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IN BRIEF

TARGETED THERAPIES

Alisertib tested in patients with solid tumours

The results of a phase I/II study reveal that the selective aurora kinase A inhibitor alisertib might be an effective treatment of a range of solid tumours. Following oral administration of alisertib, partial responses to therapy were detected in some patients with breast (18%), small-cell lung (21%) or non-small-cell lung (4%), gastroesophageal (9%), or head and neck cancers (9%). In total, 43% of patients reported serious adverse events. Further testing, in phase III clinical trials, is required to establish the efficacy of alisertib.

Original article Melichar, B. *et al*. Safety and activity of alisertib, an investigational aurora kinase A inhibitor, in patients with breast cancer, small-cell lung cancer, non-small-cell lung cancer, head and neck squamous-cell carcinoma, and gastro-oesophageal adenocarcinoma: a five-arm phase 2 study. *Lancet Oncol.* doi:10.1016/S1470-2045(15)70051-3

GENETICS

New genomic alterations detected in pancreatic cancer

An investigation using whole-genome sequencing and copy-number variation analysis of 100 pancreatic ductal adenocarcinomas has identified several new candidate genes that might act as 'drivers' of pancreatic carcinogenesis. These candidates include PIP_3-dependent RAC1 guanine nucleotide exchange factor (*PREX2*) and lysine-specific demethylase 6A (*KDM6A*). A substantial number of the tumours analysed had focal amplifications of targetable oncogenes (such as *HER2*, *MET and FGFR1)*; however, none of these specific amplifications was highly prevalent.

Original article Waddell, N. *et al*. Whole genomes redefine the mutational landscape of pancreatic cancer. *Nature* **518**, 495–501 (2015)

BREAST CANCER

Meta-analysis reveals new breast cancer risk loci

A new meta-analysis of genome-wide association studies consisting of >15,000 women of European ancestry with breast cancer has identified 15 new breast cancer-susceptibility loci. Using association analyses, probable gene targets of these susceptibility loci were identified at 18q12.3 and 1q21.1. Inclusion of these new genetic loci in polygenic evaluations of familial breast cancer risk might result in an improvement in our ability to discriminate between women with a high risk and low risk of breast cancer.

Original article Michailidou, K. *et al*. Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nat. Genet.* doi:10.1038/ng.3242

PAEDIATRIC CANCER

Adrenocortical cancer mutations are prognostic for survival

Findings from whole-genome, whole-exome and/or transcriptome sequencing of 37 paediatric adrenocortical tumours have demonstrated the prognostic importance of specific mutations. 100% of tumours had *IGF2* overexpression, and the majority (78%) had *TP53* mutations. The presence of concomitant mutations was found to be predictive of clinical outcome; in particular, the presence of concomitant somatic *ATRX* and germline *TP53* mutations was associated with significantly worse event-free survival and higher disease stage.

Original article Pinto, E. M. *et al*. Genomic landscape of paediatric adrenocortical tumours. *Nat. Commun.* doi:10.1038/ncomms7302