studies investigating the inhibition of c-kit in patients with AML are ongoing.

Original article Advani AS *et al.* (2008) Increased c-kit intensity is a poor prognostic factor for progression-free and overall survival in patients with newly diagnosed AML. *Leuk Res* **32:** 913–918

High *BAALC* expression is indicative of poor survival in acute myeloid leukemia

High *BAALC* expression is known to be a predictor of poor outcome in patients with cytogenetically normal acute myeloid leukemia (CN-AML). Langer *et al.* investigated the relationship between *BAALC* and other genetic markers of poor prognosis in 172 patients with CN-AML who were <60 years old.

Patients with high *BAALC* expression were more likely than those with low expression to have *FLT3* internal tandem duplication (44% vs 28%), *MLL* partial tandem duplication (15% vs 3%), *NPM1* wild-type alleles (48% vs 17%), *CEBPA* mutations (32% vs 10%), and high *ERG* expression (45% vs 29%). After controlling for other significant variables, high *BAALC* expression was an independent predictor of poor response to treatment (odds ratio 0.27 for complete remission) and overall survival (hazard ratio 1.84); *BAALC* was not, however, an independent predictor of disease-free survival.

Gene-expression profiling revealed that high *BAALC* expression was associated with upregulation of stem-cell markers and of genes involved in drug-resistance mechanisms such as *ABCB1*, which encodes P-glycoprotein. An inverse correlation was seen between expression levels of the putative *BAALC*-binding microRNA miR-148a and *BAALC*. Additionally, lower levels of miR-148a were observed in patients with CN-AML than in healthy individuals.

The authors conclude that high *BAALC* expression is associated with a less-differentiated gene signature and independently predicts poor treatment response and survival in patients with CN-AML. MicroRNA miR-148a might be a negative regulator of *BAALC* expression.

Original article Langer C *et al.* (2008) High BAALC expression associates with other molecular prognostic markers, poor outcome, and a distinct gene-expression signature in cytogenetically normal patients younger than 60 years with acute myeloid leukemia: a Cancer and Leukemia Group B (CALGB) study. *Blood* **111:** 5371–5379

Extent of poorly differentiated carcinoma is an effective grading tool

The TNM and WHO classification systems grade tumors into four categories according to degree of cell differentiation; however, the grades are defined on the basis of subjective judgment, which can differ between clinicians. A major problem with these systems is that the definition of the least differentiated tumor grade has not been standardized. Ueno and colleagues, therefore, considered how the extent of poor differentiation could be used to grade tumors and predict patient outcomes.

Data were analyzed from 1,075 Japanese patients (average age 62 years, 624 male) with advanced colorectal cancer who underwent tumor resection. Poorly differentiated regions were defined strictly as those with no glandular structure. Grade categories were based on the total area of poorly differentiated cells, as viewed under a microscope: tumors with <10 clusters of ≥5 poorly differentiated cells were classified as grade I (161 patients); tumors with ≥10 such clusters as grade II (575 patients); and tumors with poorly differentiated cells covering the entire microscopic field at 40 × magnification as grade III (339 patients). Patients with grade I tumors had the best prognosis, with a 99.3% 5-year cancer-specific survival rate, compared with 86.0% and 68.9% for grade II and III tumors, respectively.

In comparison with the WHO and TNM grading systems, which define poorly differentiated tumors as those with 'some' gland formation or mucin production, Ueno *et al.* believe that quantification of regions without glandular formation provides objective results, and could be a practical system for tumor grade standardization and selection of optimal postoperative therapy.

Original article Ueno H *et al.* (2008) Histological grading of colorectal cancer: a simple and objective method. *Ann Surg* **247:** 811–818

Identification of malignant thyroid tumors by differential gene expression

Thyroid tumors can often be difficult to identify as benign or malignant by cytological examination.