INPLASY

Newborn Concurrent Hearing and Genetic Screening for hearing impairment in China: A Systematic Review and Meta-analysis

Corresponding author:
Pan Xie

13699615056@163.com

Author Affiliation:
MianYang Maternity & Child Healthcare Hospital.

Pan, K; Shang, ZR; Liu, JL; Wen, YD; Luo, J; Zou, D; Wang, AC; Li, T; Liao, LY; Xie, P.

ADMINISTRATIVE INFORMATION

INTRODUCTION

*R*eview question / Objective This study employs a systematic review methodology to conduct a meta-analysis of the included literature, analyzing the rate of hearing screening pass and genetic screening fail (UNHS pass/ genetic fail), aiming to investigate the advantages of combining newborn hearing and genetic screening for hearing impairment in China.

Rationale This study employs a systematic review methodology to conduct a meta-analysis of the included literature, analyzing the rate of hearing screening pass and genetic screening fail (UNHS pass/genetic fail), aiming to investigate the advantages of combining newborn hearing and genetic screening for hearing impairment in China.

Condition being studied The subjects were newborns.

METHODS

Search strategy "newborn" "neonate" AND "hearing loss" "deaf" AND "hearing screening" AND "genetic screening".

Participant or population Newborns.

Intervention Combination of neonatal hearing and gene screening.

Comparator Not applicable.

Study designs to be included Observational study.

Eligibility criteria The inclusion criteria were as follows: (1) Original research; (2) The subjects were newborns; (3) The research detection technology is the combination of neonatal hearing and gene screening; (4) The number of screened genes is not less than 3; (5) The original data is complete, and

relevant data can be extracted directly or indirectly for statistics; (6) The language limit is English.Exclusion criteria: (1) Duplicate published studies; (2) incomplete data or unavailability of data; (3) Animal experiment; (4) case report, review and systematic review; (5) Non-universal neonatal hearing and gene screening; (6) The number of screened genes is less than 3.

Information sources Electronic databases.

Main outcome(s) The number of cases that passed the hearing screening but failed the genetic screening including GJB2, SLC26A4 and MT-RNR1.

Data management All data were processed with the statistical software STATA 15.1 (12). For the synthesis analysis of the primary outcomes, we calculated the weighted mean effect size and its 95% confidence interval (CI) for each study result to estimate the overall impact of combined screening on the detection rate of newborn hearing loss. When facing multiple studies reporting the same outcome measures, we utilized forest plots to visually display the effect size and its confidence interval for each study, as well as the total effect size after combining all studies. A heterogeneity test of P>0.1, I2>50% indicated that all studies were homogeneous; P5% indicated that studies differed and a difference sensitivity analysis was performed to identify sources of difference. A random-effects model was applied This meta-analysis used a random effects model to summarize the effects. The funnel plot method and the Egger test were used to investigate publication bias.

Quality assessment / Risk of bias analysis The cross-sectional Research Quality evaluation scale recommended by Agencyfor Health Research and Quality (AHRQ) in the United States was used to evaluate the quality of the included literatures, which consisted of 11 items. Use the "yes", "no" and "not clear" categories respectively, with "1", "0" and "0" marks respectively. The total score is 0 to 11 points, of which 0 to 3 is classified as low quality, 4 to 7 as medium quality, and 8 to 11 as high quality. The meta-analysis is performed according to the report items and the relevant items in the meta-analysis Checklist (PRISMA Checklist) that are preferred in the system evaluation.

Strategy of data synthesis All data were processed with the statistical software STATA 15.1 (12). For the synthesis analysis of the primary outcomes, we calculated the weighted mean effect

size and its 95% confidence interval (CI) for each study result to estimate the overall impact of combined screening on the detection rate of newborn hearing loss. When facing multiple studies reporting the same outcome measures, we utilized forest plots to visually display the effect size and its confidence interval for each study, as well as the total effect size after combining all studies. A heterogeneity test of P>0.1, I2>50% indicated that all studies were homogeneous; P5% indicated that studies differed and a difference sensitivity analysis was performed to identify sources of difference. A random-effects model was applied This meta-analysis used a random effects model to summarize the effects. The funnel plot method and the Egger test were used to investigate publication bias.

Subgroup analysis Non.

Sensitivity analysis We did a sensitivity analysis to exclude each of these trials one by one, and then did a combined analysis of the remaining trials.

Language restriction English.

Country(ies) involved China.

Keywords Newborn concurrent hearing and genetic screening; Newborn hearing screening; Deafness genes; Systematic review; Meta-analysis.

Contributions of each author
Author 1 - Ke Pan - Author 1 drafted the manuscript.
Author 2 - Zhirong Shang - The author drafted the manuscript.
Author 3 - Jialin Liu - The author drafted the manuscript.
Author 4 - Yidong Wen - The author provided statistical expertise.
Author 5 - Jing Luo - The author contributed to the development of the selection criteria, and the risk of bias assessment strategy.
Author 6 - Dan Zou - The author contributed to the development of the selection criteria, and the risk of bias assessment strategy.
Author 7 - Aichun Wang - The author participated in data extraction.
Author 8 - Tao Li - The author participated in data extraction.
Author 9 - Lingyan Liao - The author participated in data extraction.
Author 10 - Pan Xie - The author read, provided feedback and approved the final manuscript.