

MicroRNAs: The Key Regulatory Molecule and the Evidence of Cross-Kingdom Regulation

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MicroRNAs are basically a conserved class of short non-coding RNAs, ranging from 18-21 nucleotides that regulate gene expression post-transcriptionally by base pairing to complementary sequences in the 3' UTR of target mRNAs. They play a very important role in most cellular processes and their dysregulation has been linked to various diseases and also serves as a novel class of biomarkers for the diagnosis of cancer and other diseases.

In plants, the microRNAs are mostly employed in the development and defense processes and functions as negative regulators of gene expression by targeting mRNAs for cleavage or translational repression. Recently, an exogenous plant microRNA MIR168a is reported to specifically target mammalian Low Density Lipoprotein Receptor Adapter Protein 1(LDLRAP1) mRNA (Zhang *et al.* 2012). This finding was confirmed by the fact that plant miRNAs are 2'-O-methyl modified at their 3' end, which makes them resistant to sodium periodate, whereas human miRNAs have free 2' and 3' hydroxyl group making them sensitive to sodium periodate (oxidizing agent). Also, experimental animals having diet rich in plant sources are found to have high level of exogenous plant miRNA in their serum.

These results have raised the question that whether the plant miRNAs can regulate human gene expression or not? However, the advances in the genome sequencing and annotation have shown that some percentage of our genome has similarity with microorganisms. These findings also reveal the importance of evolutionary relationships in different kingdoms, studies are needed to explore further in detail.