NOVEL PROGNOSTIC SNP IN CN-AML

Recent work has identified a single nucleotide polymorphism (SNP) as a novel prognostic marker in cytogenetically normal acute myeloid leukemia (CN-AML). Frederik Damm and colleagues located this SNP in the mutational hotspot of Wilms tumor 1 (*WT1*) in individuals with CN-AML and found it to be an independent predictor of a favorable outcome in these patients. *"WT1* has been an interesting gene in hematology for almost 20 years, and we wanted to conduct a combined analysis on *WT1* expression and mutations," comments Damm.

The researchers sequenced exon 7 and exon 9 of WT1 in 249 patients with CN-AML and 50 healthy controls, and analyzed the data for associations between mutations in the WT1 sequence and disease outcome. Damm's team found the minor allele of the SNPtermed rs16754 (WT1^{AG/GG})—in 25.7% of patients with CN-AML and 36% of healthy participants. Overall, although SNP rs16754 was not associated with disease susceptibility, it was favorably prognostic in individuals with CN-AML, and predicted relapse-free survival (hazard ratio (HR) 0.49, 95% CI 0.3-0.81, P=0.005) and overall survival (HR 0.44, 95% CI 0.27–0.74, P=0.002). By contrast, no other molecular marker (including NPM1 or CEBPA) could identify a favorable prognosis in these patients.

Interestingly, the prognostic strength of SNP rs16754 was elevated in patients classified as high-risk on the basis of *NPM1/FLT3*-internal tandem duplications, a finding that might have important clinical utility. "As highrisk patients normally undergo bone marrow transplantation, with the risk of transplant-related mortality, it is of clinical importance to identify patients who are likely to benefit from a bone marrow transplantation," concludes Damm, who predicts that "our study might help to address this issue".

Rowan Higgs

Original article Damm, F. *et al.* Single nucleotide polymorphism in the mutational hotspot of *WT1* predicts a favorable outcome in patients with cytogenetically normal acute myeloid leukemia. *J. Clin. Oncol.* **28**, 578–585 (2010)

RESEARCH HIGHLIGHTS