teachers guide

Molecular evidence for evolution 4:
Viral evolution

Components

	NAME	DESCRIPTION	AUDIENCE
	Viral evolution teachers guide	This guide explains how to use bioinformatics tools within the Influenza Research Database to build students' understanding of molecular evidence for evolution.	teachers
	Influenza background sheet	This background sheet for teachers describes the structure and reproduction of influenza viruses.	teachers
	Investigating influenza background sheet	This background sheet for teachers describes how influenza viruses evolve, and mechanisms of antigenic drift and shift. It also provides an introduction to bioinformatics and the Influenza Research Database.	teachers
	Fighting the 'flu fact sheet	This fact sheet describes the structure of influenza viruses and how they evolve through antigenic shift and drift.	students
	Influenza – an evolving problem! worksheet	This activity sheet guides students through interactive use of the Influenza Research Database.	students

Purpose

Students develop an understanding of how databases may be used to map changes in influenza viruses as they evolve.

Outcomes

Students understand that:

- there are different types of influenza virus that affect different animal species;
- evolution can occur rapidly in viruses, through mechanisms of antigenic drift and antigenic shift;
- mutations or changes in nucleotide sequences of viruses mean hosts may not recognise a virus; and
- online databases, such as the Influenza Research Database, enable scientists to track strains of viruses and map evolutionary changes, as they occur.

Activity summary

ACTIVITY	POSSIBLE STRATEGY
Students read the fact sheet, *Fighting the 'flu*, to provide background information for an online database activity.	individually or in pairs
Students work through the activity, *Influenza – an evolving problem!*, answering questions.	individually or in pairs

Teacher notes on the Influenza Research Database

The Influenza Research Database used in *Influenza – an evolving problem!* is an authentic research tool. It is used to determine directions of influenza evolution and to identify emerging new strains. As the database is complex it is recommended that teachers work through the activity before giving it to students. The activity is structured and includes screen shots to make the database straightforward to use.

Each student will need to log into the database and set up a workbench. Teachers may want to demonstrate this.

Influenza type A, segment 4, has been selected for this activity. This segment of RNA codes for the protein haemagglutinin, which is a surface protein used to identify influenza strains. After completing the activity, another phylogenetic tree may be generated using segment 6 which codes for neuraminidase.

Students answer questions as they work through the database and produce a phylogenetic tree for selected strains of influenza. Their phylogenetic tree will reveal how genetically different, due to antigenic shift, the 2009 strains of influenza were from earlier strains, thus explaining why so many people became sick. Immune memory is raised in the introduction to the activity. It may be necessary to elaborate on this topic, focusing on immunisation and why it's recommended that influenza vaccination is repeated each year.

Students should be able to complete the activity in the worksheet, *Influenza – an evolving problem!* in about one hour.

Technical requirements

The teachers guide, background sheets, worksheet, and fact sheet require Adobe Reader (version 5 or later), which is a free download from get.adobe.com/reader/.

The Influenza Research database requires a compatible Javascript-enabled web browser. Minimum browser requirements are Internet Explorer 6.0, Netscape 8.0, Firefox 1.5 or Safari 1.2.

Check with your IT support person if Java is enabled on your computers, as it is required to display aligned sequences and phylogenetic trees. A message 'Missing plug-in' or a blank space where data should be displayed probably indicates problems with your version of Java or security settings. Macintosh users may find Firefox less restrictive than Safari.

You can check that the browser you are using supports Java by going to http://www.java.com/testjava/

Acknowledgements

More information

World Health Organisation, Influenza (Seasonal), fact sheet number 211, April 2009, retrieved January 2013 from www.who.int/mediacentre/factsheets/fs211/en/

Virus WAtch is a weekly electronic publication by the Communicable Disease Control Directorate (CDCD) and key collaborators. It provides a brief summary of General Practice and sentinel surveillance data on influenza-like and other illnesses to alert health care workers in WA to important circulating viruses. www.public.health.wa.gov.au/3/487/3/virus_watch_homepage.pm

SPICE resources and copyright

Associated SPICE resources

Molecular evidence for evolution 4: Viral evolution
may be used in conjunction with related SPICE
resources to teach the topic of molecular evidence for
evolution.

DESCRIPTION	LEARNING PURPOSE
Molecular evidence for evolution (overview)	
Molecular evidence for evolution 1: Mammal evolution A card game engages student interest in evidence used to determine evolutionary relationships between eutherians (placental mammals).	**Engage**
Molecular evidence for evolution 2: Primates Students use interactive learning objects to explore how anatomical evidence may be used to determine relatedness.	**Explore**
Molecular evidence for evolution 3: Evolutionary trees The use of molecular evidence to determine relatedness between species is explained. Students draw evolutionary trees to represent relatedness.	**Explain**
Molecular evidence for evolution 4: Viral evolution Students use the Influenza Research Database to investigate virus evolution. This bioinformatics database is an authentic research tool used to compare genetic sequences of virus strains, and to construct cladograms to draw conclusions about their relatedness.	**Elaborate**

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NEALS