

SWINE HEALTH

Title: African Swine Fever Virus: a bioinformatics resource to support comparative genomics for vaccine and virulence studies. – **NPB #15-123**

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Scientific Abstract

All ASFV researchers require access to the viral genome sequences. However, the access provided by NCBI gives only FASTA or GenBank files of the data, which are static text files. If only a few genomes were sequenced, managing the data in this way would be tedious but perhaps manageable. However, there are currently 16 completed and publically available and probably in the order of 100-200 due to be sequenced in the next three years. This quantity of data certainly requires storage in a dedicated database with integrated tools to make the analysis, not only efficient, but possible at all.

The poxvirus database and bioinformatics resource, previously managed at www.virology.ca, was modified so that it could be run from a cloud computer resource at WestGrid.ca. This is the western portion of Compute Canada, a Canadian academic research compute centre that serves all research facilities in the country. The purpose of this move was:

- 1) platform stability – more secure backups.
- 2) platform portability – much easier to move the system to other platforms if required (e.g. when I retire).
- 3) expandability – more powerful resources available if required.

We also created a new model for annotation of the ASFV multi-gene families to enable better consistency in the annotation of these genes in preparation for the sequencing of large numbers of genomes.

Finally, we began an out-reach campaign to make researchers in the ASFV community aware of the project and to ask for their input on the proposed annotation scheme.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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