Meeting Report: 34th Annual Conference of the Malaysian Society for Biochemistry and Molecular Biology & 3rd Asean Biochemistry Conference

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The 34th Annual Conference of the Malaysian Society for Biochemistry and Molecular Biology was held on the 7th and 8th October 2009 at the Prince Hotel, Kuala Lumpur, Malaysia. This meeting report describes the aims of the meeting, the main topics of the presentations, and the highlights of the conference. The meeting was open to presentations on various topics pertaining to biochemistry and molecular biology. The topics concentrated on Agricultural Biochemistry and Biotechnology, Genomics and Proteomics, Protein Structure, Function and Regulation, Gene Expression and Regulation, Biochemistry and Molecular Biology of Diseases, Environmental Biochemistry and Biotechnology, Nutrition and Clinical Biochemistry, Natural Products and Drug Discovery, Molecular Systematics, Bioinformatics, Plant Molecular Biology, Pharmacogenomics and a special session on Carbohydrate Biochemistry under the umbrella programme of the 3rd Asean Biochemistry Conference. Over the course of the conference, there were five plenary presentations, seven invited speakers, twenty five oral presentations as well as eighty five posters presented covering the topics listed above.

Mimicking nature's approach in creating devices with similar functional complexity is one of the ultimate goals of scientists and engineers [1]. Ille Gebeshuber described biomimetics as the knowledge transfer from biology to technology. She elaborated on the Biomimicry Innovation Method, a highly successful biomimetics design approach to identify nature's best practices for novel approaches to address global challenges. An example of an investigation on the best practices formed is the integrity of the cell that depends on its ability to separate inside from outside and yet at the same time allows massive transport of matter in and out the cell. Nature has elegantly met this challenge by developing membranes in the form of lipid bilayers in which specialized and highly efficient transport proteins are incorporated [2]. Thus, can we mimic biological membranes and create membrane-based sensor and/or separation devices? Gebeschuber proposed that to accelerate scientific and technological breakthroughs in biomimicry, we should aim at having a context of knowledge that involves a pipeline from "know-why" to "know-how" to "know-what".

Copy-number variation (CNV) – the presence of additional or missing segments of chromosomes in some individuals – has been found to be abundant in humans and adds another dimension of variation to the genome. The first CNVs in humans were discovered in the early 1900s and found to be widespread throughout all populations, with a range of striking but largely benign phenotypic consequences [3]. Copy-number variants have already been associated with some diseases and disease susceptibilities and are proving to be as if not more significant as sequence polymorphisms in this respect. Paul Dear introduced the intricacies of copy-number variation and the relationship to single nucleotide polymorphisms (SNPs). With CNVs added to SNPs information, the human genome has ceased to exist as a defined entity and is instead becoming a fluid continuum. Although earlier estimates predicted 0.1–1% of sequence differences that distinguish one human from another, current CNV analysis has demonstrated that 5% of the genome is already known to display CNV [4]. How does this newly appreciated variability affect our view of the genome and the search for the genomic basis of human variation and disease? Most CNVs are deemed to have either no phenotypic consequences or only subtle or benign ones. If they had significant effects, the deleterious alleles would have been largely selected out of the population or would be defined as mutations and found in a small number of heterozygotes and in an even smaller number of affected individuals [3]. CNVs appear to be comparable to the majority of SNPs in that selective pressure has weeded out most CNVs other than those that are benign or subtle in their effects or that confer a mixture of beneficial and harmful effects depending on their genomic and environmental context.

Glucansucrases are produced principally by *Leuconostoc mesenteroides* and oral *Streptococcus* species, but also by the lactic acid bacteria (Lactococci, Lactobacilli). They catalyse the synthesis of high molecular weight D-glucose polymers, named glucans, from sucrose. In the presence of efficient acceptors, they catalyse the synthesis of low molecular weight oligosaccharides [5]. Bauke Dijkstra, an eminent industrial enzymologist from the University of Groningen, The Netherlands, talked about the structural and functional

characterization of *Lactobacillus reuteri* glucansucrase. His work involved the crystallization and X-ray crystallography of the enzyme, both in its native state as well as in complex with sucrose and maltose. Van Hijum *et al.* [6] had previously reviewed the glucansucrases of the glycoside hydolase family 70 whereby the enzyme has an α-amylase-like barrel catalytic domain that is circularly permutated, different from that of the catalytic domain of other members of the α-amylase family. The functional analysis of the structures analysed by Dijkstra's group also demonstrated that a number of other characteristics common to α-amylases did not hold true for the glucansucrase and concluded that large conformational changes might play an important role in modulating linkage specificity.

Keeping to the theme of Carbohydrate Biochemistry, Marc van der Maarel delivered a plenary on the exploration and exploitation of starch-active glucanotransferases. Starch is a major storage product of many economically important crops such as wheat, rice, maize, tapioca, and potato. A large-scale starch processing industry has emerged in the last century. In the past decades, we have seen a shift from the acid hydrolysis of starch to the use of starch-converting enzymes in the production of maltodextrin, modified starches, or glucose and fructose syrups. Currently, these enzymes comprise about 30% of the world's enzyme production [7]. Van der Maarel provided a comprehensive review of what is currently known on the biochemistry of amylases and how they react on starch as well as their potential industrial applications.

The fifth plenary speaker presented work in progress at the Universiti Kebangsaan Malaysia on understanding the host response to infection by the tropical pathogen *Burkholderia pseudomallei.* Sheila Nathan began by reviewing the current status of host-pathogen interaction studies using various models. One of the host models discussed at length was the nematode *Caenorhabditis elegans.* As an experimental system, *C. elegans* offers a unique opportunity to interrogate in vivo the genetic and molecular functions of human disease-related genes [8]. The *C. elegans* model has several distinct advantages, including a completely sequenced genome that shares extensive homology with that of mammals, ease of cultivation and storage, a relatively short lifespan and techniques for generating null and transgenic animals. However, the ability to conduct unbiased forward and reverse genetic screens in *C. elegans* remains one of the most powerful experimental paradigms for discovering the biochemical pathways underlying human disease phenotypes. The identification of these pathways leads to a better understanding of the molecular interactions that perturb cellular physiology, and forms the foundation for designing mechanism-based therapies. Sheila Nathan discussed a genome-wide analysis of *C. elegans* infected by *B. pseudomallei* that demonstrated an enrichment of genes including those in the metabolism functional category and defense-related genes. Contrary to this, genes involved in the aging process, lipid metabolism and response to oxidative stress were robustly repressed. These genes were distinctly different from those previously reported for other bacterial pathogens and Nathan's group have gone on to propose a novel mechanism by which *B. pseudomallei* suppresses the host immune defense via targeting the intestinal GATA transcription factor ELT-2 and the subsequent down regulation of ELT-2 targets.

M.S. Kanthimathi, the first of the invited speakers described the ability of extracts of the woody herbaceous plant *Cyrtandra cupulata* (Gesneriaceae) to suppress oxidative and carcinogenic properties. In addition, the plants were also shown to possess wound healing, enhancement of lipogenesis, anti-inflammatory and contraceptive properties. Tey Beng Ti talked about life and death in an animal cell bioreactor emphasizing on the occurrence of apoptosis, a highly regulated and active cell death mechanism. He also discussed the progress in the development of solutions to improve cell culture productivity and robustness of industrially important cell lines through modulation of apoptosis. Ni Nyoman Tri Puspaningsih (Airlangga University, Indonesia) spoke on the expression system of bifunctional Arabinofuranosidase/ Xylosidase from *Geobacillus thermoleovorans* IT-08. The biochemical characteristics of the recombinant enzylme were described in detail and the enzyme shows promising potential. Rosli Illias followed this presentation by describing the improvement of CGTase product specificity by protein engineering. Engineering was aided by rational design and the availability of 3D modeling structures and succeeded in increasing the Cyclodextrin production ratio. Two further talks during the 3rd Asean Biochemistry Conference session by Ganden Supriyanto and Osman Hassan described the photometric cholesterol biosensor as well as the characteristics and digestability of "empty-fruit-bunches" following pretreatment, respectively. EFB pretreated with glycerol was shown to produce higher yield of glucose when compared to EFB treated with ethanol and alkali solution. The final invited speaker was Lim Yang Mooi (University Tuanku Abdul Rahman) whose work on phytochemicals and their role in cell signaling regulation proposed that the anti-inflammatory properties of maslinic acid could be attributed to the inhibition of COX-2 expression through the down regulation of NFκB and AP-1 activation via the suppression of upstream Protein Kinase C phosphorylation.

A total of fourteen oral presentations were made over the 4 scientific sessions. The first session was focused on data generated using 'omics and bioinformatics technologies as well as studies on the effects of natural compounds on cells. Of particular mention is the pattern matching algorithm NASSAM that uses graph theory to efficiently search databases of nucleic acid structures to locate known or novel base triple interactions in RNA structures (Mohd Firdaus Raih, Universiti Kebangsaan

Malaysia - UKM). Covering the theme of Carbohydrases and Biomass Utilization were several presentations on a number of fungal derived enzymes with industrial potential, particularly glucanase (Farah Diba Abu Bakar, UKM) and cellulose (Fadzillah Kamaluddin, UKM) for processing of palm oil wastes. The final scientific session was divided into genomics-based sequence analysis as well as biochemical characterization of phytochemicals.

References

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