



Microarray analysis refines classification of non-medullary thyroid tumours of uncertain malignancy

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Résumé en anglais	<p>Conventional histology failed to classify part of non-medullary thyroid lesions as either benign or malignant. The group of tumours of uncertain malignancy (T-UM) concerns either atypical follicular adenomas or the recently called 'tumours of uncertain malignant potential'. To refine this classification we analysed microarray data from 93 follicular thyroid tumours: 10 T-UM, 3 follicular carcinomas, 13 papillary thyroid carcinomas and 67 follicular adenomas, compared to 73 control thyroid tissue samples. The diagnosis potential of 16 selected genes was validated by real-time quantitative RT-PCR on 6 additional T-UM. The gene expression profiles in several groups were examined with reference to the mutational status of the RET/PTC, BRAF and RAS genes. A pathological score (histological and immunohistochemical) was estimate for each of the T-UM involved in the study. The correlation between the T-UM gene profiles and the pathological score allowed a separation of the samples in two groups of benign or malignant tumours. Our analysis confirms the heterogeneity of T-UM and highlighted the molecular similarities between some cases and true carcinomas. We demonstrated the ability of few marker genes to serve as diagnosis tools and the need of a T-UM pathological scoring.</p>
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