Comparison of two Next Generation sequencing platforms for full genome sequencing of Classical Swine Fever Virus

Fahnøe, Ulrik; Pedersen, Anders Gorm; Höper, Dirk; Beer, Martin; Rasmussen, Thomas Bruun

Published in:
ABSTRACTS

Publication date:
2013

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):

General rights
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.
EPIZONE ABSTRACTS

7th Annual Meeting
‘Nothing permanent, except change’
1 - 4 October 2013
Brussels

Hosted by
CODA - CERVA
www.epizone-eu.net
D 2 - POSTER: Comparison of two Next Generation sequencing platforms for full genome sequencing of Classical Swine Fever Virus

Fahnøe, Ulrik¹; Pedersen, Anders Gorm²; Höper, Dirk³; Beer, Martin³; Rasmussen, Thomas Bruun¹

DTU Vet¹; DTU Systems Biology²; FLI³

Key words: Classical Swine Fever Virus, Next Generation Sequencing, platform comparison, Variant analysis

Next Generation Sequencing (NGS) is becoming more adopted into viral research and will be the preferred technology in the years to come. We have recently sequenced several strains of Classical Swine Fever Virus (CSFV) by NGS on both Genome Sequencer FLX (GS FLX) and Iontorrent PGM platforms. In this study, we analyzed NGS data of virus rescued from a CSFV C-strain vaccine strain cDNA clone. The virus analyzed was obtained from a 4th and a 12th passage of rescued virus in SFT cell culture, which had shown a difference in growth kinetics between the passages, and NGS analysis was chosen in order to look for molecular differences. Identical RT-PCR products were run on both GS FLX and an Iontorrent PGM platform for comparison. The NGS data was compared by quality and the percentage mapped reads. Results showed good quality of reads for both platforms and a close to 100% of the reads mapped to the consensus sequence. Additionally, we got an average sequence depth for the genome of 4000 for the Iontorrent PGM and 400 for the FLX platform making the mapping suitable for single nucleotide variant (SNV) detection. The analysis revealed a single non-silent SNV A10665G leading to the amino acid change D3431G in the RNA-dependent RNA polymerase NS5B. This SNV was present at 100% frequency in the 12th passage and only at 55% in the 4th passage, which could explain the difference in growth kinetics between the passages.