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Prognosis and response to therapy can be efficiently predicted by a combination of cytogenetic aberrations, detected by interphase-FISH in newly diagnosed multiple myeloma patients

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Introduction: The detection and interpretation of cytogenetic abnormalities in Multiple Myeloma is of critical importance for prognosis and risk stratification.

Objectives: To determine the role of cytogenetic aberrations in classification, risk stratification and predicting therapy response.

Material & Methods: FISH studies using commercially available DNA probes were retrospectively carried out in 342 *de novo* multiple myeloma patients on purified CD138 positive plasma cells.

Results: Cytogenetic abnormalities by FISH were detected in 65% (221/342) patients. The incidences of aberrations were monosomy 13/del (13q) in 35% hyper-diploidy in 33%, IgH translocations in 30%, gain (1q21) in 21% and monosomy 17/TP53 deletion in 7% patients. Patients' median age was 55.5 years (range, 27 to 84 years) with male preponderance. IgH translocation group ($P < 0.042$) and TP53 deletion ($P < 0.052$) were identified as high-risk group due to correlation with advanced disease, ISS stage III, whereas chromosome 13 aberrations were associated with high plasma cells ($P < 0.043$). Lower response rates were observed in patients with high risk cytogenetic abnormalities: t (4; 14) ($P < 0.008$), t (14; 20) ($P < 0.032$) and gain (1q) ($P < 0.003$). Median survival can be commented on further follow up.

Conclusions: Lower Incidence of chromosome 13 aberrations, t (11; 14) and lower median age, as compared to Western population, is probably due to geographic heterogeneity. Deletion (17p13), t (4; 14), t (14; 20) and gain (1q21) were independent high-risk prognostic factors, can predict lower response rates to therapy, are more likely to relapse early, thus need more intensive treatments. Interphase-FISH can efficiently detect poor prognostic markers thus helping in risk stratification aiding in treatment decisions and better patient management.

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