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IN BRIEF

BREAST CANCER

Assay for sentinel lymph node avoids second surgery

In patients with breast cancer, if the lymph node is involved, second surgery in the form of axillary lymph-node (ALN) resection is carried out, which can delay adjuvant treatment. In a retrospective study of 381 patients with early stage breast cancer, 100 patients were assessed using conventional histopathology, and 281 patients were assessed using the intraoperative one-step nucleic acid amplification (OSNA) assay. The OSNA assay for intraoperative SLN analysis allowed immediate ALN resection, significantly reduced the re-intervention rate (9% versus 39%) and accelerated the initiation of adjuvant therapy. Thus, OSNA avoids the need for second surgery, and reduces the time to adjuvant therapy.

Original article Klingler, S. *et al.* Using one-step nucleic acid amplification (OSNA) for intraoperative detection of lymph node metastasis in breast cancer patients avoids second surgery and accelerates initiation of adjuvant therapy. *Ann. Oncol.* doi:10.1093/annonc/mdt160

GENETICS

Methylation patterns in thyroid cancer identified

The global patterns of aberrant DNA methylation in thyroid cancer have been determined for the first time using DNA arrays. Encompassing the major tumour subtypes, the study identified 262 genes that are hypermethylated in differentiated papillary tumours, and 13 that are hypomethylated; in follicular tumours, 352 hypermethylated and 21 hypomethylated genes were detected. By contrast, anaplastic and medullary tumours had greater levels of hypomethylation than hypermethylation. Eight genes of interest were affected by aberrant methylation: the potential tumour suppressors *ADAMTS8*, *HOXB4*, *ZIC1* and *KISS1R* and oncogenes *INSL4*, *DPPA2*, *TCL1B* and *NOTCH4*.

Original article Rodríguez-Rodero, S. *et al.* DNA methylation signatures identify biologically distinct thyroid cancer subtypes. *J. Clin. End. Met.* doi:10.1210/jc.2012-3566

GENETICS

New susceptibility loci for testicular cancer identified

Two new studies have added to the body of knowledge on the chromosomal loci associated with testicular germ cell tumour (TGCT), which is known for high familial risk. The first, a meta-analysis, involved the analysis of >900 men with TGCT and >1,900 controls included in three genome-wide association studies (GWAS). The study identified four previously unknown loci for this cancer type (4q22.2, 7p22.3, 16q22.3 and 17q22), all of which contain genes plausibly involved in germ cell development, chromosomal segregation and DNA repair. The second study revealed nine loci by GWAS on >300,000 single nucleotide polymorphisms from >900 patients and >4,900 controls. The loci identified account for an additional 4–6% of the familial risk of TGCT to what was previously known. *DAZL* and *PRDM14*, which are involved in germ cell development and specification, respectively, are located in these mutational ‘hot spots’ and might be implicated in the disease.

Original articles Chung, C. C. *et al.* Meta-analysis identifies four new loci associated with testicular germ cell tumor. *Nat. Genet.* doi:10.1038/ng.2634 | Ruark, E. *et al.* Identification of nine new susceptibility loci for testicular cancer, including variants near *DAZL* and *PRDM14*. *Nat. Genet.* doi:10.1038/ng.2635