BPM1 protein is involved in plant development and stress responses by regulating de novo DNA methylation

P-01.4-25

N. Bauer[I], L. Markulin[II], M. Jagić[I], T. Vuk[I], S. Vitko[I], A. Škiljaica[I], M. Tokić[I], V. Vičić-Bočkor[I], Ž. Vidaković-Cifrek[I], D. Leljak-Levanić[I]

[I]associate professor, Zagreb, Croatia, [II]Department of Biology, Faculty of Science, University of Zagreb, Zagreb, Croatia

A member of a small family of *Arabidopsis thaliana* MATH-BTB proteins, BPM1 functions as a substrate-specific adaptor of a cullin3-based E3 ubiquitin ligase complex. Its N-terminal MATH domain binds target proteins and designates them for ubiquitination and subsequent proteasomal degradation. Recent studies reported that BPM1 mediates proteasomal degradation of transcription factors (ERF/AP2, R2R3 MYB and Homeobox) and phosphatases (PP2Cs). By using immunoprecipitation, TAP-tag purification, fluorescence-lifetime imaging microscopy, yeast-2-hybrid, pull down and microscale thermophoresis we confirmed BPM1 interaction with DMS3 and RDM1, key regulators of *de novo* DNA methylation in *A. thaliana*. Chromatin immunoprecipitation was used to determine regions of overlap between DMS3 and BPM1 chromatin binding sites. The DNA methylation status of identified regions was analysed by pyrosequencing after bisulphite conversion in *A. thaliana* plants overexpressing *BPM1,* in plants with downregulated *BPMs* as well as in DNA methylation mutants. Methylation patterns were assessed during plant development and after exposure to different abiotic stresses. Our results indicate that BPM1 does not participate in degradation of DMS3 and RDM1. Rather, it seems BPM1 recruits DNA methylation machinery to specific chromatin positions for *de novo* DNA methylation establishment.