

s8a.m9.p3 Structure of the matrix protein of VSV. M. Gaudier¹, Y. Gaudin² & M. Knossow¹ (1) *L.E.B.S. C.N.R.S. 91198 Gif sur Yvette France* (2) *Laboratoire de Génétique des Virus C.N.R.S. 91198 Gif sur Yvette France*.
Keywords: virus, matrix protein, structure.

The matrix protein of vesicular stomatitis virus (VSV M protein : 229 AA, 26 kDa) acts as a multifunctional protein in the viral cycle. Firstly, it plays a central role in viral assembly and budding ; secondly, it has been shown to inhibit the transcription of the viral genome ; lastly, it is directly involved in some of the VSV cytopathic effect and in virus induced inhibition of transcription of host genes.

Crystals of the M protein were obtained in presence of PEG 2000 monomethyl-ether. They diffract at least to a resolution of 1.96 Å and a full diffraction data set has been measured on the F.I.P. beamline of the ESRF. The structure was determined by SIRAS using the program SHARP ; a single isomorphous derivative containing methyl-mercuric chloride was sufficient. A model of the protein was built after solvent flipping in SOLOMON (CCP4 suite). This model is being refined.

We will describe the structure obtained and define the functional sites of M, based on the known locations of mutations that affect the functions of this protein.

s8a.m9.p4 Crystal structure of two pathogenesis-related proteins of class PR10 from yellow lupine. J. Biesiadka, G. Bujacz, M. M. Sikorski, M. Jaskolski, A. B. Legocki. *Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland*.
Keywords: lupine protein, allergens, X-ray structure.

Proteins of PR10 class are abundant in roots of yellow lupine (*Lupinus luteus*), but in the aerial parts of the plant their expression level is low and can be significantly increased upon the pathogen invasion¹. Similar situation was observed in many other plants in which their presence was reported. PR10 proteins are generally induced by the stress-related factors, including pathogenic invasion, wounding, UV radiation or some chemical compounds, and the expression pattern vary between plant species or between the gene family members. Many members of PR10 family are abundant in specific plant organs (pollen grains, fruits, roots) and have been previously recognized as a strong and common allergens. The biological function of the PR10 proteins is unknown.

Two lupine proteins, LIPR10.1A and LIPR10.1B, sharing 75 % identity, crystallized in relatively high protein and salt concentrations, both in orthorhombic spacegroup², and diffraction data was collected with the resolution 1.95 Å and 2.25 Å, respectively. Structure was solved by the molecular replacement method using structure of birch pollen allergen³ (45 % identity) as a probe. All three proteins have similar fold, consisting of the seven-stranded β-sheet, partially surrounding the long, C-terminal α-helix. Two additional, short helices are located near N-terminus. The C-terminal helix, however, occupies different position in all three structures and additionally in both lupine proteins it is curved. The comparison of three homologous structures led us to the discovery of cavity, that can be responsible for the protein activity. The pocket is located between highly conserved and well ordered glycine-rich loop 45-50 and connection of two N-terminal helices. The side chains directing to the cavity lumen appeared to be also conserved and together with the carbonyl oxygen from the glycine-rich loop could be responsible for ligand binding.

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