Clin. Lab. 2023;69:1-2

ORIGINAL ARTICLE

A Meta-Analysis of Polymerase Chain Reaction for Prosthetic Joint Infection Diagnosis

Sang-Yeob Lee [1, 2, *], Min-Chul Cho [3, *], Yong-Han Cha [4], Chan Ho Park [5], Jung-Taek Kim [6], Jun-Il Yoo [7]

** Sang-Yeob Lee and Min-Chul Cho contributed equally to this work*
[1] Department of Biomedical Research Institute, Gyeongsang National University Hospital, Jinju, South Korea
[2] Department of Theriogenology and Biotechnology, College of Veterinary Medicine, Gyeongsang National University, Jinju, South Korea
[3] Department of Laboratory Medicine, Korea University Guro Hospital, Korea University College of Medicine, Seoul, South Korea
[4] Department of Orthopedic Surgery, Eulji University Hospital, Daejeon, South Korea
[5] Department of Orthopedic Surgery, New Daesung Hospital, Bucheon, South Korea
[6] Department of Orthopedic Surgery, Ajou University School of Medicine, Ajou Medical Center, Suwon, South Korea
[7] Department of Orthopedic Surgery, Inha University Hospital, Incheon, South Korea

SUMMARY

Background: **One of the most dangerous side effects of joint replacement for the hip, knee, shoulder, and elbow is prosthesis joint infection (PJI). Polymerase chain reaction (PCR) has been considered a promising method for PJI diagnosis due to its short diagnostic time and high sensitivity. Although several PCR methods such as multiplex PCR and broad-range PCR are useful diagnostic methods for detecting microorganisms causing PJI, values of different PCR methods for the diagnosis of PJI remain unclear. Thus, the objective of this study was to perform a meta-analysis of different PCR methods in the diagnosis of PJI to determine their diagnostic characteristics including sensitivity and specificity.**

Methods: **The following data were extracted: PCR method, number of patients, sample site and type, diagnosis standard, true positive, false positive, false negative, and true negative. Pooled sensitivity, specificity, positive likelihood ratio, negative likelihood ratio, and diagnostic odds ratio were calculated. Meta-regression analysis was conducted to assess heterogeneity. Subgroup analysis was also performed to assess effects of several variables on meta-analysis results.**

Results: **The current study showed that pooled sensitivity and pooled specificity were 0.70 (95% CI: 0.67 - 0.73) and 0.94 (95% CI: 0.92 - 0.95), respectively. Results of subgroup analysis indicated that sequencing method showed the lowest sensitivity (0.63, 95% CI: 0.59 - 0.67). However, after excluding studies using tissue samples directly, sequencing method showed higher sensitivity (0.83, 95% CI: 0.73 - 0.90) than other PCR methods (0.74, 95% CI: 0.69 - 0.78).**

Conclusions: **The main significance of this study was that we attempted to classify accuracies of several PCR methods and found that sequencing with a reliable sampling method could be used as an early screening strategy for PJI. Further comparisons for PCR technologies are needed to evaluate their cost effectiveness and diagnostic procedures, not just diagnostic values, to discover the optimal one for PJI diagnosis.**
(Clin. Lab. 2023;69:xx-xx. DOI: 10.7754/Clin.Lab.2022.220833)

Correspondence:
Jun-Il Yoo, MD. PhD
Department of Orthopaedic Surgery
Inha University Hospital
27, Inhang-Ro, Jung-Gu
22332, Incheon
South Korea

Phone: +82-890-3663
Email: furim@daum.net

Manuscript accepted September 9, 2022

Supplementary Data

Meta-Regression(Inverse Variance weights)

Var	Coeff.	Std. Err.	p - value	RDOR	[95%CI]
Cte.	3.254	0.7868	0.0025	----	----
S	-0.215	0.2741	0.4530	----	----
sequencing	0.345	1.0134	0.7415	1.41	(0.14;13.98)
U-ITI	-0.360	1.2192	0.7744	0.70	(0.04;11.00)
multiplex PCR					
multiplex PCR	0.093	1.1483	0.9373	1.10	(0.08;14.74)

Tau-squared estimate = 1.0003 (Convergence is achieved after 7 iterations)
Restricted Maximum Likelihood estimation (REML)

No. studies = 14
Filter OFF
Add 1/2 to all cells of the studies with zero

Meta-Regression(Inverse Variance weights)

Var	Coeff.	Std. Err.	p - value	RDOR	[95%CI]
Cte.	3.638	0.6285	0.0002	----	----
S	-0.182	0.2376	0.4604	----	----
no_tissue	0.082	0.8285	0.9231	1.09	(0.17;6.88)
-no sequencing					
tissue	-0.741	0.7215	0.3287	0.48	(0.10;2.38)
-no sequencing					

Tau-squared estimate = 0.8035 (Convergence is achieved after 5 iterations)
Restricted Maximum Likelihood estimation (REML)

No. studies = 14
Filter OFF
Add 1/2 to all cells of the studies with zero

Meta-Regression(Inverse Variance weights)

Var	Coeff.	Std. Err.	p - value	RDOR	[95%CI]
Cte.	3.056	0.4979	0.0001	----	----
S	-0.312	0.2467	0.2349	----	----
tissue	-0.168	0.7539	0.8277	0.85	(0.16;4.53)
-sequencing					
no_tissue	1.160	0.8242	0.1898	3.19	(0.51;20.01)
-sequencing					

Tau-squared estimate = 0.7428 (Convergence is achieved after 7 iterations)
Restricted Maximum Likelihood estimation (REML)

No. studies = 14
Filter OFF
Add 1/2 to all cells of the studies with zero

Figure S1. Meta-regression analysis using Meta-DiSc software.