INPLASY

Meta-analysis Protocol: Gut Microbiota Alterations in Pancreatic Cancer Patients

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ADMINISTRATIVE INFORMATION

Support - None.

Review Stage at time of this submission - Preliminary searches.

Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 11 July 2023 and was last updated on 11 July 2023.

INTRODUCTION

Review question / Objective This study aims to characterize the alterations in the gut microbiota of pancreatic cancer patients compared to healthy individuals.

Condition being studied Pancreatic cancer.

METHODS

Participant or population Pancreatic cancer patients.

Intervention 16S rRNA sequencing technique is employed to test the texonomy of gut bacteria between pancreatic cancer patients and healthy controls.

Comparator Healthy subjects were selected as controls based on age, sex, body mass index, and dietary habits matching those of the pancreatic cancer patients.

Study designs to be included Case-control studies or cohort studies.

Eligibility criteria (1) Study population diagnosed with pancreatic cancer, regardless of histological type; (2) Investigation of the gut microbiota in patients with pancreatic cancer; (3) Clinical studies with a control group are required; (4) Full-text access is available; (5) No language restrictions apply.

Information sources PubMed, EmBase, Cochrane Library, and Web of Science.

Main outcome(s) Compared to the healthy controls, pancreatic cancer patients exhibited specific characteristics in their gut microbiota, including alpha diversity and the relative abundance of microbial taxa at the phylum to species levels.

Quality assessment / Risk of bias analysis We will use the Newcastle-Ottawa Scale (NOS) to conduct quality assessments of all the literature, including experimental group selection,

comparability and exposure level of factors in observational studies. The total score is 9, and a higher score indicates higher research quality.

Strategy of data synthesis Both fixed-effects model and random-effects model will be used to assess the alpha diversity and relative abundances of gut microbiota in PC group. Statistical heterogeneity was detected using Stata software (version 15.1). Based on an I square value less than 50% or greater than 50%, the literature was classified was having low or high heterogeneity, respectively. When heterogeneity was high (>50%), the random-effects model was applied. When heterogeneity was low (<50%), the fixed-effects model was used.To assess publication bias, we will apply Begg's test and sensitivity analysis using Stata software (version 15.1).

Subgroup analysis None.

Sensitivity analysis The sensitivity analysis will be conducted by the Stata (version 15.1).

Country(ies) involved China.

Keywords pancreatic cancer, gut microbiota, dysbiosis, alpha diversity, meta-analysis.

Contributions of each author
Author 1 - Dachuan Jin - Drafted the manuscript.
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