Gene expression profile of MTC in relation to RET mutation status

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Aim of the study: Medullary thyroid cancer (MTC) arises from parafollicular C and occurs as hereditary (20% of all cases) and sporadic form. Hereditary type is a consequence of *RET* proto-oncogene germline mutations. Strong genotype-phenotype manifestation is correlated with different sites of *RET* mutation. The aim of study was to evaluate whether the differences in gene expression profile are related to the particular *RET* mutation.

Methods: Fresh-frozen tumor samples from 60 MEN 2 patients and 21 *RET* negative MTC patients were collected. Germline mutation screening was performed according to standard diagnostic algorithm. *RET* somatic mutations were analyzed among sporadic MTC patients and twenty one exons of *RET* gene were directly sequenced. Gene expression profile was analyzed in 34 MTC samples using Gene Chip 1.0 ST Arrays (Affymetrix). An independent set of 26 MTC samples was used for QPCR validation.

Results:

Hierarchical clustering did not show any global differences in gene expression profile between type of *RET* mutation, however, supervised analysis revealed 10 genes differentially expressed between tumor samples with mutation at *RET* codon 634 and 918. We select 5 genes for QPCR validation and confirmed 3 of them as deregulated. Additionally we also did not find significant changes between hereditary and sporadic MTC.

Conclusion:. The differences in gene expression profile of slightly are dependent of RET site mutation.

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