Global MicroRNA Profiling of Small Intestinal Neuroendocrine Carcinomas and Establishment of a Method to Study Serum MicroRNA Expression from the Same Malignancies

Conclusions

The small intestinal neuroendocrine carcinoma (SI-NEC) microRNA (miRNAs) profile provides potential pivotal miRNAs. They may be involved in tumor progression and have a role in novel therapeutic targets development. One of the major goals is to extend this study to blood samples to overtake patient’s tissue specimens collection.

Aims

To provide an exclusive miRNAs profile on SI-NECs at different stage of disease and identify miRNA expression from patient blood samples.

Background

miRNAs are posttranscriptional regulators and function either as tumor suppressors or oncogenes in a variety of cells. MiRNAs may play a critical role in development, diagnosis and progression of SI-NECs.

Results

The Global miRNA profile shows that nine miRNAs significantly altered their expression between primary tumors and metastases. QRT-PCR analysis from laser capture microdissected (LCM) tumor cells detected five upregulated miRNA expression in LCM tumor cells versus immuno LCM normal enterochromaffin (EC) cells. Whereas, four miRNAs were downregulated in LCM tumor cells. We also investigated miRNA expression from serum samples by QRT-PCR analysis. In addition, the nine deregulated miRNAs are expressed at different level on five human NET cell lines.

Material & Methods

1. Total RNA from 15 SI-NEC specimens (5 primary tumors, 5 mesentery metastases and 5 liver metastases) to perform genome-wide Affymetrix GeneChip® miRNA arrays.

2. In silico data have been validated by QRT-PCR analysis from LCM normal EC cells and LCM tumor cells.

3. SI-NEC serum samples were also used to validate our findings.

4. Five human NET cell lines were profilied as potential cellular models for further functional studies.