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Background. Genetic anomalies (GA) are primary link of pathogenesis in MM. GA lead to formation of clonal plasma cells, which has different phenotype.

Aim. To estimate the incidence of GA and their correlation with clonal plasma cells’ phenotype in patients with ND MM.

Methods. We analysed 22 patients with ND MM (median age 57 years, range 38-80; male/female – 1:1.75). Cytogenetic analysis was performed on bone marrow samples using standard GTG-method. Metaphase FISH analysis was performed according to the manufacturer’s protocol using DNA probes: LSI 13(RBL)13q14, IGH/CCND1, IGH/FGFR3, LSI TP53 (17q13.1). 8-color immunophenotypic by flow cytometry using antibody to CD45, CD38, CD138, CD56, CD19, CD20, CD27 and CD117 antigens.

Results. Translocation t(11;14) was detected in 3/14 (21.4%) patients, del(13q) – 2/14 (14.3%), t(11;14) – 3/14 (21.4%), hypodiploidy – 1/20 (5%), del(17p) – 0% patients. Clonal plasma cells’ phenotype CD38+CD138+CD45– was detected in 100%. Expression CD56+ was revealed in 11/22 (50%) patients, CD19+ in 9/22 (40.9%), CD117+ in 5/22 (22.7%), CD20+ in 1/22 (4.5%), CD27+ in 1/22 (4.5%). The frequency of GA didn’t depend on clonal plasma cells’ phenotype and was 27.3%(3/11) in CD56+ phenotype, 23.8%(5/21) – CD20–, 23.8%(5/21) – CD27–, 23.5%(4/17) – CD117–, 23%(3/13) – CD19–, 22.2%(2/9) – CD19+, 20%(1/5) – CD117+, 18.2%(2/11) – CD56–, 0%(0/1) – CD20+, 0%(0/1) - in CD27+ phenotype. Patients of standard risk group according to mSMART 2.0 with GA had CD19-negative plasma cells’ phenotype vs. CD19-positive phenotype in patients of intermediate and high-risk groups (p<0.05). 3-years overall survival in standard risk group with CD19– phenotype was 92.3%, CD19+ – 77.7% (p<0.05).

Conclusion. Identification of GA, which has adverse forecast, correlates with CD19+ plasma cells phenotype. The combined definition of plasma cells phenotype and GA can improve the system of risk stratification in MM.