Novel and classical molecular pathways identified in pituitary tumorigenesis using mRNA profiling.

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SCOPE

To identify novel molecular pathways involved in pituitary tumorigenesis using mRNA expression profiles.

METHODS

• RNA extracted from 8 pituitary tumours (5 NFPA, 2 GH-secreting tumours, 1 Prolactin/TSH-co-secreting) and pooled normal pituitary control RNA were used for microarray RNA expression analysis on Affymetrix HuGene 1.0 ST Chip.

• Microarray data was analyzed using GeneScript GX 11.0 and network analysis was carried out using the Ingenuity Pathway Analysis (IPA) software.

• Data from microarrays was verified using RNA from 30 pituitary tumours (20 NFPA, 6 GH-secreting, 2 PRL-secreting and 2 ACTH-secreting tumours) using quantitative PCR of key genes involved in the networks identified by the IPA.

RESULTS

3. Canonical Pathways involved in Pituitary Adenomas

Wnt Pathway was involved in all pituitary adenomas types.

CONCLUSIONS

• Microarrays coupled with qPCR are a useful tool in characterizing tumour types.

• Classical pathways were confirmed by microarray and IPA, namely the cAMP signalling, PI3K cascade and Wnt signalling pathways (1,2).

• Wnt pathway inhibitors are greatly down-regulated however, canonical signalling through β-catenin appears unaltered.

• Novel pathway identified include the AHR signalling, GABA receptor signalling and p53 signalling pathways among others.

References


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