Zahra Jalali Sefid Dashti et al., J Mol Biomark Diagn 2015, 6:4
http://dx.doi.org/10.4172/2155-9929.C1.026

OMICS International
conferenceseries.com

6th International Conference on
Biomarkers & Clinical Research
August 31-September 02, 2015 Toronto, Canada

Detection of novel genetic variants associated with *Mycobacterium tuberculosis* drug resistance

Zahra Jalali Sefid Dashti[1], **Ruben van der Merwe**[2], **Samantha Sampson**[2], **Rob Warren**[2] and **Alan Christoffels**[1]
[1]University of the Western Cape, South Africa
[2]Stellenbosch University, South Africa

Tuberculosis (TB) is an infectious disease caused by bacteria belonging to the *Mycobacterium tuberculosis* complex (MTC). The global burden of disease based on the World health organization (WHO) estimates suggests 9.4 million new TB cases worldwide, with the majority of the estimated cases occurring in Africa and Asia. In spite of the existing challenge with the multidrug resistant (MDR) TB, TB control faces another dilemma; extensively drug resistant (XDR) TB a situation where the pathogen is resistant to the four most effective anti-TB drugs rifapincin, isoniazid, an aminioglycoside and a fluoroquinolone. Deciphering the molecular basis of drug resistance has become a research priority, as this information will guide the development of new molecular based diagnostics as well as providing insight into new drug targets. In line with this, we carried out the assembly and functional annotation of a relatively large dataset with 400 M. tuberculosis genomes using reference based assembly approach. Variant calling methods including GATK (Haplotypecaller), Samtools and FreeBayes were used to identify SNPs that map to specific phenotypic categories such as XDR, MDR, and drug susceptible. This data provides a knowledge base for drug resistance marker discovery.

Biography

Zahra Jalali Sefid Dashti has completed her PhD at the South African National Bioinformatics institute (SANBI), University of the Western Cape. She is currently a Post-doctoral researcher at the same institute. Her research expertise is in the next generation sequencing data analysis of infectious diseases such as sleeping sickness and tuberculosis.

zahra@sanbi.ac.za

Notes: