INPLASY

Genetic Alterations in Extramedullary Leukemia among Acute Myeloid Leukemia Patients: Insights from a Cohort Study and Meta-analysis

INPLASY202380091

doi: 10.37766/inplasy2023.8.0091

Received: 21 August 2023

Published: 21 August 2023

Suvijak, U[1]; Sasinipa, T[2]; Kamolchanok, K[3]; Tarinee, R[4]; Sujitra, P[5]; Thanapon, K[6]; Nattawut, L[7]; Weerapat, O[8].

Corresponding author:
Weerapat Owattanapanich

weerapato36733@gmail.com

Author Affiliation:
Division of Hematology, Department of MedicineFaculty of Medicine, Siriraj Hospital, Mahidol University.

ADMINISTRATIVE INFORMATION

Support - No financial support for the research, authorship, and/or publication of this article.

Review Stage at time of this submission - Piloting of the study selection process.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY202380091

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 21 August 2023 and was last updated on 21 August 2023.

INTRODUCTION

Review question / Objective 1. The primary objective of this analysis was to determine the incidence of each mutation in AML patients with EML. 2. The secondary objective was to compare the mutational statuses of AML patients with and without EML.

Rationale MS commonly manifests in extramedullary sites such as the skin, bones, soft tissues, and gall bladder. However, some studies also document its occurrence in rarer locations, including the pleura, penis, and vulva. The prognosis for MS patients tends to be unfavorable and can vary based on the location of the lesion and its molecular attributes. In contemporary diagnostic approaches, Next-generation sequencing (NGS) has become an instrumental tool for detecting mutations in AML patients, including those with MS. The NPM1 mutation is the most common mutation found in MS, along with other common mutations and fusion genes such as KRAS, NRAS, KIT, CEBPA, IDH1, IDH2 mutations, RUNX1::RUNX1T1, and CBFB::MYH11. Nevertheless, discrepancies exist regarding the reported incidence of each mutation in MS across different studies.
Consequently, this systematic review and meta-analysis endeavor to compile and analyze data regarding the incidence of each mutation from all pertinent sources. Our objective is to gain a deeper understanding of the specific characteristics and precise prevalence of genetic mutations in AML patients presenting with extramedullary leukemia (EML).

Condition being studied AML with EML.

METHODS

Search strategy Six researchers independently searched for published articles from their inception through August 1, 2023, using the EMBASE,

Medline, and Scopus databases. The search incorporated terms such as "acute myeloid leukemia," "extramedullary," "granulocytic sarcoma," "myeloid sarcoma," and "leukemic cutis". For a comprehensive search strategy, our systematic review and meta-analysis strictly followed the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-analysis) guidelines.

Participant or population All acute myeloid leukemia(AML) with extramedullary leukemia(EML) patients.

Intervention Not applicable.

Comparator Not applicable.

Study designs to be included We included retrospective or prospective cohort studies centered on AML with EML.

Eligibility criteria We included retrospective or prospective cohort studies centered on AML with EML. We excluded reviews, case reports, and case series consisting of fewer than 10 cases.

Information sources EMBASE, Medline, and Scopus electronic databases.

Main outcome(s) The incidence of genetic mutations in AML patients with EML.

Additional outcome(s) The mutational statuses of AML patients with and without EML.

Data management Four researchers independently assessed the titles and abstracts of the retrieved studies. They also undertook a manual review of the references in the selected studies to pinpoint any additional pertinent research. In instances of disagreement about the inclusion of certain studies, a consensus was reached with the mediation of two investigators.

Quality assessment / Risk of bias analysis Two researchers independently evaluated the included studies' quality using the Newcastle-Ottawa quality assessment scale.

Strategy of data synthesis We conducted the data analysis utilizing the Review Manager 5.4 software provided by the Cochrane Collaboration (London, United Kingdom). The Inverse Variance method was employed to compute pooled odds ratios (ORs) and their corresponding 95% confidence intervals (CIs) for each gene across the studies . Given the anticipated variability among the incorporated studies, a random-effects model was favored over a fixed-effects model in this meta-analysis. We evaluated statistical heterogeneity with Cochran's Q test and quantified its extent using the I2 statistic. Depending on the I2 values, heterogeneity was classified as either insignificant (0-25%), low (25-50%), moderate (50-75%), or high (75-100%) . For transparency and procedural clarity, we registered our study protocol with the International Platform of Registered Systematic Review and Meta-analysis Protocols (INPLASY) network under the registration number.

Subgroup analysis Not performed.

Sensitivity analysis Not performed.

Language restriction English.

Country(ies) involved Thailand.

Keywords Acute myeloid leukemia; Myeloid sarcoma; Extramedullary leukemia; genetic mutation; meta-analysis.

Contributions of each author

Author 1 - Suvijak Untaaveesup - design the study, collect the data, drafted the manuscript and prepared the final version.
Author 2 - Sasinipa Trithiphen - collect the data, drafted the manuscript and prepared the final version.
Email: sasinipa.tri@gmail.com
Author 3 - Kamolchanok Kulchutisin - designed the study and collected the data.
Author 4 - Tarinee Rungjirajittranon - designed the study and collected the data.
Author 5 - Sujitra Panyoy - designed the study and collected the data.
Author 6 - Thanapon Kaokunakorn - designed the study and collected the data.
Author 7 - Nattawut Leelakanok - designed the study and statistical analysis.
Author 8 - Weerapat Owattanapanich - design the study, collect the data, statistical analysis, drafted the manuscript and prepared the final version.
Email: weerapato36733@gmail.com