Abstract #768

The MicroRNAs (miRNAs) expression in benign urological diseases: a systematic review

Hypothesis

The exact molecular and cellular processes that cause benign urological diseases in the stromal and epithelial components of the urinary tract are yet unknown. Reviewing and analysing the data linking microRNAs (miRNAs) in the pathophysiology of benign urological conditions, including overactive bladder (OAB), bladder outlet obstruction (BOO), bladder pain syndrome/ interstitial cystitis (BPS/IC), and Lower urinary tract dysfunction (LUTD) is the objective of the current systematic review.

Study Design

Evidence including all case-control, cohort, and cross-sectional studies that measure participants' MicroRNA as a biomarker for benign urological diseases has been gathered On January 2024, through searching MEDLINE via PubMed, Scopus, Web of Science, Embase, and ProQuest databases with the following search strategy: ((((((bladder[Title/Abstract]) OR (urinary[Title/Abstract])) NOT ((((("neoplasms"[MeSH Terms]) OR (neoplasm* [Title/Abstract])) OR (cancer* [Title/Abstract])) OR (tumor*[Title/Abstract]))) OR (neurogenic[Title/Abstract])) OR ((("lower urinary tract symptoms"[MeSH Terms]) OR ("urinary incontinence" [MeSH Terms])) OR ((lower urinary tract [Title/Abstract]) OR (lower urinary tract symptom[Title/Abstract]) OR (urinary incontinence[Title/Abstract]) OR (LUTS[Title/Abstract])))) OR ((((detrusor[Title/Abstract])) OR (("urinary bladder, overactive"[MeSH Terms]))) OR (overactive bladder[Title/Abstract]))) AND ((((("micrornas"[MeSH Terms]) OR (microRNA[Title])) OR (miRNA[Title])) OR (miR[Title])) thorough search of the PubMed, Scopus, Web of Science, Embase, and ProQuest databases. Studies considered eligible that present information on the reference Gene, profile type, and serum levels of microRNA from patients diagnosed with benign urological disease including benign prostate hyperplasia (BPH) or benign prostate enlargement (BPE), overactive bladder (OAB), and bladder outlet obstruction (BOO). These studies were appraised by the quality assessment checklist of the Joanna Briggs Institute (JBI).

Results:

A total of 4,587 records related to miRNAs in urological diseases and their diagnostic significance were retrieved. Of these, we identified 28 records for our systematic study. The most frequently associated miRNA was 92a-3p identified which was found upregulated in OAB diagnosis. In BOO, miR-146a-5p was identified to be upregulated. miR 146a-5p was upregulated in BO, and for other benign conditions, different miRNAs were reported.

491-5p miRNAs were found deregulated in OAB-related studies. We expected other miRNAs to have the same trend in the OAB studies. In SUI miR-93 was the most frequent downregulated miRNA. The other reported miRNAs had similar frequencies. JBI appraisal checklists based on the study design (Cohort, Case-control, and cross-sectional), were used to assess the diagnostic accuracy of the eligible studies. The risk of bias for the included articles is shown in Table 1. We found that all reports met the criteria for a high-quality score. Specifically, they were well described and adequately answered the quality questions. Regarding the risk of bias, more studies had a representative spectrum of patients, including clear selection criteria.

Interpretation of Results

When it comes to the early detection and treatment of benign urological conditions, 92a-3p, miR-21, miR-199a-5p, and miR-146a-5p, and 491-5p have the potential to be employed as both a biomarker and a therapeutic target. The creation of pre-RNA or anti-RNA molecules within carrier vehicles that may be safely administered to patients should be made possible by technological advancements.

Table 4. Quality assessment of the included studies based on JBI critical appraisal tool.

Study	Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Overall
Case-Control											
S. H. Yang	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Yes	Yes	Included
M. von Siebenthal	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Included
F. Urabe (letter to editor)	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Unclear	Yes	Included
M. Schneider (ABSTRACT)	Yes	Yes	Yes	Yes	Yes	Unclear	Unclear	Unclear	Unclear	Yes	Included
V. Sanchez-Freire (ABSTRACT)	Yes	Yes	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Yes	Included
X. Liu	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Unclear	Yes	Included
S. Liu	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Unclear	Yes	Included
J. M. Hotaling (ABSTRACT)	Yes	Yes	Yes	Yes	Yes	No	No	Unclear	Unclear	Unclear	Included
A. Hashemi Gheinani 2014 (ABSTRACT)	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Yes	Included
A. Hashemi Gheinani 2016 (ABSTRACT)	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Yes	Included
A. Hashemi Gheinani 2015 (ABSTRACT)	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Unclear	Included
A. Hashemi Gheinani 2019 (ABSTRACT)	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Unclear	Included
A. Hashemi Gheinani 2017 (ABSTRACT)	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Yes	Included
A. H. Gheinani 2017	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Included
A. H. Gheinani 2014 (abstract)	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Yes	Included
A. H. Gheinani 2016 (abstract)	Yes	Unclear	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Yes	Included
A. H. Gheinani 2021	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Included
A. H. Mossa (abstract)	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Unclear	Yes	Included
Cohort											
T. Overholt (abstract)	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	Yes	Unclear	Yes	Included
I. Koeck 2018	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Included
A. Hashemi Gheinani 2018 (abstract)	Unclear	Yes	Yes	Unclear	Unclear	Yes	Yes	Yes	Unclear	Unclear	Included
A. Hashemi Gheinani 2017 (abstract)	Yes	Yes	Yes	Unclear	Unclear	Yes	Unclear	No	Unclear	Unclear	Included
Cross-Sectional											
T. S. Worst	Yes	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes			Included
T. Tanaka	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes			Included
E. Firat	Yes	Yes	Yes	Yes	Unclear	Unclear	Yes	Yes			Included

Conclusion

92a-3p, miR-21, miR-199a-5p, and miR-146a-5p, and 491-5p have the potential to be employed as both a biomarker and a therapeutic target.

References

1. Kimura T. [Non-coding Natural Antisense RNA: Mechanisms of Action in the Regulation of Target Gene Expression and Its Clinical Implications]. Yakugaku Zasshi. 2020;140(5):687-700.
2. Vos PD, Leedman PJ, Filipovska A, Rackham O. Modulation of miRNA function by natural and synthetic RNA binding proteins in cancer. Cell Mol Life Sci. 2019;76(19):3745-52.
3. Matsuyama H, Suzuki HI. Systems and Synthetic microRNA Biology: From Biogenesis to Disease Pathogenesis. Int J Mol Sci. 2019;21(1).
4. Iles J, Fehlmann T, Fischer U, Backes C, Galata V, Minet M, et al. An estimate of the total number of true human miRNAs. Nucleic Acids Res. 2019;47(7):3353-64.

Salehi-Pourmehr H, Hajebrahimi Sakineh , Atayi M, Mahdavi N, Mostafaei Hadi
Tabriz University of Medical Sciences, Tabriz, Iran