

1st IFRcC/SIGn Winter School on Advanced Immunology

Osaka University Immunology Frontier Research Center (IFReC) and the Singapore Immunology Network (SIGn) provide a new educational and networking venue for young researchers interested in immunologic research. In January 2012, they will organize a four-day intensive series of immunology lectures for Ph.D. students and recent post-doctoral fellows. The first Winter School will be held at the Westin Awaji Island Resort & Conference Center in Awaji City, Japan and will alternate annually between Japan and Singapore in the following years.

The preliminary program of the Winter School consists of 14 sessions, including Microbial Infection, Innate Receptors and Innate Cells, Lymphocyte Development, Cellular Trafficking, Lymphocyte Memory, Differentiation of Effector T cells, Nod-like Receptors in Immunity and Disease, Autoimmunity, Mucosal Immunity, Allergy, DC and Antigen Presentation, Vaccination and Immunotherapy, Lymphocyte Signaling and Antibody Therapy.

The ultimate goal for the newly launched school is to achieve a major academic focal point in the field of immunology. The organizers aim to provide opportunities for both international and domestic students to explore their own interests in immunology, and to foster a new generation of scientists who will lead and challenge the boundaries of immunological science in the future. Ph.D. students and post doctoral fellows (no more than three years since obtaining the Ph.D. degree) are eligible to participate and are invited to apply. The organizing committee will select 40 participants who will then be required to present a poster and short oral presentations. Accommodation and travel expenses will be covered by the school.

More information and application documents are available on the website: <http://ifrec-sign-winterschool.org>.

2nd Congress of Biochemistry and Cell Biology in Cracow

The Polish Cell Biology Society and the Polish Biochemical Society invite you to participate in the Second

Congress of Biochemistry and Cell Biology that will be held on September 5-9 2011 in Cracow, Poland. The event is organized in collaboration with the Jagiellonian University and the University of Agriculture in Cracow.

Sessions held during the Congress will cover a wide variety of topics, including molecular oncology, gene therapy, biogenesis and functions of small RNAs, biochemistry of reproduction, molecular and cellular neurobiology, immune response: from cell trafficking to enzymatic regulation, stem cells in tissue engineering, bioenergetics and advances in plant biochemistry. Among the invited speakers will be leading specialists from Polish and foreign institutions.

The first joint Congress of the Polish Biochemical Society and the Polish Cell Biology Society, held in Olsztyn in 2008, had an impressive scientific program: 60 lectures, 51 oral presentations and 494 posters were presented. It attracted over 900 participants. The Organizing Committee expects that the Second Congress will attract an even larger audience. Apart from the scientific sessions, general meetings of the Polish Biochemical Society and the Polish Cell Biology Society members will be also held.

A complete list of invited speakers, the Congress program and the registration form are available on the website: <http://kbbk2011.pl>.

6th Annual Meeting *Biofuels 2011*

In October 2011, specialists from the biofuel industry and research will meet in Amsterdam to participate in the 6th Annual Meeting *Biofuels 2011– Capitalise on the Global Biofuels Opportunity*. The meeting is organized by the World Refining Association (WRA).

Biofuels 2011 conference is dedicated to overcoming the key issues of sustainability, commercialization and supply chain traceability requirements for global biofuels. The conference will reflect a biofuels market which is undergoing a revival following the legislative developments, new projects getting underway around the world, and significant corporate investments being made.

The organizers list several issues which are going to be discussed during *Biofuels 2011* conference, including

new projects within the bioethanol and biodiesel sectors, infrastructure and production related developments, meeting sustainability criteria and certification challenges, practical suggestions for meeting the EU Renewable Energy directive targets, individual country programs for meeting government requirements and partnership opportunities between the public and private sectors. Robert Gmyrek, Director of the Biofuels Department at the PKN Orlen S.A., is one of the conference keynote speakers. At the closing of the first day of *Biofuels 2011*, the World Refining Association will announce winners of Biofuels awards in three categories: "Bioethanol corporation of the year", "Biodiesel corporation of the year" and "Biofuels technology of the year".

For detailed information about this event visit the meeting's website: <http://www.wraconferences.com/2/4/articles/277.php>.

Conferences on personalized medicine in 2012

Two important congresses on personalized medicine will be held at the beginning of 2012. In January "The fourth Personalized Medicine World Conference (PMWC) 2012" will take place in the United States and will be followed by the Italian "Up Close and Personalized, International Congress on Personalized Medicine" in February.

The PMWC is a fully-integrated conference on Personalized Medicine which brings together all aspects of business, government, healthcare-delivery, research and technology into one information-rich, two-day conference. Annually it has over 1000 attendees from academia, healthcare and industry. It provides an exhibition opportunity for companies, which ranges from the emerging to the public, to promote products and services. Interestingly, as a side event, a PMWC's "Most Promising Company" Competition is going to be held, with the aim to award the most unique and innovative privately-owned companies from the field of therapeutics, diagnostics and information technology.

The second event, "Up Close and Personalized, International Congress on Personalized Medicine", will be particularly focused on the examination of the essential clinical, genomic, proteomic, metabolomic, pharmacogenomic and biomarker data necessary to predict, prevent and treat major medical conditions concerning metabolism (diabetes and obesity), cardiovascular complications and cancer. Importantly, one of the key the-

mes will be to explore bio-informatic tools, algorithms, artificial intelligence techniques, decision support systems and other new platforms for predicting clinical outcome and better adjustment of the treatment to the individual patient.

The registration for both events is already open. More details are available on the websites: <http://www.pmwc2012.com> and <http://www.upcp.org>.

Genome-wide atlas of transcription during maize development

A team of scientists from the University of Wisconsin-Madison and Michigan State University have developed a comprehensive atlas of global transcription profiles across the developmental stages and plant organs in maize. The 'corn atlas' was published in the May issue of *The Plant Journal*. The study described in the paper serves as a valuable resource for gene discovery and functional characterization of maize.

To understand how the underlying genome sequence results in specific plant phenotypes, information on the temporal and spatial transcription patterns of genes is crucial. In order to elucidate this issue, researchers grew more than 600 corn plants at the UW-Madison West Madison Agricultural Research Station during summer 2008 and collected, on a daily basis, samples for gene expression profiling. They profiled transcript levels using RNA samples from 60 diverse tissues representing 11 major organ systems and varying developmental stages of the maize plant. The organ systems included germinating seed, root, whole seedling, stem and shoot apical meristem, internodes, cob, tassel and anthers, silk, leaf, husk and seed. The harvested tissues were immediately frozen in liquid nitrogen and, after RNA extraction, gene expression profiling was performed using NimbleGen platform. Clustering of maize tissues based on global gene expression profiles resulted in the formation of groups of biologically related tissues. Interestingly, 44.5% of the probe sets were expressed in all tissues, indicating a substantial overlap of gene expression among plant organs.

"The atlas is basically the whole landscape of the plant's transcriptome. It contains information about all of the genes in corn – where they're expressed and when they're expressed", says Rajandeep Sekhon, the

study's co-lead author, a research associate in the Great Lakes Bioenergy Research Center at UW-Madison. Such atlases, which already exist for rice and *Arabidopsis*, have proven useful in the studies on key genes involved in important biological processes.

References

Sekhon R.S. et al. (2011) *Genome-wide atlas of transcription during maize development*. Plant J. 2011 Feb 7. doi: 10.1111/j.1365-313X.2011.04527.x. [Epub ahead of print] University of Wisconsin-Madison website: <http://www.news.wisc.edu>.

p53 inactivation may lead to increased glucose consumption in cancer cells

In March 2011, *Nature Cell Biology* published an interesting article on glucose metabolism in p53-deficient cancer cells. In the *Letters* section, Jiang and co-workers presented their work entitled "p53 regulates biosynthesis through direct inactivation of glucose-6-phosphate dehydrogenase".

That study identified an important regulatory role of the tumor suppressor p53, which is the most frequently mutated gene in human tumors. Jiang and co-workers showed that p53 regulates glucose-6-phosphate dehydrogenase (G6PD), the first and rate-limiting enzyme of the pentose phosphate pathway (PPP). In a normal cell, p53 suppresses glucose consumption, NADPH production and biosynthesis through the PPP. Through this regulation, p53 strictly controls the metabolic pathways that are critical for both glucose catabolism and biosynthesis. Jiang and co-workers investigated the after-effect of p53 loss in HCT116 human colon cancer cell line. They demonstrated enhancement of the oxidative PPP flux and a strong increase in glucose consumption in p53^{-/-} cells. It has been previously described that cancer cells consume large quantities of glucose and primarily use glycolysis for ATP production, even in the presence of adequate oxygen. This metabolic signature called the Warburg effect enables cancer cells to direct glucose to biosynthesis, supporting their rapid growth and proliferation. The presented study elucidates the little known genetic background of the Warburg effect.

Reference

Jiang P., Du W., Wang X., Mancuso A., Gao X., Wu M., Yang X. (2011) *p53 regulates biosynthesis through direct inactivation of glucose-6-phosphate dehydrogenase*. Nat. Cell Biol. 13(3): 310-316; Epub 2011 Feb 20.

Woodland strawberry genome sequenced

The complete genome of woodland strawberry was recently published in *Nature Genetics* by a team of 71 scientists. The report presents the genome sequence of the diploid strawberry *Fragaria vesca* ssp. *vesca* accession Hawaii 4 (National Clonal Germplasm Repository accession # PI551572). The sequence was achieved using exclusively short-read technologies and was assembled without a physical map or reference genome.

According to the report, *F. vesca* has the smallest sequenced plant genome, even smaller than this of *Arabidopsis*. It consists of 240 Mb, while the gene prediction modeling identified 34 809 genes. Interestingly, genes that are critical to valuable agricultural traits, such as *inter alia* flavor, nutritional value and flowering time have been defined.

Fragaria vesca shares substantial sequence identity with the cultivated strawberry (*Fragaria* × *ananassa*) and other economically important rosaceous plants such as apple, rose, peach and cherry. Like *Arabidopsis*, *F. vesca* is rapidly transformable, grows with a small footprint and has a short generation time from seed to seed, which are all characteristics that make it particularly useful for functional genomics research. Deciphering the woodland strawberry genome is the first step to gain an insight into economically important traits of other fruits in the Rosaceae family, especially the disease resistance, developmental control, fruit flavor and quality.

Reference

Shualey V. et al. (2011) *The genome of woodland strawberry (Fragaria vesca)*. Nat. Genet. 43(2): 109-116; Epub 2010 Dec 26.