Patients with plasma cell myeloma (AKA multiple myeloma, MM) are divided into three risk groups based on their cytogenetic findings: high risk, intermediate risk and standard risk. Per current recommendation, all patients with plasma cell myeloma should undergo cytogenetic evaluation (preferably FISH analysis) at diagnosis if possible due to its importance in risk stratification.

With the advent of Fluorescence in Situ Hybridization (FISH) studies and with the increasing number of probes used for various abnormalities, it has become clear that nearly all patients with plasma cell myeloma have one or more abnormalities that can be detected by this methodology. FISH studies are particularly useful when the plasma cell number is low. If the sample contains less than 20% plasma cells, conventional cytogenetic analysis may fail due to low proliferative rate of myeloma cells, thus underestimating cytogenetic aberration in MM. In those cases, the sample will undergo enrichment for plasma cells for FISH testing to ensure higher sensitivity. If the sample is sufficient, both FISH testing and conventional cytogenetic analysis will be performed.

Based on the above rationales, TriCore Reference Laboratories offers an algorithm for plasma cell myeloma by FISH testing in order to detect significant cytogenetic abnormalities associated with this disease.

Abnormalities such as t(4;14), t(14;16), del 17p, and CDKN2C/CKS1B predict for significantly shortened survival in patients with newly diagnosed MM. Therefore, the initial FISH panel offered at TriCore Reference Laboratories will include probes for the above-mentioned high risk abnormalities:

P53 (17p13)/CEP7
IgH/FGFR3 (4;14)
IgH/MAF (14;16)
CDKN2C/CKS1B (1p32.3/1q21.3)

Among those probes, testing for P53 takes the highest priority and will be prioritized in cases with limited specimen. If the specimen is sufficient, all the probes will be performed simultaneously.

If any of the above cytogenetic abnormalities becomes positive, subsequent testing for trisomy may be performed as the presence of trisomy in patients with high risk abnormality may ameliorate the usual adverse impact associated with these prognostic markers to some degree:

Chromosomes 5, 9, and 15 (probes 5p/CEP9/CEP15)

If IgH is rearranged, MAF B break apart probe for t(14;20) and IgH/CCND1 (11;14) are available upon request. t(14;20) is infrequent and is associated with poor prognosis. IgH/CCND1 (11;14) is associated with lymphocytic morphology and/or CD20 coexpression. It is one of the most common cytogenetic abnormalities in MM and can be served as a marker for minimal residual disease monitoring.

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