

# The Science of Significant Protection Explained

## Genetic Characterization of Recent Equine Influenza Outbreaks

Influenza viruses are constantly undergoing genetic changes. Understanding these genetic changes—known as antigenic drift—through ongoing surveillance and sequencing of isolates is critical to evaluating and improving the efficacy of equine influenza vaccines.

## Genome Sequencing

Sequencing of the influenza virus is focused on the hemagglutinin (HA) and neuraminidase (NA) glycoproteins found on the surface of the virus. HA is the most important because it is the target for serum neutralizing antibodies generated by influenza vaccines. Through this process of comparing genetic sequences we can make informed decisions regarding:

- How well an equine influenza vaccine might protect against a particular influenza virus
- The genetic variations (mutations) that appear when viruses begin spreading more easily or causing more severe diseases
- How closely equine influenza viruses are ‘related’ to one another (e.g., homology)
- How equine influenza viruses are evolving

Florida ‘13 was responsible for a significant disease outbreak in well-vaccinated horses. **Sequencing and homology of recent outbreaks in 2018 and 2019 demonstrates Florida ‘13 is highly relevant to equine influenza circulating today in our U.S. horse population.**<sup>1</sup>

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**Homology Defined:** The existence of shared ancestry between a pair of structures or genes.

**Genome Sequencing Defined:** The process that determines the order or sequence of the RNA nucleotides (e.g., A, C, G, U) in each of the genes present in the virus’s genome.

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<sup>1</sup> Data on file. Merck Animal Health.

## Equine Influenza: PIVOTAL ROLE OF HA GLYCOPROTEIN

Different strains of EIV can be compared by sequencing the hemagglutinin (HA) glycoprotein. Hemagglutinin contains the receptor binding sites that enable the influenza virus to attach to host cells. If antigenic drift decreases binding with the HA glycoprotein at these “key sites,” there may be either a total lack of or reduced protection.

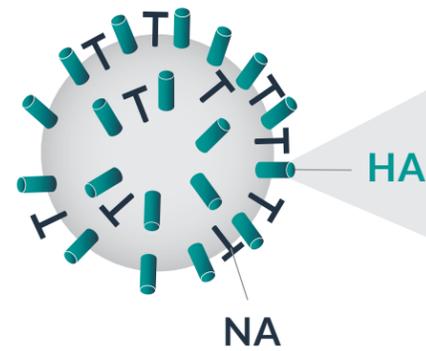


Figure 1. - Equine Influenza Surface Proteins. Influenza strains are named based on the hemagglutinin (HA) and neuraminidase (NA) surface glycoproteins.

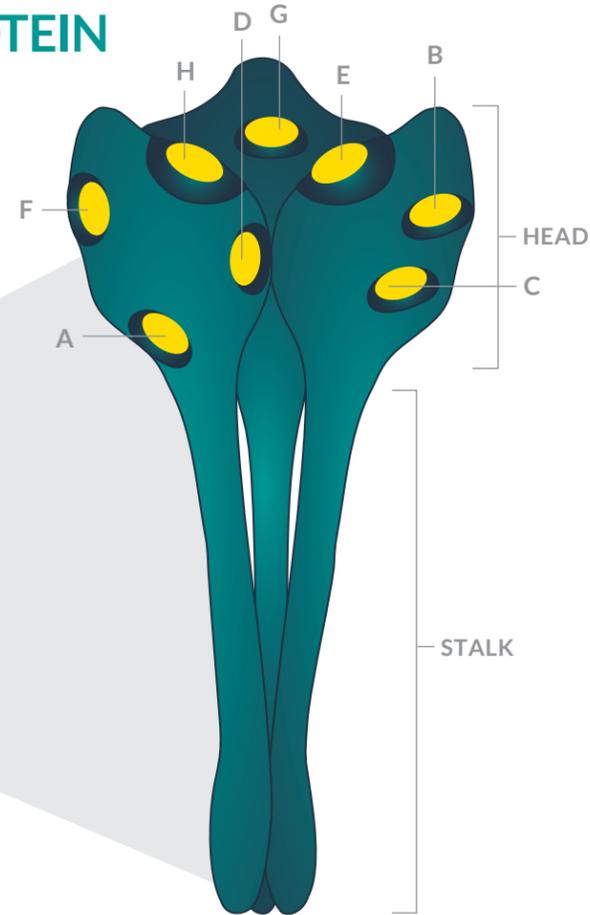
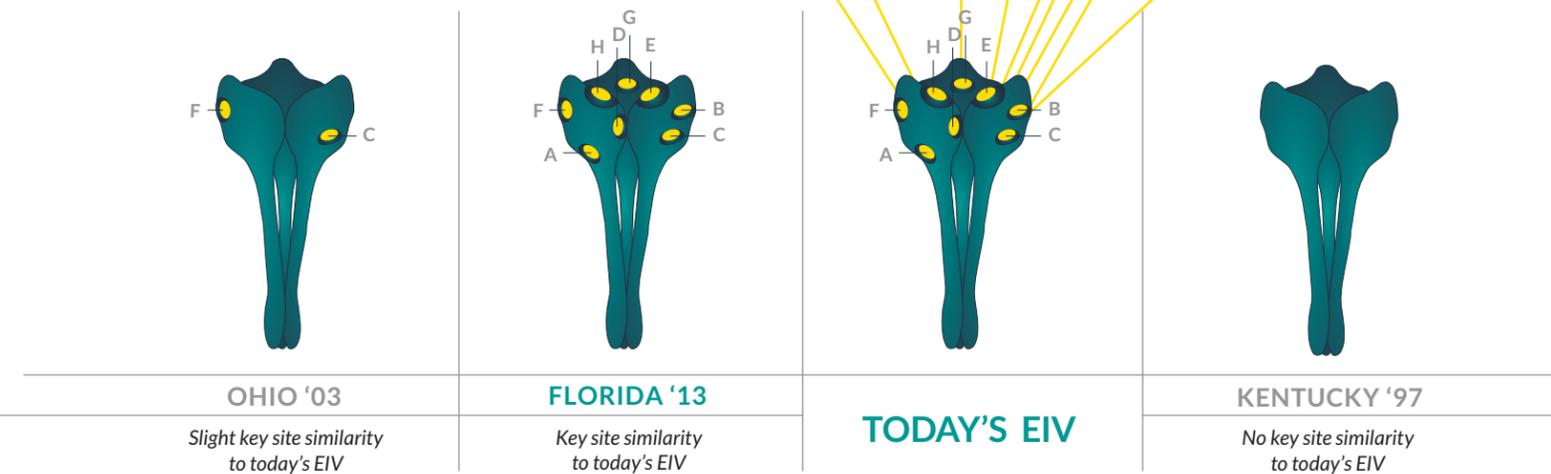


Figure 2. - Key antigenic sites of the HA glycoprotein

## Comparing Today's EIV Isolates at Eight Key Sites

Key site location plays a vital role in unraveling amino acid differences.



## EIV Sequencing Homology of Recent Outbreaks Compared to Florida '13<sup>2</sup>

Sequencing of recent positive equine influenza samples submitted through the Merck Animal Health Equine Respiratory Biosurveillance Program shows a very high degree of homology (or similarity) to Florida '13.

This demonstrates the relevance of Florida '13 to influenza strains currently circulating throughout the United States and causing disease in the field.

SAMPLE	FL '13 REFERENCE	OUTBREAK STATE
FL-13 reference	100.00	Florida
Horse 1	98.50	Pennsylvania
Horse 2	98.69	Missouri
Horse 3	98.88	Ohio
Horse 4	98.88	Arizona
Horse 5	98.69	Tennessee
Horse 6	99.21	Missouri
Horse 7	98.50	Florida
Horse 8	98.67	New York
Horse 9	98.73	Ohio
Horse 10	98.69	Washington
Horse 11	98.99	Texas

Sample submissions collected from equine influenza outbreaks over an 11-month period (April 2018–February 2019). Table shows homology—or similarity—of sample vs. Florida '13, expressed as a percentage. All samples are >98.50% similar to Florida '13. All are Clade 1 viruses.

<sup>2</sup>Data on file. Merck Animal Health.

## Sequencing Data Reinforces Florida '13 as Highly Relevant Equine Influenza Strain<sup>3</sup>

- Demonstrated similarity to isolates from recent outbreaks**
  - >98.50% sequencing homology
  - Spans multiple age groups, breeds and other signalment parameters
  - Broad geographic distribution of cases
  - Representative of real-life challenge and sick horses
- Key site similarity to today's equine influenza**
  - Ohio '03 shows only slight key site similarity to today's EIV
  - Kentucky '97 shows no key site similarity to today's EIV

<sup>3</sup>Data on file. Merck Animal Health.



## When Surveillance Comes Full Circle

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Our industry benefits. The Merck Animal Health Biosurveillance Program has delivered more than a decade of important ongoing surveillance data on infectious upper respiratory disease in horses. With it we've gained one of the largest collections of equine influenza isolates ever compiled in the U.S., allowing us to identify and monitor current strains of equine influenza and—ultimately—improve influenza protection through identification of antigenic drift and isolation of a new influenza strain.<sup>4</sup> Florida '13 is highly relevant and similar to the influenza circulating today.

## Only in PRESTIGE<sup>®</sup> Vaccines

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PRESTIGE equine vaccines continue to set the standard in safety and efficacy you've come to expect along with new influenza strains (including Clade 1 and Clade 2 viruses).

- Florida '13 Clade 1
- Richmond '07 Clade 2
- Kentucky '02 (maintained from previous vaccine line)

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For more information, contact your Merck Animal Health sales representative at 800-521-5767, or Veterinary Professional Services at 866-349-3497.

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<sup>4</sup>Merck Animal Health and University of California, Davis School of Veterinary Medicine (Nicola Pusterla). Infectious Upper Respiratory Disease Surveillance Program. Ongoing research 2008–present.

**The Science of  
Healthier Animals**

