

The Mechanisms of Non Coding RNA and Micro RNA in Asthma Pathogenesis

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DESCRIPTION

The large group of heterogeneous RNAs known as long non-coding RNAs (lncRNAs) has a variety of important role in various biological and developmental processes. A class of RNA molecules known as non-coding RNAs (ncRNAs) does not convert into proteins. Small non-coding RNAs called MicroRNAs (miRNAs). MicroRNAs are defined as single-stranded Non-Coding RNAs (ncRNAs) approximately 20 nucleotides in length that are endogenously expressed and regulate gene expression at the post-transcriptional level. Thousands of MicroRNA has been identified in flies, plants, and mammals. The conserved structure and biogenesis of these RNA species control the material to understanding microRNA (miRNAs) regulate gene expression. The biogenesis of Long Non-Coding RNAs (lncRNAs) occurs in the nucleus core is the synthesis of protein coding transcripts. Long Non-Coding RNAs (lncRNAs) promotes the epigenetically marked with histone modifications as well as bound and controlled by transcriptional factors inclining toward or hampering gene expression.

Struggling to breathe, chest constriction, irregular expiratory airflow limitation, and coughing are all symptoms of asthma, a chronic airway inflammatory illness. Airway remodeling, airway inflammation, and airway hyperresponsiveness are some of its significant features. Asthma pathophysiology remains extremely complicated, and the specific pathways are still incomplete. According to reports, Long Non-Coding RNAs (lncRNAs) have a significant impact on asthma and function as modulators of a variety of pathological symptoms of the disease. Long Non Coding RNA (lncRNAs) are non-protein coding records with a length of not less than 200 nucleotides and are generally divided into antisense Long Non-Coding RNAs, pseudo genes Long Non-Coding RNAs, intronic Long Non-Coding RNAs (lncRNAs) and intergenic Long Non-Coding RNAs by protein-coding gene sequencing and gene position.

The mechanism of MicroRNAs are bond with argonaut proteins, dicer and trans-activation reaction RNA-binding protein

to form the RNA-Induced Silencing Complex (RISC). In deficient correlative sequences, they bind to mRNA to translation inhibition. In case of complete reciprocal sequences, they bind to 3' Untranslated Regions (UTR) of mRNA to mRNA degradation. Also, they can bind to transcription elements to coregulate the transcription of genes.

The mechanism of long non coding RNAs is directly bound to the genes to translation inhibition, binding modifications, and mRNA degradation. Competitive Endogenous RNA (ceRNA) that has the microRNA (miRNAs) reaction component to sponge the microRNA (miR) to further prevent mRNA degradation and enhances the mRNA expression.

Long non-coding RNAs additionally intervene chromatin remodeling for chromatin modification and function as a RNA decoy that binds to the transcription elements to regulate the downstream signaling pathways. They collect Ribonucleoprotein (RNP) complexes to regulate protein stability. Compared to MicroRNA, the mechanistic characterization of Long Non-Coding RNAs (lncRNAs) is rather poor. This is because Long Non-Coding RNAs (lncRNAs) can regulate gene expression at multiple levels within the cell through complex molecular mechanisms.

Airway remodeling is a significant connection over asthma, is closely associated with a wide range of structural and functional cells in the airway route, including fibroblast activation, epithelial cell enhancement. Long Non-Coding RNAs are involved in asthma progression, mediate multiple signaling pathways, act as biomarkers of asthma phenotypes, but also function as regulators of airway inflammation, remodeling and glucocorticoid sensitivity. Long Non-Coding RNA expression was demonstrated to remarkable differences in the peripheral blood of children with refractory and controlled asthma. Macrophages are the most abundant immune cells in asthma pathogenesis and the related cytokines, chemokine's and transcription factors balance the progression of asthma.

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