Randomized Treatments for Myelodysplastic Syndrome and Related Disorders: A Comprehensive Component Network Meta-Analysis of Randomized Controlled Trials

E. ZERZAN [1], **K. JINDAL** [2], **A. SUMRANI** [3], **A. BHATIA** [4], **H. NAGAMALLU RAJASEKAR** [5], **L. PATEL** [6], **N. GOSWAMI** [7], **M. LLERENA VARGAS** [8]

1. The University of Texas at Austin, Texas, USA
2. Government Medical College, Patiala, Punjab, India
3. Hamdard Institute of Medical Science and Research, Delhi, India
4. Jawaharlal Nehru Medical College, Maharashtra, India
5. Sri Ramachandra Institute of Higher Education and Research, Tamil Nadu, India
6. GMERS Medical College and Hospital, Sola, Gujarat, India
7. Indira Gandhi Government Medical College, Nagpur, Maharashtra, India
8. Universidad Tecnológica Equinoccial, Pichincha, Ecuador

INTRODUCTION

Myelodysplastic syndromes (MDS) are heterogeneous hematologic malignancies with limited and evolving treatment options.[1] Numerous randomized trials have evaluated pharmacological and combination therapies, but comparisons across treatments remain challenging.[1]
We conducted a systematic review and network meta-analysis of randomized trials to compare treatments for MDS and related malignancies. Outcomes included remission, survival, and death with the present analysis focused on complete remission. A component network meta-analysis was also performed to assess the contribution of individual treatment components.[2]

AIM

To compare the efficacy of randomized treatment strategies for myelodysplastic syndromes (MDS) and related malignancies using network and component network meta-analysis, with complete remission as the primary outcome.

METHOD

Searches identified 14904 records, including 5894 from Embase, 3597 from Scopus, 2042 from Cochrane CENTRAL, 1971 from PubMed, and 1400 from ClinicalTrials.gov. After deduplication in Covidence, 5262 records were imported for title and abstract screening. Full-text assessment was performed for 833 articles, and 88 articles were included for data extraction. (Figure 1)
The most common reasons for full-text exclusion were duplicate records and absence of available results, accounting for 504 and 73 exclusions, respectively. This screening pathway reflects a large evidence base refined through multiple stages before quantitative synthesis.

CONCLUSIONS

Network meta-analysis identified several treatment strategies associated with higher odds of complete remission compared with best supportive care, with **glasdegib plus cytarabine** showing the largest point estimate.
This review combines broad trial identification, structured screening, detailed extraction, and treatment level synthesis across a complex therapeutic landscape. Its findings may support future guidelines, whereas the contrast between regimen- and component-level effects leaves key clinical questions for the full review to resolve.

RESULTS

Of 29 included studies, 15 studies evaluating 14 interventions contributed to the primary connected complete remission network. 14 interventions included supportive care, conventional care, single-agent hypomethylating therapy, cytarabine-based regimens, and multiple combination strategies. A component network meta-analysis separated combination regimens into 13 active components, allowing both whole-regimen and component-level interpretation. (Figure 2)

Compared with best supportive care, higher odds of complete remission were observed for azacitidine, azacitidine plus lenalidomide, azacitidine plus vorinostat, panobinostat plus azacitidine, APR-246 plus azacitidine, decitabine, decitabine plus valproic acid, and glasdegib plus cytarabine. The largest point estimate was seen with glasdegib plus cytarabine, followed by APR-246 plus azacitidine, decitabine plus valproic acid, and panobinostat plus azacitidine. (Figure 3)

At the component level, azacitidine, decitabine, and glasdegib showed statistically significant associations with complete remission.

Heterogeneity and inconsistency were not detected, with $\tau 2=0$, I2=0%, total Q=0.28, P=0.9637, within-design Q=0.14, P=0.7099, and between design Q=0.14, P=0.9315.

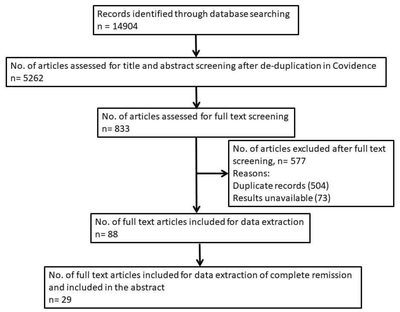

Figure 1: PRISMA flowchart

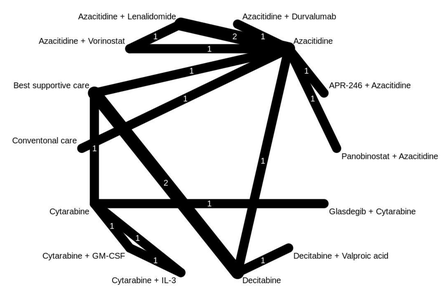

Figure 2: Network plot

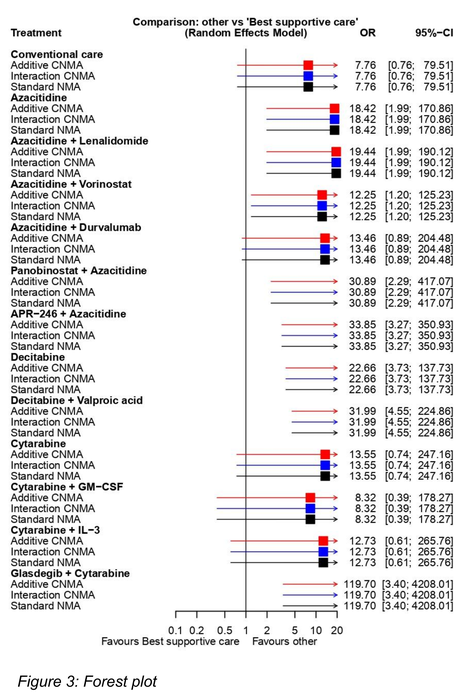

Figure 3: Forest plot

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CONTACT INFORMATION

Emi Zerzan: emikzerzan@gmail.com
Kridhay Jindal: kridhayjindal2@gmail.com
Arushi Sumrani: arusum2010@gmail.com

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Complete references for included studies and supplementary study characteristics are available from the authors upon request.