

# Characterization of sponge homolog of human metastasis suppressor DRG1

P-01.1-06

S. Beljan<sup>I,II</sup>, K. Dominko<sup>II</sup>, A. Talajić<sup>II</sup>, M. Radić<sup>III</sup>, M. Herak Bosnar<sup>III</sup>, K. Vlahovićek<sup>I</sup>, H. Ćetković<sup>II</sup>

<sup>I</sup>University of Zagreb, Faculty of Science, Department of Biology, Division of Molecular Biology, Zagreb, Croatia, <sup>II</sup>Ruder Boskovic Institute, Division of Molecular Biology, Laboratory for Molecular Genetics, Zagreb, Croatia, <sup>III</sup>Laboratory for Protein Dynamics, Division of Molecular Medicine, Ruder Boškovic Institute, Zagreb, Croatia

Cancer is known as a disease of multicellular animals caused by the errors within the multicellular system, leading to the proliferation of “selfish” cell lines. Research of ancestral homologs of cancer-related genes in humans has gained more popularity in recent years since comparative genomic studies have confirmed that many homologs of human genes were already present in simple metazoans. From an evolutionary point of view, the development of cancer is most likely related to the development of multicellularity and the appearance of true tissues and organs. Despite their simple morphology, with only a few cell types and without true tissues and organs, sponges possess complex genomes harboring many genes highly similar to their vertebrate homologs. Therefore, they provide an excellent model for studying the evolution of different genes that were most possibly present in the genome of the animal ancestor. Our research focuses on metastasis suppressor genes. Metastasis suppressors inhibit metastasis formation without affecting primary tumor growth. Bioinformatics analyses have shown that homologs of metastasis suppressors were probably already present in the last common ancestor of all animals. To better understand the basic role of ancestral metastasis suppressor homolog, we analyzed the sponge homolog of the main metastasis suppressor gene: developmentally-regulated GTP-binding protein 1 (DRG1). Our bioinformatics and phylogenetic analyses showed that these proteins are conserved across animals. Transfection of sponge and human cells revealed the intercellular localization of DRG1 proteins. The proteins were then overexpressed in *E. coli* and confirmed by Western blot and the protein GTP-binding properties by a GTPase activity assay. Further biochemical and biological characterization is in progress. These results will provide a better understanding of the intracellular processes related to the metastasis suppression and pathology of cancer and metastasis.