



An Optimized, More Efficient Method for Characterizing Microorganisms and Viruses Using Metagenomics

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The Wisconsin Alumni Research Foundation is seeking commercial partners interested in implementing a more sensitive, streamlined method for characterizing microbes using metagenomics. Characterization of microbes and other microorganisms in biological samples enhances veterinary and human diagnostics and enables the identification of contaminants within bodily fluids, food, water, soil and industrial processes.

Overview

Metagenomics is the study of genetic material from environmental samples for detecting microbes, especially pathogens. It is increasingly used within clinical and industrial settings. While metagenomics offers invaluable information, inefficiencies and other limitations in sample processing and computational analysis hinder its use. To date, users of this approach lack a reliable, efficient method for preparing, analyzing and interpreting their metagenomic data.

The Invention

Two scientists at UW-Madison have created a “pipeline” that quickly prepares and efficiently processes metagenomic data for the identification of microbes within a given sample. This optimized method enables more and faster comparisons to be made using a curated database that increases the sensitivity of the analysis.

The power of this new approach starts with the *in silico* translation of nucleotide sequences into protein sequences, which reduces the time per comparison of each sequence within the database from 30-60 minutes to just 2-5 minutes. This technology is more effective compared to commonly used nucleotide-based methods and streamlines the bioinformatic analysis, making it less labor intensive and computationally involved. Additionally, this technology is versatile and can be applied to data from multiple metagenomic sequencing platforms.

Applications

- Improves bioinformatic analysis of metagenomic data for use in various sectors
- Provides reliable and sensitive identification and characterization of protein sequences

Key Benefits

- No comparable technology is available on the market.
- Offers comprehensive characterization of ALL microorganisms present in a sample
- Use of protein sequence comparisons increases the sensitivity and speed of the analysis
- Provides a less complex analysis pipeline
- No sample data needed de novo to yield meaningful results, which delivers an unbiased analysis.

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Stage of Development

The development of this technology was supported by the WARF Accelerator Program. The Accelerator Program selects WARF's most commercially promising technologies and provides expert assistance and funding to enable achievement of commercially significant milestones. WARF believes that these technologies are especially attractive opportunities for licensing.

Additional Information

For More Information About the Inventors

- [Tony Goldberg](#)

Tech Fields

- [Animals, Agriculture & Food : Food safety & quality.](#)
- [Diagnostics & Biomarkers : Diagnostics](#)
- [Medical Devices : Diagnostics & monitoring tools](#)
- [Research Tools : Detection](#)
- [Research Tools : DNA & RNA tools](#)
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For current licensing status, please contact Jennifer Gottwald at jennifer@warf.org or 608-960-9854

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