Microarray analysis has now identified a panel of genes that are differentially expressed in benign and malignant thyroid tumors; this information could assist in the diagnosis of 'suspicious' or 'indeterminate' thyroid lesions.

Prasad *et al.* analyzed samples from 94 thyroid tumors, 50 of which were benign (13 adenomatoid nodules, 13 follicular adenomas, 13 Hürthle cell adenomas and 11 lymphocytic thyroiditis nodules) and 44 were malignant (13 papillary thyroid carcinomas, 13 follicular variant papillary thyroid carcinomas, 13 follicular carcinomas and 5 Hürthle cell carcinomas). Compared with benign tumors, 33 of the 15,745 genes included in the analysis were significantly overexpressed and 42 were underexpressed in malignant tumors. Prediction and cross-validation models suggested that the genetic analysis was 73% sensitive and 82% specific for the prediction of malignancy; the positive predictive value was 78%. Validation of 12 of the differentially expressed genes was carried out by real-time reverse transcription polymerase chain reaction: validated genes included *HMGA2*, *PLAG1*, *SPOCK1*, *CEACAM6*, *LRRK2*, *RAG2* and *AGTR1*.

Western blotting and immunohistochemistry confirmed the overexpression of HMGA2 protein in malignant tumors—HMGA2 was detected in 26 of 30 papillary thyroid carcinomas, 13 of 16 follicular variant papillary thyroid carcinomas, and 11 of 14 follicular carcinomas. Most benign tumors were negative for HMGA2 expression.

The results of this study indicate that these 12 genes could be used to develop a panel of markers that could be used to distinguish malignant from benign thyroid lesions.

Original article Prasad NB *et al.* (2008) Identification of genes differentially expressed in benign versus malignant thyroid tumors. *Clin Cancer Res* **14:** 3327–3337

Family history influences post-treatment survival in patients with advanced colon cancer

A family history of colorectal cancer in a first-degree relative (parent or sibling) is associated with an increased risk of developing the disease; however, it is uncertain whether family history influences recurrence or survival in patients with advanced colon cancer. Chan and colleagues investigated the outcomes of patients with stage III colon cancer who provided detailed information on their family history of colorectal cancer.

Data were analyzed from 1,087 patients enrolled in the Cancer and Leukemia Group B (CALGB) 89803 study who received adjuvant chemotherapy after surgical resection of the primary tumor. A total of 195 (17.9%) patients reported a family history of colorectal cancer in a first-degree relative. During follow-up (median 5.6 years), the incidence of cancer recurrence or death was significantly lower in the 195 patients with a family history of colorectal cancer (29%, 95% CI 23–36%) than in the 892 without a family history (38%, 95% CI 35–42%). Further reductions in the risk of cancer recurrence and mortality were observed as the number of affected relatives increased. The link between family history and outcome was independent of tumor characteristics.

The authors suggest that a number of genetic and environmental factors might influence the relationship between family history and post-treatment outcome, and they recommend further studies to determine the mechanisms responsible for reducing recurrence and mortality in patients with colon cancer who have a family history of colorectal cancer.

Original article Chan JA *et al.* (2008) Association of family history with cancer recurrence and survival among patients with stage III colon cancer. *JAMA* **299:** 2515–2523

© 2008 Macmillan Publishers Limited. All rights reserved