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Clinical significance of next-generation sequencing (NGS) for advanced cancer

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Introduction & Aim: Target therapy plays an important role in the treatment of advanced cancer and NGS could detect gene mutation accurately and high through-put. The present study aimed to detect the paraffin tissue samples of advanced cancer utilizing next-generation sequencing platform and discuss the related clinical significance.

Method: The paraffin tissue samples of 93 cases with advanced cancer were collected in the department of medical oncology, Shaanxi Province People's Hospital between 2011-9-1 and 2016-9-30. We detected 428 common mutation sites of 16 cancer related genes by Ion Torrent PGM platform and searched information on the official website of the clinical trials and FDA.

Result: 120 missense mutation sites were found, TP53 was the most common missense mutation site. In addition to TP53, the most common missense mutation site in lung cancer, colorectal cancer, gastric cancer, ovarian cancer and cervical cancer is EGFR (25.7%, 9/35), KRAS (31.6%, 6/19), KDR (50%, 3/6), KRAS (28.6%, 2/7) and KDR (60.0%, 3/5) respectively. 70 cases (75.3%, 70/93) have one or more missense mutation site, 93.8% (15/16) of the tested genes have small molecular inhibitor or monoclonal antibodies which are developing, 75% (12/16) of the tested genes have the target drugs which have been approved by FDA for specific cancer and 68.8% (11/16) of the tested genes have target drugs which have not been approved.

Conclusion: The frequency of missense mutation in advanced cancer is high and the mutation pattern is different in different cancer. For advanced cancer, individual target therapy based on the next-generation sequencing has broad prospects.

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