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INPLASY

Feasibility and utility of endoscopic ultrasound-guided tissue acquisition for comprehensive genomic profiling of pancreatic cancer: A systematic review and meta-analysis

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ADMINISTRATIVE INFORMATION

Support - None.

Review Stage at time of this submission - Preliminary searches.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY2023120005

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 01 December 2023 and was last updated on 01 December 2023.

INTRODUCTION

Review question / Objective What is the feasibility and practicality of using endoscopic ultrasound-guided tissue acquisition for the comprehensive genomic profiling of pancreatic cancer?

Condition being studied In the realm of diagnosing pancreatic cancers, endoscopic ultrasound (EUS)-guided fine-needle aspiration (EUS-FNA) and EUS-guided fine-needle biopsy (EUS-FNB) play vital roles. Comprehensive genomic profiling (CGP), conducted through next-generation sequencing, has become a crucial aspect of precision medicine for pancreatic cancers. While there has been an increasing trend in conducting CGP analysis using EUS-FNA/FNB specimens for pancreatic cancer, the clinical success rate of CGP analysis remains suboptimal. Additionally, It is important to understand not only the specimen collection factors, but also the specimen processing factors that can increase the success rate of CGP testing.

METHODS

Search strategy The main key search words are “pancreatic neoplasms”, “endoscopic ultrasound”, “FNA”, “FNB”, “genetic profile”, and “NGS”.

Participant or population Pancreatic ductal adenocarcinoma tissue acquired through endoscopic ultrasound-guided fine-needle aspiration/biopsy and subjected to genetic profiling analysis.

Intervention Patients diagnosed with pancreatic ductal adenocarcinoma from whom tissue samples were obtained via endoscopic ultrasound-guided fine-needle aspiration/biopsy and subsequently underwent comprehensive genetic profiling analysis.

Comparator Not applicable.

Study designs to be included All prospective or retrospective studies.

Eligibility criteria Inclusion: (1) studies conducting a genetic profile analysis on pancreatic ductal adenocarcinoma (PDAC) tissue obtained through EUS-FNA/B; (2) studies analyzing at least five cancer-related genes including K-ras and p-53.Exlucsion: (1) studies only assessing tissue adequacy or measuring DNA quantity without sequencing data; (2) studies targeting pancreatic cystic lesions, pancreatic neuroendocrine tumor, or pancreatic lesion of uncertain diagnoses; (3) studies conducting immunohistochemistry or transcriptome analysis: (4) articles that were either not written in English or were case series (n<10), letters, commentaries, or review papers.

Information sources We will conduct a comprehensive systematic literature search in PubMed, EMBASE, and the Cochrane Library.

Main outcome(s) Success rate of sequencing.

Additional outcome(s) Detection rates of four major driver and actionable genes, and concordance rates with other samples or methods.

Quality assessment / Risk of bias analysis The Newcastle-Ottawa scale.

Strategy of data synthesis Pooled results with corresponding 95% confidence intervals (CIs) will be calculated using the random effects model recommended by DerSimonian and Laird.

Subgroup analysis Subgroup analyses and meta-regression will be performed to identify the sources of heterogeneity among the studies (e.g. region, EUS type, specimen type, sample preprocessing method, and minimum DNA requirements).

Sensitivity analysis Not applicable.

Language restriction English.

Country(ies) involved Republic of Korea.

Keywords pancreatic cancer, endoscopic ultrasound, genomic profile.

Dissemination plans We will publish a systematic review and meta-analysis.

Contributions of each author
Author 1 - Seung Bae Yoon.
Author 2 - Sung Woo Ko.
Author 3 - Hyun Yang.

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