Maarten Rudolph Leerkes, J Mol Genet Med 2015, 9:3
http://dx.doi.org/10.4172/1747-0862.C1.009

OMICS International
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3rd International Conference on
Genomics & Pharmacogenomics
September 21-23, 2015 San Antonio, USA

Discovery of novel molecular targets in SIV infected non-human primates serve as models for human HIV drug targeting

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We have analyzed RNAseq data in the context of re-annotating the genome of African green Monkeys (AGM). RNA-seq experiments were designed to answer questions regarding the mechanisms underlying the lack of disease progression in these natural Simian Immunodeficiency Virus (SIV) hosts which are still poorly understood. Although the AGM genome is available, it is poorly annotated. The rhesus genome is also available for dual-genome predictions and although it has its own limitations, it can be used in combination with RNA-seq data to re-annotate the AGM genome. The patas monkey is an interesting third primate study model but does not have a reference genome available and depends on *de novo* assembly of RNA-seq reads to be analyzed. *De novo* assembly compared with genome-based splicing detection helps cross-validate methods. Cross-species comparisons can shed light in more detail on resistance mechanisms related to SIV and HIV infections. RNA-seq studies focusing on splicing signatures are an essential tool for both genome re-annotation and biomarker discovery. As such, this is of interest for upcoming RNA-seq studies with the objective to more accurately define how specific splicing signatures render African green monkeys resistant to progressive SIVagm infection. This is promising in the discovery of novel molecular targets in the process of SIV infection and can serve as a model for human HIV targets and thus serves as a compelling example that impacts genomic advances on global health.

Biography

Maarten Rudolph Leerkes is an accomplished Bioinformatics Scientist at NIH-BCBB (Bioinformatics and Computational Biosciences Branch). He works on developing novel quantitative biology methods. He has worked on identifying molecular signatures for disease prognosis and treatment prediction in patient sub-populations in biotech industry as well as on product development including study design for product validation in clinical settings. His PhD, Post-doctoral and research experiences span academia as well as biotech industry settings where he focused on the use of bioinformatics to interpret sequencing data (NGS) and to find patterns that can be extrapolated into diagnostic tools for improving treatment for patients.

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