FROM THE FDITORS









SARAH SETON-ROGERS







TERESA VILLANUEVA

t is often claimed that the use of protein biomarkers will provide the means to 'personalize' the treatment of cancer patients. A plethora of proteomics-based papers have identified potential biomarkers for predicting prognosis, classifying tumours and identifying responders to specific therapies. But why are so few biomarkers used in the clinic?

Proteomics techniques have improved substantially in the past decade, and this has allowed researchers to screen various types of samples, including formalin-fixed paraffin-embedded tissue samples (see the Science and Society article on page 646), for changes in the cancer proteome that could be used to classify patients. However, the need for effective validation and standardization of procedures to improve reproducibility, sensitivity and specificity is impeding the translation of biomarkers to the clinic. As discussed on page 605, this process might be improved through the use of established clinical assays to detect biomarkers. In addition, the Timeline article on page 652 suggests that the cancer proteome could be better characterized and translated to the clinic through large collaborative projects.

Of course, biomarkers are not the only application of proteomics to cancer research. For example, as discussed on page 618, proteomic techniques are being used to more precisely characterize altered signal transduction pathways in tumour cells. Proteomics-based methods can also be applied to drug development (see the Review on page 630) and tumour pathology to acquire detailed molecular and spatial information, as detailed on page 639. So perhaps proteomics, rather than biomarkers, could be the answer to the personalized care of cancer patients.

This issue focuses on the different applications of proteomics to cancer research, as well as the issues surrounding this field, and is available online at www.nature.com/nrc/focus/proteomics.

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