256. EXPRESSION OF THE MIR-1 MOLECULE IN PATIENTS WITH UTERINE LEIOMYOSARCOMA

Victor Cernat[1], Mathias Stope[2], Dominique Könsgen[3], Karoline Diesing[4], Luise Wiegank[5], Alexander Mustea[6]

1 Department of Surgery, University Medicine Greifswald, Ferdinand-Sauerbruch-Strasse, 17475 Greifswald, Germany

2 Department of Urology, University Medicine Greifswald, Ferdinand-Sauerbruch-Strasse, 17475 Greifswald, Germany

3 Department of Gynecology and Obstetrics, University Medicine Greifswald, Greifswald, Germany-Strasse, 17475 Greifswald, Germany

4 Department of Gynecology and Obstetrics, University Medicine Greifswald, Greifswald, Germany-Strasse, 17475 Greifswald, Germany

5 Department of Gynecology and Obstetrics, University Medicine Greifswald, Greifswald, Germany-Strasse, 17475 Greifswald, Germany

6 Department of Gynecology and Obstetrics, University Medicine Greifswald, Greifswald, Germany-Strasse, 17475 Greifswald, Germany

Background: The uterine leiomyosarcoma represents the most frequent malignant gynecologic mesenchymal tumor that often develops distant metastases. The diagnosis of these tumors is nowadays still a challenge and the direct implication of the small non-coding RNAs (MicroRNAs) in gene expression, tumor initiation and tumor progression has already been revealed in scientific studies. Because the aberrant microRNA (miRNA) expression patterns show a diagnostic value as tumor markers, we aimed to identify the gene expression level of miRNA-1 (miR-1) and the protein targets in uterine leiomyosarcoma.

Methods: Using the specific cell line - SK-UT-1 with similar biological characteristics of the uterine leiomyosarcoma tissue, in comparison to ovarian carcinoma cell lines: OVCAR-3, TOV-21 and SK-OV-3, and cell lines of mouse heart-muscle (HL-1), we were able to perform real time PCRs and RNA-Isolation arrays, transient and stabile transfection programs with lipofectamine reagents. Tissue samples of uterine leiomyosarcoma and healthy uterus were again analyzed by means of transfection and isolation arrays. The electrophoresis using protein targets of the miR-1 (p38 and ERK 1/2 widely expressed protein kinase intracellular signaling molecules and involved in functions including the regulation of meiosis, mitosis, und postmitotic functions) was also integrated.

Results: The analysis of the SK-UT-1 cell line have shown significant differences in comparison to the other studied cell lines, respectively a reduced expression of the miR-1 molecules. The same results were observed in the process of transfection and electrophoresis of the human tissues, where the lowest expression of the miR-1 was evidenced in the uterine leiomyosarcomas. The specific protein targets of miR-1 have shown positive Western Blot signals.

Conclusions: The miR-1 non coding molecules may improve our understanding of disease development, progression and gene expression of the uterine leiomyosarcoma. Further prospective translational studies in order to evaluate miR-1 as a prognostic factor are needed.

Key words: MIR-1, leiomyosarcoma, Western Blot.

257. MATURITY ONSET DIABETES OF THE YOUNG: CURRENT TRENDS AND CONCEPTS

Covantev Serghei

Scientific adviser: Perciuleac Ludmila, PhD, Associate Professor, Department of Molecular Biology and Human Genetics, *Nicolae Testemitanu* State University of Medicine and Pharmacy, Chisinau, Republic of Moldova

Introduction: Diabetes is a worldwide problem with polygenic etiology and high rate of mortality and morbidity. By 2030 the number of individuals with diabetes worldwide may rise to 472 million. Eighty per cent of them will be in low and middle income countries. In some of these countries diabetic drugs and insulin are inaccessible or rather expensive which eventually affect the whole healthcare system. Nevertheless 10% of patients with type 1 and 5% of patients with type 2 diabetes have a monogenic form of this disease.

Materials and methods: We studies a case series of patients with maturity onset diabetes of the young (MODY) with the review of the literature of the last 10 years using PubMed and Scopus.

Discussion results: Nationwide studies show that the prevalence of MODY ranges from about 1% to 35% of all diabetes mellitus cases. Current data describes 11 types of MODY. The most frequent are MODY 1, 2 and 3. To date, several transcriptional factors and an enzyme are Associated with MODY. There are several characteristic traits that may help to diagnose the disease without molecular methods. Such include diabetes diagnosed before 45 years, negative β-cell antibodies, less than 30 years of age, no insulin resistance, family history of diabetes, detectable C-peptide more than 0,2 nmol/l outside the honeymoon period, GST more than 0.2 nmol/l.

Conclusion: In Republic of Moldova there are approximately 80 thousand diabetic patients, which mean that they represent somewhere 50% of the endocrine diseases. Some of these patients may have MODY diabetes which requires different treatment options and has a better clinical prognosis then type 1 and 2 diabetes mellitus.

Key Words: monogenic forms of diabetes, HNF-4a, GCK, HNF-1a.