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# PROFILING METHYLATION AND DEMETHYLATION ENZYMES IN VARIOUS PLASMA CELLS AND IN UNSORTED CELL POPULATION OF MULTIPLE MYELOMA PATIENTS

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**Objective:** DNA methyltransferases (DNMTs) including DNMT1, DNMT3A and DNMT3B, catalyze the transfer of methyl groups to cytosine position 5, and play an important role in epigenetic regulation, which could be involved in pathogenesis of multiple myeloma (MM). Active DNA demethylation occurs during 5-methylcytosine through TET (Ten Eleven Translocation) enzyme-mediated oxidation removal, and this process is necessary for the epigenetic reprograming of genes and is directly involved in tumor progression.

**Methods:** Expression profiles of demethylation enzymes of TET protein family and DNA methyltransferases were determined from three independent repeats in untreated myeloma cell lines: NCI-H929, MM1S, OPM2, U266 and lymphoma cell lines JURKAT, C7. RNA was isolated from unsorted cell population in the bone marrow aspirate of 20 multiple myeloma patients, and from each experiment with cell lines. Followed prepared cDNA was used for DNMT1, DNMT3A, DNMT3B, and TET1, TET2, TET3 expression analysis using quantitative real-time PCR.

**Results**: Multiple myeloma cells from tested myeloma cell lines, and in comparison to used lymphoma cell lines show decreased expressions of all DNMTs, especially in de novo DNMT3A and DNMT3B is very low. In tested myeloma cell lines, the TET1 expression is undetectable, TET2 and TET3 expressions are also very low. Similar expression profiles of methylatin and demethylation genes we obtained from samples of multiple myeloma patients. Although the TET3 expression is higher compared to TET1 and TET2, their expressions in multiple myeloma are also very low. In addition to three analyzed DNMTs, the DNMT3B expression is the lowest in multiple myeloma patients.

Conclusion: Our study indicates down regulation of both methylation and demethylation mechanisms in multiple myeloma, and is the first approach data available of this type of tumor malignancy.

## Biography

Katerina Smesny Trtkova works as a research fellow at University Palacky Olomouc, Czech Republic. She has solved grant project focused on multiple myeloma epigenetics together with several Ph.D and Diploma students.

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