phase and blast crisis (AP and BC) of CML may show additional oncogene aberrations and pronounced anaemia manifested by an increase in organomegaly and blast count. The abnormal expression of some proto-oncogenes which may accompany or even precede BC of CML warrants their study. Aim. The follow-up of oncogene expression during the course of CML. Methods. We studied 85 patients (pts.) with the median age of 50 (15-82). At the commencement of the study, 63 pts. were in CP, 25 in an AP, and 31 in the BC. The temporal expression (percentage positivity per 1000 analysed cells) of c-kit, c-myc, H-Ras, cyclin A1, p53, bcl-2 and VEGF proto-oncogene proteins over the course of CML was studied using the immunohistochemical technique which utilizes relevant monoclonal antibodies. It was correlated with the laboratory (Hb, WBC and platelet counts, and the percentage of blasts) and clinical parameters (organomegaly, duration of CP, AP, and BC) of disease progression. Results. The level of c-kit expression differed significantly in time with the largest values observed in the BC (x2, p=0.025). The level of anti-apoptotic protein bcl-2 increased significantly with the progression of CML (x2, p=0.005). Conversely, the expression of c-myc was highest in CP (x2, p=0.035). The expression of VEGF protein was most pronounced in an AP (ANOVA, p=0.033). There was no significant difference in the level of expression of H-Ras, cyclin A1 and p53 over the course of CML. The level of VEGF expression correlated inversely with degree of organomegaly (Pearson, r=-0.406, p=0.011). The c-kit expression correlated directly with the extent of marrow fibrosis (Spearman, r=0.407, p=0.000). High expression of VEGF correlated with a longer duration of CP (log rank, p=0.0304) and with a longer overall survival (log rank, p=0.042). Conclusion. The significance of changes in oncogene expression, estimated by a histochemical approach over the course of CML, has an important influence on the course and treatment with imatinib. The details of the temporally-related changes in oncogene protein expression in leukemic cells require the study at the molecular level.

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**PI90 BCR-ABL CHRONIC MYELOID LEUKEMIA PARTLY RESEMBLING CHRONIC MYELOMONOCYTIC LEUKEMIA IN A YOUNG PATIENT TREATED WITH IMATINIB**

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Background. In Ph-positive CML, the breakpoint on the BCR gene nearly always occurs within the major breakpoint cluster region (M-bcr), and the BCR-ABL fusion gene encodes a protein of 210 kDa molecular weight (P210). In most Ph-positive ALL, by contrast, the breakpoint on chromosome 22 occurs within the first intron of the BCR gene, or minor bcr (m-bcr). In these cases, the first BCR exon is fused to ABL exon 2 (e1a2 junction) and a BCR-ABL protein of 190 kDa is formed (P190). This form of CML was reported as having some unusual clinical and haematological features, partly resembling chronic myelomonocytic leukemia (Melo et al., 2001). We describe a 24 year-old female admitted to our hospital in July 2005 with leukaemia, when she volunteered as a blood donor. She was assymptomatic, with only splenomegaly detected on physical examination. The peripheral blood examination showed a WBC count of 29,7×10^9/L, basophilia (4%), mononucleosis (5%) and a platelet count of 713×10^9/L. No pseudo-Pelger-Huet hypolobulation or periph-

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**THE E19A2 BCR-ABL BREAKPOINT: MORE FREQUENT THAN OTHER ATYPICAL BCR-ABL VARIANTS IN CHRONIC MYELOGENOUS LEUKEMIA?**

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In the vast majority of patients diagnosed as having chronic myelogenous leukaemia (CML) and t(9;22), the breakpoint on chromosome 22 occurs in the major region of the BCR gene (M-BCR); this translocation usually results in a hybrid BCR-ABL mRNA with a b2a2 and/or b3a2 junction, which encodes a p210 fusion protein proved to be involved in the mechanism that underlines the chronic phase of CML. Here, we report 7 newly diagnosed chronic phase CML patients with an unusual e19a2 BCR-ABL transcript. The BCR breakpoint in this type of rearrangement occurs downstream from M-BCR, in the µ-BCR region, between exons e19 (c5) and e20 (c4). This novel translocation, previously reported in our group in only few patients, results in the transcription of e19a2 type BCR-ABL fusion mRNA, which is translated into a p230-KD BCR-ABL protein. We observed that in some patients e19a2 was associated with neutrophilic leukaemia while in the other patients the rare rearrangement was associated with a classical CML in chronic phase. In particular, in a 45-year-old male hemoglobin was 14.7 g/L, white blood cell count 71.8×10^9/L, neutrophils 64%, lymphocytes 8%, monocytes 2%, eosinophils 3%, basophils 5%, metamyelocytes 7%, myelocytes 9%, promyelocytes 2% and platelet count 277×10^9/L. In a 30-year-old female hemoglobin was 9.4 g/L, white blood cell count 108×10^9/L, neutrophils 60%, lymphocytes 4%, monocytes 4%, eosinophils 0.9%, basophils 4.2%, promyelocytes 9%, myelocytes 20% and platelet count 9.9×10^9/L. In all 7 patients cytogenetic analysis of 20 bone marrow

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