



Monitoring Viruses in Human Blood Using Particle Selection and Shotgun Sequencing

Rapid detection of viral epidemics, biological threats, or leukemia

New viral infections in humans appear to be emerging at an increasing rate. The safety of the blood supply is currently maintained by selective screening of donors, pathogen reduction, and nucleic acid and antibody testing for known viruses including human immunodeficiency virus (HIV), hepatitis B virus (HBV), hepatitis C virus (HCV), human T cell lymphotropic virus (HTLV), and West Nile virus (WNV). Established monitoring systems have made the blood supply extremely safe from the transmission of these known viruses.

The largest potential threats for infection of the blood supply or community are posed by novel pathogens, which would escape the current screening techniques. In addition, viral infection has been implicated in some long-



term illnesses that manifest with non-infective symptoms (e.g., childhood acute leukemias). The inability to identify novel viral DNA chains by comparison with viruses present in healthy populations has hindered our ability to: 1) identify novel viral threats and infections, and 2) link early infections from unknown viruses to subsequent maladies.

Dr. Forest Rohwer has developed a technique to identify the complete viral community in human blood through DNA selection and shotgun sequencing. This methodology does not rely on conserved sequences being present within viral communities, so it is appropriate for identifying completely novel viral types in blood samples. In addition, it does not use representative differential amplification (RDA), which requires a high level of viremia to be present before the virus can be recovered.

The method employs selection based on the physical properties of viruses combined with sequence-independent amplification and cloning. It has already been established and used to

discover novel anellovirus sequences in the blood of healthy donors.

Future research will focus on characterizing the viral communities of healthy humans. This information will be used to identify novel pathogens as they emerge, as well as to identify *in utero* infective agents thought to contribute to the development of childhood acute leukemia.

Benefits

- Identifies novel viruses
- Not restricted by low viral DNA count, abundance of host and mitochondrial DNA, or absence of conserved genes

Applications

- Monitoring of blood supply contamination
- Early identification of biological threats or novel viral outbreaks
- Screening for novel viruses that may generate subsequent cancers (e.g., childhood acute leukemias)

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