TESTICULAR CANCER

Identifying occult metastatic seminoma using two small RNAs

Researchers have identified a number of small RNAs that are differentially expressed in testicular tumours from patients with nonmetastatic and metastatic disease. Michael Abend and colleagues report that detection of just two of these small RNAs can completely discriminate between nonmetastatic and metastatic disease.

About 30% of men with clinical stage 1 testicular seminoma are estimated to harbour occult metastases and, therefore, experience recurrence after orchidectomy. The ability to identify these patients before they undergo surgery would enable clinicians to tailor adjuvant treatment or follow-up monitoring accordingly, but the lack of appropriate predictive factors currently prevents such stratification.

Abend and colleagues used next-generation sequencing to search the genome for small RNAs that could differentiate between nonmetastasized seminoma and metastatic disease (lymphogenic, occult or either). They analysed testicular tumour samples from five patients with nonmetastatic seminoma who had not received any adjuvant treatment and did not experience progression for at least 2 years, five patients who presented without visible metastasis and did not receive adjuvant therapy but later experienced retroperitoneal progression and five patients who presented with lymphogenic metastasis (clinical stage IIb–c).

Univariate analysis revealed 35, 32 and 38 small RNA species that were differentially expressed between nonmetastatic seminoma and lymphogenic, occult and combined subtypes, respectively. Using support vector machines, the investigators found that various combinations of two small RNAs could completely distinguish each metastatic subtype from nonmetastasized seminoma; 125 combinations were able to identify lymphogenic and 53 combinations differentiated occult metastasis from nonmetastatic disease.

Despite the small sample size of this study, the authors believe their findings
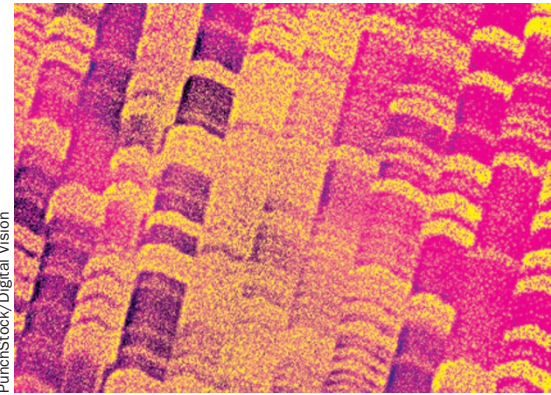
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have considerable diagnostic potential for the prediction of metastasis and treatment decision-making. They hope their candidate small RNAs will be validated in larger studies.

Sarah Payton

Original article Ruf, C. G. *et al.* Discriminating metastasised from non-metastasised seminoma based on transcriptional changes in primary tumours using NGS. *Br. J. Cancer* doi:10.1038/bjc.2014.134