ARABINOGALACTAN-PROTEINS FROM ECHINACEA PURPUREA: CHARACTERIZATION, LOCALIZATION AND IMMUNOMODULATING PROPERTIES

© Classen B.

Pharmaceutical Institute, Dept of Pharmaceutical Biology, University of Kiel, Gutenbergstr. 76, 24118 Kiel, Germany

Arabinogalactan-proteins (AGPs) are macromolecular glycoproteins belonging to the putative active compounds of Echinacea preparations (1). (β -D-Glc), Yariv phenylglycoside specifically binds to most plant AGPs and has been used to isolate AGPs from pressed juice of the aerial parts of Echinacea purpurea L. Moench (Asteraceae). The carbohydrate moiety has been classified as type II arabinogalactan consisting of a backbone of 1,3,6-Galp and 1,3-Galp, with branched side chains composed of 1,3,6-Galp, 1,6-Galp,1,5-Araf, terminal Araf and terminal GlcAp. In the protein part, AGP from pressed juice showed an amino acid sequence rather untypical for AGPs with predominantly contiguous arrangement of three to four Hyp residues in blocks (2). For microscopic localization of AGPs in fresh plant tissue, a new method has been developed. Antibodies against Yariv's reagent have been generated in rabbits and used for immunofluorescent labeling of plant tissue. Xylem tracheary elements showed very strong labeling of the cell wall, especially at the inner side of the wall and in the area of pit canals. Preparations of pressed juice from *Echinacea purpurea* are used as herbal medicinal products with immunomodulating properties. *In vitro*, AGP from the pressed juice of herbal material showed complement stimulating activities (3) as well as binding to human leukocytes (4).

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UBIQUINOL IS ANTIHYPOXANT AND CELL ENERGIZER OF THE NEW GENERATION

© Dadali Vladimir A.¹, Makarov Valery G.²

¹North-West State Medical University named after I. I. Mechnikov, Saint-Petersburg, Russia ²Institute of experimental pharmacology, Saint-Petersburg, Russia

Coenzyme Q (CoQ) is low molecular component of mitochondrial electron transport chains that functions as molecular shuttle between next some enzymatical complexes: NADH-CoQ-reductase (complex I); succinate-CoQ-reductase (complex II); ubiquinol (CoQH₂)cytochrome C-reductase (complex III) that with complex IV (cytochrome C-oxidase) realize transformation of carbohydrates, fats and proteins molecular energy into rich energy compounds ATP. CoQ functions in form of quinone redox-cycle (Q-cycle) where oxidized form of CoQ (ox CoQ) via intermediate free radical and anion forms is transformed by enzymaticaly into its active reduce form — ubiquinol (CoQH₂). Mitochondrial Q-cycle functions so effectively that stimulates transmembrane proton transfer and ATP synthesis twofold more intensively than simple one stage redox process. But redox processes in system (ox) CoQ-CoQH₂ take place not only in mitochondrion but in another membrane structures — lysosomes, Goldgi and plasma membranes and serum LDL. In lysosomes Q-cycle takes part in proton transfer in pH-dependent activation of lysosomal proteases for the degradation of worked off cell proteins. Another site of (ox) CoQ-CoQH₂ action is endosomal pynocytoses that regulates transport of Fe⁺² by transferrin into cell cytoplasma. In plasma membranes system (ox) CoQ-CoQH₂ activates of Na⁺/H⁺ antiportal proton transfer that with ATP-dependent ion transport determine intracell ion homeostasis. In LDL CoQ (in Co-QH₂ form) defenses cholesterol and another lipid components from peroxidation. Q-Cycle determines antioxidant-prooxidant functions of CoQ but CoQH, only is single stable antioxidant form of CoQ. Moreover it is single enzymatically regenerated endogenic lipid antioxidant. From point of view of CoQH₂ formation three enzymatic systems are important: a) NADH-CoQ-oxidoreductase; b) NADH-cytochrome b₅-reductase; c) NADH/NADPHoxidoreductase (DT-diaphorase). But DT-diaphorase only reduces at once (ox) CoQ in to CoQH₂ by twoelectron transport. Another two enzymes reduce (ox) CoQ via one-electron transfer to semiguinone-radical CoQ⁻ that is generated by interaction of CoQH₂ with lipid radicals. Besides of right radical scavenging action Co-