

TITLE: Structural insights into the infection cycle of plant viruses

Summary: RNA viruses have very compact genomes. They usually overcome this size limitation by expressing proteins with multiple functions. Typical representatives of such viruses are from the genus Potyvirus, the most abundant group of pathogenic RNA viruses in plants, whose members have major economic impacts on crop yields worldwide (Scholthof et al., DOI: 10.1111/J.1364-3703.2011.00752.X). We determined the cryo-EM structure of the potyvirus potato virus Y (PVY) and corresponding virus-like particles (Kežar et al., DOI: 10.1126/sciadv.aaw3808). Here we have shown for the first time how the intrinsic structural plasticity of the only viral structural protein, the coat protein (CP), is important for its ability to perform multiple functions, as it is involved in almost every phase of the viral infection cycle. This is enabled by its structural properties, post-translational modifications and competitive interactions with other viral as well as host components in the infected cell (Ivanov & Mäkinen, <http://dx.doi.org/10.1016/j.coviro.2012.10.001>). We are interested in the structural basis (details) of these complex interactions. We are collaborating with colleagues from the National Institute of Biology (Slovenia, Prof. Dr. Kristina Gruden) and University of Helsinki (Finland, Prof. Dr. Kristiina Mäkinen), who are experts in biology of potyviruses, to combine in planta studies with our integrative structural biology approaches to gain high-resolution insight into the mechanisms of action of viral and hijacked host proteins and their complexes during the viral cycle. We do this by (1) a bottom-up approach by studying individual proteins and their complexes produced in vitro, and by (2) direct purification of protein/protein or protein/RNA complexes from plants formed during the potyviral infection cycle.

Research techniques used: Molecular biology, biochemistry, biophysics, structural biology (NMR, X-ray crystallography, cryo-EM), plant biology, bioinformatics, computational chemistry. All these methodological approaches are combined to provide an integrated structural and mechanistic insight into complex biological systems.

The reason why the topic is innovative: The existence of our planet depends on plants. To find efficient ways to protect them, we need to know the basic molecular mechanisms behind plant diseases. Using state-of-the-art methodological approaches, we are studying complex interaction networks between viral and plant host molecules to build new structural and mechanistic models for the biological molecules and complexes involved in the different phases of the viral infection cycle. This knowledge is necessary to develop new strategies to protect plants from viral diseases. Moreover, since most of these viral proteins contain locally disordered regions, they have a high potential to form polymorphic and architecturally interesting nano-sized complexes (especially in the case of CP (virus-like particles)), which represents a potential for use in biotechnology (vaccine development, drug delivery, etc.) or for the development of hybrid materials with tailored properties.

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