

Abstracts for the Ninth International Workshop on Multiple Endocrine Neoplasia (MEN2004)

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several genes involved in growth regulatory pathways, including RB1, DAPK and GADD45g and is associated with gene silencing. To identify novel genes subject to this epigenetic change we used methylation-sensitive arbitrarily primed PCR (MsAP-PCR). We isolated several sequences that showed differential methylation in pituitary tumours relative to normal pituitary. For one of these novel sequences, isolated from chromosome 22, we found that the majority of pituitary adenomas, irrespective of subtype, failed to express the transcript as determined by qRT-PCR. We next performed function studies through transfection analysis in the AtT20 cell lines. Enforced expression of the cDNA encoding this novel gene had no discernible effects on proliferation or cell viability, however, cells expressing this construct showed a threefold increase in apoptosis, as determined by acridine orange staining and TUNEL labelling, compared to those harbouring an empty vector control. Apoptosis was preceded by an increase in active caspases and was reversible in the presence of z-VAD-fmk. The pituitary tumour derivation and role in apoptosis of this gene led us to assign it the acronym PTAG. The ability of cells, showing reduced expression of PTAG, to evade or show a blunted apoptotic response may underlie oncogenic transformation in both the pituitary and other tumour types.

O5

Familial isolated pituitary adenomas

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Familial pituitary adenomas have been characterized in the settings of multiple endocrine neoplasia type 1 (MEN1) and Carney complex (CNC). Furthermore, isolated familial somatotropinomas have been reported. Interestingly, we have observed other pituitary phenotypes not linked to these previous syndromes, suggesting a new entity: familial isolated pituitary adenomas (FIPAs). To get further clinical and genetic insight of FIPAs, a retrospective European multicentre study was undertaken. A hundred and forty cases (56 males and 84 females) have been identified in 64 families, including prolactinomas (40%), GH-omas (34%), clinically non-secreting adenomas (16%), ACTH-omas (5.7%) and gonadotrophinomas (4.3%). FIPAs represented less than 2% of all pituitary adenomas followed in the centre involved in the study. There were 54 families with two patients, 8 with three, and two with four affected members. A direct familial relationship (siblings and/or parents/offsprings) was the most frequently encountered (75%), and, where at least two generations were present, the mean age at diagnosis was significantly lower in the second generation compared to the first one (50.3 ± 15 vs 29.7 ± 10.6 , $P < 0.001$). The main biochemical features of FIPAs were also compared to a control series of sporadic pituitary adenomas.

The mean age at diagnosis was 38 ± 16 years. During follow-up (10 ± 8 years) no MEN-1 nor CNC-associated features was observed. From a genetic point of view, sequencing of the MEN-1 gene in at least one affected patient in each family allowed to exclude a pituitary-restricted form of MEN-1 in all FIPAs subgroups, and sequencing of the PKARIA gene for Carney complex was also normal in all tested kindreds ($n = 14$).

We suggest, on the basis of clinical, epidemiological and genetic data, that FIPAs represent a new entity. Further molecular studies should help to clarify FIPAs' etiology, plan relative familial screening and provide new insights into the pathogenesis of pituitary adenomas.

O6

Prevention of medullary thyroid carcinoma

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Formerly, multiple endocrine neoplasia (MEN) type 2a or familial medullary thyroid carcinoma (FMTC) were detected by clinical examination or biochemical testing. Currently, direct DNA analysis for mutations in the RET protooncogene is the preferred method of diagnosis. Regardless, affected patients are candidates for total thyroidectomy (TT), since virtually all will develop MTC.

In screening new kindreds with MEN 2a or FMTC, one finds disease in family members of various ages. We sought to compare clinical outcomes in patients whose MTC was diagnosed either below 25 years of age or above 50 years of age.

Our clinic, as part of a molecular screening program, performed TTs on 61 patients with MEN 2a (57) or FMTC (4). All patients were under 24 years of age and had no physical evidence of MTC. Our clinic also performed TTs on 39 patients over 50 years of age (36 with MEN 2a and 3 with FMTC), who were identified during screening of kindreds with hereditary MTC. The MTC was diagnosed either by direct DNA analysis ($n = 2$), elevated plasma CT levels ($n = 29$) or a nodule in the neck ($n = 8$). In the immediate postoperative period stimulated plasma CT values were either undetectable or within the normal range in all 61 patients under 25 years of age. Postoperative testing was performed immediately postoperatively in 30 of the 39 patients over 50 years of age and CT values were undetectable or within the normal range in 15 patients (50%) but elevated above the normal range in 15 patients (50%).

Currently, TT appears to be preventative or curative therapy for patients with MEN 2a and FMTC. The therapy is most often preventative when performed in young patients, whose only detectable abnormality is a mutation in the RET protooncogene.

O7

Consortia experiences – can we cure MTC?

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Medullary thyroid carcinoma (MTC) is a rare tumour characterized by the occurrence of two different variants, sporadic and hereditary, and the development of early lymphatic and haematogenous metastases. Although patients with occult metastasis and persistent hypercalcaemia may have a favourable long-term course [1], distant metastases and locoregional lymph node metastases (LNMs) are proven risk factors of local recurrence and impaired survival [2,3]. The aim of this study was to identify risk factors of postoperative persistent hypercalcaemia in sporadic and hereditary MTC based on single centre as well as multicentric studies.

Pre- and postoperative calcitonin levels and extent of disease: Preoperative calcitonin levels have shown to be correlated as well with the T-category, as with N- and M-categories [4–6]. Also postoperative calcitonin levels paralleled with the extent of disease. In patients with 10 or more LNM biochemical are could not be achieved. Remarkably, calcitonin normalization occurred only in about 70% of pT1, and nodal-negative patients, respectively