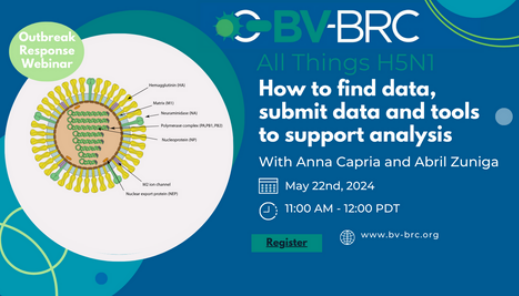


What's New

We're thrilled to reach out to our users with some exciting updates to share. Firstly, our tools and service section has undergone a revamp, offering a smoother experience and improved accessibility.

Genomics	Metagenomics
Genome Assembly	Taxonomic Classification
Genome Annotation	Metagenomic Binning
Comprehensive Genome Analysis (β)	Metagenomic Read Mapping
BLAST	
Primer Design	Transcriptomics
Similar Genome Finder	RNA-Seq Analysis
Genome Alignment	Expression Import
Variation Analysis	
Tn-Seq Analysis	Utilities
	Fastq Utilities
	ID Mapper
Phylogenomics	Viral Tools
Bacterial Genome Tree	SARS-CoV-2 Genome Analysis
Viral Genome Tree	SARS-CoV-2 Wastewater Analysis
Gene/Protein Tree	Influenza Sequence Submission
	Influenza HA Subtype Conversion
Protein Tools	Subspecies Classification
MSA and SNP Analysis	Sequence Feature Variant Types
Meta-CATS	
Proteome Comparison	Outbreak Tracker
Protein Family Sorter	Influenza H5N1 2024
Comparative Systems	SARS-CoV-2

Next, our outbreak surveillance includes information about the current H5-N1 2.3.4.4b cases; [check that out here](#). Speaking of H5N1- we will have a webinar on May 22nd at 11:00 am PT. [Register Here](#). The webinar will focus on influenza A and how you can search for data and submit sequences and tools for analyzing data- all within the BV-BRC.



Additionally, we've expanded our virus classification with the inclusion of new viruses for sub-species categorization. We're also venturing into wastewater surveillance to bolster early detection capabilities.



Finally, we are highlighting the success of the Viral Sub-species classification workshop, and we urge you to join the conversation on the [BV-BRC Reddit](#).

Website Updates

Data and Metadata Updates

- CDS Counts for Phages: Resolved issue of missing CDS counts for phages, enhancing data completeness.
- Assembly Accessions: Completed missing assembly accessions for bacterial, archaeal, and phage genomes, improving data integrity.
- Protein Structures: Additional protein structures from PDB were added, enriching available data resources.

Analysis Services Enhancements

- New Service: Introduced the [SARS-CoV-2 Wastewater Analysis Service](#), facilitating environmental surveillance..
- [FastqUtils Service](#): Implemented bug fixes and enhancements, including minimap and hostile detection improvements.

Website and UI Enhancements:

- Tools and Services Menu Update: The menu now has a dedicated section for specialized viral services. The new [SARS-CoV-2 Wastewater Analysis Service](#) has also been added for easier access.
- Advanced Search in Surveillance: Added "pathogen_type" to advanced search options in Surveillance for enhanced filtering capabilities.
- Additional Options in Surveillance: Included "treatment_type" in additional options and grid display within Surveillance, providing more comprehensive data presentation.
- Serology Grid Improvement: Made the "test_interpretation" column visible in the Serology grid, improving data visibility and interpretation.

Documentation Updates:

- New Tutorial: Published a new tutorial for the Compare Region Viewer tool. Access it at: [Compare Region Viewer Tutorial](#)
- [Taxonomic Classification Service Tutorial Series](#): Introduced a video tutorial series for the Taxonomic Classification Service, offering comprehensive guidance on its usage and functionalities.

AMR Data Updates

This month, the BV-BRC team updated the antimicrobial resistance (AMR) metadata collection from 91,028 genomes to 122,157 genomes with some form of antimicrobial susceptibility test (AST) data. The collection consists of data were collected from over 300 publications and data sourced from NCBI. The AST collection is comprised of laboratory measurements in the form of minimum inhibitory concentrations and zones of inhibition as well as susceptible, intermediate, and resistant determinations based of community accepted breakpoints. The data and are available at ftp.bvbr.org/RELEASE_NOTES/PATRI_C_genomes_AMR.txt.

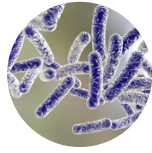
Wastewater Surveillance Updates

We are excited to unveil the [SARS-CoV-2 Wastewater analysis](#) service! It is an end to end pipeline to detect and quantify SARS-CoV-2 lineages and variants of concern (VOC) from wastewater samples. This service analyzes raw short amplicon reads.

The service writes a comprehensive report including data visualizations, time series analyses, analysis statistics and any warnings generated during the analysis. This service uses iVar, Samtools, FastQC, MultiQC and Freyja.

Sub-Species Tool Updates

The [Sub-Species Classification](#) tool now incorporates updated comprehensive data on various viruses, including those from the Adenoviridae and Paramyxoviridae families. This includes complete genome sequences and genomic DNA analysis for Human mastadenovirus A, B, C, E, and F from the Adenoviridae family, as well as Measles morbillivirus and Mumps orthorubulavirus from the Paramyxoviridae family. These updates facilitate maximum likelihood placement.

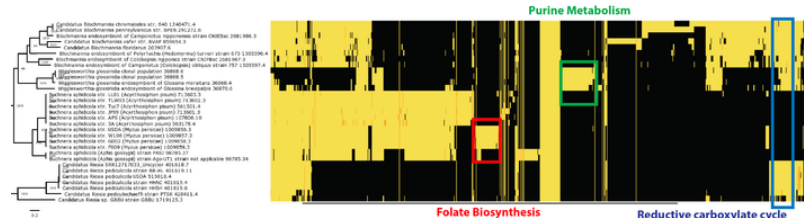


BV-BRC BACTERIA SPOTLIGHT

Buchnera 93 Complete, 30 Plasmid, 19 WGS
Buchnera, found in aphids, are symbiotic bacteria that are crucial for the insect's survival. Named for Paul Buchner, the founder of systematic symbiosis research, these bacteria have very small genomes (600 to 650 kb) and have been hypothesized to have undergone genomic decay as they adapted from a free-living existence to an intracellular environment. They were used in the first molecular characterization of a symbiotic bacterium, carried out by Paul Baumann. Symbiotic bacteria can be analyzed with these BV-BRC tools:

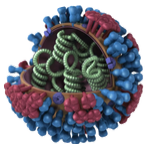
- [Genome Assembly](#)
- [Genome Annotation](#)
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- [RNA-Seq Analysis](#)



If you zoom in- you can see one of a phylogenetic tree generated by our service, and how BV-BRC data can be combined to do unique analysis. This figure is showing the trees, the protein families (heatmap), and the genes involved in metabolic pathways (annotations) all together. The phylogenetic trees can be visualized right on the data table that is central to the BV-BRC- a great way to visualize bacterial data.

BV-BRC VIRUS SPOTLIGHT



H5N1 Influenza 2.3.4.4b

On the next page read all about the current H5N1 outbreak which is impact many species around the US and world. This is also currently highlighted in our outbreak pages- which are described in the next section and can be found here.

Outbreak Updates

The BV-BRC now has outbreak pages to monitor and document outbreaks, ensuring the retention of pertinent information regarding currently circulating outbreaks. By incorporating this new feature, we hope to give you timely and actionable insights. It is accessible on the home page and the tools and services tab. Currently this tool includes H5N1 and SARS-CoV-2. [Check out H5N1 page now!](#)

Viral Sub-Species Classification Workshop



The Viral Sub-species classification workshop was an immense success with incredible conversation and great speakers. The meeting was an unqualified success, but this is of course, only the first step.

Our goal is to compile a sensible, usable plan to track and name the evolution of viral pathogens in real-time during a disease outbreak. This will then inform and empower the many stakeholders interested in using the information on these evolving lineages, serving as the basis for their response.

Our next steps will involve preparing a meeting summary and then turning that into a manuscript describing the meeting and outlining our collective recommendation for how best to design and implement a future response framework.

Session One, led by Elliot Lefkowitz, tracked virus evolution and its impact on sub-species. Dr. Richard Neher discussed RNA virus spread, followed by Dr. Bette Korber's insights on SARS-CoV-2 and HIV variants.

Session Two, moderated by Dr. Rodney Brister, explored RNA and DNA virus complexity. Dr. Justin Bahl discussed RNA virus evolution, Dr. Tavis Anderson spoke on influenza A virus, and Dr. Jens Kuhn covered Filovirus nomenclature.

Session Three, moderated by Dr. Conrad Schoch, explored diverse perspectives on virus classification, featuring discussions on Influenza, SARS-CoV-2, and virus classification from Dr. Derek Smith and Dr. Peter Simmonds, respectively.

Session Four, moderated by Dr. Richard Scheuermann, delved into classification schemes, featuring discussions from Dr. Jens H. Kuhn on ICTV taxonomy, Dr. Krista Queen about GISAID classification, Dr. Áine O'Toole, on the Pango system development, and its future beyond the SARS-CoV-2 pandemic from Dr. Rachel Colquhoun.

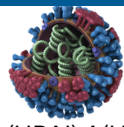
Session Five, moderated by Dr. Eneida Hatcher, focused on tools for viral evolution classification. Dr. Cornelius Roemer discussed Clade and lineage assignment, Dr. Angie Hinrichs presented USHER and autolin, and Dr. Christian Zmasek discussed BV-BRC sub-species classification tools.

Session Six, moderated by Indresh Singh, explored analytical and visualization tools for studying virus evolution during outbreaks. Dr. Eneida Hatcher discussed NCBI Virus and Taxonomy, Dr. Philippe Le Mercier presented Virus sub-species in ViralZone and UniProtKB, and Dr. Andrew Warren discussed viral mutational spectra visualization.

Session Seven, led by Dr. Paul Eder, addressed public health responses. Dr. Brown discussed NIAID's disease prevention efforts, Dr. Beck shared CDC's perspective, Dr. Rosamund Lewis explored viral evolution's impact on pox outbreaks, and Dr. Xiong (Sean) Wang provided insights from the Minnesota Department of Health on virus surveillance.

More information and complete summaries to come on the BV-BRC website.

H5N1 Indepth Report



H5N1 Influenza 2.3.4.4b

In 2020, highly contagious bird flu (HPAI) A(H5N1) 2.3.4.4b viruses emerged from existing strains and spread mainly through migrating birds across Africa, Asia, and Europe, causing significant wild bird deaths and poultry outbreaks. By late 2021, these viruses reached North America and later South America in 2022. They've also affected other animals like mammals, with a recent outbreak in a mink farm in Spain. Since 2020, six human cases of A(H5N1) linked to the 2.3.4.4b clade have been reported to WHO. This assessment focuses on the latest strains of A(H5N1) from the 2.3.4.4b clade.

Influenza A Taxonomy

- Realm: Riboviria
- Kingdom: Orthornavirae
- Phylum: Negarnaviricota
- Subphylum: Polyoviricota
- Class: Insthoviricetes
- Order: Articulavirales
- Family: Orthomyxoviridae
- Genus: Alphainfluenzavirus
- Species: Alphainfluenzavirus influenzae
- Sub-species: H5N1 , 2.3.4.4b

Influenza A

Influenza A virus, a member of the Orthomyxoviridae family, is a significant etiological agent of influenza, an acute respiratory illness with substantial global impact. Characterized by its enveloped structure housing a segmented, negative-sense single-stranded RNA genome, this virus exhibits remarkable genetic plasticity, facilitating rapid evolutionary adaptation and strain diversification.

Replication Cycle

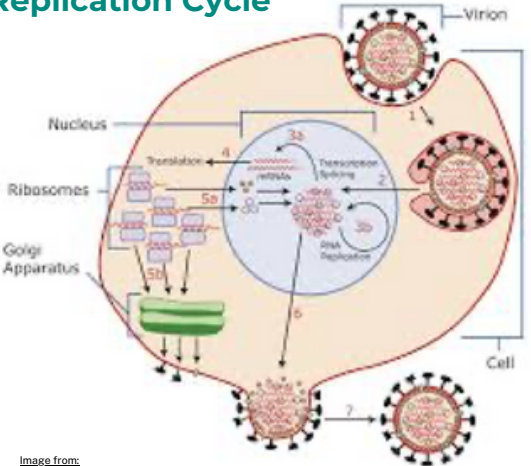
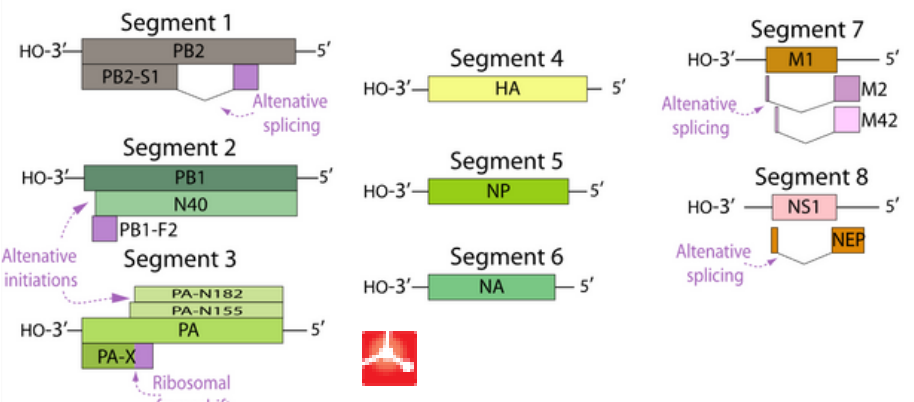


Image from: [https://bio.libretexts.org/Bookshelves/Microbiology/Microbiology_\(Boundless\)/09%3A_Viruses/9.09%3A_Negative-Strand_RNA_Viruses_in_Animals/9.9C%3A_Replicative_Cycle_of_Influenza_A](https://bio.libretexts.org/Bookshelves/Microbiology/Microbiology_(Boundless)/09%3A_Viruses/9.09%3A_Negative-Strand_RNA_Viruses_in_Animals/9.9C%3A_Replicative_Cycle_of_Influenza_A)

Influenza Genomic Structure



Segmented ssRNA(-) linear genome, encapsidated by nucleoprotein (NP). Contains 8 segments coding for a total of 12-14 proteins depending on strains. Segment sizes range from 890 to 2,341nt. Genome total size is 13.5Kb Image from Viralzone.

H5N1 History

Influenza A subtype H5N1, commonly known as avian influenza or bird flu, has garnered significant attention due to its potential to cause severe illness in both birds and humans. Originating primarily in wild birds, H5N1 can occasionally infect domestic poultry, posing significant economic and public health concerns. In humans, H5N1 infections are rare but have been associated with high mortality rates, making it a focus of pandemic preparedness efforts. The virus is known for its ability to undergo genetic reassortment & evolve into novel strains with pandemic potential. Continuous surveillance and research are crucial for monitoring H5N1 activity, understanding its transmission dynamics, and developing effective control measures to mitigate the risk of widespread outbreaks.

Disease Manifestation

In humans- Influenza A virus spreads efficiently via respiratory droplets, efficiently exploiting host respiratory epithelial cells as its primary replication site. Key to its pathogenic prowess is the virus's capacity for antigenic drift and shift, which evades host immune surveillance, precipitating periodic epidemics and potential pandemics.

Clinical manifestations of influenza A infection encompass a spectrum of symptoms, including fever, malaise, myalgia, respiratory distress, and complications such as pneumonia. The severity of disease often correlates with host factors, including age, immune status, and underlying health conditions.

BV-BRC Tools

- [Genome Annotation](#)
- [BLAST](#)
- [Primer Design](#)
- [Similar Genome Finder](#)
- [Viral Genome Tree](#)
- [Gene/Protein Tree](#)
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- [Taxonomic Classification](#)
- [Metagenomic Binning](#)
- [Subspecies-Classification](#)
- [Sequence Submission](#)

H-N DECODED

Influenza A viruses are further classified into subtypes based on their surface proteins: hemagglutinin (H) and neuraminidase (N). For example, H5N1, H3N2, etc.

Epidemiology

Influenza is a well studied virus which has lots of previous work done to understand and monitor mutations that may affect virus transmissibility, virulence, and antigenic properties, which could impact vaccine efficacy.

