Dokumenttyp: journal article

Autor(en) des Beitrags:
Paschka, P; Du, J; Schlenk, RF; Gaidzik, VI; Bullinger, L; Corbacioglu, A; Späth, D; Kayser, S; Schlegelberger, B; Krauter, J; Ganser, A; Köhne, CH; Held, G; von Lilienfeld-Toal, M; Kirchen, H; Rummel, M; Götze, K; Horst, HA; Ringhoffer, M; Lübbert, M; Wattad, M; Salih, HR; Kündgen, A; Döhner, H; Döhner, K

Titel des Beitrags:
Secondary genetic lesions in acute myeloid leukemia with inv(16) or t(16;16): a study of the German-Austrian AML Study Group (AMLSG).

Abstract:
In this study, we evaluated the impact of secondary genetic lesions in acute myeloid leukemia (AML) with inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CBFB-MYH11. We studied 176 patients, all enrolled on prospective treatment trials, for secondary chromosomal aberrations and mutations in N-/KRAS, KIT, FLT3, and JAK2 (V617F) genes. Most frequent chromosomal aberrations were trisomy 22 (18%) and trisomy 8 (16%). Overall, 84% of patients harbored at least 1 gene mutation, with RAS being affected in 53% (45% NRAS; 13% KRAS) of the cases, followed by KIT (37%) and FLT3 (17%; FLT3-TKD [14%], FLT3-ITD [5%]). None of the secondary genetic lesions influenced achievement of complete remission. In multivariable analyses, KIT mutation (hazard ratio [HR] = 1.67; P = .04), log(10)(WBC) (HR = 1.33; P = .02), and trisomy 22 (HR = 0.54; P = .08) were relevant factors for relapse-free survival; for overall survival, FLT3 mutation (HR = 2.56; P = .006), trisomy 22 (HR = 0.45; P = .07), trisomy 8 (HR = 2.26; P = .02), age (difference of 10 years, HR = 1.46; P = .01), and therapy-related AML (HR = 2.13; P = .14) revealed as prognostic
factors. The adverse effects of KIT and FLT3 mutations were mainly attributed to exon 8 and tyrosine kinase domain mutations, respectively. Our large study emphasizes the impact of both secondary chromosomal aberrations as well as gene mutations for outcome in AML with inv(16)/t (16; 16).