EVALUATION OF CYTOGENETIC BIOMARKERS FOR RISK STRATIFICATION IN MULTIPLE MYELOMA PATIENTS ELIGIBLE FOR BONE MARROW TRANSPLANTATION IN A NORTHEASTERN BRAZILIAN STATE

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Multiple myeloma (MM) is a malignant hematologic neoplasm characterized by the deregulated clonal proliferation of plasma cells in the bone marrow, leading to the abnormal production and secretion of monoclonal immunoglobulin. MM is estimated to account for approximately 1% of all cancers. Among risk markers, cytogenetic abnormalities are predictive of diagnosis and prognosis in MM.This study aimed to evaluate the presence of key cytogenetic biomarkers using conventional cytogenetics and fluorescence in situ hybridization (FISH) targeting t(4;14)(p16;q32), t(11;14)(q13;q32), and del(17p) in treated MM patients eligible for bone marrow transplantation in a northeastern Brazilian state. Between Feb/24 and May/25, 30 patients were analyzed 56% female and 44% male with a mean age of 68 years. Conventional cytogenetic analysis was performed in 13 patients, five of whom (38.5%) presented abnormal karyotypes. FISH was performed in all patients and identified TP53 deletion in five patients (17%), gain of IGH gene signals in one patient (3.3%), and FGFR3 gene amplification in one patient (3.3%), associated with a karyotype showing t(8;22)(q24;q21).Analysis of clinical outcomes in relation to cytogenetic alterations revealed that all five patients with FISH abnormalities were eligible for transplant: one underwent transplant and is currently at D+365 with VGPR status; one underwent two transplants and experienced disease progression; one was contraindicated for autologous transplant due to chronic liver disease, had disease progression, initiated daratumumab therapy, but was lost to follow-up; and two are awaiting transplant scheduling.Patients with abnormal karyotypes but normal FISH results were diagnosed with monoclonal gammopathy of undetermined significance and were not transplant candidates. One patient presented both karyotypic and FISH abnormalities, is transplant-eligible, and is awaiting consultation for pre-conditioning.Additionally, six patients with normal karyotype and FISH underwent transplantation: two achieved complete response (CR) by D+180, three showed very good partial response (VGPR) by D+180, and one experienced post-autologous transplant relapse and remains on lenalidomide therapy. Del(17p) (TP53) occurs in approximately 20% of MM cases and is considered a high-risk secondary cytogenetic marker, associated with poor prognosis. Alterations involving the IGH gene are observed in about 55% of cases, primarily via translocations, with isolated gene amplifications being less frequent. The FGFR3 gene, when involved in the t(4;14)(p16;q32) translocation, leads to gene overexpression, contributing to resistance to standard therapies. Isolated amplification of FGFR3 is rare and its prognostic significance in MM remains unclear.Therefore, identifying cytogenetic biomarkers at diagnosis and during pre-transplant assessment is critical for accurate risk stratification and effective therapeutic decision-making.

KEYWORDS: ultiple Myeloma, Risk Stratification, Cytogenetics