

GENETICS

Identifying CUP tumours with PCR

A prospective trial has shown that gene-expression profiling can predict the tissue of origin from biopsy specimens of patients with carcinomas of unknown primary site (CUPs), and this information can direct therapy towards improving overall survival.

Patients with CUPs tend to do worse than those with identifiable malignancies because they are treated with 'empiric' chemotherapy (for example, cytotoxic agents). "As treatments for various solid tumours continue to develop and diverge, the benefit of accurate identification of the tissue of origin and subsequent site-specific treatment will continue to increase," investigator John Hainsworth explained. Of the 289 patients enrolled, enough tissue was harvested from 252 and a 92-gene PCR assay made a prediction for 247 (98%). Of these, 194 patients went on to receive treatment based on this information. Median survival time was 12.5 months, which compares favourably against the typical 9-month median survival of patients treated empirically.

Outcomes were also better when considering subsets of patients. For example, the PCR assay predicted the site of origin with a probability $\geq 80\%$ in 95 patients (49% of those who received directed treatment). These patients did significantly better than the remaining patients with probabilities $< 80\%$ (12.5 months versus 10.8 months).

Despite these promising results, some questions remain unanswered. "We will compare the predictions of three assays in a large group of biopsies from patients with CUP," Hainsworth continues, "and hope to determine whether actionable mutations occur frequently in the CUP population to further direct treatment."

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Original article Hainsworth, J. D. *et al.* Molecular gene expression profiling to predict the tissue of origin and direct site-specific therapy in patients with carcinoma of unknown primary site: a prospective trial of the Sarah Cannon Research Institute. *J. Clin. Oncol.* <http://dx.doi.org/10.1200/JCO.2012.43.3755>