



ZAJEDNIČKI SEMINAR

Ponedjeljak, 26. rujan 2016., 14:00 sati (točno)

PMF-Fizički odsjek, Bijenička cesta 32, Predavaonica 201

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The many faces of MATH-BTB proteins in plants

The MATH-BTB protein family is common to both animals and plants. It is a phenomenon that *Arabidopsis* and human genomes encode only few members (six and two, respectively) of the MATH-BTB protein family but in some plant and animal organisms, the same protein family has expanded more than 10-fold. The first functionally characterized MATH-BTB protein is Mel26 from *Caenorhabditis elegans* which is a key regulator required for the first asymmetric zygote division. Three different plant MATH-BTB genes, from maize, wheat and *Arabidopsis thaliana* were selected due to their exclusive/strong expression during plant reproduction and functionally characterized in our work. A gametophyte/zygote specific *ZmMAB1* gene from maize is expressed in both the female and male germline and its silencing leads to defects in spindle organization and chromosome segregation during gametophyte development. The zygotic induced gene *TaMAB2* encodes a protein that asymmetrically co-localises with microtubuli around the nuclear envelope, what suggests its role in organizing the assembly and proper position of microtubular spindles during asymmetric cell divisions of zygote. Moreover, zygote deposited TaMAB2 is always inherited to the large basal cell after first asymmetric zygotic division. The asymmetric inheritance indicate that the protein might be involved not only into establishment of asymmetry but also into the cell specification in two-celled embryo.

Both *ZmMAB1* and *TaMAB2* as well as other yeast, animal, and plant BTB-domain containing proteins interact with Cullin 3-based E3 ligases and are involved in ubiquitin -dependent degradation pathway. In addition to Cullin 3-related functions, *Arabidopsis* MATH-BTB protein *AtBPM1*, localizes predominantly in nucleolus of plant cells indicating a Cullin3 independent function. We identified, by mass spectrometry and other protein interaction analysis, that *AtBPM1* interacts with proteins involved in RNA-directed DNA methylation which represent a novel, yet undiscovered function of MATH-BTB protein in regulation of DNA methylation.

Dunja Leljak-Levanić je izvanredna profesorica Biološkog odsjeka PMF-a. Problematika kojom se bavi je razvojna biologija biljaka u sklopu koje se najveći opus istraživanja odnosi na biljnu somatsku i zigotnu embriogenezu. Njezina istraživanja pružaju prve dokaze da se embriogeneza može potaknuti neovisno o biljnim regulatorima rasta. Analizom regulatornih mehanizama indukcije i razvitka

somatskih embrija pokazuje da su oni povezani s reverzibilnim promjenama metilacije DNA i stresom. Istraživanja biljne zigotne embriogeneze temelje se na iskustvu u mikromanipulaciji muškog i ženskog gametofita biljaka. Utemeljenjem postupka izolacije jajne stanice, zigote i ranih embrija pšenice *in vivo* D. Leljak Levanić ukazuje na set gena uključenih u aktivaciju embriogenog razvitka. Funkcionalnom karakterizacijom proteina porodice MATH-BTB razjasnila je njihovu ulogu u regulaciji asimetrične diobe stanica tijekom oplodnje i embriogeneze. Kao dobitnica stipendije i projekta Alexander von Humbolt Dunja Leljak-Levanić usavršavala se na Zavodu za razvojnu biologiju i biotehnologiju Sveučilista u Hamburgu, nakon čega svoju suradnju nastavlja na Zavodu za biologiju i biokemiju biljaka Sveučilišta u Regensburgu, Njemačka.