PET predicts progression or relapse in patients with advanced Hodgkin lymphoma

One of the main goals of treatment for patients with Hodgkin lymphoma is to reduce treatment toxicity while maintaining its efficacy. The HD15-PET trial performed by the German Hodgkin Study Group (GHSG) evaluated the negative predictive value of ^{18}FDG-PET in patients with HL who were treated with chemotherapy.

This substudy of the HD15 trial included patients with Hodgkin lymphoma who had received 6–8 cycles of cyclophosphamide, adriamycin, etoposide procarbazine, prednisone, vincristine and bleomycin (BEACOPP). Of 817 patients available for this interim analysis, 311 patients had residual tumor ≥2.5 cm as assessed by CT, among whom 66 had ^{18}FDG-PET results indicative of active disease (PET-positive) and 245 had ^{18}FDG-PET results indicative of inactive disease (PET negative). PET-positive patients received 30 Gy radiotherapy to residual masses, while PET-negative patients were followed up without radiotherapy. Progression-free survival 12 months after ^{18}FDG-PET was 85% and 96% for PET-positive and PET-negative patients, respectively ($P = 0.011$). The negative predictive value of PET was defined as the proportion of PET-negative patients without relapse, progression, or radiotherapy within the 12 months after ^{18}FDG-PET, and its value was 94% (range, 91–97%).

The authors suggest that PET-negative patients with HL do not need to receive radiotherapy after chemotherapy, and that omission of radiotherapy does not increase the risk for early relapse or progression.

Original article Kobe C *et al.* (2008) Positron emission tomography has a high negative predictive value for progression or early relapse for patients with residual disease after first-line chemotherapy in advanced-stage Hodgkin lymphoma. *Blood* **112:** 3989–3994

Novel gene signature predicts outcome in patients with cytogenetically normal AML

In patients with acute myeloid leukemia (AML), chromosomal abnormalities can affect gene-expression profiles and, therefore, genes that have been identified as having a predictive role might not represent suitable prognostic factors for outcome in patients with cytogenetically normal AML (CN-AML). Metzeler *et al.* recently reported a 66-gene signature that predicts overall survival in patients with CN-AML.

The authors analyzed data from 163 adult patients with CN-AML who were enrolled in the AMLCG 1999 trial and had received intensive induction and consolidation chemotherapy. Gene-expression profiling was performed using microarrays. A supervised principal components analysis identified 86 probe sets that corresponded to 66 genes significantly associated with overall survival. When the authors analyzed the treatment outcomes in an independent group of 79 CN-AML patients, a high-risk genotype score was a significant negative prognostic factor for overall survival and event-free survival ($P = 0.002$ and $P = 0.001$, respectively). Moreover, in patients in complete remission, a high-risk genotype score was associated with reduced relapse-free survival ($P = 0.025$). In a validation cohort of 64 patients treated in the CALGB 9621 study, this risk score was also negatively associated with overall survival and event-free survival ($P < 0.001$). Patients with a high-risk score in complete remission had reduced relapse-free survival ($P < 0.001$). After adjusting for age, the ratio between *FLT3* alleles with internal tandem duplications: wild type and *NPM1* mutation status, and the gene-expression score continued to predict overall and event-free survival.

This novel gene signature predicts outcome in patients with CN-AML. Future studies assessing its clinical utility in AML patients with aberrant karyotypes are warranted.

Original article Metzeler KH *et al.* (2008) An 86-probe-set gene-expression signature predicts survival in cytogenetically normal acute myeloid leukemia. *Blood* **112:** 4193–4201

Computer-aided detection is an alternative to double-reading mammography

Single-reading mammography is standard practice in the US and computer-aided systems have been widely implemented to improve detection of breast cancer. In many European countries use of two readers to interpret the mammogram is standard practice and this double-reading increases the rate of detection for small tumors.