

VIROCAP: ENHANCED, EFFICIENT VIROME SEQUENCING WITH METAGENOMIC CAPTURE PROBES

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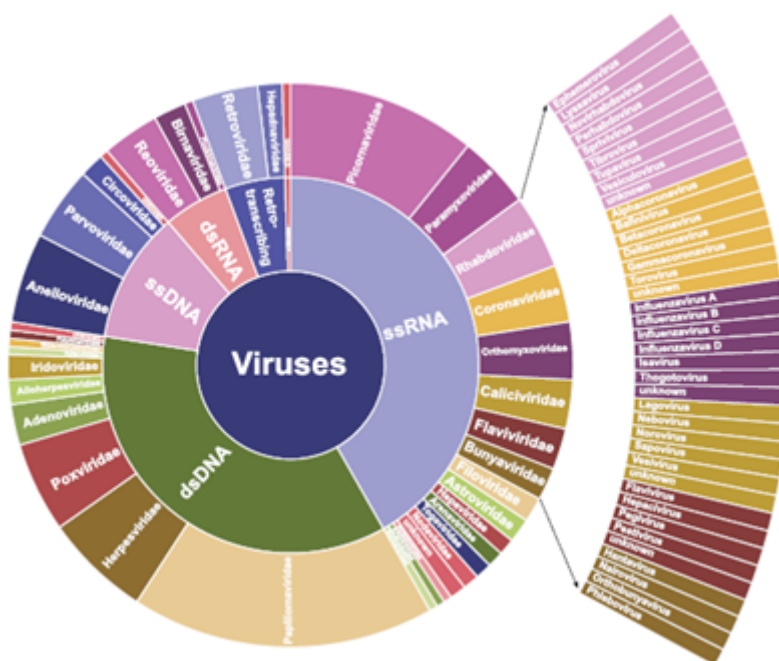
[Hardin, Clyde "Frank"](#)

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Technology Description

A team of researchers at Washington University developed “ViroCap”, a patented capture probe technique for sensitive, comprehensive, in-depth metagenomics analysis vertebrate viruses. This invention could enhance traditional metagenomics shotgun sequencing (MSS) with the potential for a clinical diagnostics tool that can simultaneously detect viruses and provide immediate characterization, including taxonomic assignment, strain typing, virulence characteristics and anti-viral drug resistance genotyping.

Traditional gold-standard assays for virus detection (e.g., PCR and microarray testing) are either extremely low throughput or require *a priori* knowledge of the exact viral sequence. Newer MSS techniques enable more in-depth metagenomics studies of the virome. However, because MSS samples have a small proportion of viral nucleic acids compared to the more abundant host and other non-viral DNA, this approach is much less sensitive and may yield insufficient data for detailed analysis. To address these issues, ViroCap provides a solution-based capture technique with probes that hybridize to thousands of viral nucleic acid sequences and enrich the sample prior to next generation sequencing. This broad-based analysis can detect and characterize virtually any virus that infects people and animals, even at low levels. ViroCap consistently and strikingly enhances MSS, with several hundred-fold increases in the percentage of viral reads. This technology could be used in both research and diagnostics settings and could be especially useful in situations with an elusive diagnosis or when the cause of a disease outbreak is unknown.



Taxonomic distribution of target genomes included in initial ViroCap studies.

Stage of Research

The inventors demonstrated the sensitivity and efficiency of ViroCap capture and enrichment using a library of nucleic acid probes computationally designed to detect 34 virus families (both DNA and RNA viruses). Results from two sets of human clinical samples comparing standard MSS to MSS following ViroCap enrichment demonstrated that ViroCap: increased viral reads 674- and 296-fold; increased medial breadth of coverage from ~2% to >75%; and could detect viral sequences with up to 58% variation.

Publications

- Wylie, T. N., Wylie, K. M., Herter, B. N., & Storch, G. A. (2015). [Enhanced virome sequencing through solution-based capture enrichment](#). *Genome Research*, gr-191049.
- [New test detects all viruses that infect people, animals](#). The Source, Sept. 29, 2015

Applications

- **Diagnosics** – metagenomic analysis for broad detection and characterization of known and novel viruses in clinical and epidemiological samples (e.g., outbreak investigations and disease surveillance)
- **Research** – reagents and kits for high-throughput studies to characterize viromes, for example in disease etiology studies of humans and animals

Key Advantages

- **In-depth, sensitive and efficient**
 - reduced time and cost of testing because assay is highly multiplexed and eliminates sequencing of host/non-viral DNA
 - broader analysis and much higher throughput than gold-standard PCR testing with comparable sensitivity
 - sequence analysis easily identifies viral subtypes to characterize strain, virulence, and anti-

viral drug resistance profiles in each sample tested

- **Broad, comprehensive detection:**

- detects all vertebrate viruses
- viral reads increased several hundred fold over traditional MSS
- no *a priori* knowledge needed to determine which viruses to sequence
- potential for low-abundance or new strain discovery
- enables a new, higher-resolution view of eukaryotic DNA and RNA viruses in the microbiome

Patents

- [Compositions and methods for detecting viruses in a sample](#) (U.S. Patent No. 10,597,736)
- Additional patent application pending

Related Web Links

- **Kristine Wylie** - [Profile](#), [Lab](#)
- **Todd Wylie** - [Profile](#)
- **Gregory Storch** - [Profile](#)