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SEQUENCE, SECONDARY STRUCTURE, AND PHYLOGENETIC CONSERVATION OF MicroRNAs in MIR182 microRNA 182 [HOMO SAPIENS (HUMAN)]

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Abstract
Introduction: The secondary structure and sequence of the miRNA are both conserved. Because it is conserved across species, we can infer that it serves a purpose and that it is probably involved in important regulatory functions. It is important to comprehend MIR182's sequence, secondary structure, and evolutionary conservation since doing so sheds light on its biological function and suggests potential implications for a number of biological processes and disorders.
Materials and methods: Selection of microRNA 182, sequence retrieved from NCBI, sequence analysis using mirBASE, conservative analysis using the Consurf server, secondary structure prediction of MIR182 by RNA fold server.
Results: The input sequence which is analyzed using mirBASE shows that the sequence is highly conserved as well as phylogenetically conserved and the secondary structure is predicted using the RNA fold server.
Discussion: The conservation of miR-182 across different species provides insights into its functional importance, miR-182 is highly conserved, it suggests that it plays crucial roles in biological processes across various organisms
Conclusion: The input sequence of the Homo sapiens region containing MIR182 was predominantly conserved.

Keywords: MicroRNA’s, MIR-182, Homo Sapiens, Conservation, Secondary structure

Introduction:
Small, non-coding RNA molecules known as microRNAs (miRNAs) are essential for post-transcriptional gene control. They have been linked to a number of biological functions, including apoptosis, cell differentiation, development, and disease pathogenesis (1). MicroRNA 182 (MIR182), one of these miRNAs, has been the subject of in-depth study because of its potential importance in human biology and disease. MIR182 is a member of the miR-183/96/182 cluster, which is highly conserved among other species and is found on human chromosome 7(2). Three mature miRNAs are encoded by this cluster: miR-183, miR-96, and miR-182, the latter of which is the main subject of this investigation. These miRNAs have been linked to the regulation of a number of biological functions, including cancer, immunological responses, and neural development (3). MiR-182 is translated from its gene as a primary miRNA (pri-miRNA) in the nucleus, similar to other microRNAs. To create the mature miR-182 molecule, this pri-miRNA is first converted into a precursor miRNA (pre-miRNA). The RNA-induced silencing complex (RISC), where the mature miRNA is loaded, is where the miRNA performs its regulatory functions (4).
MiR-182 is known to target particular mRNA molecules by attaching to complementary sequences, which are typically present in the 3' untranslated region (UTR) of the mRNA. It is possible for miR-182 to inhibit gene expression when it attaches to its target mRNA (5) . Inhibiting translation or encouraging mRNA decay are two ways to achieve this control. Developmental processes, neuronal function, and cell cycle regulation are just a few of the biological activities that MiR-182 has been linked to (6). The nervous system, where it affects the growth and upkeep of neurons, has been discovered to place a special emphasis on its significance. MiR-182 can function as an oncogene in specific circumstances, increasing the growth and survival of cancer cells (6,7). Depending on the precise context and target genes involved, it may also play a tumor-suppressive effect in other situations, MiR-182 and other microRNAs have drawn interest as possible diagnostic and therapeutic targets because of their participation in disease processes (8). By controlling the expression of genes involved in immune cell activity and cytokine generation, miR-182 can modify the immune response. MiR-182 dysregulation has been linked to autoimmune disorders and inflammatory illnesses (9). According to research, miR-182 may be involved in the control of insulin secretion and pancreatic beta-cell activity. Diabetes has been associated with dysregulation of miR-182 expression, which may aggravate poor glucose metabolism (10).
Uncovering MIR182's functional importance requires an understanding of the sequence, secondary structure, and phylogenetic conservation of this gene in Homo sapiens. In order to better understand the function of MIR182 in human biology, the objective of this study is to present a thorough analysis of these features. The research's prediction of MIR182's secondary structure is a critical component. Because it controls how a microRNA interacts with the target mRNA molecules, a microRNA's secondary structure is crucial to how well it performs its intended function. We can learn more about the stability and functionality of MIR182 by predicting the secondary structure (11,12).
By comprehensively investigating the sequence, secondary structure, and phylogenetic conservation of MIR182, this research aims to provide valuable insights into the molecular mechanisms and biological roles of this microRNA in Homo sapiens. Such knowledge is essential for understanding its potential as a therapeutic target or biomarker in various human diseases and cellular processes. Understanding these aspects of MIR182 is essential for unraveling its role in human biology (11). The aim of this study is to investigate the functional significance of MIR182 by studying its sequence, secondary structure as well as its phylogenetic conservation.

Materials and methods
The present study was done in the department of Forensic Odontology in Saveetha Dental College for the duration of 3 months
Retrieval of miR-182 Sequence
The sequence of miR-182 was retrieved from the National Center for Biotechnology Information (NCBI) database. The accession number or identifier for the miR-182 sequence (NG_023385.1) was used for retrieval.
Sequence Analysis
Sequence analysis was performed using the miRBase database . The miR-182 sequence obtained from NCBI was cross-referenced with the miRBase database to confirm its identity and obtain additional information about the microRNA.
Conservation Analysis
The conservation analysis of miR-182 was conducted using the Consurf server. This analysis involved aligning the miR-182 sequence with homologous sequences from different species to assess the degree of conservation. The output from the Consurf server provided a conservation score for each nucleotide position within miR-182.
Secondary Structure Prediction
The secondary structure of miR-182 was predicted using the RNAfold server . The miR-182 sequence was input into the server, which utilized algorithms to predict the most likely secondary structure of the microRNA, including stem-loops and hairpin structures.

Result
The sequence that was retrieved from the NCBI using the reference sequence NG_023385.1 with reference sequence gene on chromosome 7 and sequence and conservation analysis was done using Consurf.

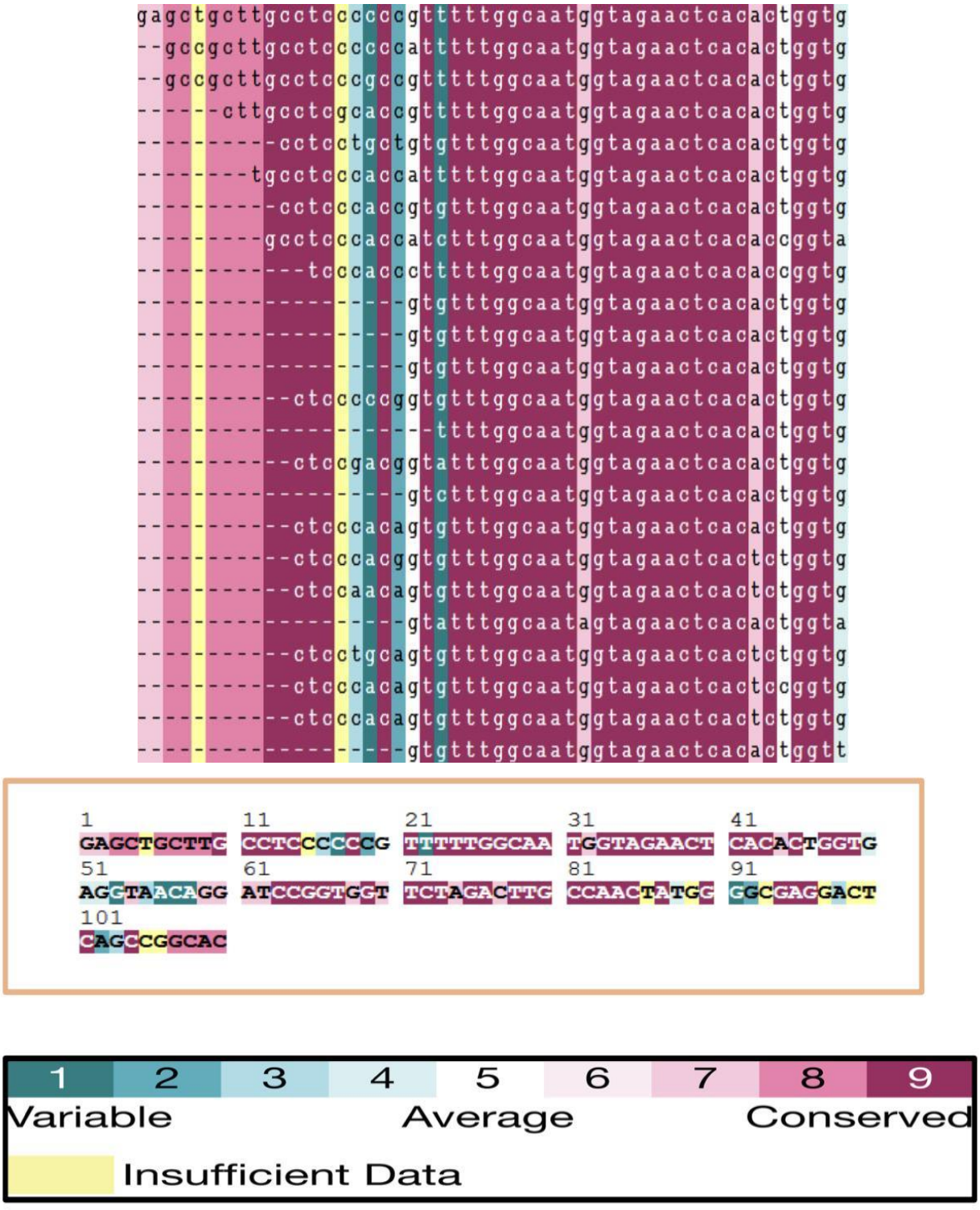

fig. 1) Sequence and conservation analysis 1

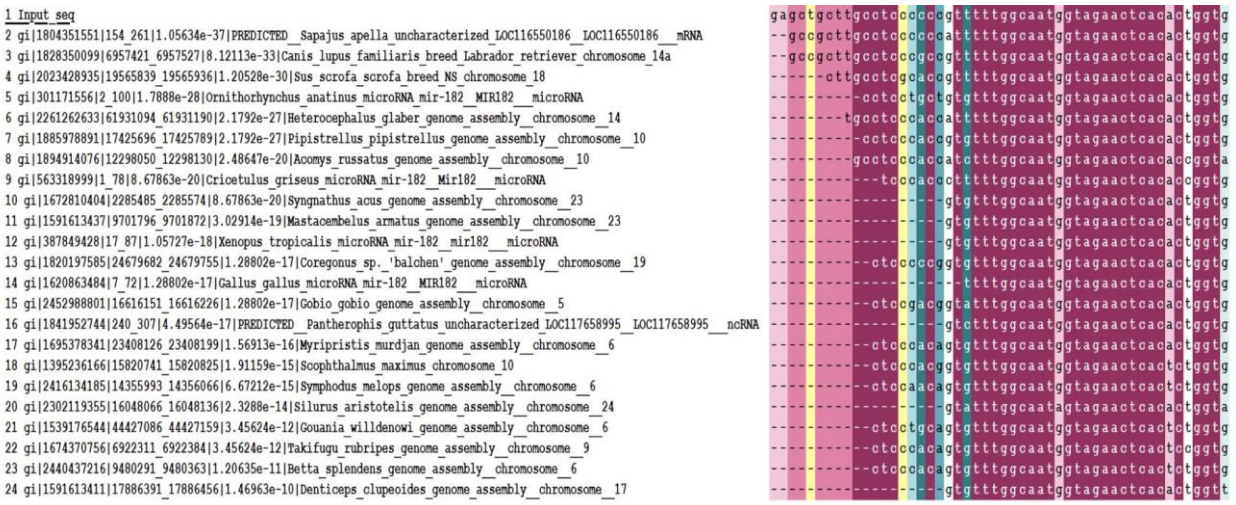

fig.2)

Sequence and conservation analysis 2

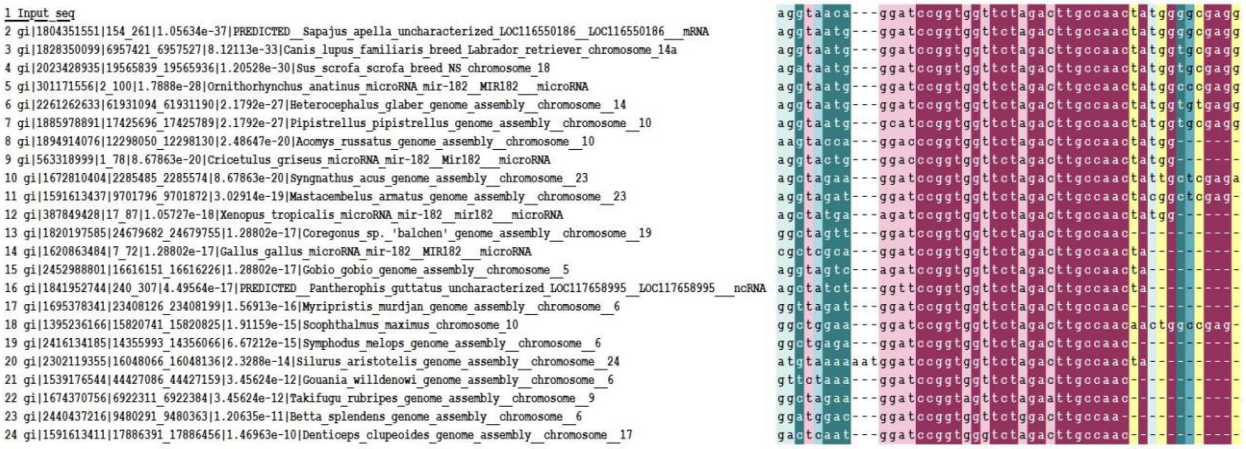

fig. 3) Sequence and conservation analysis 3

fig. 4) Sequence and conservation analysis 4

fig.5) Phylogenetic Conservation of MicroRNAs in MIR182 microRNA 182

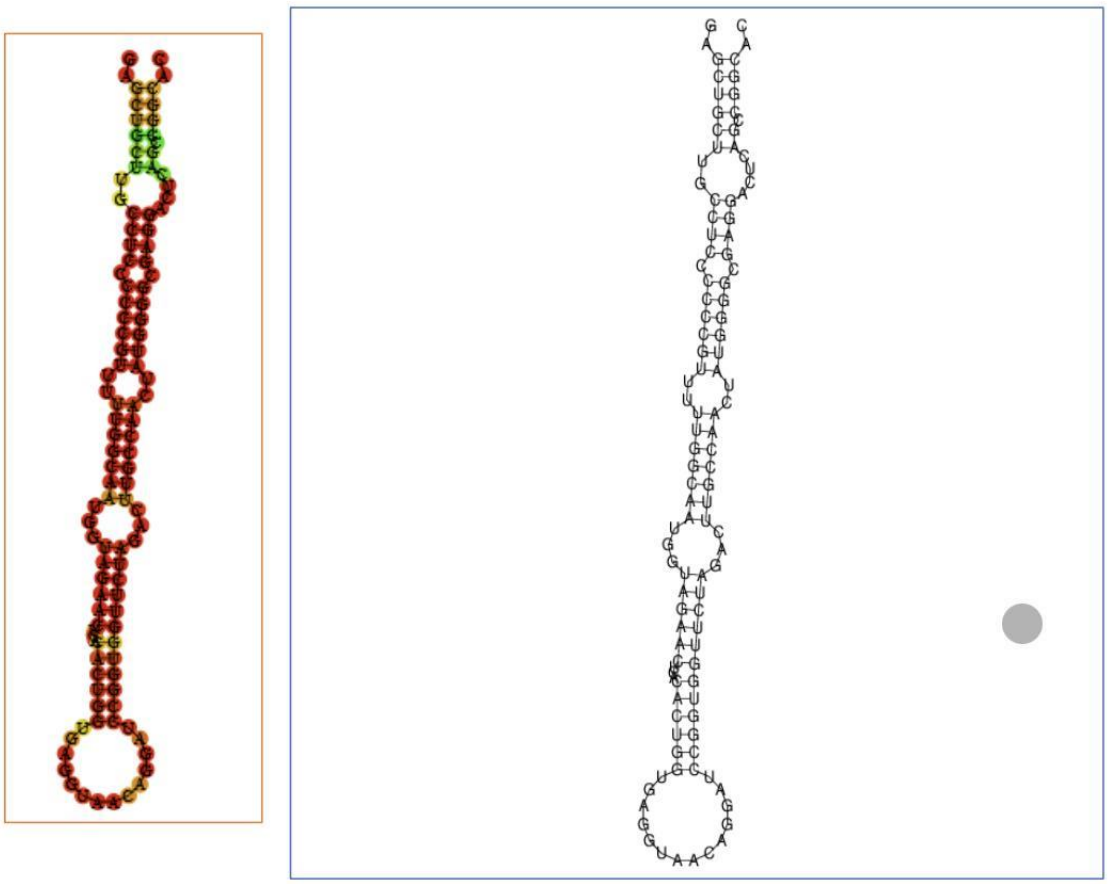

fig. 6) Secondary structure prediction of MIR182 by RNAFOLD SERVER

Discussion:
The conservation of miR-182 across different species provides insights into its functional importance, as seen in the sequence and conservation analysis in figures 1-4 miR-182 is highly conserved; it suggests that it plays crucial roles in biological processes across various organisms. As seen in figure 5, the sequence analysis is highly phylogenetically conserved which is of significance since MIR 183 being conserved across different species suggests that it plays crucial roles in biological processes across various organisms. In a study done by Shweta Dambal in 2015 it is claimed that both the sensory organs and circadian rhythm, which are both important conserved evolutionary traits seen in the animal kingdom, depend on the expression of the miR-183 cluster .

This cluster is extremely specialized to the sensory organs. Maybe it is because of this role in development that there has been conservation for 600 million years, which correlates with our findings since our study proves that MIR182 is highly conserved (13). A study by Marsha L. Pierce states that The sensilla of Drosophila and C. elegans as well as the innervated areas of invertebrate deuterostomes express members of the miR-183 family, which correlates with the highly phylogenetically conserved data in our study implying that miR-182 is being a crossed various species and not only in homo sapiens (13,14).

A study done by Patrizia Perri in 2012 claims that miRNAs are arranged in the genome in close proximity, with the same orientation, and are transcribed as a polycistronic structure from a particular promoter, enabling them to cooperate in the same regulatory network. For instance, the developmental expression patterns of all three miRNAs in the cluster mir-182/miR-96/miR-183 in sensory cells of vertebrates and invertebrates are comparable (13–15).

This corresponds with our study on how understanding the secondary structures of a microRNA can help understand the evolutionary implication of highly conserved genes. A study in 2013 done by Keerthana Krishnan claimed that an array of human breast cancer samples have high expression levels of miR-182-5p, emphasizing the possible oncomir function of this gene, this shows that with better understanding of the gene using secondary structure prediction we can explore the therapeutic potential and possible prevention (16).

Conclusion:
As seen in the results it can be inferred that the input sequence of the Homo sapiens region containing MIR182 was predominantly conserved; it suggests that this microRNA likely plays important roles in gene regulation, development, and disease. Studying its functions can lead to a better understanding of biology and potential therapeutic applications as seen in the studies referred to in the discussion.
The scope of future research on MIR182 includes disease associations, sequence/structural analysis, and therapeutic potential. By exploring these aspects, researchers can deepen our understanding of the biological roles of MIR182 and uncover its potential implications in health and disease.

Conflict of Interest:
The author reported the conflict of interest while performing this study to be nil.

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