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Evaluation of the Sensitivity and Specificity of MicroRNA in the Diagnosis of Cervical Cancer: A Systematic Review and Meta-analysis

Evaluación de la Sensibilidad y Especificidad del MicroRNA en el Diagnóstico del Cáncer Cervical: Una Revisión Sistemática y Meta-análisis

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Abstract

Objectives: New regulatory RNAs called microRNAs are about 22 nucleotides in length. Also, a number of human cancers are also caused by microRNAs; which function both as oncogenes and suppressors. We evaluated the sensitivity and specificity of MicroRNA in diagnosing cervical cancer in the present study.

Methods: A search of the international databases PubMed, Scopus, Science Direct, ISI, Web of Knowledge, and Embase of keywords related to the study objectives was conducted until March 2023. A fixed effect model with the inverse-variance method was used to calculate effect size (95% confidence interval). The meta-analysis was performed using STATA/MP. V17 software.

Results: A meta-analysis was conducted using nine articles in the present study. The sensitivity of microRNA-21 for diagnosis of cervical cancer was 86% (ES: 0.86 [95% CI: 0.70, 1.01]), specificity of microRNA-21 to diagnose cervical cancer was 84% (ES: 0.84 [95% CI: 0.68, 1.00]. The AUC of microRNA-21 on tissue models to diagnose cervical cancer was 85% (ES: 0.85 [95% CI: 0.69, 1.02].

Conclusions: According to the present meta-analysis and the role of microRNA-21 in cervical cancer progression, and considering its relationship with clinic pathological factors, it can be considered a differential marker with high sensitivity and specificity.

Key words: Diagnosis, Neoplasms, Sensitivity and Specificity, Uterine Cervical Neoplasms.

Resumen

Objetivos: Los nuevos ARN reguladores denominados microARN tienen una longitud de unos 22 nucleótidos. Además, varios tipos de cáncer humano también son causados por microARN; que funcionan tanto como oncogenes como supresores. Evaluamos la sensibilidad y especificidad de MicroRNA en el diagnóstico de cáncer de cuello uterino en el presente estudio.

Métodos: Se realizó una búsqueda en las bases de datos internacionales PubMed, Scopus, Science Direct, ISI, Web of Knowledge y Embase de palabras clave relacionadas con los objetivos del estudio hasta marzo de 2023. Se utilizó un modelo de efectos fijos con el método de la varianza inversa para calcular tamaño del efecto (intervalo de confianza del 95%). El metanálisis se realizó con STATA/MP. programa V17.

Resultados: Se realizó un metanálisis utilizando nueve artículos en el presente estudio. La sensibilidad del microARN-21 para el diagnóstico de cáncer de cuello uterino fue del 86 % (ES: 0,86 [IC del 95 %: 0,70, 1,01]), la especificidad del microARN-21 para el diagnóstico del cáncer de cuello uterino fue del 84 % (ES: 0,84 [IC del 95 %: 0,68, 1,00]. El AUC de microARN-21 en modelos de tejido para diagnosticar cáncer de cuello uterino fue del 85 % (ES: 0,85 [IC del 95 %: 0,69, 1,02].

Conclusiones: De acuerdo con el presente metaanálisis y el papel del microARN-21 en la progresión del cáncer de cérvix, y considerando su relación con factores clínico patológicos, puede considerarse un marcador diferencial con alta sensibilidad y especificidad.

Palabras clave: Diagnóstico, Neoplasias, Sensibilidad y Especificidad, Neoplasias del Cuello Uterino.

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Introduction

The fourth most common cancer among women is cervical cancer. In 2018, 570,000 new cases occurred, which is 7.5% of all women's deaths from cancer, and annually more than 311,000 deaths from cervical cancer occur worldwide, more than 85% of which occur in less developed societies¹. The World Health Organization has estimated that in 2030, this cancer will kill about 474,000 women annually, and low- and middle-income countries will suffer 95% of these deaths². Cervical cancer screening (Pap smear test) by detecting abnormal changes in cervical cells that may lead to cervical cancer if not treated, and also by detecting the presence of certain types of human papillomavirus (HPV) that cause fundamental changes in the Cervix and eventually lead to cancer, it prevents cancer^{3,4}. HPV 16 and HPV 18 strains cause approximately 70% of cervical carcinoma cases^{5,6}. The findings of the studies have shown that, in addition to the mentioned cases, personal and sexual health, having several sexual partners, poverty, a history of sexually transmitted infections, smoking, immune deficiency, contraceptive pills, and early initiation of sexual intercourse can cause the disease, help people with cervical cancer⁷⁻¹¹.

Based on the available evidence, microRNAs can also play a role in cervical carcinogenesis¹². MicroRNAs are a large subgroup of 18-25 nucleotide non-coding RNAs that are evolutionarily conserved. Several studies have determined that microRNAs play a critical role in cancer initiation and progression¹³. Depending on the type of mRNAs they inhibit, microRNAs can suppress tumors or inhibit oncogenesis¹⁴. Proliferation and invasion of cells are stimulated by microRNA-21, while the process of apoptosis is inhibited¹⁵. Growth, programmed death, differentiation, and cell proliferation are all regulated by microRNA interactions with target genes, and microRNAs have been directly implicated in cancer development¹⁶. Cancer samples show abnormal expression of many microRNAs based on their structure and function¹⁷.

The expression of microRNAs is also associated with functional differences between tumor types and stages of cancer¹⁸. The expression of miRNA is associated with clinical and biological characteristics of tumors, such as tissue type, differentiation, invasion, and response to treatment¹⁹. Human serum or plasma can be studied to identify cancer miRNAs and tumor cells without the use of invasive methods. miRNAs can be used as diagnostic markers by examining human serum or plasma. Malignant cells are easily available, except for leukemia^{20,21}. Early diagnosis of cancer can be enhanced by using miRNAs closely related to malignant phenotypes as diagnostic markers²². As most common cancer screening methods are not able to detect the disease early, a key aspect of the timely diagnosis of cancer is the identification of tumor miRNAs in the bloodstream during the gradual

progression of the disease. Many studies have indicated that microRNA-21 plays an oncogenic and anti-apoptotic role²³. Based on the findings of studies in patients with cervical cancer, the level of microRNA-21 increases, which can effectively diagnose cervical cancer as a diagnostic biomarker²⁴⁻²⁶. In many studies, increased expression of microRNA-21 has been investigated in all types of cancers, especially cervical cancer; However, the findings of the studies are not consistent, and there are many challenges; Therefore, in the present study, an attempt has been made to investigate the results of microRNA increased expression studies as a diagnostic and prognostic method in cervical cancer in order to provide stronger evidence. Therefore, MicroRNA was evaluated to determine its sensitivity and specificity for the diagnosis of cervical cancer in the current study.

Methods

Search strategy

The present study was conducted using the PRISMA 2020 checklist²⁷. Searches were conducted in the international databases PubMed, Scopus, Science Direct, ISI, Web of Knowledge, and Embase using keywords related to the study objectives; all articles were reviewed until March 2023. The PICO strategy (Population, Intervention, Comparison, and Outcomes) is summarized in **table I**. Keywords and the Mesh terms:

(((((("Neoplasms"[Mesh] OR "Early Detection of Cancer"[Mesh]) OR "Neoplasms/diagnosis"[Mesh]) OR "Uterine Cervical Neoplasms "[Mesh]) AND "MicroRNAs"[Mesh]) OR ("Biomarkers"[Mesh] OR "Biomarkers, Tumor"[Mesh])) AND "Diagnosis"[Mesh]) AND "Sensitivity and Specificity"[Mesh].

Table I: PICO strategy.

PICO strategy	Description
Р	Population: Patients with cervical cancer
I	Intervention: microRNA-21
С	Comparison: healthy controls
0	Outcome: Sensitivity and Specificity

Data collection

First, a checklist including the author's name, publication year, study design, sample size, Cancer stage, and MicroRNA was prepared. The study data were entered in this checklist and summarized in Table II. The sensitivity and diagnostic specificity data of the studies were extracted and used for meta-analysis. Two independent, blinded reviewers screened each record, and a third person retrieved each report. The selection of articles was based on inclusion and exclusion criteria.

Inclusion and Exclusion criteria

Only articles published in English, prospective and retrospective studies, case-control studies, miRNA

models based on qRT-PCR data, and reported diagnostic performance data were included. Case studies, case reports, and review articles; studies without access to the full text were excluded from the study.

Risk assessment

The quality of studies was measured using Diagnostic Accuracy Studies (QUADAS-2)²⁸. In this tool, four areas of patient selection, index test, reference standard, and schedule are examined; Assessment of bias is rated as "high," "low," and "uncertain."

Data analysis

I2 coefficients were used to estimate potential heterogeneity between studies. Low heterogeneity is defined as values less than 50%, moderate heterogeneity is defined as values between 50% and 75%, and high heterogeneity is defined as values greater than 75%. A fixed effect model with the inverse-variance method was used to calculate the effect size (95% confidence interval). STATA/MP. Meta-analysis was conducted using V17 software.

Results

Study selection

402 articles were found utilizing keywords in the initial search, and they were all entered into EndNote X8 software; Duplicate articles, articles with inappropriate and inconsistent titles, and other reasons were removed, then the abstracts of 372 articles were reviewed, 304 articles were removed (based on the inclusion and exclusion criteria). The full text of 68 articles was reviewed. Articles whose full text was incomplete had incomplete data, articles that were not in line with the objectives of the study were excluded, and finally, nine articles were selected (**Figure 1**). All the steps of searching and reviewing the articles were done by two blind observers and evaluated by a third observer.

Study characteristics

One prospective study and eight case-control were selected and included in the present meta-analysis. A total of 1324 patients (Experimental: 707; Control: 617); **table II** shows a summary of the data extracted.

Table II: Full-text demographic data extracted from selected studies.

Figure 1: PRISMA 2020 Checklist.



Risk assessment

All studies had high quality (low risk of bias).

Diagnostic accuracy Subgroup meta-analysis

The AUC of MicroRNA to diagnose cervical cancer was 82% (ES: 0.82 [95% CI: 0.75, 0.88], (l^2 =0%; p =0.98; low heterogeneity) (**Figure 2**). According to subgroup meta-analysis AUC of microRNA-21 to diagnose cervical cancer was 84% (ES: 0.84 [95% CI: 0.74, 0.93], (l^2 =0%; p =0.86; low heterogeneity).

n	Study. Years	Study Design	Source of MiRNAs	Number of Patients		Cancer Stage	MicroRNA	
				Cancer Group	Control Group			
1	Aftab et al., 202129	Prospective	Tissue	40	30	I-IV	miR-21, miR-199a, and miR-155-5p	
2	Du et al., 202030	Case-control	Serum	140	140	1-11	miRNA-29a, miRNA25, miRNA-486-5p	
3	Ruan et al., 202031	Case-control	Serum	68	57	NR	microRNA-21 and microRNA-124	
4	Zamani et al., 202032	Case-control	Tissue	50	46	NR	miR-21 and miR29-a	
5	Qiu et al., 202024	Case-control	Serum	112	90	I-IIA	miR-21	
6	Ma et al., 201933	Case-control	Plasma	97	87	1-11	miR-21	
7	Zhu et al., 2018 ³⁴	Case-control	Tissue	25	23	NR	miR-21-5p, miR-34a	
8	Park et al., 201735	Case-control	Tissue	Serum	50	I-IIA	MiR-9, miR-21, and miR-155	
9	Jia et al., 201536	Case-control	Serum	123	94	III	miR-21, -29a, -25, -200a and -486-5p	

Figure 2: AUC of MicroRNA to diagnose cervical cancer.

Study				AUC with 95% CI	Weight (%)
miR-21				5. T. T. T. S. Mark	1000
Aftab et al., 2021				0.97 [0.77, 1.17]	10.81
Ruan et al., 2020				0.72 [0.52, 0.92]	10.81
Zamani et al., 2020				0.85 [0.07, 1.63]	0.68
Qiu et al., 2020				0.78 [-0.00, 1.56]	0.68
Ma et al., 2019	-			0.79 [-5.09, 6.67]	0.01
Zhu et al., 2018				0.87 [0.48, 1.26]	2.70
Park et al., 2017				0.83 [0.63, 1.03]	10.81
Jia et al., 2015				0.82 [0.62, 1.02]	10.81
Heterogeneity: I ² = 0.00%, H ² = 1.00				0.84 [0.74, 0.93]	
Test of $\theta = \theta$; Q(7) = 3.22, p = 0.86					
miR-199a					
Aftab et al., 2021				0.71 [0.51, 0.91]	10.81
Park et al., 2017				0.72 [0.52, 0.92]	10.81
Heterogeneity: 1 ² = 0.00%, H ² = 1.00		1		0.72 [0.58, 0.85]	
Test of θ = $\theta_j;$ Q(1) = 0.01, p = 0.94					
miR-155-5p					
Aftab et al., 2021				0.83 [0.44, 1.22]	2.70
Heterogeneity: I ² = 100.00%, H ² = 1.00		٠		0.83 [0.44, 1.22]	
Test of θ = $\theta_{\rm c}$ Q(0) = -0.00, p = .					
miR29-a					
Du et al., 2020				0.66 [0.27, 1.05]	2.70
Zamani et al., 2020	-	_	_	0.85 [-5.03, 6.73]	0.01
Jia et al., 2015				0.90 [0.70, 1.10]	10.81
Heterogeneity: I ² = 0.00%, H ² = 1.00		+		0.85 [0.68, 1.03]	
Test of $\theta = \theta$; $Q(2) = 1.15$, $p = 0.56$					
miRNA25					
Du et al., 2020				0.88 [0.68, 1.08]	10.81
Heterogeneity: I* = 100.00%, H* = 1.00		1		0.88 [0.68, 1.08]	
Test of $\theta = \theta$; $Q(0) = -0.00$, $p = .$					
miRNA-486-5p					
Du et al., 2020		-		0.92 [0.14, 1.70]	0.68
Heterogeneity: I* = 0.00%, H* = 1.00				0.92 [0.14, 1.70]	
Test of $\theta_i = \theta_j; \ Q(0) = 0.00, \ p = .$					
microRNA-124					
Ruan et al., 2020		-		0.76 [-0.02, 1.54]	0.68
Heterogeneity: I* = 100.00%, H* = 1.00		•		0.76 [-0.02, 1.54]	
Test of 8 = 8; Q(0) = 0.00, p = .					
miR-34a					
Zhu et al., 2018				0.87 [0.48, 1.26]	2.70
Heterogeneity: I" = 100.00%, H" = 1.00		•		0.87 [0.48, 1.26]	
Test of 8 = 8; Q(0) = 0.00, p = .					
Overall		E.		0.82 [0.75, 0.88]	
Heterogeneity: I ^z = 0.00%, H ^z = 1.00					
Test of $\theta = \theta$; Q(17) = 7.33, p = 0.98					
Test of group differences: Q,(?) = 2.96, p = 0.89	_				
	-5	0	5	10	
Eined affacts inunsta-unsistence model					

The AUC of microRNA-21 on tissue models to diagnose cervical cancer was 85% (ES: 0.85 [95% CI: 0.69, 1.02], (I²=0%; p =0.99; low heterogeneity) (**Figure 3**). AUC of microRNA-21 on serum models to diagnose cervical cancer was 79% (ES: 0.79 [95% CI: 0.61, 0.98], (I²=0%; p =0.92; low heterogeneity) (**Figure 3**). AUC of microRNA-21 on plasma models to diagnose cervical cancer was 79% (ES: 0.79 [95% CI: 020, 1.38], (I²=0%; p =0.92; low heterogeneity) (**Figure 3**).

Sensitivity and specificity

The sensitivity of microRNA-21 to diagnose cervical cancer was 86% (ES: 0.86 [95% CI: 0.70, 1.01], (I²=0%; p = 1.00; low heterogeneity) (**Figure 4**). Specificity of microRNA-21 to diagnose cervical cancer was 84% (ES: 0.84 [95% CI: 0.68, 1.00], (I²=0%; p = 0.86; low heterogeneity) (**Figure 5**).

Figure 3: AUC of MicroRNA to diagnose cervical cancer.

Study					AUC with 95% CI	Weight (%)
Tissue						
Aftab et al., 2021		_		-	0.88[0.49, 1.27]	9.23
Zamani et al., 2020		+			0.84 [0.64, 1.04]	36.92
Zhu et al., 2018	12				0.96 [0.18, 1.74]	2.31
Park et al., 2017				-	0.83 [0.24, 1.42]	4.10
Heterogeneity: I ² = 0.00%; H ² = 1.00			-		0.85 [0.69, 1.02]	
Test of $\theta = \theta$: Q(3) = 0.11, p = 0.99						
Serum						
Ruan et al., 2020		-		_	0.91 [0.32, 1.50]	4.10
Qiu et al., 2020			-		0.78 [0.58, 0.98]	36.92
Jia et al., 2015	-				0.82[0.04, 1.60]	2.31
Heterogeneity: I' = 0.00%, H' = 1.00		-	-		0.79[0.61, 0.98]	
Test of $\theta_{\rm c}$ = $\theta_{\rm c}$ Q(2) = 0.17, p = 0.92						
Plasma						
Ma et al., 2019				_	0.79[0.20, 1.38]	4.10
Heterogeneity: I ² = 100.00%; H ² = 1.00			-	-	0.79[0.20, 1.38]	
Test of $\theta_{\rm c}$ = $\theta_{\rm c}$ Q(0) = -0.00, p = .						
Overall			•		0.82 [0.71, 0.94]	
Heterogeneity: I ² = 0.00%, H ² = 1.00						
Test of $\theta = \theta$. Q(7) = 0.51, p = 1.00						
Test of group differences: $Q_{1}(2) = 0.22$, $p = 0.89$	_		- 1	Le		
Fixed-effects inverse-variance model	0	.5	1	1.5	2	

Figure 4: Sensitivity of microRNA-21 to diagnose cervical cancer.

microRNA-21 Study					Sensitivity with 95% CI	Weight (%)
Aftab et al., 2021		_			0.88 [0.49, 1.27	16.29
Ruan et al., 2020		-		_	0.91 [0.32, 1.50	7.24
Zamani et al., 2020		-	-		0.84 [0.64, 1.04	65.16
Zhu et al., 2018	1.4				0.96 [0.18, 1.74	4.07
Park et al., 2017					0.83 [0.24, 1.42	7.24
Overall Heterogeneity: $I^2 = 0.00\%$, $H^2 = 1.00$ Test of $\theta_i = \theta_i$: $Q(4) = 0.15$, $p = 1.00$			*		0.86 [0.70, 1.01	1
Test of 0 = 0: z = 10.60, p = 0.00	0	.5	i	1.5	2	

Figure 5: Specificity of microRNA-21 to diagnose cervical cancer.

microRNA-21 Study				v	Specificity with 95% CI		
Aftab et al., 2021			-	0.98	[0.59, 1.37]	16.29	
Ruan et al., 2020	_	-		0.60	[0.01, 1.19]	7.24	
Zamani et al., 2020		2	-	0.85	[0.65, 1.05]	65.16	
Zhu et al., 2018	-		•	0.78	[-0.00, 1.56]	4.07	
Park et al., 2017	-	-		0.72	[0.13, 1.31]	7,24	
Overall				0.84	[0.68, 1.00]		
Heterogeneity: I ² = 0.00%, H ² = 1.00							
Test of $\theta_1 = \theta_1$: Q(4) = 1.32, p = 0.86							
Test of 6 = 0: z = 10.42, p = 0.00	, 0	.5	i	1.5			
ixed-effects inverse-variance model							

Discussion

In patients with cervical cancer, the expression of microRNA-21 may act as a diagnostic marker. An increase in microRNA-21 results in a reduction in tumor suppressor protein expression and an increase in oncogenic protein expression^{35,37,38}. Considering these roles, microRNA-21 can be a suitable option for investigating cancer and metastasis development. The increased expression of microRNA-21 in cancer tissues makes it useful for early

metastasis detection and follow-up. Because oncogenic and apoptotic properties of this microRNA affect tumor cells, it causes a disturbance in the apoptosis pathway, which favors the survival of cancer cells³⁹.

In the present study, subgroup meta-analysis showed that the diagnostic accuracy of microRNAs in cervical cancer diagnosis is acceptable. Also, microRNA-21 was used in articles more than other microRNAs; for this reason, its sensitivity and specificity were investigated. Became; Meta-analysis showed that the sensitivity and specificity of microRNA-21 in cervical cancer diagnosis is high. Also, subgroup meta-analysis showed that the AUC of microRNA-21 on tissue models to diagnose cervical cancer is higher than serum and plasma models. There was low heterogeneity between studies, so the present study provides strong evidence, and the selected studies were of high quality. One of the weaknesses of the present study was that only one prospective study was investigated, and no randomized clinical trial study was found. The present study observed that microRNAs are potential cancer biomarkers, and the diagnostic importance of microRNA-21 in cervical cancer was well-defined. Also, other studies have shown that microRNA-21 has high sensitivity and specificity in diagnosing other cancers⁴⁰⁻⁴². Changes in the expression levels of miRNAs can be stably and easily measured in tumor tissues, plasma, serum, and urine samples²⁹. Meta-analysis studies have shown that in patients with

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all types of cancers, microRNA-21 is an important and independent prognostic biomarker for patient survival^{43,44}. It has been well studied that MicroRNA-21 is one of the most well-known microRNAs. On the other hand, this microRNA plays an oncogenic role by turning off a series of essential genes that lead to cancerous cells. This microRNA is found in a variety of cancers⁴⁵.

Conclusion

Considering the results of the present meta-analysis and the low heterogeneity between studies, the present study provides strong evidence. Based on the present metaanalysis and the role of microRNA-21 in the progression of cervical cancer, and considering its relationship with clinicopathological factors, it can be considered a differential marker with high sensitivity and specificity. Also, cervical cancer patients can benefit from this noninvasive method for early diagnosis. MicroRNA-21 has an oncogenic role, and by measuring its amount in patients' tissue, it is possible to check the progress of cancer.

Conflict of Interest

The authors declared that there is no conflict of interest.

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