



NACIONALNI INŠTITUT ZA BIOLOGIJO

Večna pot 111, SI-1000 Ljubljana

National Institute of Biology kindly invites you to attend the lecture:

"Comparative and functional genomics of phytoplasmas - emerging plant pathogens "

**by Martina Šeruga Musić, PhD, University of Zagreb, Faculty of Science,
Department of Biology
(Croatia)**

**The lecture will take place on Thursday, the 2nd April 2015,
at 12:00 in the Lecture Hall B5
of the Biological Centre, Večna pot 111, Ljubljana.**

Abstract:

Phytoplasmas (genus '*Candidatus* Phytoplasma') belong to a group wall-less bacteria from the class *Mollicutes* along with mycoplasmas, spiroplasmas and achleoplasmas. These intracellular pathogens have a unique life-style successfully manipulating their plant and insect hosts and needing both hosts for survival and dispersal in nature. Phytoplasmas affect numerous plant species worldwide causing significant economic losses in agriculture, viticulture and fruit production. They induce dramatic perturbations in plant development; however, the understanding of all mechanisms underlying phytoplasma pathogenicity is far from complete. Phytoplasma axenic cultivation is still unsuccessful probably due to their small genomes (680-1600 kbp) devoid of many genes thought to be essential for cellular life-forms. Nevertheless, four phytoplasma genomes have been completely sequenced and annotated with several genome drafts also available. Comparative analyses of phytoplasma genomes revealed some unique features of these bacteria that evolved through reductive evolution due to their parasitism in a nutrient-rich environment. Although extremely reduced, the genomes are repeat-rich and some of the repeats termed potential mobile units (PMUs) have characteristics of replicative transposones. PMU1 of 20 kb is the largest most complete repeat among the PMUs in the genome of Aster Yellows phytoplasma strain Witches' Broom. It contains 21 genes encoding DNA replication and predicted membrane-targeted proteins and exists as linear chromosomal and circular extrachromosomal element with enhanced expression in insect vectors compared with plant hosts. Together with plasmids, PMUs probably contribute to phytoplasma genome size variations and high plasticity as well as to adaptation to diverse hosts. Recent breakthroughs in phytoplasma functional genomics are findings on the secreted effector molecules (SAP11, SAP54) and virulence factors (TENGU) proved for '*Ca. P. asteris*' subclade members. The pathogen effectors generally influence plant development, signalling pathways and also modify plant-insect interactions. Furthermore, genomic findings paved the way to identifying phytoplasma species-specific variable genes, such as *vmp* (variable-membrane protein) genes, that can be useful in epidemiological and pathogenicity studies through genotyping of phytoplasma strains by Multilocus Sequence Typing strategies.

Kindly invited!