



Technology Transition Workshop | *Steven A. Hofstadler, Ph.D.*

# ***High-Throughput Analysis of Amplified Nucleic Acids with Mass Spectrometry: The Ibis™ Platform***

# **Outline**

- **The challenge of broad pathogen detection**
- **The Ibis™ approach**
  - Principle of operation
- **Bacterial detection and strain typing**
  - Group A strep – direct throat swab analysis
- **Viral detection and strain typing**
  - Influenza
    - Pandemic influenza detection and strain typing
- **Integrated platform**

# *The Pathogen Detection Arena*

- Biological weapons defense is not just about anthrax
- Food safety is not just about E. coli 0157
- Hospital associated infections are not just due to Staph. aureus
- There are numerous naturally occurring infectious diseases
- Over 1000 agents known to infect humans\*
  - 217 virus species
  - 538 bacterial species
  - 307 fungi
  - 66 parasitic protozoa
- Additional plant and animal pathogens not counted
- Numerous strain variations
- Potential bio-engineered organisms

\*Taylor et al, Phil. Trans. R. Soc. Lond. B (2001) 356, 983-989

# Mainstream Bioagent Detection Today

- Culture techniques
  - Detects a subset of all pathogens
  - Can take multiple days (weeks)
- Single agent nucleic acid tests
  - One test for each agent (smallpox, anthrax, plague, etc.)
  - Need too many tests
  - Fail to detect newly emergent pathogens
- There is currently no good method to detect organisms that have never been seen before



Nucleic acid tests (NAT's)



# **Bacterial Threat Symbols**

## **Microbial Rosetta Stone Database**

 NIAID Category A Priority Pathogen

 NIAID Category B Priority Pathogen

 NIAID Category C Priority Pathogen

 HHS Select Agent

 USDA High Consequence Animal Pathogen

 USDA High Consequence Plant Pathogen

 Validated Biological Weapon

 Potential Biological Weapon

 Validated Biocrime Agent

 Globally Important Human Pathogen

 Medically Important Human Pathogen

 Important Animal Pathogen

 Important Plant Pathogen

 High Potential For Bioengineering

 Zoonotic Agent

 Toxin

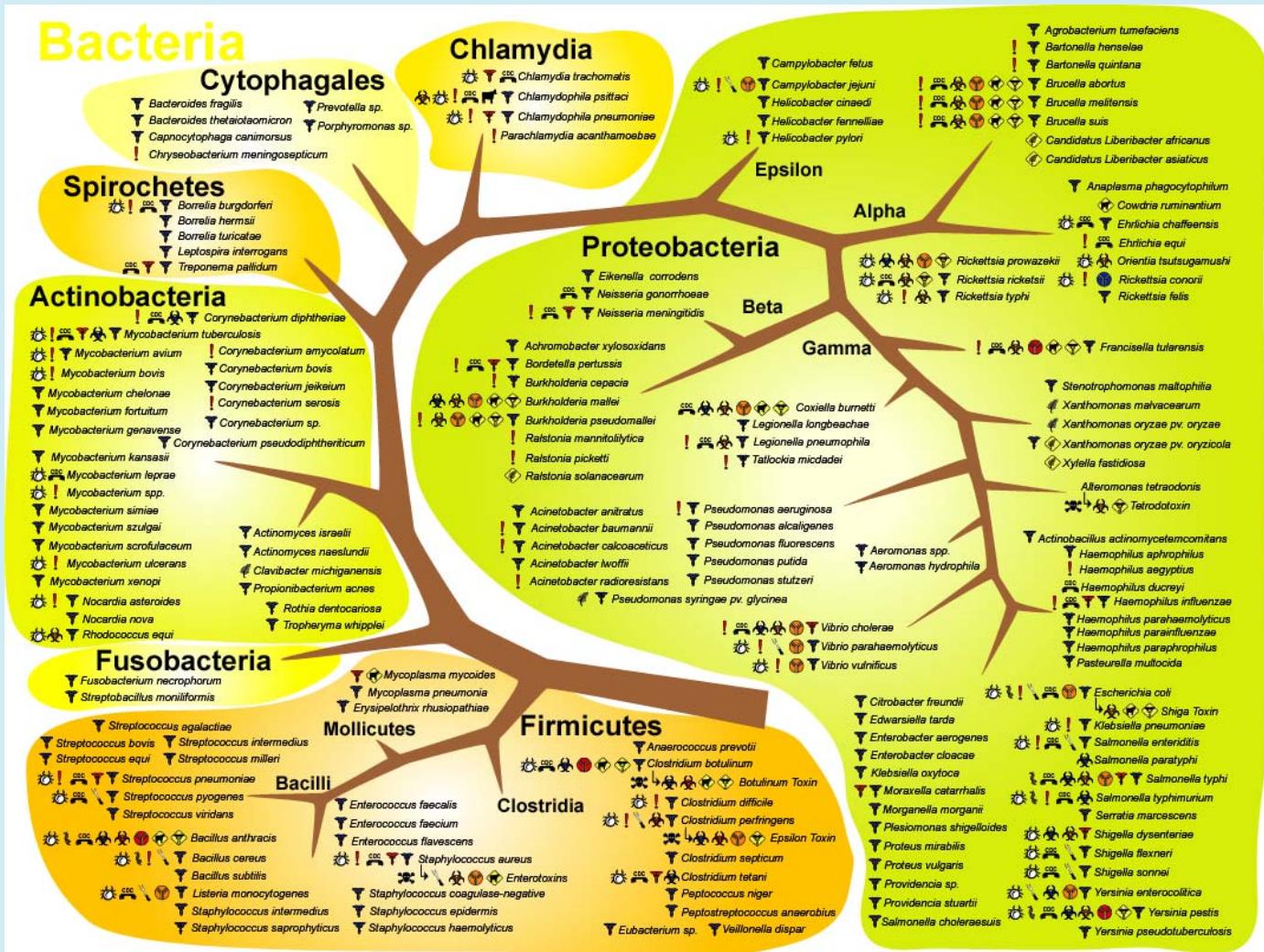
 CDC Notifiable Agent

 Principal Foodborne Pathogen

 Emerging Infectious Agent

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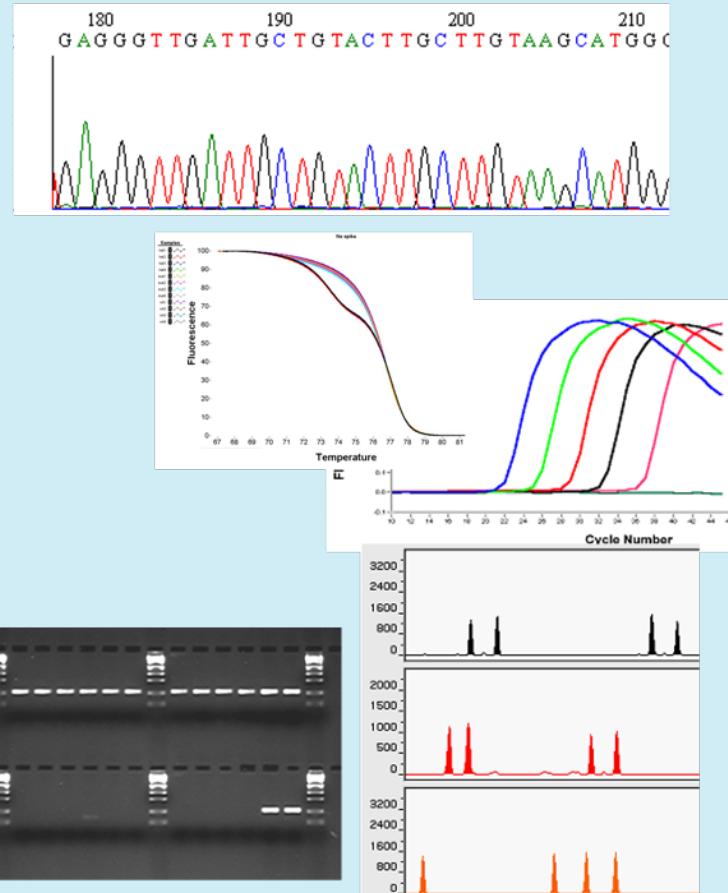
# *Why Detect and/or Type Microorganisms via Nucleic Acids?*

- All living things rely on DNA and/or RNA to propagate
  - All infectious agents\* contain DNA and/or RNA
  - Bacteria, viruses, fungi, protozoa
- DNA and RNA are unique among biomarkers in that they can be amplified (e.g. PCR, WGA, NASBA, etc)
  - From trace amounts of sample
  - From highly degraded samples
  - From samples in complex backgrounds
- NO CULTURE REQUIRED
- Some genetic differences do not result in phenotypic differences
  - e.g. rRNA, VNTRs, SNPs
- Range of specificity can be “tuned” for different applications
  - “Name that Bug”: Broad range primers
  - “Genotype/Strain-type that Bug”: species specific primers
  - “Profile that Bug”: drug resistance, virulence markers, etc.

\* Except those nasty prions!

# *Interrogation of Amplified Nucleic Acids*

- Sequencing
  - “Gold Standard”
- Fluorescent intercalating dye
- Hybridization
  - Specific probe with FRET pair
- DNA microarray
- Melting profiles
- Electrophoresis
  - Slab gels
  - Capillary gel electrophoresis
- **WHAT ABOUT MASS?**



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- **Identification and Strain Typing of Bacterial and Viral Pathogens using High Performance Mass Spectrometry: The Ibis™ Concept**

- DARPA
- CDC
- NIAID
- Department of Homeland Security

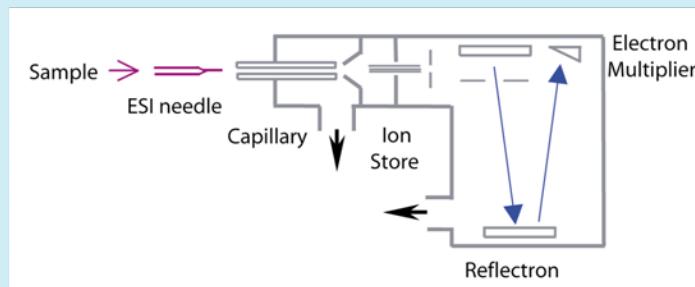
# The Ibis™ Approach to Pathogen ID and Strain-Typing

## STEP 1 Identify genomic regions for identification:

Variable DNA sequences flanked by conserved sequences

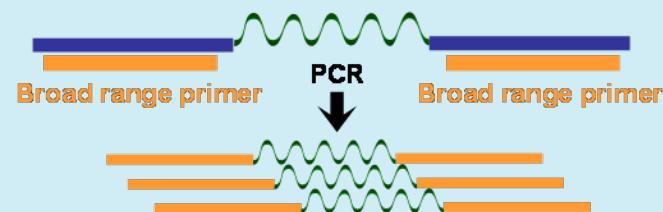


## STEP 3 Measure nucleic acid: ESI-TOF



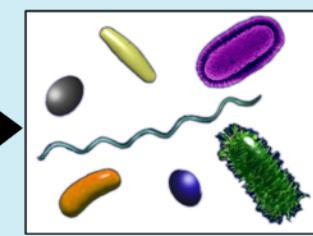
## STEP 2 Amplify nucleic acids to measure:

Use broad-range, unbiased PCR primers



## STEP 4 Identify the organisms: Base-composition fingerprints

**As: 17  
Gs: 30  
Cs: 11  
Ts: 61**



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# Broad Range Priming in Bacteria

**STEP 1**

Primers bind to conserved regions present in ALL (or groups of) bacteria

Primer pair	GGATTAGATAACCTGGTAGTCC	CGCCTGGGAGTACGGCC
E. coli	ACGCCGTAAACGATGTCGACTTGGAGGTTGTGCC-CTTGA-GGCCTGGCTCCGGAGCTAACCGCTTAAGTCGAC	
Cox. burnetii	ACGCCGTCAACGATGAGAACTAGCTGTTGGGAAG--TTCA-CTTCCTTAGTAGCGAAGCTAACCGCTTAAGTTCTC	
Leg. pneumophila	ACGCTGTTAAACGATGTCAACTAGCTGTTGGTTAT-ATGAAAATAATTAGTGGCCAGCAAACGGATAAGTTGAC	T
Ricket. prowazekii	ACGCCGTAAACGATGAGTGCTAGATATCGGAGG--ATTCT--CTTCGGTTTCGGCAGCTAACGCATTAAGCACTC	T
Mycb. tuberculosis	ACGCCGTAAACGGTGGGTACTAGGTGTTGGGTTCTTCCTGGGATCCGTGGCTAGCTAACGCATTAAGTACCC	
Trep. pallidum	ACACAGTAAACGATGTACACTAGGTGTTGGGC---ATGA--GTCTGGCGCCGACCGAACGCATTAAGTGTAC	T T
Bacillus anthracis	ACGCCGTAAACGATGAGTGCTAAGTGTAGAGGG-TTCCGCCCTTAGTGCTGAGCTAACGCATTAAGCACTC	
Staph. aureus	ACGCCGTAAACGATGAGTGCTAAGTGTAGGGGG-TTCCGCCCTTAGTGCTGAGCTAACGCATTAAGCACTC	A
Staph. epidermidis	ACGCCGTAAACGATGAGTGCTAAGTGTAGGGGG-TTCCGCCCTTAGTGCTGAGCTAACGCATTAAGCACTC	A
Strep. agalactiae	ACGCCGTAAACGATGAGTGCTAGGTGTTAGGCC-TTCCGGGGCTTAGTGCCGAGCTAACGCATTAAGCACTC	A
Strep. mutans	ACGCCGTAAACGATGAGTGCTAGGTGTTAGGCC-TTCCGGGGCTTAGTGCCGAGCTAACGCATTAAGCACTC	A
Strep. pneumoniae	ACGCTGTTAAACGATGAGTGCTAGGTGTTAGGCC-TTCCGGGGCTTAGTGCCGAGCTAACGCATTAAGCACTC	A
Strep. pyogenes	ACGCCGTAAACGATGAGTGCTAGGTGTTAGGCC-TTCCGGGGCTTAGTGCCGAGCTAACGCATTAAGCACTC	A

Region varies in different

kinds of bacteria

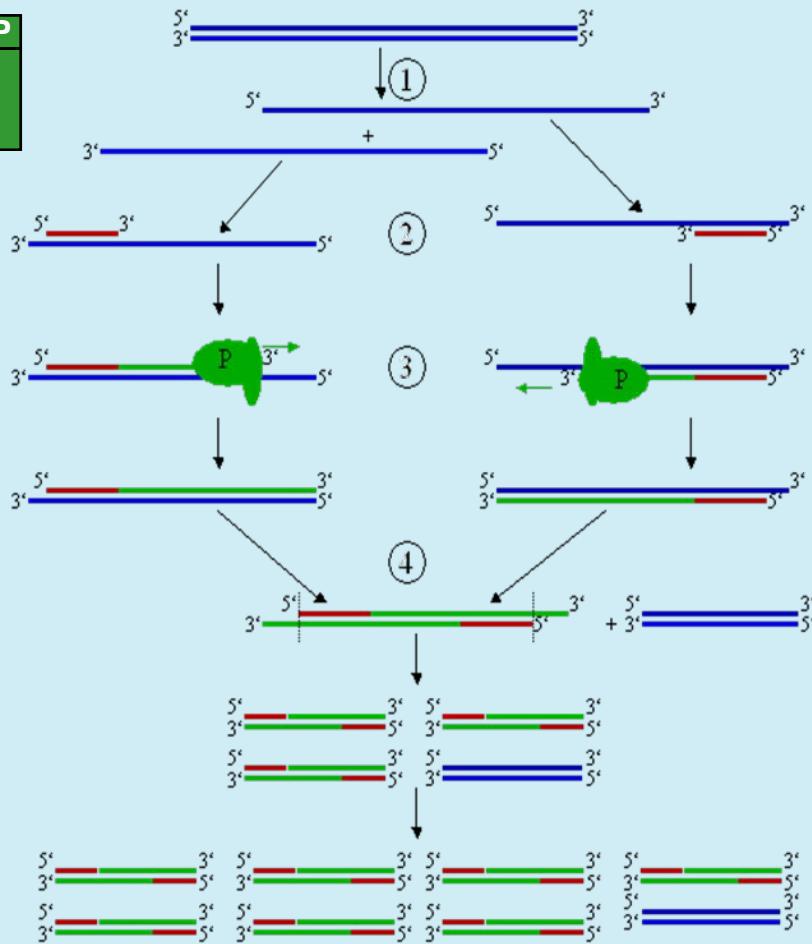
$$\Delta [A_w G_x C_y T_z]$$

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# The Polymerase Chain Reaction (PCR)

## STEP 2



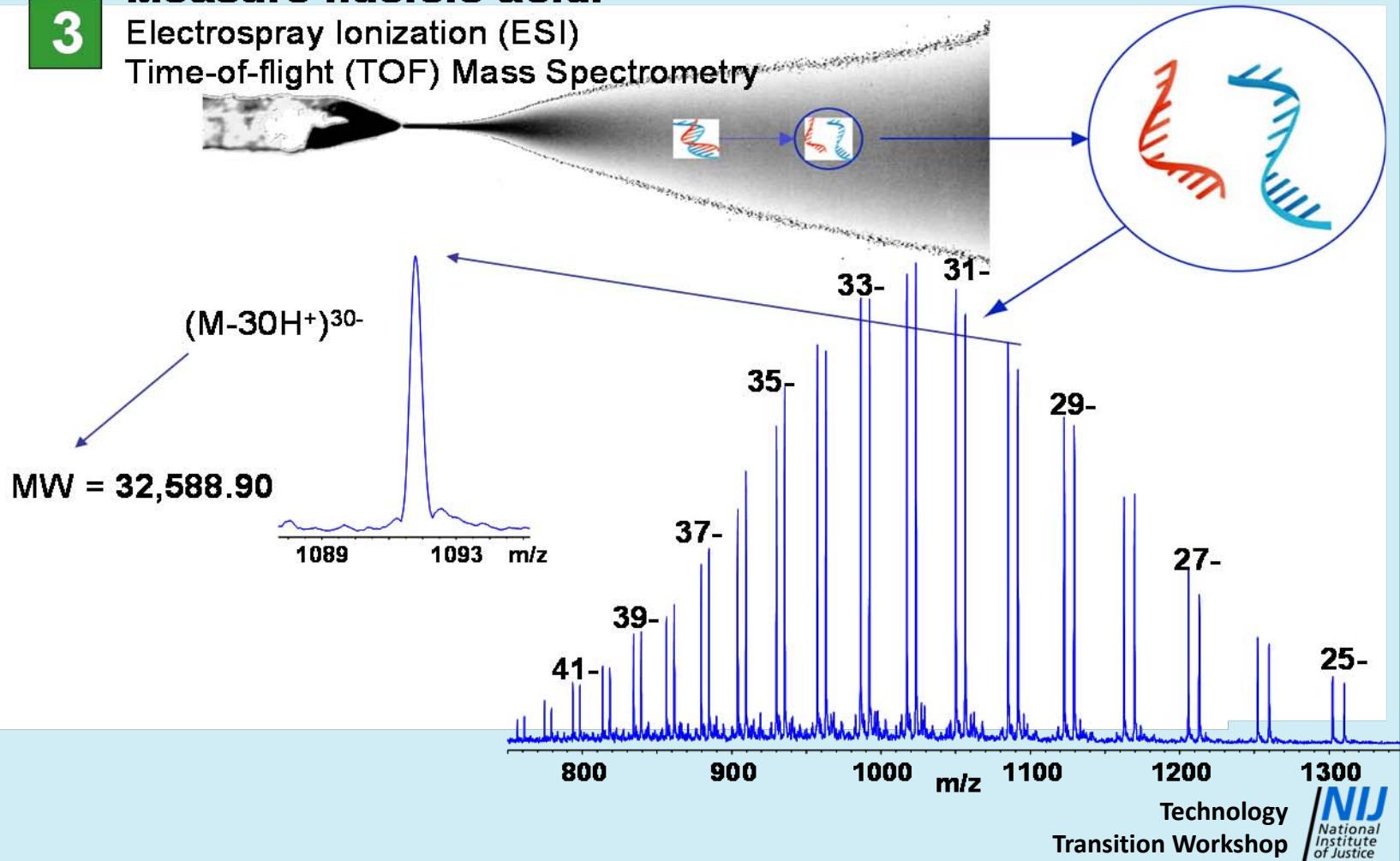
- Performed using primers designed for broad coverage
- PCR cycling conditions tolerate mismatches on initial cycles
- All primer pairs designed to work under identical PCR conditions
- Each well contains an internal calibrant
- Generally don't multiplex broad range primers (e.g. 16S and 23S rDNA)
- Multiplexing of more specific primers common (e.g. strain typing, drug resistance, virulence)

# Automated ESI-TOF of PCR Amplicons on T5000

STEP  
**3**

## Measure nucleic acid:

Electrospray Ionization (ESI)  
Time-of-flight (TOF) Mass Spectrometry



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# Masses to Base Composition

STEP

4



Penny = 2.500 g

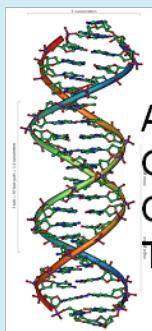
Nickel = 3.950 g

Dime = 2.268 g

Quarter = 5.670 g



Weight = 4.6 grams  
 $\therefore$  2 dimes

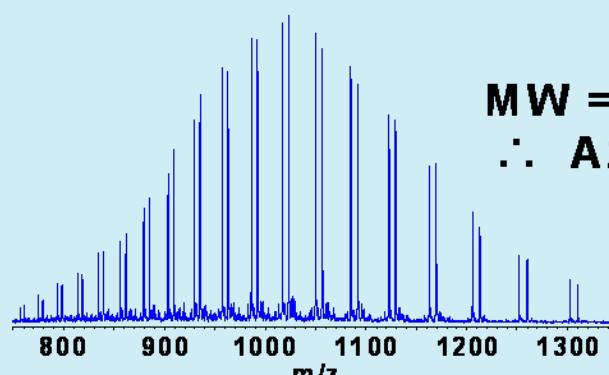


A = 313.0576 amu

G = 329.0526 amu

C = 289.0464 amu

T = 304.0461 amu



Mass spectrum

MW = 32,588.90 amu  
 $\therefore$  A28 G29 C25 T24

Requires 25 ppm  
mass measurement error

Math takes into account  
Watson-Crick base pairing

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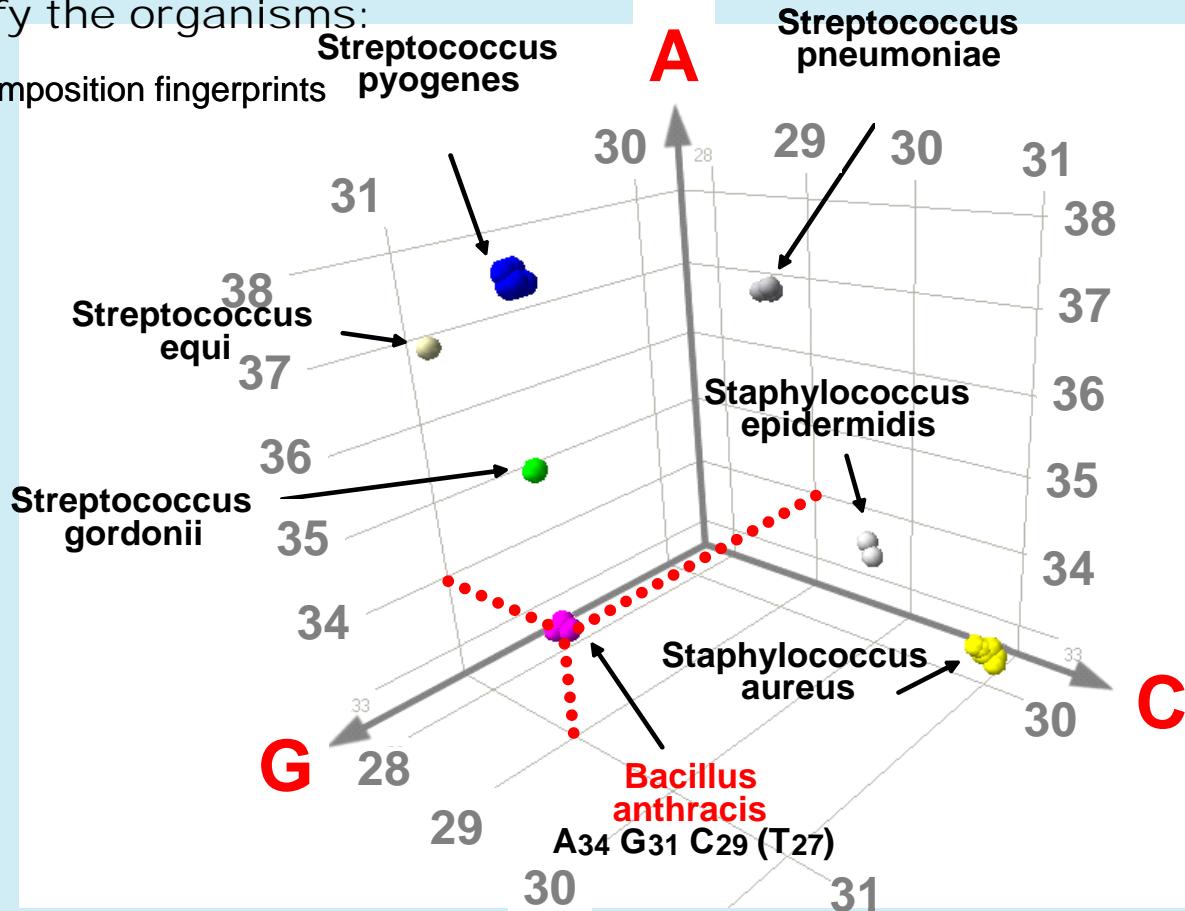
# Derived and Expected Base Compositions

## Primer 356 (*RplB*) Expected Products

STEP  
**4**

Identify the organisms:

Base-composition fingerprints



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# ***Broad Pathogen Detection***

**Instead of asking; “Is pathogen X in my sample?”, we ask: “Which pathogen, or pathogens, are in my sample?”**

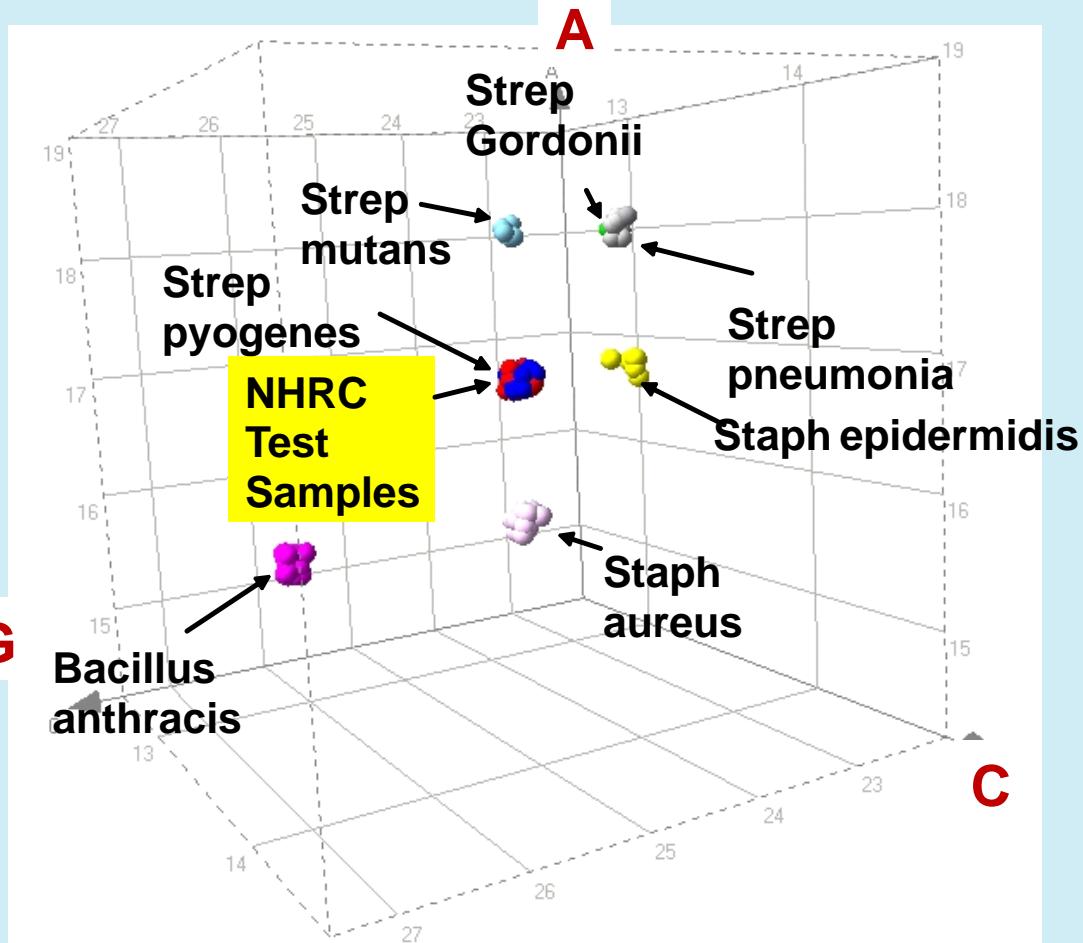
# **Group A Streptococcus (GAS)**

## **Outbreaks in Military Settings**

- **Outbreaks of group A strep at MCRC 2002/2003**
  - Highly virulent strain
  - One death, 160 hospitalized
  - Training activities suspended
- **Initial analysis of post-culture samples**
  - 80 samples sent from NHRC, Dr. Kevin Russell, December 20, 2002
  - “Hijacked” some BW air surveillance plates
- **Follow up surveillance at multiple military bases**
- **Direct analysis of throat swabs without culture**

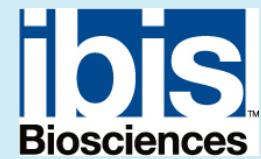
Ecker et al. *Proc. Nat. Acad. Sci. USA*, (2005) 102(22), 8012-17

# *Primer 17 (a 23S Primer)* *Observed Products (from Culture)*



All primers of all samples consistent with *S. pyogenes*

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# *Direct Analysis of Throat Swab\**

\*Repeat swab positive on culture for *Streptococcus pyogenes*

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# **Primer 349: 23S rDNA 1826-1924**

***From an Interesting Throat Swab***

**Ecker et al. Proc. Nat. Acad. Sci. USA, (2005) 102(22), 8012-17**

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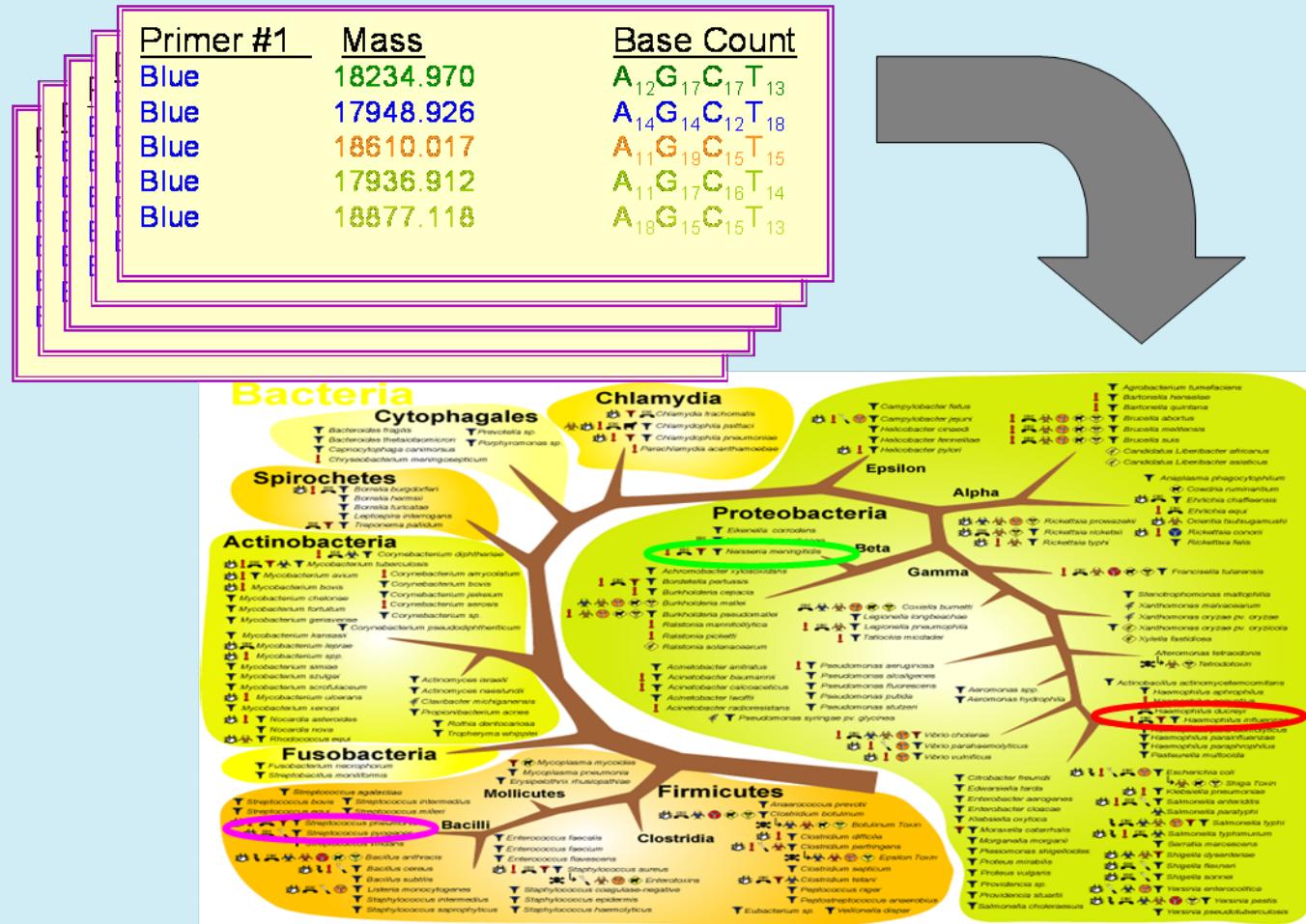


# *Multi-primer Triangulation*

Ecker et al. *Proc. Nat. Acad. Sci. USA*, (2005) 102(22), 8012-17

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# Haemophilus influenzae, Neisseria meningitidis, Streptococcus pyogenes (Ratio 4/2/1, 1.5 X 10<sup>6</sup> genomes/swab)



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# ***Conclusions of Pneumonia Study\****

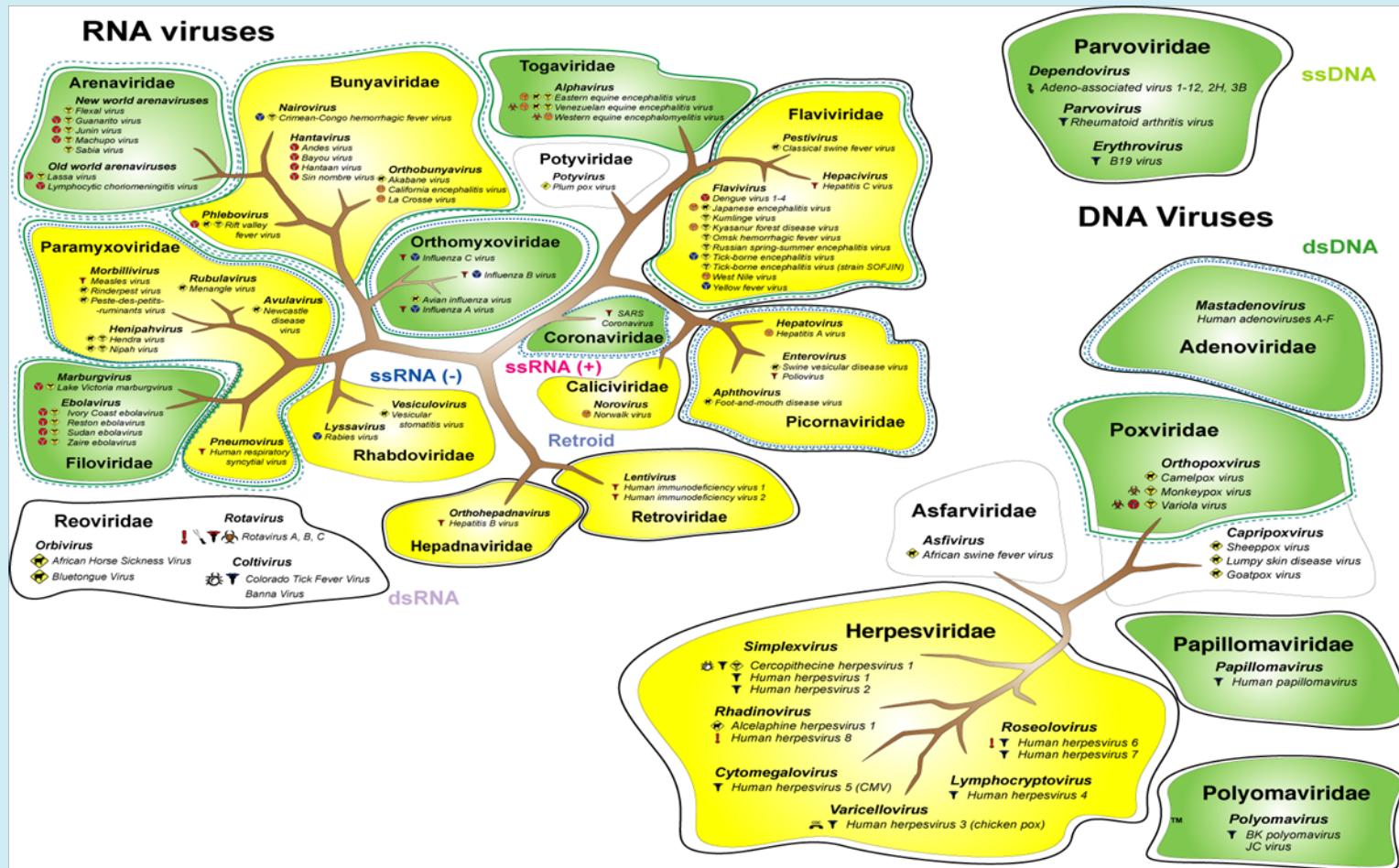
- Primary pathogen:
  - **Streptococcus pyogenes (GAS)**
  - Known virulent strain
- Secondary pathogens:
  - **Haemophilus influenzae**
  - **Neisseria meningitidis**
- Five other military facilities
  - Determined these sites had a mixture of strain types
- Throughput
  - >200 / samples per day

\*Ecker et al. (2005) Proc. Natl. Acad. Sci. Vol. 102: p8012-8017

# *Virus Identification and Typing*

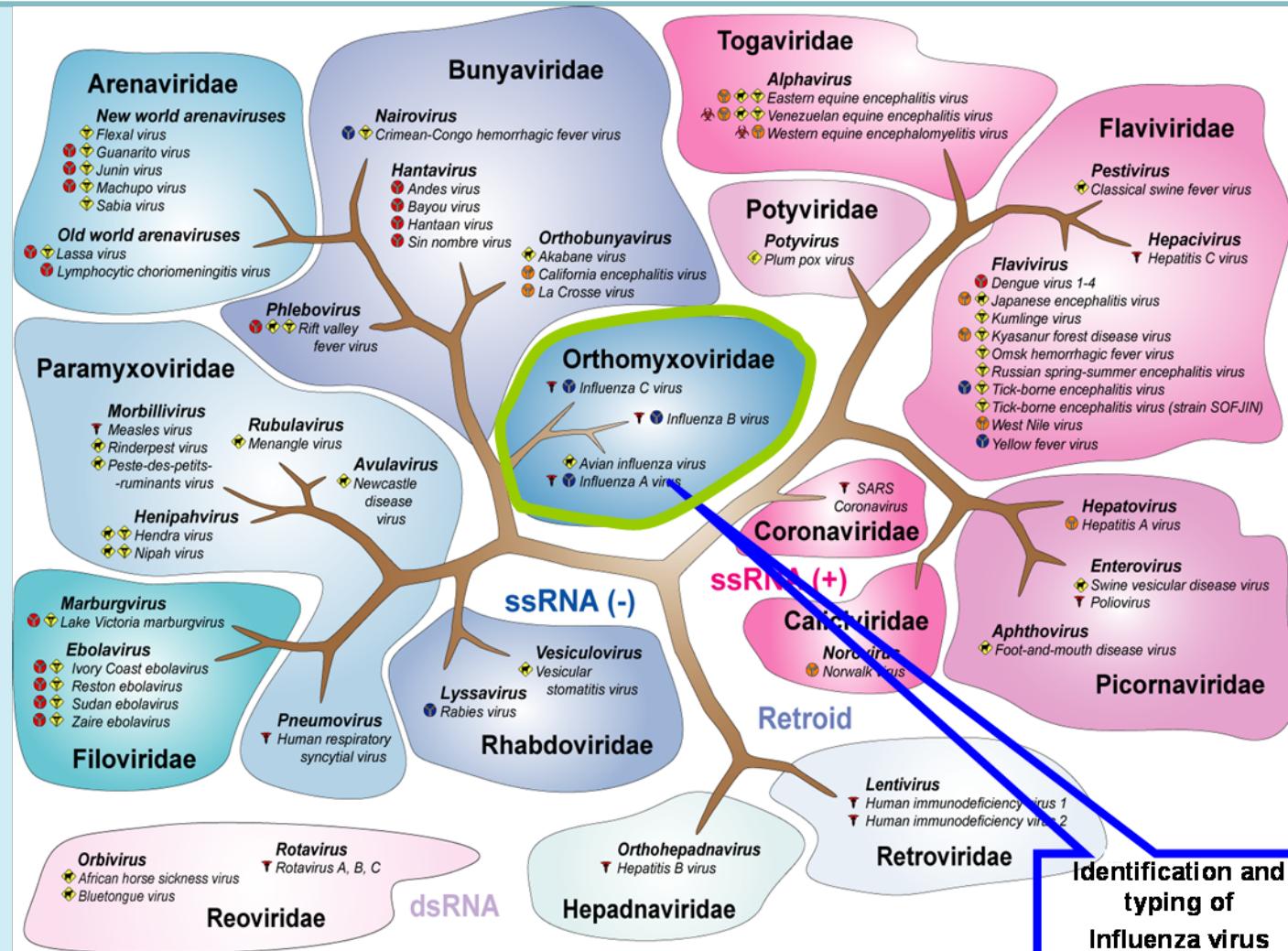
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# Viral Coverage



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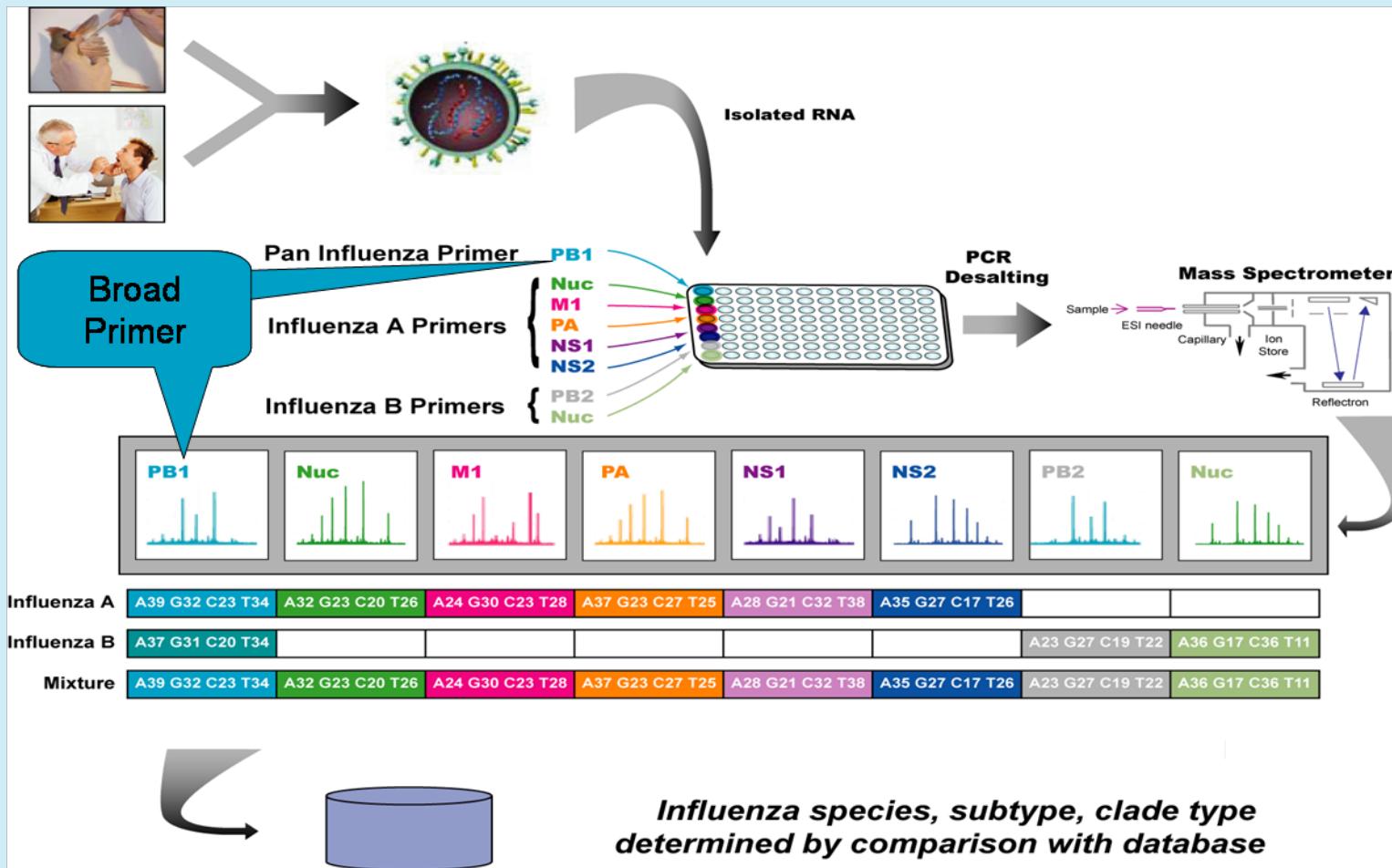
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## *Influenza Virus Surveillance: Project Collaborators*

- **CMDR Kevin Russell M.D., Naval Health Research Center, San Diego, CA**
- **Kirsten St.George, MAppSc, PhD, New York State Department of Health, Slingerlands, NY**
- **Charlotte Gaydos, Dr.P.H. and Rich Rothman, M.D. Johns Hopkins University, Baltimore, MD**
- **Stan Lemon M.D. , University of Texas Medical Branch, Galveston, TX**
- **Wendy Sessions. M, SV (ASCP), Texas Department of State Health Services**
- **Dave Stallknecht and Ginger Goekjian, College of Veterinary Medicine, University of Georgia**

# Ibis™ Influenza Virus Assay



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# Pan Influenza Primer Polymerase PB1 Primer

The diagram shows a sequence alignment of the Pan Influenza Primer Polymerase PB1 Primer across various influenza subtypes. The sequence is numbered from 1300 to 1420. A blue arrow points to a segment from 1390 to 1400, which is highlighted in red. A blue bracket above the sequence indicates a 6 nucleotide deletion in the Influenza B and C group, spanning positions 1390-1405. The alignment includes sequences for Human, Swine, Canine, Equine, and Avian subtypes.

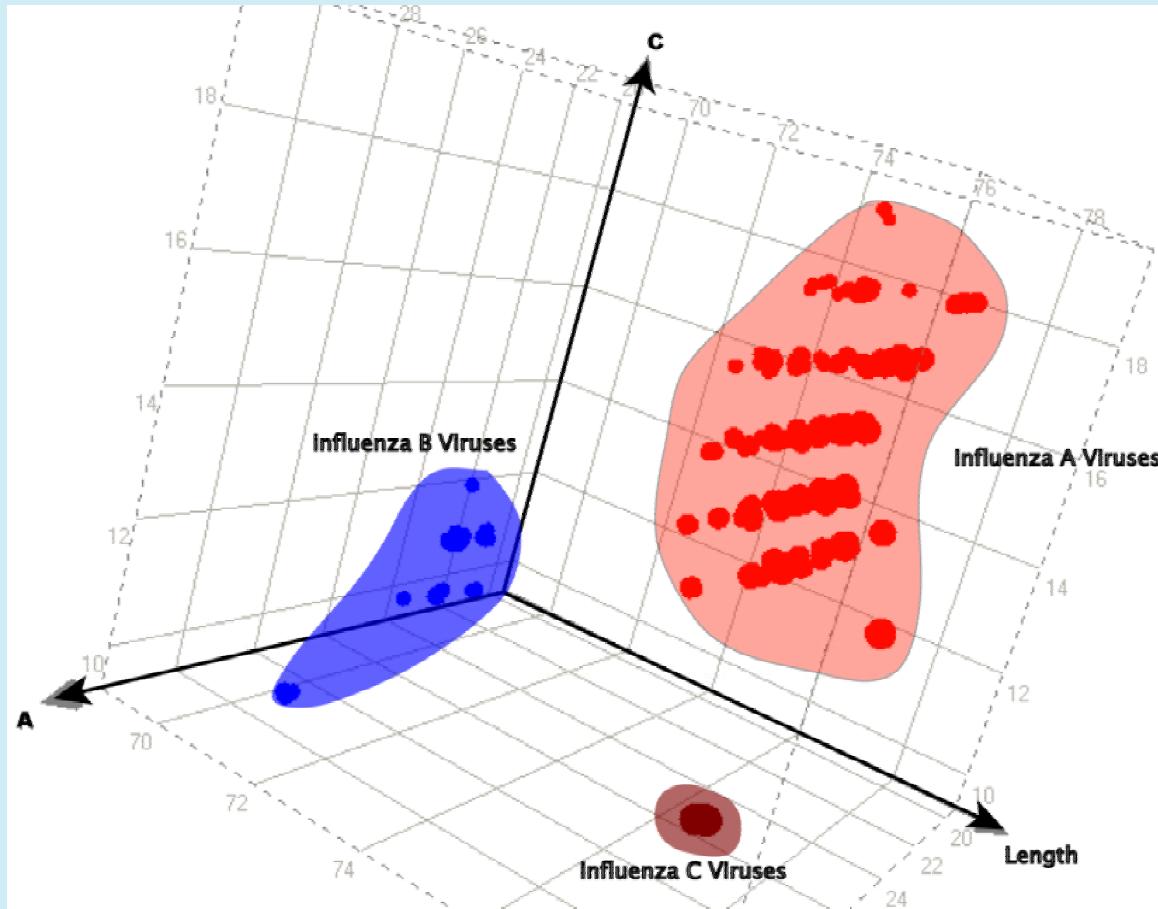
	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420
2798 VIR2798 FLU ALL_P	-TGTCTTGGAATGATGGGCATGTT										GGGATGGACTCCAATCCTCTGATGA-		
REFERENCE 1918Flu_H1N1	CA.C.....	CAATATCTAACCACTGTATTAGCGCTCCATCCTGAATCTTCGACAAAACAGATACACCAAGACTACTTACTGGT.....	T..T....T.....T										
Human H1N1 (gi 3248991)	CA.C.....	CAATATCTAACCACTGTATTAGCGCTCCATCCTGAATCTTCGACAAAACAGATACACCAAGACTACTTACTGGT.....	T..T....T.....T										
Human H1N1 (gi 3248971)	CA.C.....	CAATATCTAACCACTGTATTAGCGCTCCATCCTGAATCTTCGACAAAACAGATACACCAAGACTACTTACTGGT.....	T..T....C..T										
Human H1N1 (gi 3144213)	CA.C.....	CAATATCTAACCACTGTATTAGCGCTCCATCCTGAATCTTCGACAAAACAGATACACCAAGACTACTTACTGGT.....	T..T....C..T										
Human H1N1 (gi 1814083)	CA.C.....	CAATATCTAACCACTGTATTAGCGCTCCATCCTGAATCTTCGACAAAACAGATACACCAAGACTACTTACTGGT.....	T..T....G.....T										
Swine H1N1 (gi 3249551)	AA.C.....T	TAACATGCTAACCGACTGTGTTGGCTGTTCATCTTAAATCTGGACAGAAGGATACACCAAGACTGCTTATGGT.....	C..T....G.....T										
Swine H1N1 (gi 20068032)	CA.....	TAACATGCTAACCGACTGTGTTGGCTGTTCATCTTAAATCTGGACAGAAGGATACACCAAGACTGCTTATGGT.....	T.....C										
Swine H1N2 (gi 3815472)	CA.C....G	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAGAACATACTGGT.....	G.....C..T										
Swine H1N2 (gi 3815471)	CA.C....G	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAGAACATACTGGT.....	G.....C..C..T										
Human H2N2 (gi 3249491)	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAGAACATACTGGT.....	C.....C										
Human H2N2 (gi 3249651)	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAAACNACATACTGGT.....	C.....C										
Human H2N2 (gi 3778501)	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAAACNACATACTGGT.....	C.....C										
Human H2N2 (gi 3778503)	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAAACNACATACTGGT.....	C.....C										
Human H3N2 (gi 3778544)	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAAACNACATACTGGT.....	T.....T										
Human H3N2 (gi 3778545)	CA.....T	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAAACNACATACTGGT.....	T.....T										
Human H3N2 (gi 3778545)	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAAAATACACCAAAACNACATACTGGT.....	T.....T										
Swine H3N2 Influenza_A	CA.....	TAACATGCTGACTACAGITCTGGAGCTCTCAATCTGAATCTGGACAAAAGAGGTACACCCAGCACATCTGGT.....	G..T....T.....C										
Swine H3N3 (gi 5207815)	CA.C.....	CAACATGCTAACCTGGGTTTAGGAGTCTCGATCTGAATCTGGACAAAAGAGGTACACCCAGCACATCTGGT.....	T.....C										
Equine H3N8 Influenza	CA.....C	CAACATGTTGACCACTGTGCTGGCTATCCATTAATAAACCTGGGCCACAGGAAATACACAAAGAACCATACTGGT.....	T..G....A..C..C										
Equine H3N8 Influenza	CA.....C	CAACATGTTGACCACTGTGCTGGCTATCCATTAATAAACCTGGGCCACAGGAAATACACAAAGAACCATACTGGT.....	T..G....A..C..C										
Canine H3N8 (gi 710842)	CA.....C	CAACATGTTGACCACTGTGCTGGCTATCCATTAATAAACCTGGGCCACAGGAAATACACAAAGAACCATACTGGT.....	T..G....A..C..C										
Canine H3N8 (gi 710842)	CA.....C	CAACATGTTGACCACTGTGCTGGCTATCCATTAATAAACCTGGGCCACAGGAAATACACAAAGAACCATACTGGT.....	T..G....A..C..C										
Swine H4N5 Influenza_A	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	C.....T										
Human H5N1 (gi 1392538)	CA....A..G	TAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	G..T....T.....T										
Human H5N1 (gi 8307772)	CA....A..G	TAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	G..T....T.....T										
Avian H5N1 (gi 2884968)	CA.....	CAATATGCTGACTACAGITCTGGAGCTTCATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	C.....T										
Avian H5N1 (gi 2884968)	CA.C.....	CAACATGCTCACTACAGITCTGGAGCTTCATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	C.....T										
Swine H5N1 (gi 5151215)	CA.....	CAACATGCTGACTACAGITCTGGAGCTTCATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	C.....T										
Swine H5N1 (gi 5412651)	CA.....	CAACATGCTGACTACAGITCTGGAGCTTCATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	C.....T										
Human H7N7 Influenza_A	CA.....C	CAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	T..G....A..C..T										
Avian H7N7 Influenza_A	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	G..T....T.....T										
Avian H9N1 (gi 313395)	CA.....G	CAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	A..C....T										
Avian H9N1 (gi 313395)	CA.....G	CAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	A..C....T										
Avian H9N2 (gi 5782314)	CA.....	CAACATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	T.....T										
Swine H9N2 (gi 5592586)	CA.....	CAATATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	T.....T										
Swine H9N2 (gi 5592586)	CA.....	CAATATGCTAACCTGGGTTTAGGAGTCTCAATCTGAATCTGGACAAAAGAGGTACACCAAACACCATATCTGGT.....	T.....T										
Influenza_B_virus_(gi	G..CG.....A	TAATATGCTATCTACCGTGTGGAGTAGCCGCACTA-GCTATC	T.....T										
Influenza_B_virus_(gi	G..CG.....A	TAATATGCTATCTACCGTGTGGAGTAGCCGCACTA-GCTATC	G..T....T										
Influenza_B_virus_(gi	G..CG.....A	TAATATGCTATCTACCGTGTGGAGTAGCCGCACTA-GCTATC	G..T....T										
Influenza_B_virus_(gi	G..CG.....A	TAATATGCTATCTACCGTGTGGAGTAGCCGCACTA-GCTATC	G..T....T										
Influenza_B_virus_(gi	G..CG.....A	TAATATGCTATCTACCGTGTGGAGTAGCCGCACTA-GCTATC	G..T....T										
Influenza_B_virus_(gi	G..CA.....A	TAATATGCTATCTACCGTGTGGAGTAGCCGCACTA-GCTATC	G..T....T										
Influenza_C_virus_(gi	ACC.GGA.....C.T	CAACATGCTAACAGTTGGACTAAGTACATATTATGCTATGAGAAGA	T.....C										
Influenza_C_virus_(gi	ACC.GGA.....C.T	CAACATGCTAACAGTTGGACTAAGTACATATTATGCTATGAGAAGA	T.....C										

6 nucleotide deletion

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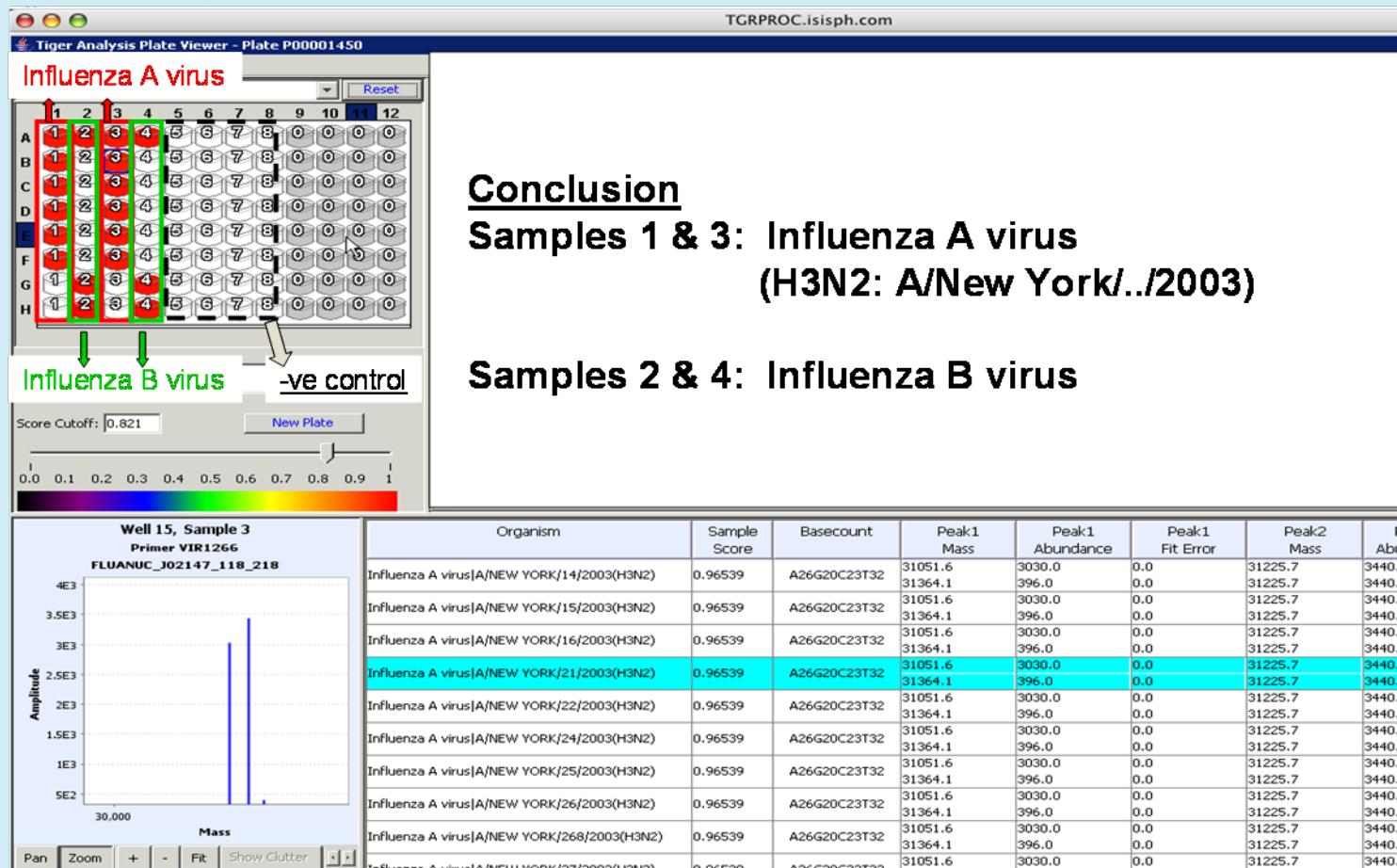


# Pan Influenza Primer Polymerase PB1 Primer PP2798 - Base Composition



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# Influenza Virus Assay Results Example



# *Human Influenza – Blinded Samples*

Source	Location	Collection Dates	Sample type	No. of Samples
Naval Health Research Center	MCRD, San Diego Ft. Leonard Wood, Ft. Sill, Ft. Benning, Lackland AFB	1999-2005	Throat swabs, nasal swabs, nasal washes	317
Johns Hopkins University Medical Center	Baltimore, MD	2003-2005	Nasal aspirates	229
NY State Dept. of Health	Throughout NY	1999-2005	Nasal aspirates, BAL, tracheal aspirates, throat swabs	100
TX State Dept. of Health	Throughout TX	2005-2006	Throat swabs, nasal washes	10
Total				656

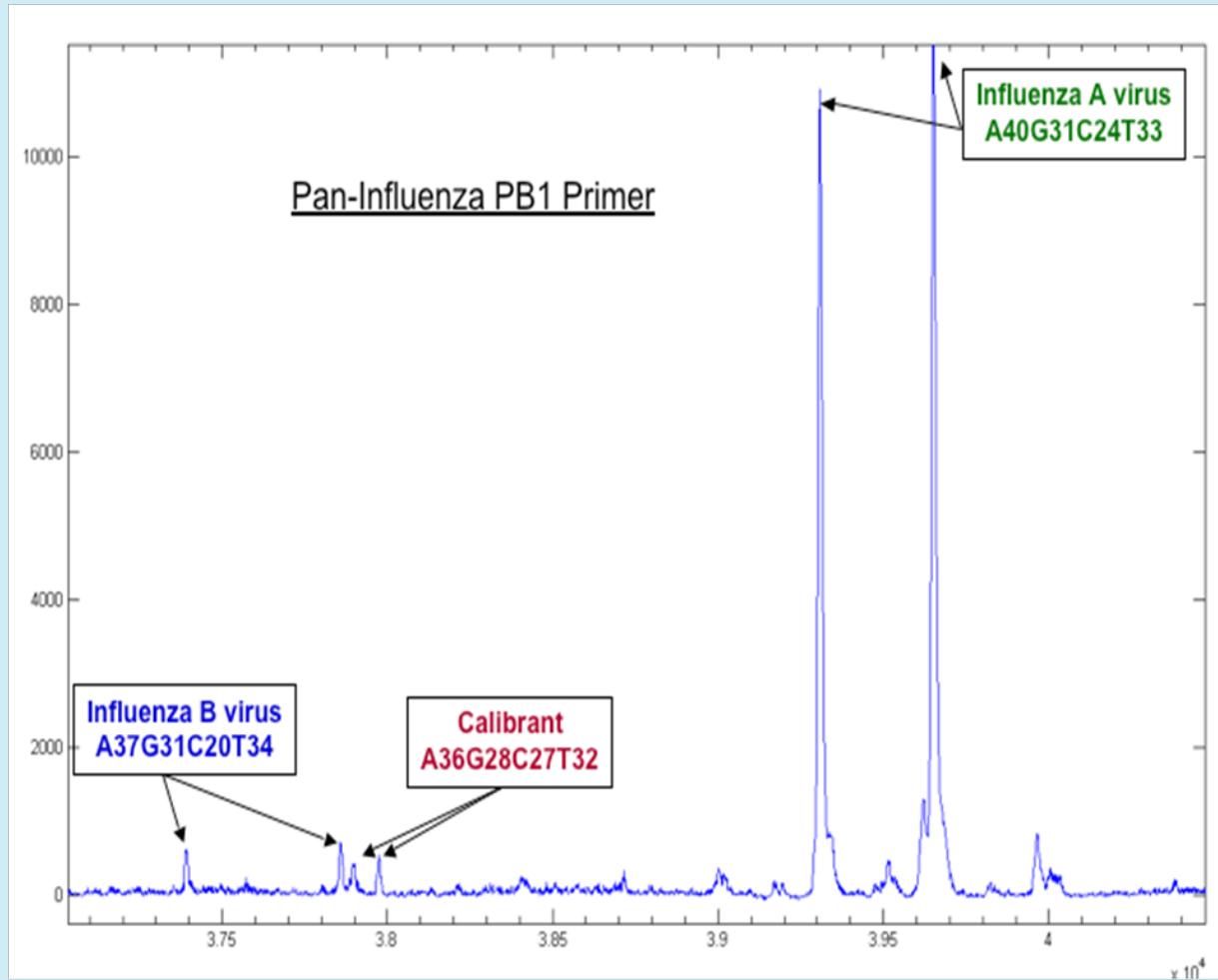
–Correctly identified all Influenza A types

- 149 H3N2
- 34 H1N1
- 67 Influenza B

Influenza	
Sensitivity	96.8%
Specificity	97.5%
PPV	96.0%
NPV	98.0%

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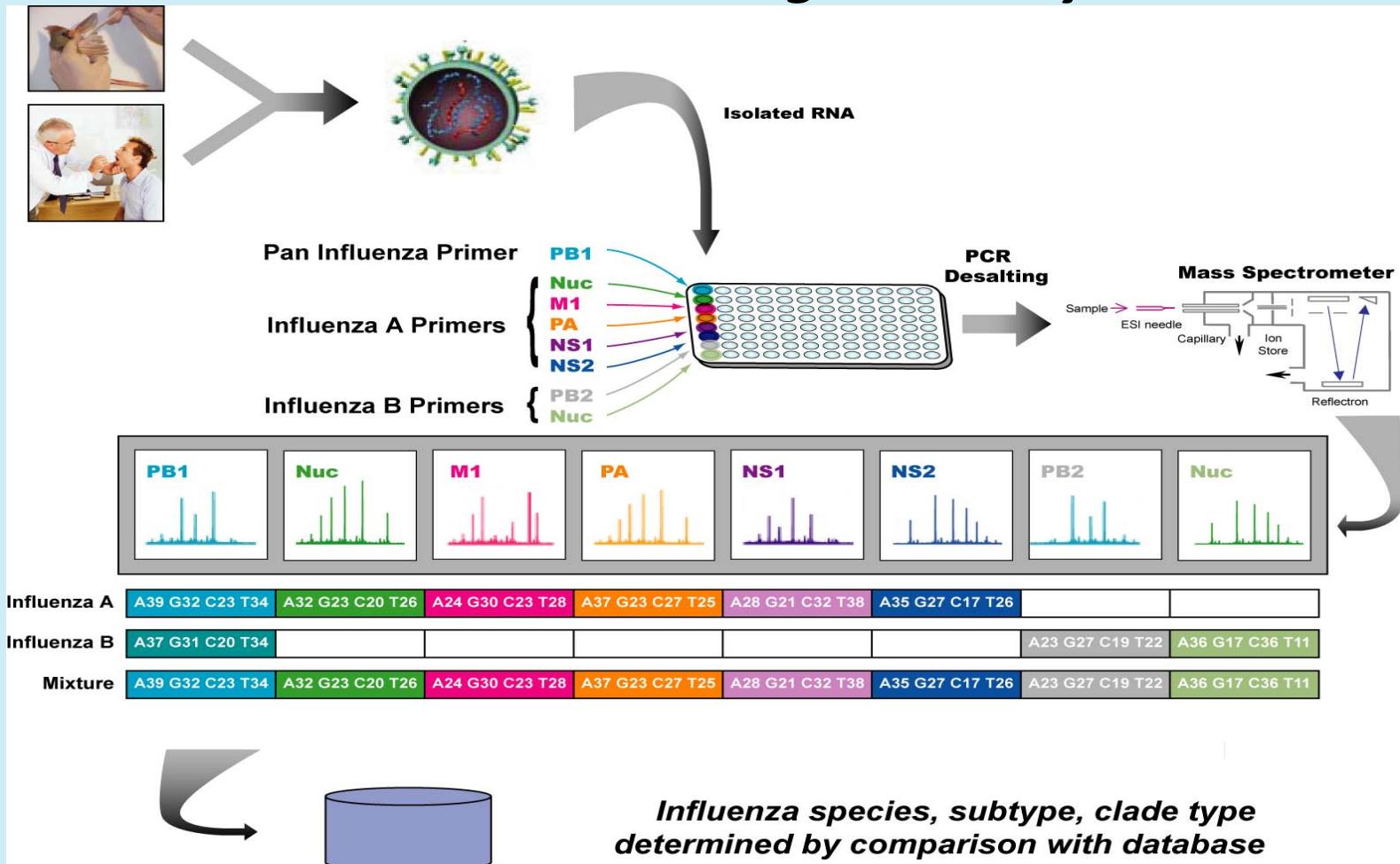
# *Detection of Mixed Infections*



# *Validation Study Test Isolates from Diverse Sources*

- **24 human influenza isolates**
  - **18 influenza A**
  - **6 influenza B**
- **63 avian influenza isolates**
  - **16 different avian species**
    - Chicken, duck, goose, egret, teal,....
  - **28 distinct H/N types**
    - **29 HIGHLY PATHOGENIC H5N1 isolates**
  - **8 worldwide geographic locations**
    - North America, Africa, Asia
- **4 swine influenza isolates**
- **1 equine influenza isolate**

# Avian Flu Detection: No Change in Assay or Primers



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# *Avian Influenza Virus Detection: University of Georgia Samples*

- **24 avian influenza virus isolates collected over a six-year period**
  - Different host species: mallard, seagull, teal,...
  - Different combinations of H and N subtypes: H12N4, H3N8...

# Avian Influenza Virus Detection: University of Georgia Samples

<b>SCWDS ID#</b>	<b>Serotype</b>	<b>Species</b>	<b>Location</b>	<b>Date</b>
AI00-1412	H6N1	REKN	Bower's Beach, DE	5/25/00
AI00-1794	H12N4	RUTU	Bower's Beach, DE	5/20/96
AI00-2150	H12N5	RUTU	Villas, NJ	5/15/96
AI00-629	H7N9	RUTU	Port Mahon, DE	5/19/96
AI02-262	H2N4	RUTU	Mispillion Harbor, DE	5/22/98
AI02-690	H2N9	RUTU	Reed's Beach, NJ	5/22/98
AI03-128	H9N7	RUTU	Reed's Beach, NJ	5/20/99
AI03-128	H9N7	RUTU	Reed's Beach, NJ	5/20/99
AI03-755	H9N5	RUTU	Mispillion Harbor, DE	5/20/99
AI04-127	H10N7	RUTU	Bower's Beach, DE	5/19/00
AI05-415	H3N8	RUTU	Fortescue Beach, NJ	5/21/01
AI05-415	H3N8	RUTU	Fortescue Beach, NJ	5/21/01
AI05-669	H11N8	RUTU	Reed's Beach, NJ	5/25/01
AI05-784	H11N6	RUTU	Reed's Beach, NJ	5/25/01
MN00-283	H5N2	MALL	Thief Lake, MN	9/10/96
MN00-382	H5N3	MALL	Thief Lake, MN	9/10/96
MN98-115	H4N8	MALL	Roseau Co., MN	09/ /1998
MN98-115	H4N8	MALL	Roseau Co., MN	09/ /1998
MN98-66	H6N5	MALL	Roseau Co., MN	09/ /1998
MN99-160	H4N6	MALL	Roseau Co., MN	/ /1999
MN99-17	H7N7	MALL	Roseau Co., MN	/ /1999
NC6412-009	H10N7	MALL	JM Futch, NC	12/20/00
NC675-075	H3N2	ABDU	Mattamuskeet, NC	12/21/00
TX01-32	H8N4	CITE	Brazoria Co., TX	2/11/97
TX01-7	H8N4	AGWT	Brazoria Co., TX	2/11/97
TX02-27	H1N4	BWTE	Brazoria Co., TX	2/18/98
TX02-75	H1N3	BWTE	Brazoria Co., TX	2/18/98

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# *Ibis™ T5000 Discrimination of Diverse Avian Influenza Virus Isolates*

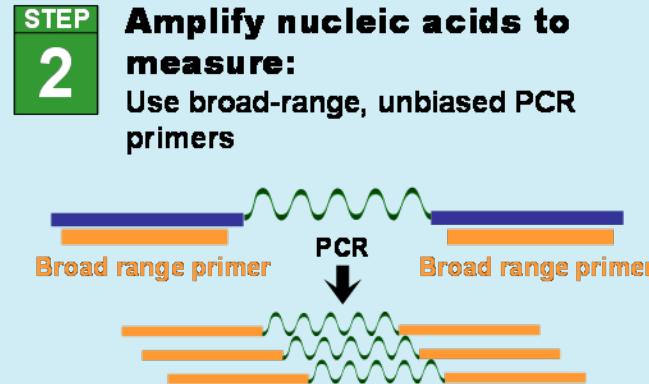
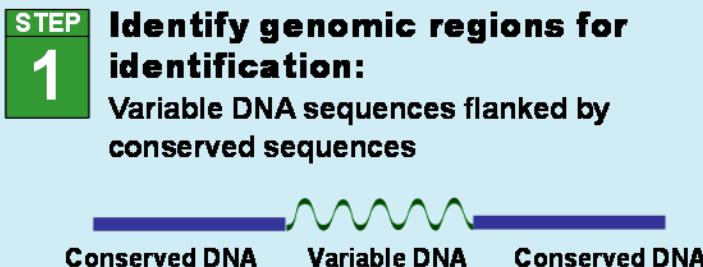
Serotype	Species	Location	Date	2798	1266	1279	1287	2775	2777
H1N3	BWTE	Brazoria Co., TX	2/18/98	A37G33C24T34	A35G22C22T22	A23G30C25T27	A35G27C28T22	A40G30C20T29	A35G27C16T27
H9N7	RUTU	Reed's Beach, NJ	5/20/99	A37G33C25T33	A37G21C20T23	A22G30C26T27	A35G26C28T23	A37G32C22T28	A34G27C18T26
H3N8	RUTU	Fortescue Beach, NJ	5/21/01	A37G34C23T34	A34G23C23T21	A23G30C24T28	A34G27C28T23	A37G32C22T28	A35G27C16T27
H3N8	RUTU	Fortescue Beach, NJ	5/21/01	A37G34C23T34	A34G24C20T23	A23G30C24T28	A34G27C28T23	A37G32C22T28	A34G27C18T26
H3N2	ABDU	Mattamuskeet, NC	12/21/00	A37G34C23T34	A34G24C21T22	A21G32C24T28	A35G26C29T22	A37G32C22T28	A34G27C18T26
H11N8	RUTU	Reed's Beach, NJ	5/25/01	A38G33C22T35	A35G22C22T22	A22G31C25T27	A34G27C28T23	A40G30C20T29	A35G27C16T27
H11N6	RUTU	Reed's Beach, NJ	5/25/01	A38G33C22T35	A35G22C22T22	A23G30C24T28	A34G27C28T23	A40G30C20T29	A35G27C16T27
H9N5	RUTU	Mispillion Harbor, DE	5/20/99	A38G33C23T34	A37G21C20T23	A24G28C23T30	A35G26C28T23	A37G32C22T28	A34G27C18T26
H9N7	RUTU	Reed's Beach, NJ	5/20/99	A38G33C24T33	A34G24C21T22	A22G30C26T27	A35G26C28T23	A37G32C22T28	A34G27C18T26
H6N5	MALL	Roseau Co., MN	09/1/1998	A39G32C22T35	A36G21C22T22	A21G32C25T27	A34G27C28T23	A40G30C20T29	A35G27C16T27
H4N6	MALL	Roseau Co., MN	/1999	A39G32C23T34	A35G22C23T21	A22G31C27T25	A34G27C28T23	A37G32C22T28	A34G27C18T26
H5N2	MALL	Thief Lake, MN	9/10/96	A39G32C23T34	A36G21C22T22	A23G31C26T25	A35G26C27T24	A37G32C22T28	A34G27C18T26
H8N4	AGWT	Brazoria Co., TX	2/11/97	A39G32C23T34	A36G22C21T22	A24G28C25T28	A34G27C28T23	A37G32C22T28	A34G27C18T26
H7N7	MALL	Roseau Co., MN	/1999	A39G32C23T34	A36G22C22T21	A20G32C27T26	A34G27C29T22	A37G32C22T28	A34G27C18T26
H5N3	MALL	Thief Lake, MN	9/10/96	A39G32C24T33	A34G24C21T22	A21G32C25T27	A34G27C28T23	A37G32C22T28	A34G27C18T26
H2N4	RUTU	Mispillion Harbor, DE	5/22/98	A39G32C24T33	A35G22C22T22	A22G31C25T27	A35G26C29T22	A37G32C22T28	A34G27C18T26
H12N5	RUTU	Villas, NJ	5/15/96	A39G32C24T33	A36G21C22T22	A21G32C24T28	A35G26C29T22	A37G32C22T28	A34G27C18T26
H7N9	RUTU	Port Mahon, DE	5/19/96	A39G32C24T33	A36G21C22T22	A21G32C24T28	A34G27C29T22	A37G32C22T28	A34G27C18T26
H2N9	RUTU	Reed's Beach, NJ	5/22/98	A39G32C24T33	A36G21C22T22	A23G30C26T26	A35G26C29T22	A37G32C22T28	A34G27C18T26
H4N8	MALL	Roseau Co., MN	09/1/1998	A40G31C22T35	A29G24C19T29	A25G28C25T27	A34G27C28T23	A37G32C22T28	A34G27C18T26
H4N8	MALL	Roseau Co., MN	09/1/1998	A40G31C22T35	A34G24C21T22	A25G28C25T27	A34G27C28T23	A37G32C22T28	A34G27C18T26
H12N4	RUTU	Bower's Beach, DE	5/20/96	A40G31C23T34	A35G23C22T21	A23G30C26T26	A35G26C29T22	A37G32C21T29	A34G27C17T27
H10N7	RUTU	Bower's Beach, DE	5/19/00	A40G31C24T33	A33G25C21T22	A23G30C25T27	A35G27C27T23	A38G31C22T28	A34G27C18T26
H10N7	MALL	JM Futch, NC	12/20/00	A40G31C24T33	A35G22C21T23	A23G30C26T26	A34G27C29T22	A37G32C22T28	A34G27C18T26
H8N4	CITE	Brazoria Co., TX	2/11/97	A40G31C24T33	A35G22C22T22	A22G30C27T26	A34G27C29T22	A40G30C20T29	A35G27C16T27
H1N4	BWTE	Brazoria Co., TX	2/18/98	A40G31C24T33	A35G22C22T22	A24G28C25T28	A35G26C28T23	A40G30C20T29	A35G27C16T27

\*Same panel was used for human Influenza detection

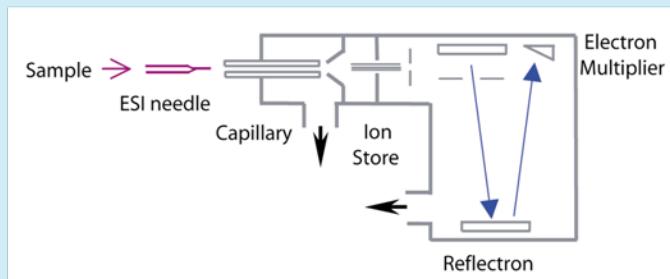
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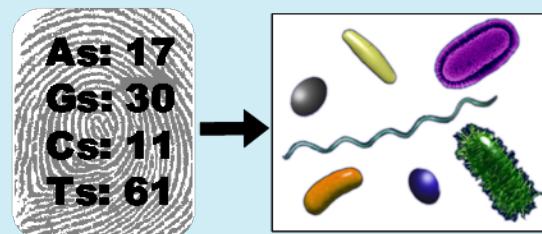
# *The Ibis™ Approach to Pathogen ID and Strain-Typing*



**STEP 3 Measure nucleic acid:**  
ESI-TOF



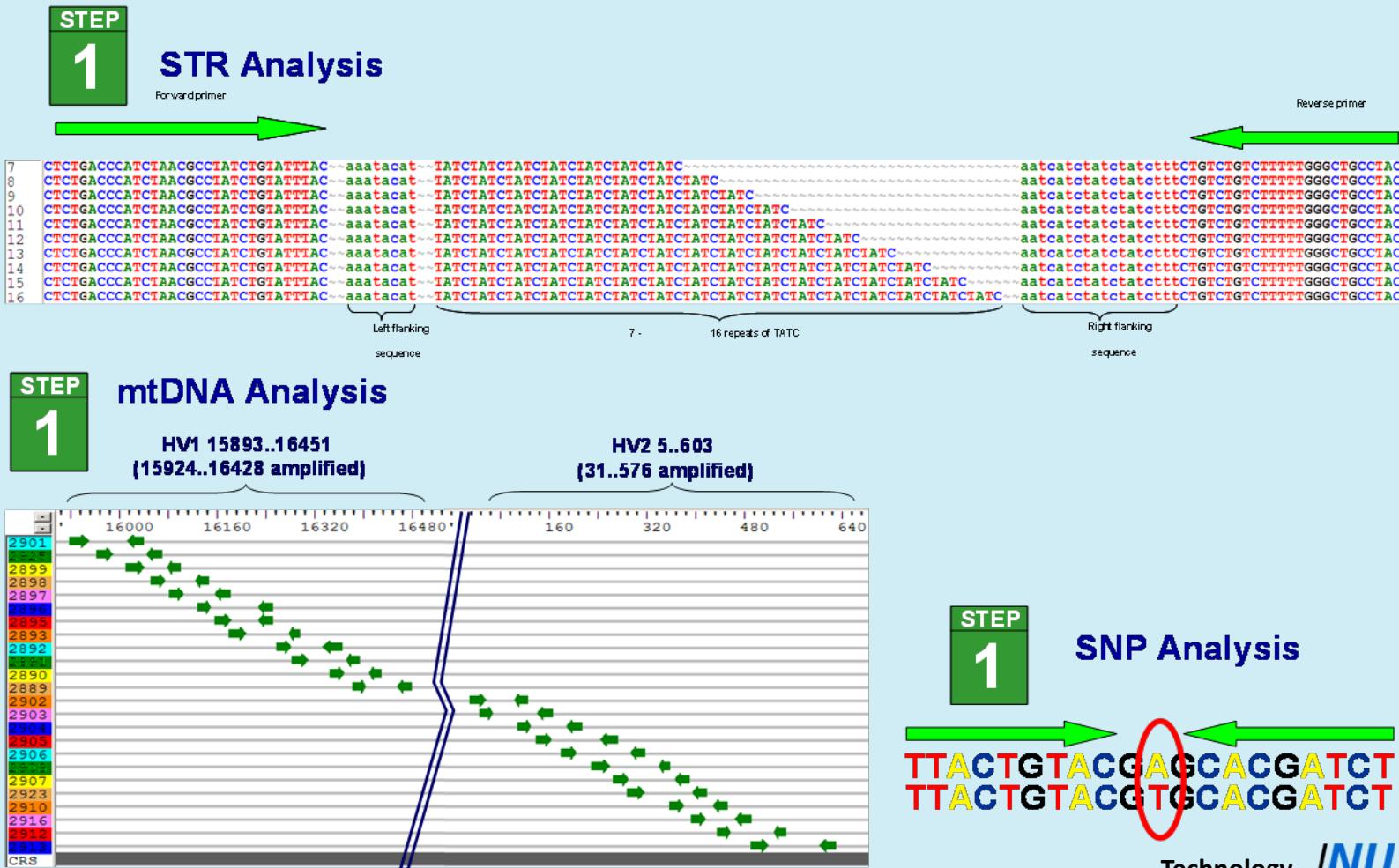
**STEP 4 Identify the organisms:**  
Base-composition fingerprints



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# PCR Primer Design for Forensic Markers



# Conclusions



- By “weighing” DNA with mass spectrometry, unambiguous base compositions can be derived
  - Remember coins and scale analogy!
- Base compositions derived from broad range primers can be used to triangulate to microbial identification
- Ibis™ platform enables broad range bacterial and viral detection
  - Broad bacterial coverage using broad range primers
    - Example: Direct analysis of throat swabs
  - All influenza (human and avian) in same assay
    - Example: Human clinical specimens and avian isolates

# **Conclusions**



- **Respiratory Virus Surveillance Assay (RVSA) provides a single test platform for six families of RNA and DNA respiratory viruses**
- **Demonstrated for bacteria and viruses without culture**
  - Also applicable to fungi, protozoa, and humans (not shown)

Instead of asking; “Is pathogen X in my sample?”,  
Ibis™ approach asks: “Which pathogen(s) are in my sample?”



# *Questions?*

# *Contact Information*

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