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meta analysis

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ABSTRACT

A systematic literature search was performed using PubMed, Embase, and WANFANG MED ONLINE databases up to March 18, 2019. All literature was analyzed using Meta Disc 1.4 and STATA 14.0 software. Diagnostic measures of accuracy of ctDNA in cervical cancer were pooled and investigated. Fifteenstudies comprising 1109 patients with cervical cancer met our inclusion criteria and were subjected to analysis.

EXTERNAL LINK

https://www.dovepress.com/diagnostic-value-of-circular-rnas-as-effective-biomarkers-for-cancer-a-peer-reviewed-article-OTT

THIS PROTOCOL ACCOMPANIES THE FOLLOWING PUBLICATION

Gu Y, Wan C, Qiu J, Cui Y, Jiang T, Zhuang Z (2020) Circulating HPV cDNA in the blood as a reliable biomarker for cervical cancer: A meta-analysis. PLoS ONE 15(2): e0224001. doi: 10.1371/journal.pone.0224001

ATTACHMENTS

diagnostic value of circular RNAs as effective biomarkers for cancer,a systematic review and meta-analysis.pdf

GUIDELINES

This meta-analysis was conducted following the criteria of Preferred Reporting Items for Systematic Review and Meta Analyses

MATERIALS TEXT

PubMed, Embase, Cochrane Library, and WANFANG medicine online databases; Meta-DiSc 1.4 and STATA 14.0 statistical software

BEFORE STARTING

First of all, we carried out task arrangement, personnel division, and their respective tasks and roles. Determine which necessary databases require query and retrieval time. Before retrieval, we searched for keywords and subject words on the website. How many research papers that can be analyzed are expected to be retrieved.

1 This meta-analysis was conducted following the criteria of Preferred Reporting Items for Systematic Review and Meta Analyses . A literature search was systematically performed using PubMed, Embase, Cochrane Library, and WANFANG medicine online databases for all relevant articles without language or regional limitations. No limitations were set with regard to the start date for publication, and the search ended on March 18, 2019. The following search terms were used: “cervical cancer AND ctDNA”, “cervix cancer AND ctDNA”, “cervical carcinoma AND ctDNA” OR “circulating DNA AND cervical cancer”. Various alterations in spelling and abbreviations were also used as search terms. Titles and abstracts were carefully screened for relevance, and duplicates were removed. The full text of each report that met the preliminary criteria was retrieved and assessed for inclusion into this meta-analysis. This meta-analysis was conducted following the criteria of Preferred Reporting Items for Systematic Review and Meta Analyses [19]. A literature search was systematically performed using PubMed, Embase, Cochrane Library, and WANFANG medicine online databases for all relevant articles without language or regional limitations. No limitations were set with regard to the start date for publication, and the search ended on March 18, 2019. The following search terms were used: “cervical cancer AND ctDNA”, “cervix cancer AND ctDNA”, “cervical carcinoma AND ctDNA” OR “circulating DNA AND cervical cancer”. Various alterations in spelling and abbreviations were also used as search terms. Titles and abstracts were carefully screened for relevance, and duplicates were removed. The full text of each report that met the preliminary criteria was retrieved and assessed for inclusion into this meta-analysis.

2 In this meta-analysis, eligible studies were selected according to these following inclusion criteria: (1) evaluated the diagnostic accuracy of quantitative analysis of ctDNA in cervical cancer; (2) the diagnostic value of ctDNA in cervical cancer was reported or could be calculated from the published data; (3) full text and all data could be retrieved and were available; (4) the techniques and target genes were clearly stated in the articles; (5) studies included at least 10 patients with cervical cancer and relevant negative controls. When the same patient population was used in several studies, only the most recent was included.In this meta-analysis, eligible studies were selected according to these following inclusion criteria: (1) evaluated the diagnostic accuracy of quantitative analysis of ctDNA in cervical cancer; (2) the diagnostic value of ctDNA in cervical cancer was reported or could be calculated from the published data; (3) full text and all data could be retrieved and were available; (4) the techniques and target genes were clearly stated in the articles; (5) studies included at least 10 patients with cervical cancer and relevant negative controls. When the same patient population was used in several studies, only the most recent was included.

3 The exclusion criteria were as follows: (1) the diagnostic or prognostic value could not be deduced from incomplete data in the studies provided; (2) repeated studies from the same study group; (3) sample size less than 10; (4) data only from experiments based on cell lines; (5) studies published in languages other than English. The exclusion criteria were as follows: (1) the diagnostic or prognostic value could not be deduced from incomplete data in the studies provided; (2) repeated studies from the same study group; (3) sample size less than 10; (4) data only from experiments based on cell lines; (5) studies published in languages other than English.

4 Two reviewers (CD Wan and YL Gu) independently reviewed and evaluated all eligible studies according to the Newcastle-Ottawa scale. In case of disagreement, the decision was made by a third researcher, and disagreement was settled through discussion. The data extracted from the basic feature table included authors’ names, country, sample type, detection method, numbers of experimental and control groups, and analysis indicators. The outcome indicators included positives, false positives, false negatives, true negatives, sensitivity, and specificity. To assess the methodological quality of each study and potential risk of bias, QUADAS-2 Guidelines were used to evaluate the quality of all articles that met the inclusion criteria [21].Two reviewers (CD Wan and YL Gu) independently reviewed and evaluated all eligible studies according to the Newcastle-Ottawa scale [20]. In case of disagreement, the decision was made by a third researcher, and disagreement was settled through discussion. The data extracted from the basic feature table included authors’ names, country, sample type, detection method, numbers of experimental and control groups, and analysis indicators. The outcome indicators included positives, false positives, false negatives, true negatives, sensitivity, and specificity. To assess the methodological quality of each study and potential risk of bias, QUADAS-2 Guidelines were used to evaluate the quality of all articles that met the inclusion criteria .

5 We used standard methods recommended for meta-analysis of diagnostic test evaluations [19]. The meta-analysis was carried out with Meta-DiSc 1.4 and STATA 14.0 statistical software. The sensitivity was defined as the proportion of patients with ctDNA presence among all patients confirmed as having cervical cancer. The specificity was defined as the proportion of patients with negative ctDNA detection among all negative control volunteers without cervical cancer. The positive likelihood ratio (PLR) was calculated as sensitivity/(1 – specificity), whereas the negative likelihood ratio (NLR) was calculated as 1 – sensitivity/specificity. DOR was calculated as PLR / NLR and was used as an indication of how much greater the chance was of having cervical cancer for patients with ctDNA presence than for those without ctDNA. These indicators were summarized using a bivariate meta-analysis model, and the threshold effect was determined by receiver operative characteristic (ROC) curve and Spearman correlation analyses; P values of less than 0.05 indicated a significant threshold effect. Heterogeneity between studies was analyzed by chi-squared and I2 tests; a P value of less than 0.1 or an I2 higher than 50% indicated the existence of significant heterogeneity [22]. Meta-regression analysis was performed to explore the sources of heterogeneity. Deek's funnel plot asymmetry test was used to test whether there was publication bias [23]. All statistical tests were two-sided, and results with P values of less than 0.05 were considered statistically significant.We used standard methods recommended for meta-analysis of diagnostic test evaluations [19]. The meta-analysis was carried out with Meta-DiSc 1.4 and STATA 14.0 statistical software. The sensitivity was defined as the proportion of patients with ctDNA presence among all patients confirmed as having cervical cancer. The specificity was defined as the proportion of patients with negative ctDNA detection among all negative control volunteers without cervical cancer. The positive likelihood ratio (PLR) was calculated as sensitivity/(1 – specificity), whereas the negative likelihood ratio (NLR) was calculated as 1 – sensitivity/specificity. DOR was calculated as PLR / NLR and was used as an indication of how much greater the chance was of having cervical cancer for patients with ctDNA presence than for those without ctDNA. These indicators were summarized using a bivariate meta-analysis model, and the threshold effect was determined by receiver operative characteristic (ROC) curve and Spearman correlation analyses; P values of less than 0.05 indicated a significant threshold effect. Heterogeneity between studies was analyzed by chi-squared and I2 tests; a P value of less than 0.1 or an I2 higher than 50% indicated the existence of significant heterogeneity [22]. Meta-regression analysis was performed to explore the sources of heterogeneity. Deek's funnel plot asymmetry test was used to test whether there was publication bias [23]. All statistical tests were two-sided, and results with P values of less than 0.05 were considered statistically significant.