



Demonstrated Sample Diversity

The Virus Counter instrument and assay were designed to work with a variety of viruses from a range of sources. The non-specific virus staining procedure employed in the assay allows the same reagents to be used regardless of the virus to be analyzed. This document summarizes many of the viruses and samples that have been analyzed with the Virus Counter.

SIMPLIFIED SAMPLE PREPARATION

A two-stain mixture containing a nucleic acid-specific stain and a protein-specific stain is used for the sample preparation process; no antibodies are needed. These dyes are virtually non-fluorescent until they bind their targets so there is no need to remove excess dye in lengthy washing steps prior to analysis. Viral proteins (e.g., capsid proteins) are labeled with a fast, one-step stain that exhibits low protein-to-protein variability. The second stain in the dye mixture is also a fast, one-step stain with a high affinity for nucleic acids. This dye works quite well with all types of nucleic acids (i.e. single or double-stranded RNA or DNA). Because of this universal, non-specific sample preparation method almost any virus can be analyzed by the Virus Counter without having to supply your own sample-specific reagents.

DEMONSTRATED EXAMPLES

A wide variety of viruses have been successfully analyzed by the Virus Counter. These include virus samples from commercial sources as well as those supplied by collaborators from fields including vaccine development, antigen production and medical research. Table 1 summarizes the diversity of virus samples that have been successfully analyzed. These include over 500 collaborator-supplied samples of influenza from a number of propagation sources in a variety of real-world suspension buffers and matrices.



SUMMARY OF VIRUS SAMPLES SUCCESSFULLY ANALYZED BY THE VIRUS COUNTER

Virus	Genome ^a	Supply Source		Source or Preparation			Notes
		Commercial ^b	Collaborator	Gradient	Cell Culture	Egg-Based	
Influenza	~15,000 nt, ssRNA	X	X	X	X	X	>30 monovalent A & B strains, "swine flu" trivalent vaccine
Parainfluenza	~15,000 nt, ssRNA		X		X		PI-3
Baculovirus	~160,000 bp, dsDNA	X	X		X		AcNPV & multiple recombinant strains
Dengue	~10,500 nt, ssRNA	X			X		Dengue Virus Type 1
Vaccinia	~194,000 bp, dsDNA		X		X		Modified Vaccinia Ankara
Coronavirus	~30,000nt, ssRNA	X			X		Human Coronavirus, NL63 (Amsterdam 1)
Rubella	~10,000 nt, ssRNA	X		X			HPV-77
Respiratory Syncytial Virus (RSV)	~15,000 nt, ssRNA	X	X	X	X		A-2 & other strains
Cytomegalovirus (CMV)	~230,000 bp, dsDNA	X			X		AD-169
Herpes simplex virus (HSV)	~150,000 bp, dsDNA		X		X		HSV-1, MacIntyre strain

^a http://www.virology.net/Big_Virology/BVHomePage.html

^b commercial sources: Advanced Biotechnologies Inc. & Microbix Biosystems Inc.

NOTES:

Viruses with genomes >9,000 bases or nucleotides should be compatible with the Virus Counter.

One virus we were not successful in analyzing was adeno-associated virus due to its small genome (~5,000 bp, ssDNA) and physical size (~20 nm diam.).

Less complex matrices (i.e. higher purity samples in a simple matrix) tend to provide better results over a wider dynamic range.