

British Association of Endocrine Surgeons Abstracts

The following abstracts were presented at the Millennium Meeting of the British Association of Endocrine Surgeons held in conjunction with the American Association of Endocrine Surgeons and the Swedish Association of Endocrine Surgeons, in London and Lille on 22–25 May 2000.

Role of frozen section, sex, age and tumour size in differentiating follicular adenoma from carcinoma: a meta-analysis

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Background: Frozen section (FS) has been the mainstay of intraoperative decision-making in thyroid neoplasms for many years. However, since the widespread use of preoperative fine-needle aspiration, the need for FS in patients with follicular neoplasms (FNs) has been debated. Preoperative features may be better at distinguishing follicular carcinoma (FC) from adenoma (FA). One reason why these issues are unresolved is because clinical studies are often too small to reach statistical significance. The purpose of this study was to combine modern trials and use the technique of meta-analysis to determine the efficacy of FS and the role of sex, age and tumour size in patients with FNs.

Methods: Inclusion criteria were published and unpublished studies between 1990 and 1999 inclusive, in which patients had a permanent pathology (PP) diagnosis of FA or FC (including Hurthle cell tumours) and underwent FS or had clinical features recorded. A pooled sample of the combined data was analysed for the prognostic variables and outcomes. $P < 0.05$ was considered significant.

Results: Nineteen studies were included. FS was evaluated in 11 studies ($n = 2204$). FS matched PP in 82 per cent of patients and was considered helpful. FS was indeterminate in 13 per cent of cases and was considered unhelpful. FS was detrimental in 4 per cent of patients. In 27 per cent of FCs, FS reported FA (false negative) and in 1 per cent of FAs, FS reported FC (false positive). Overall, FS had an 87 per cent sensitivity, 48 per cent specificity, 92 per cent positive predictive value, 35 per cent negative predictive value and 82 per cent accuracy. Clinical features were examined in ten studies ($n = 1980$). Nine studies ($n = 1780$) reported sex; 20 per cent of patients were male. A disproportionately high percentage of patients with FC were male (28 per cent) compared with female ($P < 0.001$). Two studies ($n = 548$) reported age; 36 per cent of patients were over 50 years old. A disproportionately high percentage of patients

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with FC were aged over 50 years (52 per cent) compared with those younger than 50 years ($P < 0.001$). Six studies ($n = 1620$) reported tumour size; 19 per cent of FNs were larger than 3–5 cm. A disproportionately high percentage of FCs were larger than 3–5 cm (33 per cent) compared with smaller lesions ($P < 0.001$).

Conclusion: FS is able to differentiate FC from FA in over 80 per cent of patients. It has a false-positive rate of less than 1 per cent and therefore may be trusted most when it reports a FC. In cases in which FS reports FA, male sex, age greater than 50 years and tumour size larger than 3–5 cm can be used as indicators that a FN will be a FC.

Screening for genetic aberrations in papillary thyroid cancer using comparative genomic hybridization

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Background: Papillary thyroid carcinomas (PTCs) are a heterogeneous group of neoplasms that display a wide variability in clinical behaviour. Knowledge of the genetic composition of these tumours may help improve prognostication, but is currently limited. The aim of this study was to identify the genetic composition of pathologically low-risk papillary thyroid cancers and identify differences based on age, using a powerful, genome-wide analytical technique, comparative genomic hybridization (CGH).

Methods: Tumour samples from patients with pathologically confirmed well differentiated PTC, less than 4 cm in size and without extrathyroidal extension or distant metastasis, were procured from the institutional tumour bank. CGH analysis was performed by differentially labelling tumour and normal DNA with fluorescent agents. The labelled DNAs were coprecipitated and simultaneously hybridized to normal metaphase chromosomes on glass slides. After chromosomal segregation, computerized image analysis was performed to detect fluorochrome intensity along the entire length of each chromosome. The ratio of fluorescent signal intensity was used