THE ROLE OF micro-RNA's IN NEUROPATHIC PAIN- A SCOPING REVIEW

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INTRODUCTION

Neuropathic pain can be caused by a lesion or disease of the somatosensory system characterized by pathological neuro-immune alterations.

At a molecular level, microRNAs (miRNAs) act as regulators of gene expression orchestrating both immune and neuronal processes.

Thus, miRNAs may act as essential modulators of processes for the establishment and maintenance of neuropathic pain.

However, little is known about the role of miRNAs in neuropathic pain.

OBJECTIVE: To explore and chart the literature to identify miRNAs that are dysregulated in neuropathic pain.

METHODS

This review has been reported in accordance with the preferred reporting items for systematic reviews and meta-analysis extension for scoping reviews (PRISMA-ScR) checklist (Tricco et al., 2018).

Information Source:
The lead investigator (KKS) in consultation with an experienced subject librarian developed the search strategy and searched the following electronic databases: PubMed, EBSCO , CINAHL, Cochrane Library, and SCOPUS , which were searched from inception to March 2023.

Data Management:
Articles obtained through the systematic search of the above-mentioned databases were exported and saved into reference management software (EndNote X9 Thomson Corporation) which was used throughout the review process

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Quality Assessment (including risk of bias):
JBI critical appraisal checklist was used for this purpose.

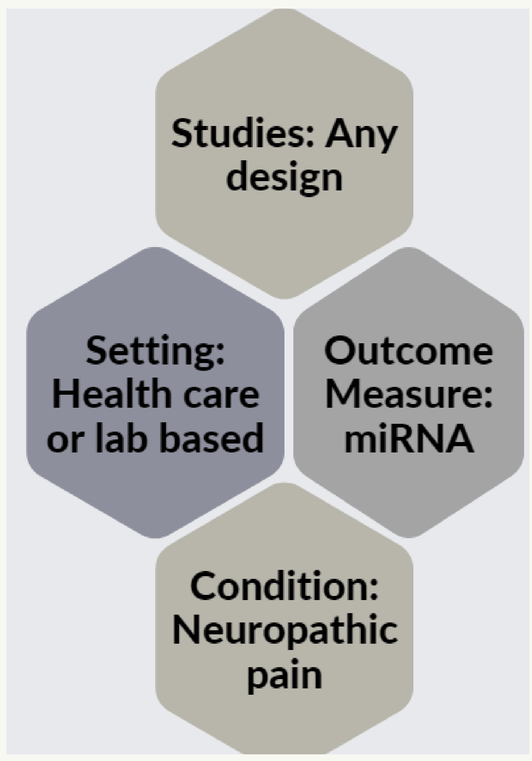

Fig 1: Eligibility Criteria

RESULTS

A total of 7 studies met our inclusion criteria and were part of the review.

A total of 384 participants informed the findings. Characteristics of studies has been shown in Figure-2.

The JBI risk of bias scores (out of 8) has been presented for individual studies (Figure-3). The overall risk of bias was considered to be 'low' (Figure- 3a).

Different miRNAs that are commonly involved in the chronic neuropathic pain conditions were identified including miR-132, miR-101 and miR-199a.

These miRNAs to be significantly associated with increased diabetic disease duration, HbA1C levels and fibrinogen levels.

DISCUSSION

Screening the maximum number of miRNAs using robust methods such as microarray or RNA- Seq may be the best way to successfully identify miRNA markers of chronic pain.

To increase specificity, it may be important to determine if an individual miRNA is expressed in "pain-specific" tissues or cells.

This could be achieved by selecting a candidate miRNA and to hypothesize its mechanism of action on the basis of bioinformatic predictions of target mRNAs.

This may require miRNA target validation as done in some of the studies included in the review.

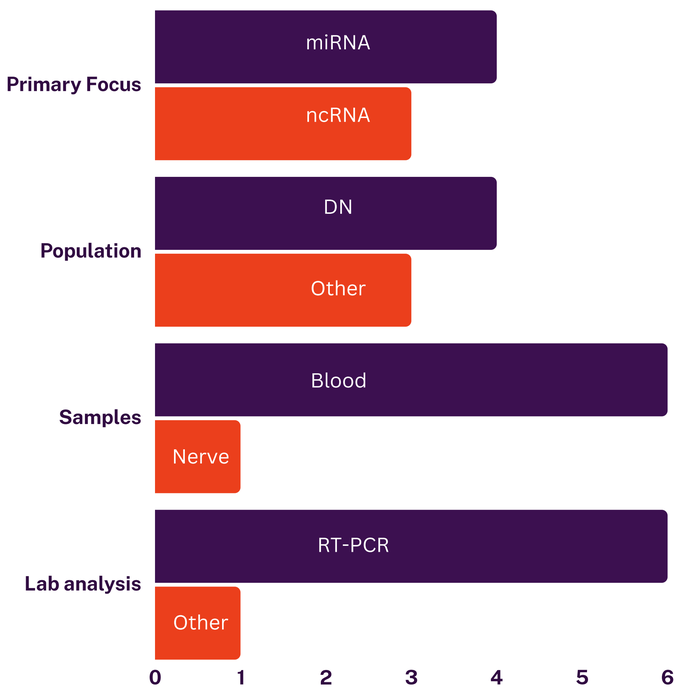

Fig 2: Key characteristics of included studies

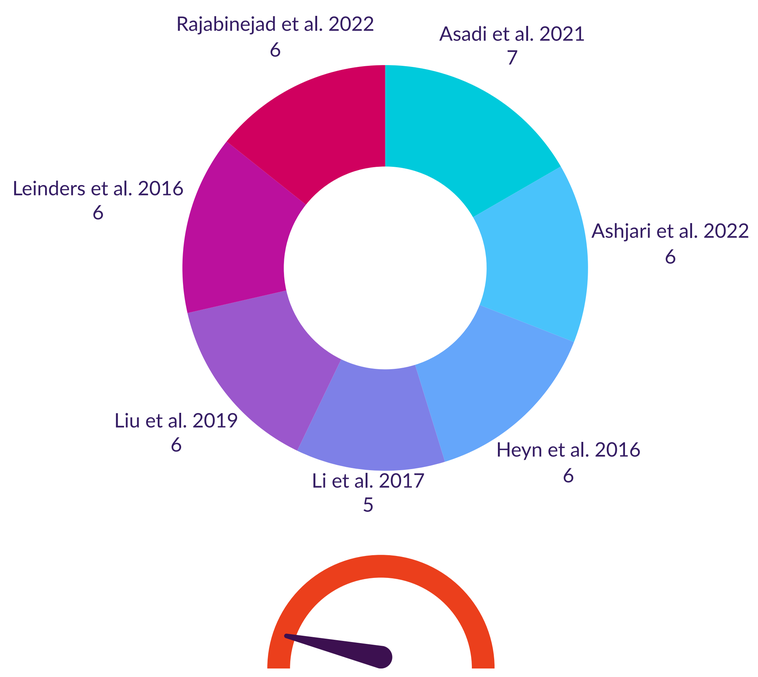

Fig 3 (top): Risk of Bias in included studies (scores out of 8).
Fig 3a (below): Overall risk of bias was 'Low'

CONCLUSION

Our review findings reveal key insights into molecular mechanisms in chronic pain states.

Promising emerging evidence shows that specific functional roles can be attributed to some miRNAs, that may facilitate translational developments.

Identifying and understanding the role of miRNAs in neuropathic pain remains an important step for potentially providing mechanism-based treatment for patients with neuropathic pain in the future.

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