

Applications

- Detection of disease-causing microbes in rivers and other environmental samples

Advantages

- Rapid and comprehensive testing
- Detailed characterization of pathogenic agents
- Better prediction of risks associated with exposure to biological agents

Inventors

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Market Need

Large rivers are impacted by disease-causing agents including bacteria, protists, worms, viruses, and harmful algae that derive from urban runoff, aging/failing sewerage, and are beginning to thrive due to nutrient pollution and climate change. Presently there are few avenues for characterizing recreational waters due to the paucity of methods to detect most of these organisms prior to reports of human illnesses related to exposure. Current water monitoring practices only serve as course indicators of potential contamination, and provide no information on the diversity, source, ecology, or evolution of waterborne disease agents.

Technology Summary

This technology presents a new direction within the field of public health genomics by applying next-generation sequencing (NGS) to rapidly and comprehensively detect disease-causing microbes in environmental samples. Created metagenome will represent the whole community of DNA and RNA sequences to document presence, distribution, and evolution of epidemiologically significant microbes. The results will have tangible public health benefits in a worldwide application. The knowledge gained and methodology developed will allow health officials to better predict risks associated with environmental exposure to biological agents.

Technology Status

Patent pending: U.S. and foreign rights available.

This technology is available for licensing to industry for further development and commercialization.