A retrospective study on cytogenetic features and prognosis of Chinese myeloma patients in a tertiary referral centre in Hong Kong

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Background

Although frequencies and significances of different cytogenetic abnormalities in plasma cell myeloma have been well documented in the Western countries, this information is relatively lacking in Chinese population. Moreover, the use of autologous stem cell transplantation and novel agents such as proteasome inhibitors and immunomodulators has increased significantly over the past 2 decades. This may change the prognostic value of cytogenetic abnormalities detected by fluorescence in-situ hybridization (FISH). Therefore the roles of FISH abnormalities in the prognosis of plasma cell myeloma need to be reevaluated in the era of novel agents. To address these issues, we studied the clinical, pathological and cytogenetic characteristics of plasma cell myeloma in a cohort of Chinese patients from Hong Kong.

Objectives

1. To analyze the pattern of FISH abnormalities in Chinese myeloma patients
2. To study the association between FISH abnormalities and baseline clinical parameters
3. To analyze the effect of FISH changes of patient's survival

Methods

The study is a retrospective cohort study. Newly diagnosed plasma cell myeloma patients with interphase FISH (iFISH) performed in Queen Elizabeth Hospital, a tertiary referral centre in Hong Kong, between August 2008 and March 2017 were included in the study. Information was collected via the electronic patient record (ePR) system of the Hospital Authority of Hong Kong for review.

Results

191 patents with a confirmed diagnosis of plasma cell myeloma were included in the analysis. 177/191 (92.7%) patients showed cytogenetic abnormalities on interphase FISH (iFISH) test. 1q21 (CKS1B) gain (88/160, 55.0%), del (13q) (97/190, 51.1%) and hyperdiploid (82/191, 42.9%) were the most common cytogenetic abnormalities, followed by t(4;14) (29/190, 15.3%), del(1p) (19/160, 11.9%), del(17p) (19/190, 10.0%), and t(14;16) (10/191, 5.2%).

	Frequency	Percentage (%)
FISH abnormalities	177/191	92.7
t(4;14)	29/190	15.3
t(14;16)	10/191	5.2
Del(17p)	19/190	10.0
Del(13q)	97/190	51.1
Loss in 1p	19/160	11.9
Gain in 1q	88/160	55.0
Hyperdiploid	82/191	42.9

Table 1: Frequencies of FISH abnormalities

We demonstrated that t(4;14), t(14;16), del(13q), 1q gain and del(1p) were adverse prognostic factors of PFS (progression free survival); while t(14;16), del(17p) and del(13q) were adverse prognostic factors of OS (overall survival).

Hyperdiploidy was both a favourable prognostic factor of PFS and OS. Among patients with high risk cytogenetic changes according to the mSMART 3.0 stratification, those with concomitant hyperdiploidy has a significantly prolonged OS but not PFS (median OS: hyperdiploid vs non-hyperdiploid: 56.8 vs 38.5 months, p=0.013; median PFS: hyperdiploid vs non- hyperdiploid: 37.7 vs 27.5 months, p=0.106).

The effects of iFISH abnormalities on PFS and OS were further assessed after adjusting for age, international staging system (ISS) and first-line therapy using multivariable-adjustment COX regression models. Of these, t(14;16) (hazard ratio [HR] 2.387 [95% confidence interval, CI: 1.086-5.248], p=0.030), del(17p) (HR 1.774 [95% CI 1.063-2.960], p=0.028), del(13q) (HR 1.684 [95% CI 1.168-2.428], p=0.005) and hyperdiploidy (HR 0.649 [95% CI 0.448-0.941], p=0.022) were statistically independent predictors of PFS in multivariate analysis; while del(17p) (HR 1.818 [95% CI 1.017-3.249], p=0.044), del(13q) (HR 2.089 [95% CI 1.335-3.270], p=0.001) and hyperdiploidy (HR 0.483 [95% CI 0.304-0.768], p=0.002) were statistically independent predictors of OS.

iFISH changes	HR of PFS	95% CI	p-value	HR of OS	95% CI	p-value
t(4;14)	1.529	0.959-2.436	0.074	1.291	0.744-2.239	0.364
t(14;16)	2.387	1.086-5.248	0.030	2.239	0.947-5.292	0.066
del(17p)	1.774	1.063-2.960	0.028	1.818	1.017-3.249	0.044
del(13q)	1.684	1.168-2.428	0.005	2.089	1.335-3.270	0.001
del(1p)	1.487	0.849-2.604	0.165	1.711	0.885-3.306	0.110
1q gain	1.336	0.846-2.036	0.178	1.310	0.780-2.203	0.308
Hyperdiploidy	0.649	0.448-0.941	0.022	0.483	0.304-0.768	0.002

Table 2: Effect estimates from multivariable-adjusted Cox regression models for the effect of FISH changes on PFS and OS after adjusting for age, ISS and first-line therapy

Conclusion

Our cohort of Chinese patients demonstrated similar patterns of FISH abnormalities compared to the western populations. The prognostic implications of FISH abnormalities were also comparable with the results found in western studies.

References

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