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EGFR overexpression and gene amplification in esophageal cancer of multiple ethnic groups in Northwest China

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To study the characteristics of epidermal growth factor receptor (EGFR) protein expression and gene amplification in esophageal cancer of multiple ethnic groups in Xinjiang and to evaluate its significances in molecular target therapy. Using immunohistochemistry (IHC) and fluorescence in situ hybridization (FISH) to detect EGFR protein expression and gene amplification combining with a retrospective study on clinical pathological characteristics of Uyghur, Chinese Han and Kazakh esophageal cancer patients' tissues were carried out. Overexpression of EGFR protein was observed in 72% of esophageal cancer tissues and it was significantly correlated with lymphatic metastasis ($P < 0.05$). EGFR gene amplification was 41.66% and was significantly correlated with tumor differentiation, lymphatic metastasis and vascular invasion ($P < 0.05$). EGFR protein expression was related to gene amplification, especially high-level expression (3^+) was significantly correlated with gene amplification ($P < 0.05$). Survival rate of patient with EGFR gene amplification was shorter than patient with no amplification (Log-rank test, $P < 0.05$), vascular invasion increased the risk of death ($P < 0.05$) in esophageal cancer patients. EGFR gene is associated with carcinogenesis, development and metastasis of esophageal cancer patients of multiple ethnic groups in Xinjiang. Combining detection of EGFR protein expression and gene amplification is a significant index in prognostic evaluation; meanwhile, it is a guide in molecular target therapy of esophageal cancer.

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