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## P890 COMBINING SKY92 GENE EXPRESSION PROFILING WITH CYTOGENETICS ACCORDING TO R2-ISS FOR MULTIPLE MYELOMA RISK CLASSIFICATION: THE FIRST PROSPECTIVE EVIDENCE

Topic: 14. Myeloma and other monoclonal gammopathies - Clinical

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### Background:

The definition of high-risk (HR) multiple myeloma (MM) is controversial. Currently, FISH is the most commonly used tool for risk stratification in MM. According to the R2-ISS, HR cytogenetics is defined as presence of del(17p), t(4;14), and/or 1q CNA. On the other hand, SKY92 gene expression profiling has been developed for detection of HR MM in clinical trials. However, data on risk stratification combining SKY92 with FISH according to R2-ISS is still missing.

#### Aims:

The aim of this study was to evaluate the HR detection using SKY92 in combination with FISH according to R2-ISS in MM.

#### Methods:

We prospectively collected bone marrow (BM) and clinical data of 258 MM patients. Cytogenetics were analyzed on purified CD138 positive MM cells by FISH, and HR cytogenetics was defined as per the current R2-ISS classification. SKY92 risk status was determined with MMprofiler gene expression assay. Whole genome sequencing (WGS) was performed to compare SKY92 and FISH.

#### **Results:**

In total, 258 patients were included in our study (NDMM: n=109; RRMM: n=149). SKY92 status was available for 216 (83.7%) patients. However, samples of 26 (17.7%) patients, who showed significantly lower bone marrow infiltration than the remaining patients (median: 20% vs 50%, *P*=0.006), did not meet the SKY92 quality control criteria. HR SKY92 was significantly enriched in RRMM (57/121, 47.1%) compared with NDMM (17/95, 17.9%) (*P*<0.0001). The percentage of patients suffering from extramedullary disease (EMD) was significantly higher in HR SKY92 (12/74, 16.2%) compared to (SR) SKY92 (8/142, 5.6%) (*P*=0.01). In RRMM, HR SKY92 was significantly more frequent in patients with  $\geq$ 4 prior lines of therapies (32/52, 61.5%) compared to those with <4 therapy lines (25/65, 36.2%) (*P*=0.009). Moreover, HR SKY92 was significantly more common in patients who received autologous SCT (48/89, 53.9%) than the remaining patients (9/32, 28.1%) (*P*=0.01), suggesting that MM-therapy including SCT may influence the expression level of different genes and, in turn, the SKY92 status. RRMM patients with HR SKY92 showed significantly shorter progression free survival (PFS) (*P*<0.0001) and overall survival (OS) (*P*<0.0001) than standard-risk (SR). In NDMM, HR SKY92 also indicated a significantly inferior PFS (*P*<0.0001) in comparison with SR.

We then combined SKY92 with FISH according to R2-ISS in 181 patients (NDMM: n=79; RRMM: n=102). We found a discrepancy between the both risk stratification systems, with 67 (37.0%) and 99 (54.7%) patients being defined as HR by SKY92 and FISH, respectively. Overall, 13 (16.4%) NDMM and 36 (35.3%) RRMM patients

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showed HR in both SKY92 and FISH ("double-HR"). After a median follow up of 10.2 months, double-HR presented a negative prognostic factor for PFS in both NDMM (P=0.0003) and RRMM (P<0.0001). Furthermore, "double-HR" patients showed the worst OS (P=0.0002) in RRMM.

To elucidate the discrepancy between FISH and SKY92, we performed WGS in 16 patients who exhibited either only HR SKY92 (n=7) or only HR FISH (n=9). Interestingly, 1 patient with bi-allelic *TP53* inactivation (del + mut) and 6 patients harbouring 1q CNA were determined as SR by SKY92 but as HR by FISH. The median PFS was not reached after a median follow up of 11.3 months in these 9 patients. Vice versa, 4 out of 7 patients with only HR SKY92 but SR FISH displayed 1q CNA, which was detected only by WGS, and del1p32 was found in 1 patients. Interestingly, we found *CRBN* mutation in 3 out of 7 patients with only HR SKY92 but SR FISH. The remaining 2 patients did not show any known HR genomic alterations, suggesting that HR MM may be associated with other factors, e.g. epigenetic modifications.

#### Conclusion:

We provide the first prospective evidence that "double-HR" (SKY92 + FISH according to R2-ISS) indicates the highest-risk MM.

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