GENETICS

Predicting outcomes in patients with neuroblastoma

The current stratification system for patients with neuroblastoma is inaccurate and often leads to patients receiving the wrong treatment. Vermeulen and colleagues sought to develop a multigene-expression signature to improve prediction of prognosis in children with neuroblastoma, a condition that often proves to be fatal. The researchers assessed 59 gene signatures and used real-time polymerase chain reaction to profile 579 patients with neuroblastoma. In total, 30 randomly selected training samples were used to build a multigene-expression signature, which was tested on 313 samples and validated on an independent cohort of 236 tumors.

With regard to predicting patients' outcomes, the signature had a performance, sensitivity and specificity of 85.4%, 84.4% and 86.5%, respectively. After controlling for the following risk factors—patients with a high molecular

risk of death and high risk of relapse or progression—multivariate analysis revealed that the signature was an independent predictor of overall survival and progression-free survival. The validation study confirmed these results.

The authors conclude that the signature can be used as an independent predictor to identify patients with increased risk. The speed of the method and the smaller amounts of starting material required are some of the important advantages of this signature compared with previously published gene-expression classifiers. These promising results should now be evaluated in large, international, prospective studies.

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Original article Vermeulen, J. *et al.* Predicting outcomes for children with neuroblastoma using a multigene-expression signature: a retrospective SIOPEN/COG/GPOH study. *Lancet Oncol.* **10**, 663–671 (2009).