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The influence of genomic contamination on the performance of illumina strand-specific RNA-Seq

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The strand-specific RNA-Seq has been broadly utilized for comprehensive transcriptome surveys, including transcripts orientation and information, which is inaccessible when using conventional RNA-Seq. To retain the strand-specificity, it is highly recommended to remove genomic DNA from the RNA template. Despite current availability of improved DNase treatment protocols, removal of genomic DNA remains a technical challenge. This step in sample preparation is particularly difficult when dealing with samples with extremely low RNA concentrations. Moreover, DNase digestion demands additional purification step, which leads to loss of up to 30% of RNA template. Therefore a question arises whether an additional step of genomic DNA removal is essential. In order to address the impact of genomic DNA contamination on strand-specificity resolution, we used a tobacco model *N. benthamiana* that was depleted in ribonuclease J and essential for chloroplast RNA surveillance. Depletion of this RNase J results in massive accumulation of chloroplast antisense RNA. In this talk, I am going to present results of our analysis of changes in expression levels of reference sense and anti-sense transcripts in relation to degree of the RNA sample contamination with genomic DNA.

Biography

Caroline Janitz is a Manager of the Next-Generation Sequencing Facility at Western Sydney University, Australia. Along with supervising her team, she is responsible for both the development and implementation of technological improvements in the NGS pipeline. She has completed her PhD in Molecular Genetics from the Freie Universität Berlin, Germany, under the supervision of Prof. Hans Lehrach, Director of the Max Planck Institute for Molecular Genetics in Berlin. Her PhD thesis focused on "An investigation of the molecular mechanism of renal damage in the course of rat hypertension using laser micro dissection and Affymetrix gene expression profiling".

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