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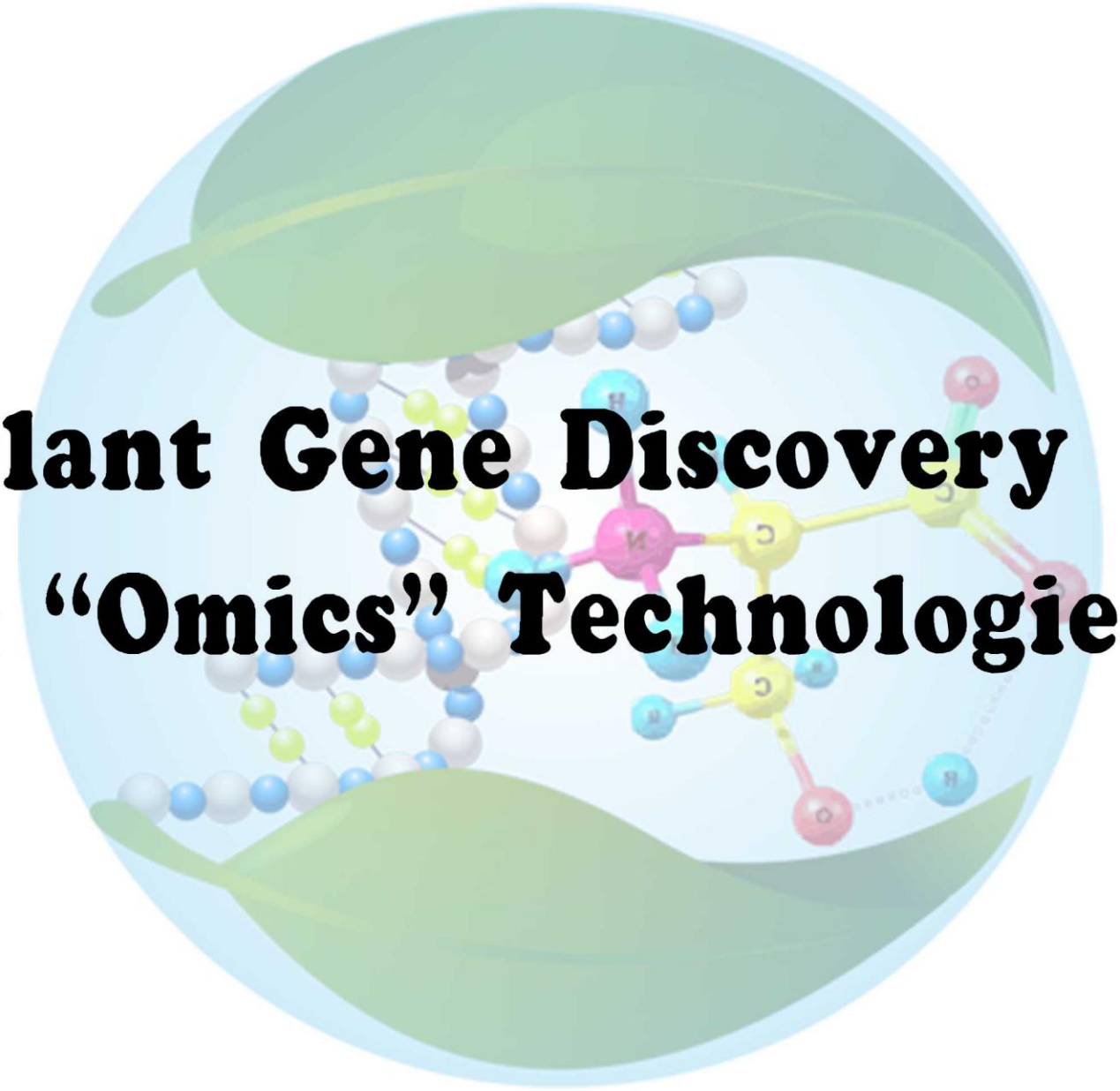

Plant Gene Discovery & "Omics" Technologies

Programme and Abstracts

Vienna, Austria
17 - 18 February 2014

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Dear Friends, Colleagues!

Welcome to the International Conference *"*Plant Gene Discovery & "Omics" Technologies*"*!

Welcome to Vienna!

Gene Discovery and "Omics" Technologies became the new mantra of modern biology. "Omics" technologies include genomics, transcriptomics, proteomics, metabolomics, phenomics and other "omics". The "-omic-" technologies are high-throughput technologies for non-targeted identification of all gene products (transcripts, proteins, and metabolites) present in a specific biological sample. The powerful modern gene discovery and "omics" technologies have opened new avenues in plant biology and crop improvement.

International Conference "Gene Discovery & "Omics" Technologies" will discuss wide range of modern technologies to discover plant gene, its function and gene products.

Vienna is located in the heart of Europe on the banks of the Danube River, and considered as one of the most important economic, cultural and touristic large cities of central Europe. Apart from providing top science, the Conference will capture the spirit of the city thanks to the central location of the venue offering a multitude of cultural events.

International Conference "**Plant Gene Discovery & "Omics" Technologies**" **to be held in Vienna on February 17-18 th, 2014** will provide leading academy and industry scientists a platform to communicate recent advances in Plant Gene Discovery & "Omics" Technologiesand an opportunity to establish multilateral collaborations.

Prof. Klaus Palme, Chair of the International Organizing Committee

Prof. Alisher Touraev, President of VISCEA, Chair of Local Organizing Committee

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N 21. Development of a TILLING Platform for Grass Pea, Lathyrus Sativus

A. Sen [1, 2], P. Emmrich [3], O. Huynh [1], F. Robson [3], M. Chatterjee [4], C. Martin [3], T. Wang [3], B. Till [1]

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Grass pea (Lathyrus sativus L.; 2n = 14) is an annual legume which belongs to the family of Leguminosae, subfamily of Papilionoideae. It is the only species widely cultivated in the genus of Lathyrus as a human food and an animal feed especially in Africa and Asia. Induced mutations have been widely used to generate a large number of functional variations in many crops for both breeding and functional genomics. Chemical mutagens such as EMS cause mainly point mutations, and are thus ideal for producing missense and nonsense mutations to alter gene function. The combination of induced mutations with high throughput discovery approaches known as TILLING is an efficient reverse-genetic tool for recovering desired alleles within a population. We are developing a TILLING platform for grass pea using EMS mutagenesis. A large M2 population has been produced for forward and reverse-genetic screening and mutation discovery optimized in a pilot study.

N 22. Isolation of Ribosomal Protein S6 Kinase Cdna of *Triticum Aestivum*

B. Smailov, A. Mursalimov, A. Bissenbaev

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The ribosomal protein S6 kinase (S6K) represents well studied effector of TOR kinase in eukaryotes and plays role in cell growth and proliferation. In the present work wheat TaS6K cDNA was identified and similarity of its product to mammalian and Arabidopsis homologues was shown by mass-spectrometric and immunological analyses. Kinase domain of TaS6K contains activation loop, hydrophobic and turn motives characteristic of S6 kinases. It was shown that Ser-466 in C-terminal HM-motif of TaS6K is a putative site of phosphorylation by T. aestivum TOR kinase. Also a higher level of activated TaS6K in wheat aleurone cells treated with gibberellic acid compared to abscisic acid was observed as an indication of possible participation of TOR signaling pathway in gibberellin-activated processes during germination of wheat grain.