

SCIENTIFIC SEMINAR ON APPLICATION OF RNA- & RAD-TAG SEQUENCING IN AGRICULTURE

DATE: 9 OCTOBER 2012 (Tue)

TIME: 10:00 AM – 12:00 PM

VENUE: INBIOSIS SEMINAR HALL, UKM BANGI



TENTATIVE PROGRAMME

10:00 am - 10:30 am

RNA SEQUENCING AND ITS POTENTIAL IN AGRICULTURE

10:30 am – 11:00 am

RAD-TAG SEQUENCING; A RAPID AND COST-EFFECTIVE GENOTYPING TOOL IN AGRICULTURE

11:00 am – 11:30 am

ANALYSIS OF RNA-SEQ DATA USING BIOINFORMATICS TOOLS

11:30 am – 12:00 pm

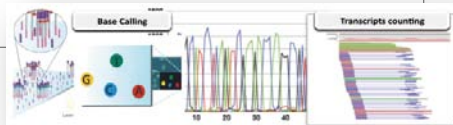
Q & A & WRAP-UP

With the advent of capillary electrophoresis (CE) based sequencing, scientists gained the ability to elucidate genetic information from any given biological system. This technology has become widely adopted but has always been hampered by inherent limitations in throughput, scalability, speed and resolution. To overcome these barriers, an entirely new technology called Next Generation Sequencing (NGS) was introduced triggering ground breaking discoveries and igniting a revolution in the world of genomics/transcriptomics science. NGS has the potential to dramatically accelerate biological and biomedical research, by enabling the comprehensive analysis of whole genome, transcriptome and gene discovery to become inexpensive, routine and widespread, rather than requiring significant production-scale efforts.

▶ RNA SEQUENCING AND ITS POTENTIAL IN AGRICULTURE

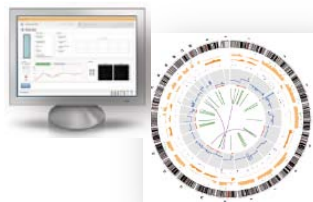
By Vahid Omidvar (Application Scientist)

RNA-Seq is a powerful tool for gene expression studies by quantifying RNA transcripts. Using Illumina's NGS technology, RNA-Seq allows scientists to count the number of reads that align to one of thousands of different cDNAs, producing results similar to those of gene expression microarrays. However, unlike hybridization-based microarrays that rely on fluorescence signal intensities, RNA-Seq counts the discrete number of reads aligned to a particular region giving a more accurate measure in expression levels. RNA-Seq is also capable of detection of alternative spliced isoforms, post transcribed editing and novel transcript variants.



Attendance confirmation should be made no later than 5 October 2012, faxed to 03 89213398, or email to hellen@sciencevision.com.my

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▶ RAD-TAG SEQUENCING; A RAPID AND COST-EFFECTIVE GENOTYPING TOOL IN AGRICULTURE By Chan Wei Hseng (Product Specialist)

Genotyping methods have traditionally been expensive and labour intensive, but new high-throughput technologies hold promise. Restriction site associated DNA (RAD) tags are a genome-wide representation of every site of a particular restriction enzyme by short DNA tags. Most organisms segregate large numbers of DNA sequence polymorphisms that disrupt restriction sites, which allows RAD tags to serve as genetic markers spread at a high density throughout the genome.



▶ ANALYSIS OF RNA-SEQ DATA USING BIOINFORMATICS TOOLS By Siew Fen (BioIT Research Associate)

RNA sequencing data analysis using bioinformatics tools are more accessible than ever. The sequencing output files (compressed FASTQ files) are the input for secondary analysis. Reads are aligned to an annotated reference genome, and those aligning to exons, genes and splice junctions are counted. Variants including cSNPs and indels can be called after the alignment step. The final steps are data visualization and interpretation, consisting of calculating gene-and transcript-expression and reporting differential expression. Depending on the analysis tools used, novel splice junctions and isoforms, rare transcript discovery and allele-specific expression can be examined within the same RNA-Seq dataset, beyond what is achievable with microarrays.

Organizer

Co-Organisers



REGISTRATION FORM

Seminar

SCIENTIFIC SEMINAR ON APPLICATION OF RNA- & RAD-TAG
SEQUENCING IN AGRICULTURE

Name (Prof./Assoc. Prof./Dr./Mr./Mrs./Ms.):	
Organization:	
Address:	
E-mail:	Tel:

Date: _____

Signature: _____

**As places are limited, early registration is recommended*

Organizer



Co-Organisers

illumina



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