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Why TP53 expression varies in lymphoma: Insights from a Bayesian meta-analysis

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OBJECTIVES/GOALS: To quantify between-study heterogeneity in TP53 expression across DLBCL studies using frequentist and Bayesian meta-analytic frameworks; estimate the association between TP53 status and cell-of-origin (GCB vs. non-GCB); and identify methodological and biological sources of variation, using study-level data. METHODS/STUDY POPULATION: Four retrospective study-level datasets (n=457) from France, Canada, Brazil, and the USA were included. TP53 status was primarily assessed by immunohistochemistry (IHC) with study-specific thresholds (20–50% positive cells). Cell-of-origin classification followed the Hans or Choi algorithms as reported by each study. We fit frequentist random effects models with REML (R metafor) and Bayesian hierarchical models (R rstan) RESULTS/ANTICIPATED RESULTS: Frequentist random effects meta-analysis indicated moderate-to-high heterogeneity ($I^2 = 66.7\%$, $p = 0.038$) and a pooled odds ratio for GCB among TP53-positive vs. TP53-negative cases of 0.953 (95% CI: 0.682–1.330). The Bayesian hierarchical model estimated P(GCB | TP53+) with a posterior mean of 0.71 (95% CrI: 0.38–0.93); study-level posterior means ranged from 0.37 to 0.53. Both approaches confirm substantial between-study variation attributable to methodological factors (IHC thresholds, COO algorithms) and biological differences DISCUSSION/SIGNIFICANCE OF IMPACT: This analysis clarifies the heterogeneity of TP53 expression in lymphoma and shows how methodological and biological variability influence results. Bayesian modeling enhances reliability in small, heterogeneous biomarker syntheses, supporting standardization of TP53 assessment and improving reproducibility in DLBCL.

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Perceptions of adolescents with insulin-dependent diabetes and their caregivers on the use of generative AI for diabetes care

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OBJECTIVES/GOALS: This study aims to assess perceptions of children with insulin-dependent diabetes and their guardians on the perceived benefits and challenges on the use of a diabetes-specific generative pretrained transformer to assist with diabetes care in insulin administration. METHODS/STUDY POPULATION: The study involved one-on-one semi-structured interviews with both adolescents aged 14-19 with insulin-dependent diabetes and their guardians. An interview guide was developed utilizing the constructs from the health information technology acceptance model. We have completed 1 interview with a caregiver with a child with diabetes. A total of 10 interviews are planned. All interviews have been or will be recorded utilizing a video conferencing platform and transcribed verbatim. The interview content will then be organized and coded using NVivo software. Thematic analysis was conducted in accordance with analysis guidelines. RESULTS/ANTICIPATED RESULTS: From initial interviews, 3 key themes have arisen regarding the use of artificial intelligence for diabetes care. First, use of large language models has been utilized in their daily life; however, there is hesitancy to utilize these resources for medical advice. A second important theme that surfaced several times was the importance of trust in the source of the artificial intelligence that she would be using since it was for medical care. Another theme was the importance of ease of use of a large language model. This theme was illustrated by being able to share with family and friends since children are often involved with multiple caregivers. It would also have to have an easy-to-use interface, such as pre-programmed personal settings and recognizable picture icons to make her more likely to use it. DISCUSSION/SIGNIFICANCE OF IMPACT: Users emphasized trust in AI sources for diabetes care, noting that clear visuals and personalization improve usability. Further interviews may reveal broader perspectives on adoption, challenges, and barriers among adolescents and caregivers with insulin-dependent diabetes.

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Use and evaluation of generative artificial intelligence for qualitative analysis in health sciences: A scoping review

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OBJECTIVES/GOALS: This is a scoping review of the use of generative AI (GenAI) for qualitative analysis in the health sciences. The primary objectives are to summarize the methods used for qualitative analysis based on the approach (e.g., inductive vs. deductive), metrics for examining GenAI's performance by approach type, and best practices for improving performance. METHODS/STUDY POPULATION: We searched six databases (PubMed, EMBASE, CINAHL, Scopus, Web of Science, and PsycINFO) using a comprehensive search string tailored to each database. We identified 5,853 unique results, of which 223 were identified as potentially relevant after review of abstracts. We will conduct a full manuscript review for each potentially relevant result to confirm inclusion, including use of GenAI for qualitative analysis of physical or mental health text data where a full-length paper is available. Two study team members will review each manuscript to confirm inclusion prior to data extraction and coding. We will also enter each manuscript into Yale Clarity, a secure GenAI platform powered by multiple large language models (e.g., ChatGPT, Claude), to examine GenAI's capacity to facilitate manuscript screening and coding. RESULTS/ANTICIPATED RESULTS: We will code included articles for: the research topic area; type of qualitative data analyzed (interview, focus group, medical chart, text-based digital or social media content); type of study (original or secondary data, review); type of qualitative analysis (thematic analysis, content analysis, grounded theory); type of approach (inductive, deductive); steps in analytic process that generative AI was used (initial open coding and sense making, final

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