Molecular testing in advanced / metastatic disease

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- There are clear national standards on which codons to test
- The results should be integrated with the diagnostic pathology, not issued as standalone molecular reports

KRAS 12
KRAS 13
KRAS 59
KRAS 61
KRAS 117
KRAS 146

NRAS 12
NRAS 13
NRAS 59
NRAS 61

BRAF 600

RAS testing of colorectal carcinoma—a guidance document from the Association of Clinical Pathologists Molecular Pathology and Diagnostics Group

Newton ACS Wong,[1] David Gonzalez,[2] Manuel Salto-Tellez,[3] Rachel Butler,[4] Salvador J Diaz-Cano,[5] Mohammad Ilyas,[6] William Newman,[7] Emily Shaw,[8] Philippe Taniere,[9] Shaun V Walsh[10]

J Clin Pathol 2014;**67**:751–757.

The Royal College of Pathologists
Pathology: the science behind the cure

Standards for integrated reporting in cellular pathology

January 2017

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- There is no good evidence for which sample to test (biopsy vs. resection vs. metastasis)
- Testing multiple blocks from the primary resection is our preferred strategy to increase the chances of detecting a mutation

Analytical Cellular Pathology 34 (2011) 61–66
DOI 10.3233/ACP-2011-0005
IOS Press

Intra-tumoral heterogeneity of *KRAS* and *BRAF* mutation status in patients with advanced colorectal cancer (aCRC) and cost-effectiveness of multiple sample testing

Take sections from up to 5 blocks of the tumour and test together

Molecular testing in advanced / metastatic disease

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- Molecular testing is currently undergoing a major overhaul

Annual Report of the Chief Medical Officer 2016

1.2 National standards and streamlined laboratory services

We need to review and improve the way that genomic medicine is organised within the NHS.

the scale of the modern NHS and the opportunities offered by genomic medicine mean it is now time to build a first-class genomic service that is scalable, future-proof and delivers value for money. The aim must be an equitable service with higher throughput and at a lower cost than is currently achieved. This can only be done through national standards and centralised genomic laboratories and related services.

This will inevitably mean fewer laboratories doing different types of work. Running fewer sequencing machines at full capacity allows sequencing to be affordable, standardised and accessible for updates. These laboratories will be different from those we had in the past, as the nature of the expertise needed in the NHS is changing. The interpretation and analysis of genomic data now involves high-powered computing, not banks of test tubes.

Likely to see more fresh tumour collection and multigene panels leading to whole genome sequencing