ABA/ASB Omics 2018

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Biophysics is the study of biological systems and processes through physics-based methods or using ideas based on physical principals (Zhou 2011). Perhaps, it is surprising to the reader that a joint meeting of the Asian Biophysics Association/Australian Society for Biophysics would contain a session dedicated to ‘omics technologies, given that the latter is commonly believed to provide researchers with a top-level view of their biological system, while biophysics approaches tend to focus on very specific molecular details. However, as we learned in the Omics session on the morning of Monday 3rd of December 2018, Omics research is highly complementary to modern biophysics, with researchers from both fields working together on projects to uncover the mechanisms driving complex biological systems.

The first session was opened by Associate Investigator Dr. Meng-Qiu Dong from the National Institute of Biological Sciences in Beijing. Chemical crosslinking and mass-spectrometry (CXMS) has recently enjoyed a resurgence in popularity as it has proved itself a complementary technique for the analysis of large protein complexes by cryogenic electron microscopy (Cryo-EM). Dr. Dong has led the development of new cross-linkers and software to improve the CXMS workflow for Cryo-EM-based structural studies (Ding et al. 2016; Gong et al. 2017; Zhang et al. 2018). In her talk today she presented exciting new work on the development of bi-functional arginine-arginine and arginine-lysine specific cross-linkers for CXMS, demonstrating their efficacy on multi-protein complexes of up to 150 kDa. These novel

cross-linkers will be extremely useful for structural studies since until now CXMS has been restricted to mostly lysine-specific cross-linkers.

The next speaker was Prof. David James from the Charles Perkins Centre at the University of Sydney. He leads the Metabolic Systems Biology Laboratory and is known internationally for diabetes metabolism research and method development for proteomics sample preparation (Fazakerley et al. 2018; Humphrey et al. 2018; Parker et al. 2019). Prof. James used his talk to discuss the future of omics technologies in the care of patients with metabolic diseases. Demonstrating his concepts using a panel of drosophila and mouse strains, he showed an enormous complexity in the response of different genomes to diet. It is the hope of Prof. James that by combining these tools with longitudinal analysis of humans, we will be able to discover new biomarkers that will be used to personalise treatments and design preventative dietary strategies tailored to each individual.

Continuing our exploration of different omics technologies, Dr. Kristin Brown from the Peter MacCallum Cancer Centre discussed the use of metabolomics to investigate the ways in which cancer cell metabolism is influenced by different stimuli, presenting her recently published and new unpublished work on the oncogenic transcriptional co-activator YAP (Cox et al. 2016, 2018). Revealing a new mechanism of crosstalk between important signalling pathways, Dr. Brown showed how YAP overexpression, which is common in human cancers, induces de novo lipogenesis, and that inhibition of de novo lipogenesis blocks YAP driven uncontrolled proliferation.

Following a brief break for morning tea, we heard from Dr. Traude Beilharz who leads the RNA Systems Biology Laboratory at the Monash University Biomedicine Discovery Institute. Dr. Beilharz discussed how she is using custom RNA-seq, proteomics and metabolomics as well as novel software and methodological approaches to understand how mRNA metabolism is regulated (Archer et al. 2016; Harrison et al. 2019; Shirokikh et al. 2017). Presenting unpublished work, Dr. Beilharz described how 3'-UTR length is

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controlled by both the rate of mRNA transcription and availability of the cleavage and polyadenylation machinery.

Dr. Nichollas Scott, an expert in glycomics (Cain et al. 2019; Harding et al. 2019) and proteomics approaches from Doherty Institute followed, presenting a new unpublished study describing tissue-specific protein:protein interactions across different tissues (Skinnider et al. 2018). In that study, Dr. Scott used a quantitative proteomics approach combining correlation profiling with stable isotope labelling of mice and mass-spectrometry to map global protein:protein interactions across seven mouse tissues. Unlike other approaches, the method used by Dr. Scott does not rely on affinity enrichment of detergent solubilised lysates, therefore, should be more representative of the interactome in vivo.

Wrapping up the Omics session for 2018, we heard from Dr. Dezeræ Cox from laboratory of Associate Prof. Danny Hatters, based in the Bio21 Institute at the University of Melbourne. Dr. Cox described her work utilising the published fluorogenic thiol-binding dye (TPE-MI), which can be used to capture a snapshot of the balance between folded and unfolded proteins in living cells (Chen et al. 2017). Dr. Cox outlined the developments and application of the TPE-MI probe for mass-spectrometry-based proteomics experiments, with a goal of being able to measure proteome foldedness following different types of protein folding stress.

Compliance with ethical standards

Conflict of interest David A. Stroud declares that he has no conflict of interest.

Ethical approval This article does not contain any studies with human participants or animals performed by the author.

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