ANALYSIS OF PROGNOSTIC MARKERS IN MULTIPLE MYELOMA BY FLOW CYTOMETER

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Introduction

Multiple myeloma (MM) is characterized by a clonal accumulation of malignant plasma cells in the bone marrow. During the neoplastic progression an initially stable clone becomes malignant via a multistep process. Our aims were to find and observe molecules (CD27, CD28, CD29) which can help the early determination of prognosis and therapeutical response. We wanted to compare the protein expression levels and the genetic aberration status of malignant plasma cells.

Methods

Bone marrow aspirate specimens were tested on a 2-laser FACS Navios (Beckman Coulter) using Navios and Kaluza softwares. 50 MM and 10 healthy patients were immunophenotyped using direct 5 and 8 color immunofluorescence stains with different combination of monoclonal antibodies (CD38, acive CD29, CD27, CD28, CD29, CD81, CD20, CD19, CD56, CD138). Our samples were screened as part of the clinical workout by fluorescence in situ hybridization (FISH) for different translocations, deletions and mutations (probes: FGFR3/IGH DC, CEP17/LSI p53, 1q21/1p36). We determined CD27, CD28, CD29 expression or activity when more than 10% of abnormal plasma cells were positive, high expression were determined when more than 50% of abnormal plasma cells were positive.

Results

CD27 showed high expression in 36% of MM cases. CD28 expression was detected in 52% of MM samples, CD29 integrin appeared in active form in 69% of MM cases. CD28 high expression level and high bone marrow infiltration showed correlation in our MM cases. This expression data were independent from each other and did not show significant correlation with genetic status of patients. Normal plasma cells were CD27 positive, CD28 negative with CD29 activation in all cases.

Conclusion

We observed a tendency in high CD28 expression and high bone marrow infiltration. The examined molecules (CD27, CD28 and CD29) showed independent expression levels from each other.

Poszter, klinikai