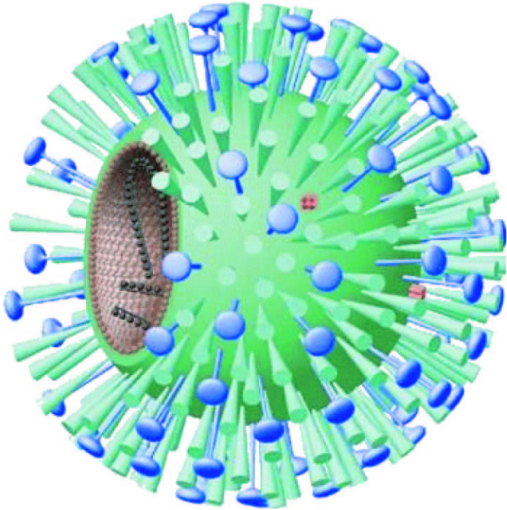


## Influenza A Virus



Model of an Influenza type A virus. Influenza viruses are enveloped RNA viruses. Recombination of segments of the viral genome may occur in hosts co-infected with different Influenza A viruses. This may give rise to new types of Influenza A viruses that may be able to exploit new hosts and cause severe disease.

### Influenza A virus

hemagglutinin (blue)  
neuraminidase (green)  
matrix protein (brown)  
courtesy [www.pasteur.fr](http://www.pasteur.fr)

## Samples

Swab	Preserved in <a href="#">sample buffer</a> (nasal swab preferred!)
Body fluids	Preserved in <a href="#">sample buffer</a>
Notes: Send all samples at room temperature, preferably preserved in sample buffer <a href="#">MD Submission form</a> .	

## Interpretation of PCR Results

High positive	
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(> 1,000 copies/ml, swab)	<b>Influenza A virus infection</b> <b>[interpretation must be correlated to clinical symptoms]</b>
<b>Low positive</b> (1-1,000 copies/ml, swab)	
<b>Negative</b>	<b>Influenza A Virus not detectable</b>

## Influenza A Virus

Three types of influenza viruses are known: A, B, and C. Humans may be infected with influenza types A, B, and C viruses. Influenza type A viruses can also infect birds, pigs, horses, dogs, and cats. Wild birds are the natural hosts for influenza A viruses ([Olson et al., 2006](#)). Influenza type A viruses are divided into subtypes and named on the basis of two proteins on the surface of the virus: hemagglutinin (HA) and neuraminidase (NA). There are 16 known HA subtypes and 9 known NA subtypes. Only some influenza A subtypes including H1N1, H1N2, and H3N2 are currently in general circulation among people. Other subtypes are found in other animal species. For example, H7N7 and H3N8 viruses cause illness in horses, and H3N8 also has recently been shown to cause illness in dogs ([Crawford et al., 2005](#)).

## Clinical Signs

Canine influenza is a highly contagious respiratory infection of dogs. Canine influenza A virus is closely related to the virus that causes equine influenza and it is thought that the equine influenza virus mutated to produce the canine influenza virus ([Crawford et al. 2005](#)). Two clinical syndromes have been seen in dogs infected with the canine influenza virus - a mild form of the disease and a more severe form that is accompanied by pneumonia.

Dogs suffering with the mild form of canine influenza develop a soft, moist cough that persists for 10 to 30 days. Some dogs have a dry cough similar to the "kennel cough" caused by Bordetella bronchiseptica/parainfluenza virus. Therefore, canine influenza virus infections are frequently mistaken for "kennel cough". Dogs with the mild form of influenza may also have a thick nasal discharge, which is usually caused by secondary bacterial infection. Dogs with the severe form of canine influenza develop high fever (104°F to 106°F) and have clinical signs of pneumonia, such as increased respiratory rate and effort. Pneumonia may also be complicated by secondary bacterial infection.

## Standard Diagnostic Methods

Acute canine influenza virus infection may be diagnosed by isolation of canine influenza virus in respiratory secretion specimens from acutely ill animals. However, isolation is time consuming and generally unrewarding. Antibodies to canine influenza virus may be detected as early as seven days after onset of clinical signs.

## Our Method

The Molecular Diagnostics Laboratory at Auburn University has developed a one-step reverse-transcriptase quantitative PCR technology targeting the highly conserved matrix gene of influenza A viruses, using swab samples (nasal swabs preferred), and fresh (not formalin-preserved or frozen) lung and tracheal tissues, or any

other specimen such as body fluids (blood, CSF, urine, etc.). Our method can detect all influenza virus A strains with highest sensitivity, and differentiates canine/equine strains from avian strains, and both these strains from human strains by the melting curve of the fluorescent probe-binding region. Further, highly accurate strain identification can be performed by DNA sequencing of PCR products.

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