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S3.3**Relapse and prediction of relapse**

Erik Stenberg
Department of Surgery, Faculty of Medicine and Health, Örebro University, Örebro, Sweden

Background

Over the last decade, bariatric and metabolic surgery has been recognized as an important step in the treatment algorithm for type-2 diabetes (T2DM). Despite early suggestions of surgery providing a potential cure for T2DM, only a small proportion of all patients who could benefit from surgery are ultimately considered for this treatment. Furthermore, the long-term effects on T2DM still remains somewhat controversial.

Methods and results

A review of the current literature as well as data from the Scandinavian Obesity Surgery Registry (SOReg) were considered. Remission of diabetes occurred for 58–89% of patients with T2DM. A higher chance of remission was reported for patients with shorter duration and a less severe disease. Age, surgical method, postoperative weight-loss, sex and socioeconomic status may also influence the chance of reaching remission. Relapse of disease was reported to occur in 19–50% of those who initially experienced remission. Longer duration and a more severe disease, as well as female sex, weight-regain, and type of surgery are associated with higher risk for relapse. Patients who eventually relapse still experience reduction in the risk for diabetes complications.

Conclusion

The chance of reaching diabetes remission after metabolic and bariatric surgery is high. While relapse is common, patients still experience long-term metabolic benefits from this type of surgery.

DOI: 10.1530/endoabs.70.S3.3

Unveiling Signatures in Pituitary Neuroendocrine Tumours**S4.1****Circulating microRNAs: from PitNET pathogenesis to diagnostics**Henriett Butz^{1,2}

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Introduction

MicroRNAs are short, single-stranded, protein non-coding RNA molecules which can be secreted into the circulation by mammalian cells. Their altered

expression pattern has been described in many different physiological and pathological conditions. In the extracellular compartments they are encapsulated within vesicles, associated to proteins or apoptotic bodies. Due to their stability they are suggested as promising circulating biomarkers. Regarding pituitary adenoma several studies have been published describing the different expression pattern of miRNAs and their role in adenomagenesis on tissue level, but only a few publications investigated circulating miRNAs.

Aim

To identify pituitary tissue-specific miRNAs in circulation comparing tissue and blood miRNA profiles reported in literature.

Methods

Data mining of available serum or plasma miRNAs detected in patients with pituitary adenomas. Reevaluation of expression data and correlation with tumor biology.

Results

Overall, a global downregulation of miRNA expression was reported in plasma samples obtained from patients with pituitary adenoma compared to healthy controls. Pituitary adenoma tissue-specific miRNAs have low abundance in plasma, minimizing their role as biomarkers. To date, only miR-143-3p was reported as plasma marker for non-functioning adenomas which level decreased following surgery.

Discussion

Circulating miRNAs in pituitary adenoma would help patient care especially in non-functioning adenoma as minimally invasive biomarkers of tumor recurrence and progression. However, technical difficulties may challenge the clinical use of miRNAs as potential biomarker and the application of standardized protocols could help their clinical utility. MiR-143-3p may predict tumor recurrence but it needs further investigation.

DOI: 10.1530/endoabs.70.S4.1

S4.2

Abstract unavailable

S4.3**Unravelling the PitNET methyloma**Antonio Pico^{1,2}

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Context

Pituitary tumorigenesis does not fit into the most common model of cancer development driven by gene mutations. Instead, epigenetic mechanisms have been widely involved. Among them, aberrant DNA methylation at CpG sites is one of epigenetic hallmarks of tumour cells. There are several methods to study the epigenetic regulation of genome activity, from DNA methylation arrays to more specific DNA methylation analysis such as pyrosequencing, Methylation-Specific PCR (MS-PCR) or MS-multiplex ligation-dependent probe amplification (MS-MLPA) of selected genes.

M & M

We studied the DNA-promoter methylation and gene expression of 35 tumour suppressor genes in 105 pituitary neuroendocrine tumors (PitNETs) by MS-MLPA and quantitative real-time PCR techniques, looking for differences among subtypes and between functional and invasive behaviour of tumors. Moreover, I revised the most relevant results published in the literature.

Results

We observed different methylation patterns among PitNET subtypes. The methylation status correlated negatively with its gene expression in some but not all methylated genes. Moreover, some genes appeared more frequently methylated in macro and invasive tumours than in micro or non-invasive ones. Finally, we found significant differences between functioning and