

MP 600 Inside into the proteome of *Chelidonium majus* latex

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Introduction

Since ancient times, *Chelidonium majus* L. (Greater Celandine), a plant from Papaveraceae family, is widely used in folk medicine in Europe and Asia. One of the most important uses of *C. majus* was the direct application of fresh milky sap (called latex) to the skin to remove warts and condylomas, which are result of human papilloma virus (HPV) infection. Moreover, the only plant virus which was shown to infect *C. majus* in its natural habitats, is cucumber mosaic virus (CMV). The aim of the study was the comparative proteomic analysis of *C. majus* shoots and latex collected from the plants inoculated with plant potyvirus comparing with the non-treated plants, as well as comparison of latex proteome in different growing conditions.

Methods

Latex were collected from plants:

- inoculated with a suspension of potyvirus strains (PVY Ny/LW),
- grown in controlled conditions,
- grown in natural habitat.

Part of samples were subjected to 2-D electrophoresis and subsequent liquid chromatography-electrospray ionization-tandem mass spectrometry (LC-ESI-MS/MS). Second group of samples were analyzed with label-free quantitative proteomic approach. Both analysis were conducted in the Mass Spectrometry Laboratory of the Institute of Biochemistry and Biophysics, Polish Academy of Sciences in Warsaw, Poland. For more precise protein identification, all collected data were searched by MASCOT software using information from *C. majus* transcriptome sequencing. For most abundant proteins, qRT-PCR was performed.

Preliminary Data

Milky sap flows out of the plant immediately after mechanical damage, which is a necessary condition for viral infection. Antiviral activity of milky sap from *C. majus* may be related to the content not only of specific alkaloids, but to activity of specific proteins. Our studies enable to identification of ca. 20 latex proteins, which among others include proteins engaged in general metabolism, nucleic acid binding proteins, i.e. glycine-rich RNA-binding protein - GRRBP and proteins related to plant defense against pathogen attack belonging to PR class. The most pronounced difference in abundance was observed for protein, which was identified as the major latex protein 28 (MLP28). The MLP28 belongs to the major latex protein family. However, the

observed protein is characterized by the different pI (ca. 4) than other proteins from this group (ca. 5.5-6.5), what suggests that it may be an isoform of MLP. Major allergen Pru ar 1 protein - another protein belonging to the Bet v 1 family as well as MLP28, were more abundant in the infected plant's latex and it may be overexpressed in response to the infection, as a component of plant defense system. We also identified few representatives of heat shock protein class (Hsp), which are well known stressed-induced group of proteins in plants.

Novel Aspect

Study demonstrated the abundance of proteins in *C. majus* latex after virus infection, with postulated antiviral activity of MLP28 protein.

Conflict of Interest Disclosure

The authors declare no competing financial interest.
