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Screening and identification of microRNA related with prognosis in patients with extra-nodal NK/T lymphomas

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Aim: The aim is to screen and identify the prognostic miRNA of patients with extranodal NK/T Cell lymphoma (ENKT).

Materials & Methods: All 82 Paraffin embedded tumor tissue blocks were obtained from ENKT patients of cancer hospital, Chinese Academy of Medical Sciences from 2010 to 2015. We analyzed the expression spectrum of miRNAs using Agilent Human miRNA Microarray Kit (V3) chip. Empirical Bayes model was used to screen the differential expression of miRNAs in ENKTs with excellent prognosis (survival >4 years) and poor prognosis (survival <3 years). Cox proportional hazards regression model was applied to identify the independent prognostic factors of ENKTs.

Results: We preliminary obtained 30 independent prognostic miRNAs related with ENKTs by comparing the miRNA expression between patients with excellent prognosis and patients with poor prognosis. And finally, 4 significant prognostic miRNAs were found when EBV infection status and age were corrected by Cox multivariate risk regression model. They are hsa-miR-210 (HR=0.44, 95% CI 0.27-0.71, P=0.0009), hsa-let-7f (HR=0.61, 95% CI 0.42-0.90, p=0.011), hsa-miR-16 (HR=0.67, 95% CI 0.47-0.93, p=0.018) and has-miR-21 (HR=0.74, 95% CI 0.56-0.99, p= 0.04).

Conclusion: In this study, we analyzed miRNA expression spectrum of large samples of ENKTs. And the results showed that hsa-miR-210, hsa-let-7f, hsa-miR-16 and has-miR-21 are independent prognostic factors in patients with ENKTs.

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