MAŁOPOLSKA CENTRE OF BIOTECHNOLOGY

Fundacja Klaster LifeScience Kraków

US Departament of Agriculture
Małopolskie Centrum Biotechnologii
Klaster LifeScience Kraków

invite you to a free seminar in the series

Think.GIN
global innovative networked

Monday, March 16th 2015, h.15.00-18.00,
Park LifeScience, ul. Bobrzyńskiego 14. Kraków,

You will have an opportunity to learn and discuss about:

Genetically modified organisms (GMO) - the current status of GMO with a worldwide view: the technology and politics around it.

Talk #1: Precise Genome Editing using Sequence-Specific Nucleases.

Presented by: **Qi, Yiping Ph.D** (East Carolina University, NC, USA)

Talk #2: Polish biotechnology 2015 - success, perspective, legislation.

Presented by: **Prof. Tomasz Twardowski** (Institute of Bioorganic Chemistry, Polish Academy of Sciences).

Registration: https://thinkgin2015ls.konfeo.com/
(Number of places limited to 100)

How to get to Lifescience Park:
By the public transportation – stop: Chmieleniec
BUS: no. 194 (Czerwone Maki - Krowodrza Górka)
TRAM: no. 11, 18, 23, 52
By car: no access by car to the building, limited parking places in surrounding.

Abstract for Talk #1.

Title: Precise Genome Editing using Sequence-Specific Nucleases

Precise genome editing has the potential to revolutionize medicine and agriculture. Sequence specific nucleases (SSNs) are critical components for precision genome editing because these enzymes are customizable “DNA scissors” that can cut DNA in a sequence specific manner. Resultant DNA breaks caused by SSNs subsequently activate DNA repair mechanisms through one of two pathways: non-homologous end-joining (NHEJ) or homologous recombination (HR). The NHEJ pathway is error-prone and can thus introduce new mutations to targeted DNA sites. The HR pathway utilizes a homologous DNA template for repair and allows precise DNA modifications such as gene replacement or insertion. Thus, SSNs can help mutate, correct or replace any sequence in almost any genome. Historically, it has been very difficult to engineer SSNs. However, recent technology advancement in the field has simplified the engineering process through the development of easily engineered SSNs and RNA guided SSNs. These are Zinc Finger Nucleases (ZFNs), Transcription Activator-like Effector Nucleases (TALENs) and the CRISPR/CAS9 nuclease system. All three classes of SSNs are promising tools for basic and applied research and will undoubtedly impact everything from the curing of genetic diseases to the making of next-generation genetically modified (GM) crops. This talk will present some applications and recent developments of these exciting genome editing tools in basic research and biotechnology.

MAŁOPOLSKA CENTRE OF BIOTECHNOLOGY

Fundacja Klaster LifeScience Kraków

US Departament of Agriculture
Małopolskie Centrum Biotechnologii
Klaster LifeScience Kraków

invite you to a free seminar in the series

Think.GIN
global innovative networked

Tuesday, March 17th 2015, h.10.00 -12.00,
Malopolska Center of Biotechnology, ul. Gronostajowa 7A, Kraków

You will have opportunity to learn and discuss about:

The technologies that potentially will revolutionize agriculture and medicine - how they are used in academia and industry.

Talk #1: Understanding maize response to herbicide stress - can we improve its growth and yield?

Presented by: **Dr Agata Tyczewska** (Institute of Bioorganic Chemistry, Polish Academy of Sciences)

Talk #2: Developing Tools for Plant Genome Editing and Gene Regulation with engineered DNA binding proteins.

Presented by: **Qi, Yiping Ph.D** (East Carolina University, NC, USA)

Registration: https://thinkgin2015mcb.konfeo.com
(Number of places is limited to 20)

How to get to MCB:
By the public transportation – stop: Ruczaj
BUS: no. 194 (Czerwone Maki - Krowodrza Górka)
TRAM: no. 11, 18, 23, 52
By car: there are parking lots available at III Campus UJ

Abstract for Talk #2.
Title: Developing Tools for Plant Genome Editing and Gene Regulation with engineered DNA binding proteins

Recent advances in genome editing tools have promised a bright future for plant research and biotechnology. These tools are based on customizable site-specific nucleases (SSNs), such as Zinc Finger Nucleases (ZFNs), TAL Effector Nucleases (TALENs) and the CRISPR-Cas9 system. All these SSNs can be engineered for recognizing specific DNA sequences, and this feature allows them to be repurposed for engineering artificial transcription factors. We have recently developed two toolkits for genome editing and gene regulation in plants. The first toolkit enables epitope or florescent tagging of endogenous plant genes, a long sought-after idea not feasible in the past. The second toolkit allows assembly of a multiplexed CRISPR-Cas9 system for genome editing and transcriptional activation or repression in plants. By working on plant species such as Arabidopsis, tobacco and rice, we have demonstrated multifaceted applications of these toolkits in reverse genetics and synthetic biology. We believe these new tools will contribute to future breakthroughs in basic research and agriculture biotechnology.