How does the Aleutian disease virus sequence database help a rancher?

Our Aleutian disease (AD) virus genome sequence database, which is the largest of its kind in the world, provides the foundation for developing an accurate virus detection method by PCR, for monitoring AD virus movement amongst ranches, and for estimating virus pathogenicity

A mink rancher who avidly follows the Aleutian Disease Research progress reports asked for a "rancher translation" of the report on virus variability in Nova Scotia. He commented "a bunch of words such as 'viral genome' or 'DNA' or 'sequence' mean nothing to me. Just tell me how the information is of any benefit to me". Here is some explanation.

Is it possible to pinpoint the origin of the AD virus that infected my ranch?
This is often the first question a mink rancher asks when his or her clean herd becomes infected with the AD virus.

There are instances where ranchers, particularly in areas with a high density of mink farms, have carefully followed recommended biosecurity measures (or they thought they had), yet mysteriously their ranch became infected with the virus.

Many ranchers vigorously test all their potential breeders at least once per year and eliminate all CIEP (counterimmunoelectrophoresis) positive animals. Yet, the virus persists on the ranch.

Where is the virus coming from? It may come from

- animals on your ranch that were undetected by CIEP testing,
- breeder animals that you purchased from an apparently clean ranch,
- other infected ranches carried in by visitors, cars, feed truck, insects, birds, etc. or even by air,
- public places where you may cross paths with folks from other infected ranches,
- wildlife populations by direct contact or by insects or birds, etc.,
- soil on your ranch where the virus could have been hiding for years,
- or from ????.

I am sure you can add to this list. Your guess is as good anyone else.

Knowledge of the sources of the virus would be a key step in the fight against the AD virus infection.

Finding the source of virus on a ranch is pretty much the same as catching criminals using fingerprints. A fingerprint of the suspect and a collection (database) of fingerprints of many criminals are required. These days DNA profiling has replaced fingerprinting, yet the basic concept has not changed. The DNA profile of the suspect and a database of DNA profiles of criminals are needed.

The same technology can be used to pinpoint the origin of the AD virus that infected a ranch. In this case, the sequence of the virus on a particular ranch is compared with a database containing the sequences of other viruses in ranched mink and wild animal populations to identify source of the virus.

Which part of the virus should be sequenced to determine the origin of a virus?
The AD virus is known to be highly variable because of its high mutation rate. This is the reason that so many different AD types were found in Nova Scotia (see my previous report). This high variability works as a 'DNA tag' for accurately identifying the source of the virus when an AD positive mink appears on a clean ranch. This is good news.

It is not practical to sequence the entire length of the virus- it would be too expensive. AD viruses have regions that are different from each other and regions that are almost similar. If incorrect sections of the virus on a ranch were compared with the database, a wrong conclusion might be reached. The key for virus identification is to determine the regions of the viral sequence that best indicate the origin of the virus. This is one of the main reasons that 92% of the AD viruses were sequenced in so many samples in Nova Scotia.

The effects of AD virus variability on the PCR (polymerase chain reaction) test
High levels of variability of the AD virus genome have a downfall. The variability may reduce the accuracy of virus detection by PCR.

PCR is a technique which multiplies a few viral copies into billions of similar copies for further testing. Every PCR test requires two primers, which work as tags or addresses for the test to be performed correctly. You will not receive your mail if your home address is incorrect on the envelope. Similarly, PCR fails to work if the primer sequence (address on the test material) is different from the target on the virus genome (home address of the virus). These two must match. Any mismatch between the primers' sequences and their targets on the virus genome causes the PCR test to fail, even if the animal is infected. This is a false negative result.

Sequencing of a large portion of the viral genome is necessary to identify regions that are similar among all viral types in Nova Scotia. It helped to find the common address for all local virus types. The information was used to develop a couple of PCR tests that can detect almost all local viruses. This is the second reason that 92% of the AD virus was sequenced.

Can we say how bad a virus is from its sequence?
Mink ranchers know that some AD viruses are nasty and cause high mortality, while others are less dangerous. All the information on the pathogenicity of a virus is present in its DNA sequence. Scientists have already identified regions of the AD viral genome that dictate, to some extent, the degree of pathogenicity of some AD virus strains. A database of viral sequences in a region can be linked to the mortality rate caused by specific virus strains, as well as to the published sequences of the viruses with known pathogenicity. It is thus theoretically possible to distinguish between the good, the bad

and the ugly, using the genome sequence database. This is the third reason for sequencing a large part of AD virus in Nova Scotia.

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