of rhodopsins as a prototype for the photonic qubit detectors. At the same time heterologous expression of visual rhodopsins (Rho) remains a challenging task due to the difficulties of the producing in functional form in the majority of expression systems. The successful expression of recombinant invertebrate visual pigment (Gq coupled Rho) was developed in HEK293 cells for honeybee, white butterfly, jumping spider.

We cloned the novel full length *octR* gene from cDNA of *Octopus vulgaris* retina [Zhgun A.A., et.al., 2015]. After the alignment and topology imposition with structure of cephalopoda Rho from *T. pacificus* [PDB ID: 2Z73; Murakami M., et.al., 2008] we designed the model of OctR topology. According this model we proposed a number of OctR variants (full length opsin, C-end fusion with eGFP, delta 390-455 mutant less cluster with polyproline-rich repeats, with 6xHis- and c-Myc epitope tags from C-end and combinations thereof) and generated a set of constructs, based on pTRE-Tight vector (Clontech, United States) for expression in HEK293 cells under doxycycline-regulated promoter. We used HEK293-G7 cell line with constitutive expression of trans-activator protein tTA for promotor pTRE (Tet-Off system) [Shubin A.V., et.al., Applied Biochemistry and Microbiology, 2013. 49(9): p. 750–755]. The preliminary results of transient expression allow us to assume the proper folding of the OctR variants in HEK293-G7 cells. The data of the developing cell lines with OctR variants and regeneration with 11-cis retinal will be reported.

Acknowledgments: Supported by RFBR Grant 16-04-01494.

P.2.1-016
Novel transmembrane protein c-Answer revealed by bioinformatic screening of genes present only in well regenerating animals

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The genetic basis of higher regenerative capacity of fishes, amphibians and reptiles, comparing to birds and mammals, is still poorly understood. Usually, it is thought that this is a result of restructuring of the corresponding regulatory network, which consists of approximately the same set of genes. We hypothesized that another cause might be a loss of some genes which are essential for regeneration. We propose a bioinformatic approach for systematic search of such genes. Our method detects genes with local synteny disruption and, vice versa, appearance of genes with specific local synteny. It examines the co-localization of homologous genes and counts the number of their copies. The method provides for flexible definition of detecting conditions and different forms of local synteny. Our algorithm outputs rather short gene lists, and quite similar lists for a wide range of parameters. Thus, we identified several genes that present only in fishes, amphibians and reptiles and revealed the genes, which demonstrated an increased expression during regeneration of tails and hindlimb buds in the model organisms, the *Xenopus laevis* tadpoles. We found out that one of these genes encodes a membrane protein, which is strongly up-regulated already at the 1st day of regeneration predominantly in the wound epithelium. As we demonstrated, this gene regulates the body appendages regeneration and also the telencephalic and eye development. We named the protein encoded by the revealed gene *c-Answer*, after cold-blooded Animals specific wound epithelium receptor-like protein. We suppose that the loss of *c-Answer* although resulted in a decrease of the regenerative capacity in birds and mammals, could be fixed by natural selection because the loss of this gene might provide new opportunities for the forebrain evolution. On the whole, local rearrangement of gene synteny is a likely driving force in many aspects of forebrain and species evolutions.

Supported by RSF14-50-00150 project.

P.2.1-017
Fluorescently labeled isopentenyladenine is a new tool for cytokinin receptor domain mapping

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Signaling of cytokinins, important plant hormones, is initiated through their perception by histidine-containing kinases (HKs). Recently, GFP-fused Arabidopsis HKs were found to be massively localized to the membrane of endoplasmic reticulum, however, their previously believed localization and function in plasma membrane has still not been disproved. Cytokinins structurally based on C6-substituted purine belong to a class of plant hormones that play important roles in many aspects of plant growth and development. To gain better insight into the dynamics of cytokinin receptor localization within the cell we developed series of cytokinin fluorescent probes. To this end, isoprenoid cytokinin N6-isopentenyladenine (iP) was accompanied with selected spacers in C2, C8 and N9 position of the adenine moiety and fluorescently labeled with nitrobenzoxadiazole (NBD) fluorescent label. The ligand properties of iP-derived probes were first assessed *in vitro* with Arabidopsis cytokinin receptors (AHK3 and AHK4) in a bacterial receptor test where the competition of a cytokinin fluoroprobe with radiolabeled tZ was measured. Although the structural changes within the fluorescent probes led mostly to significant loss of the biological activity, some probes with N9 substitution were still able to interact with the receptor binding site as revealed by our ligand binding studies. Thus, NBD-labeled iP derivatives seem like a promising tool in rapid staining procedures for visualization of the cytokinin receptor pool inside the cell. *In planta* experiments revealed that these compounds were transported to the cell cytosol and the signal was associated with several subcellular structures, most importantly with the endoplasmic reticulum, which is probably the intracellular site for hormonal cross-talks between cytokinin and other plant hormones.

This work was supported by Czech Science Foundation grant 16-04184S.

P.2.1-018
The effect of high cholesterol diet on scavenger receptor expression and fatty acid profile in cardiac tissue

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Hypercholesterolemia plays an important role in the progression of cardiovascular diseases (CVD) which is the major cause of death worldwide with highest mortality and morbidity rates. Excessive cardiac remodeling conditions result in various cell