In the news

CANCER CODE CRACKED?

The entire genome sequences of two individual cancers — one small-cell lung cancer and one melanoma — have revealed the staggering number of mutations present in tumour cells compared with normal cells from the same patient.

The research, published in *Nature*, was led by Peter Campbell, Michael Stratton and Andrew Futreal at the Wellcome Trust Sanger Institute, UK. The group is part of the International Cancer Genome Consortium, which involves 10 countries and aims to analyse the genomes of the 50 most common cancers. Campbell and colleagues identified almost 23,000 somatic mutations in the lung cancer, most of which seemed to be caused by tobacco carcinogens, and Stratton, Futreal and colleagues found more than 33,000 in the melanoma, in which, as Futreal noted, "we can see sunlight's signature writ large" (*The Independent*, 18 Dec 2009).

Although this research was hailed with headlines such as "We're winning the war on cancer" (*The Telegraph*, 18 Dec 2009) and "Scientists crack 'entire genetic code' of cancer" (*BBC News*, 16 Dec 2009), most acknowledged that much work must be done before these findings lead to improved patient care. One hurdle is identifying which mutations are 'drivers', a point emphasized by Harpal Kumar, chief executive of Cancer Research UK. "The next step will be to find out which of these thousands of mutations are just collateral damage, and which actually drive these cancers. Only then can we begin to find ways to correct or prevent them." (*The Times*, 17 Dec 2009).

Other hurdles are costs and time. Each genome pair cost around UK£60,000 (US$100,000) and took several months. This is improving, though, and Stratton was optimistic: "I can envisage a time a decade or more hence when these catalogues will become routine, and influential in selecting treatment for that individual." (*The Times*, 17 Dec 2009).

Sarah Seton-Rogers