay between initial transmission, infection, and development in the reindeer, with summer being the most likely time-period
Legendre, 2014, [8]	phenol/chloroform extraction and purelink genomic DNA extraction mini kit	N/A	cellular host <i>A. castellanii</i> purposefully infected with Pithovirus to assuage viability
Legendre, 2015, [9]	PureLink Genomic DNA Extraction Mini Kit, Platinum Pfx Taq Polymerase Kit, RNeasy Midi kit	Giant virus genomes: Mollivirus, Pandoravirus salinus, Pandoravirus dulcis, Pithovirus sibericum, Mimivirus, Megavirus chilensis and cellular host: <i>A. castellanii</i>	
Park, 2017, [10]	16S rRNA	<i>Pseudomonas</i> sp. strain PAMC 28618	
Revich, 2011, [11]	Regional models of climate change	N/A	Significant 0.1% level positive trend (rise) in temperatures, more pronounced in Center & South Yakutia, where the highest numbers of anthrax outbreaks have occurred in the last 80 years
Revich, 2012, [12]	N/A	Encephalitis, Rabies, Leptospira, Brucella, <i>Francisella tularensis</i> , <i>B. anthracis</i>	Northward expansion of tick populations with change in spatial and temporal patterns in tick bites and tick-borne encephalitis, epizootic rabies rates have increased, human leptospirosis is endemic in some areas of Russian arctic, Brucella bacteria epidemics and a pathogenic resistance to the environmental conditions, Anthrax can survive longer in the arctic environment
Rivkina, 2000, [13]	activity: high-sensitivity liquid scintillation analyzer, organic Carbon content: wet oxidation method, plate counting: sonication, unfrozen water: adiabatic and differential calorimetry	N/A	Cores 2-3 million years old depth of 8.5-25.0 m, lipid activity tracked for 550 days with temperature ranging -20 to 5 degrees Celsius
Tuorto, 2013, [14]	Stable Isotope Probing (SIP) and 16S rRNA	Bacteria from phylum Actinobacteria, Chloroflexi, Proteobacteria, subphylum Acidobacteria class Gemmatimonadetes	
Zhang, 2013, [15]	16S rRNA	multiple strains of each: <i>Arthrobacter phenanthrenivorans</i> , <i>Subtercola frigoramans</i> , <i>Glaciomonas immobilis</i>	Growth temperature range of -5 to 35 Celsius, Growth on different Media, Anaerobic Growth, Salt Tolerance, Resistance to Antibiotics and Heavy Metals, biodegradation of Hydrocarbons, and Enzyme Activity
Zhang, 2007, [16]	16S rRNA and amplified ribosomal DNA restriction analysis (ARDRA)	Bacteria from genus: <i>Nesterenkonia</i> , <i>Arthrobacter</i> , <i>Citricoccus</i> , <i>Marinibacillus</i> , <i>Sporosarcina</i> , <i>Planomicrobium</i> , <i>Bacillus</i> , <i>Mycoplana</i> , <i>Paraooccus</i>	

RESULTS

- Twenty-six studies were identified for review. Of the sixteen included for the final review, research was conducted in nine different countries. Overall, the studies suggested that global warming has increased reduction in the permafrost, which is resulting in higher metabolic activity of bacteria and viability of bacteria that has been trapped for up to millennia. Novel mutations have been noted in recognized and unidentified bacterium. Additionally, these same effects have been seen in viral strains actively affecting animals and humans living near or in permafrost regions.

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