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Prevalence and Prognostic Impact of ASXL1 Somatic Mutation in Patients with Chronic Myeloid Leukemia: A Systemic Review and Meta-Analysis

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ADMINISTRATIVE INFORMATION

Support - TBD.

Review Stage at time of this submission - Completed but not published.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY202630075

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 21 March 2026 and was last updated on 21 March 2026.

INTRODUCTION

Review question / Objective Primary question: Among patients with CML, does ASXL1 mutation affect survival and prognosis compared with wild type?

Primary objective: Evaluate association between ASXL1 mutation and CML prognosis, response to therapy and overall survival.

Secondary objectives: PFS, EFS, transformation risk, response to TKI therapy, and mutation prevalence.

P: individuals with chronic myeloid leukim

Rationale ASXL1 (additional sex combs-like 1) mutations are frequent in several myeloid malignancies and have been associated with adverse prognosis in diseases such as myelodysplastic syndromes (MDS) and acute myeloid leukemia (AML). The prevalence and prognostic impact of ASXL1 mutation in chronic myeloid leukemia (CML) — across chronic, accelerated, and blast phases, and in the era of tyrosine kinase inhibitors (TKIs) — remains unclear.

A systematic review of available evidence will clarify whether ASXL1 is a prognostic biomarker in CML and inform future research and clinical management.

Condition being studied Chronic Myeloid Leukemia (CML).

METHODS

Search strategy A comprehensive literature search was conducted by a medical librarian using the following databases: CINAHL, EMBASE, MEDLINE Ultimate, and PubMed. The search strategies applied in each database are detailed in the corresponding figure. The search was carried out up to August 2025 and was restricted to publications in the English language.

Participant or population Patients diagnosed with CML.

Intervention NA.

Comparator Patients with CML without ASXL1.

Country(ies) involved United States.

Study designs to be included Randomized controlled trials, cohort retrospective and prospective studies.

Keywords chronic myeloid leukemia, CML, myeloproliferative neoplasms, leukemia, ASXL1 mutation.

Eligibility criteria For inclusion in this systematic review and meta-analysis, studies were required to be peer-reviewed articles that examined the impact of ASXL1 mutations and the progression of chronic myeloid leukemia (CML).

Contributions of each author

Author 1 - Rita Ahmad - drafted and reviewed manuscript, provided resources, finalized methods. Email: ritaedsl@gmail.com

Author 2 - Motaz Almahmood - data curation and risk of bias assessment. Email: motazodat71@gmail.com

Author 3 - Rasha Kaddoura - provided statistical analysis. Email: rasha.kaddoura@gmail.com

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Author 12 - Sara Westall - librarian, provided initial search. Email: sara.westall@und.edu

Author 13 - Fadi Haddad - supervision and expertise. Email: fhaddad@mdanderson.org

Author 14 - Shehab F. Mohamed - supervision, mentorship, review, data curation, conceptualization. Email: shehabfareed@yahoo.com

Information sources Electronic database.

Main outcome(s) ASXL1 mutations are recurrent in chronic myeloid leukemia and are associated with significantly inferior molecular response to tyrosine kinase inhibitor therapy, particularly reduced rates of major molecular response at 12 months. While the impact on cytogenetic response appears less consistent, these findings support ASXL1 as a clinically relevant adverse prognostic biomarker in CML.

Quality assessment / Risk of bias analysis Risk of bias/quality assessment was performed independently by two reviewers using the Newcastle–Ottawa Scale (NOS) (modified as applicable for observational studies). The NOS evaluates studies across three domains: selection (maximum 4 stars), comparability (maximum 2 stars), and outcome (maximum 3 stars), with a maximum total score of 9 stars [18]. Any discrepancies between the two reviewers were resolved through discussion and consensus (with senior reviewer adjudication if needed). Based on total NOS score, studies were categorized as good quality (7–9 stars), fair quality (4–6 stars), or poor quality (0–3 stars). The detailed study-level ratings are presented in table (1) below.

Strategy of data synthesis Data extraction was performed independently by five investigators (RA, MA, AD, MR and AAM) using a standardized, predesigned extraction form. Extracted variables included study characteristics (design, country, sample size), patient demographics, disease phase distribution, ASXL1 detection method, treatment exposure, and reported outcomes. Clinical endpoints included major molecular response (MMR), complete cytogenetic response (CCyR), progression, resistance, and survival outcomes where available. Disagreements were resolved through discussion with senior reviewers.

Subgroup analysis NA.

Sensitivity analysis NA.