Nature Reviews Clinical Oncology **10**, 606 (2013); published online 3 September 2013;
doi:10.1038/nrclinonc.2013.165;
doi:10.1038/nrclinonc.2013.166;
doi:10.1038/nrclinonc.2013.167

IN BRIEF

IMAGING

MRI technique potentially predicts antiangiogenic response

A new MRI-based technique—vessel architectural imaging (VAI)—combines two magnetic resonance parameters (gradient-echo and spin-echo) to determine the haemodynamic properties of blood vessels. In doing so, the vessels can be distinguished from each other (whether arteries, veins or capillaries), the vessel radii can be measured and the oxygen level being delivered to tissues can be determined. Using the technique in patients with recurrent glioblastoma being treated with the pan-VEGF receptor inhibitor cediranib, researchers showed 10 out of 30 patients demonstrated normalization of vessel architectures after therapy onset. A further 12 patients were classified as nonresponders on the basis of VAI. Importantly, the responders had a longer median overall survival (341 days) compared with nonresponders (146 days), which suggests that VAI might be useful in selecting patients likely to benefit from antiangiogenic therapies.

Original article Emblem, K. E. *et al.* Vessel architecture imaging identifies cancer patient responders to anti-angiogenic therapy. *Nat. Med.* doi:10.1038/nm.3289

GENETICS

SNPs associated with multiple myeloma identified

A new genome-wide association study has assessed samples from more than 4,500 individuals with multiple myeloma, comparing the genetic variation against almost 11,000 controls. From this large dataset, four single nucleotide polymorphisms (SNPs) were identified that are significantly associated with this haematological malignancy. The SNPs are rs10936599 (at 3q26.2, which maps within a region that also encompasses *TERC*, the telomerase RNA component gene), rs2285803 (at 6p21.33), rs4273077 (at 17p11.2, mapping within *TNFRSF13B*, which encodes a regulator of B-cell and T-cell function) and rs877529 (at 22q13.1, which is localized to intron 2 of *CBX7*, whose product is involved in determining cell fate in development and the control of cell growth and differentiation). Combined with loci already identified, these data account for approximately 13% of the familial risk of multiple myeloma.

Original article Chubb, D. *et al.* Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. *Nat. Genet.* doi:10.1038/ng.2733

HAEMATOLOGICAL CANCER

Compromised cohesin complex in myeloid leukaemias

Using samples of acute myeloid leukaemia ($n=157$), myelodysplastic syndrome ($n=224$), chronic myelomonocytic leukaemia ($n=88$), chronic myelogenous leukaemia ($n=64$) and classical myeloproliferative neoplasm ($n=77$), researchers have identified a series of recurrent mutations and deletions, all of which are associated with the cohesin complex. The affected genes were identified using high-throughput sequencing and included *STAG2*, *SMC1A*, *RAD21* and *SMC3*, mutations and deletions of which were generally mutually exclusive. However, these mutations frequently coexisted with mutations in other genes known in myeloid neoplasms, including *TET2*, *ASXL1* and *EZH2*. The multimeric cohesin complex is involved in sister chromatid cohesion after DNA replication, DNA repair and transcriptional regulation.

Original article Kon, A. *et al.* Recurrent mutation in multiple components of the cohesin complex in myeloid neoplasms. *Nat. Med.* doi:10.1038/nm.3289