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Research Article

MICRO RNA AS KEY REGULATORS IN ALLERGIC DISEASES: EPIGENETIC MECHANISMS AND DIAGNOSTIC POTENTIAL

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Abstract
Epigenetic therapy represents a promising approach for treating allergic diseases, with microRNAs (miRs) playing a crucial role as regulatory molecules in the immune response. The aim of this study was to systematize data on miRs to elucidate the molecular mechanisms of pathogenesis in allergic diseases. A meta-analysis of 61 studies published between 2017 and 2024 was conducted, focusing on specific miRs, their targets, biochemical interactions, model organisms, and health impacts related to different allergic diseases. The study identified key miRs such as miR-21, miR-151A, miR-155, miR-202-5p, and miR-375, which regulate inflammatory processes in allergic asthma, allergic rhinitis, atopic dermatitis, and urticaria. miRs such as miR-143-3p, miR-146a, and miR-221 have dual roles in modulating inflammation, depending on the tissue and disease stage. Additionally, miRs influence the differentiation of macrophages and T-helper cells, and the production of pro- and anti-inflammatory cytokines, which are critical to the pathogenesis of allergic diseases. Specific diagnostic markers were proposed for each disease, including miR-126, miR-133a, and miR-203 for asthma and atopic dermatitis. This analysis highlights the complex role of miRs in regulating allergic responses, offering potential therapeutic targets for miR-based interventions. The findings suggest that miRs could serve as biomarkers for diagnosis and prognosis of allergic diseases. Furthermore, the ability of miRs to both exacerbate and attenuate inflammation underscores their potential as therapeutic tools in precision medicine. The novelty of this study lies in the comprehensive synthesis of miR involvement in allergic diseases, providing a clearer understanding of their dual regulatory roles.

Keywords Allergic Rhinitis, Atopic Dermatitis, Bronchial Asthma, Hypersensitivity, Transcription Factors, Urticaria

INTRODUCTION

The most common allergic diseases include atopic dermatitis, bronchial asthma, rhinitis, and allergic reactions to food. They require an individualised approach to treatment, as they have many

manifestations and are determined by various causes. The immune response is controlled by gene expression and is normally manifested by a rapid response in terms of detecting and neutralising pathogens. However, sometimes individual parts of the immune system show hypersensitivity to safe external stimuli, their own antigens, tissue destruction products. Due to excessive sensitivity, a strong inflammatory process develops, which often causes autoimmune or allergic diseases.

Most allergic diseases (including asthma and dermatitis) are of heterogeneous origin and are provoked by various pathophysiological processes. For example, asthma has two endotypes: allergic and non-allergic (Chulenbayeva et al., 2022; Hanoum et al., 2024; Melinda et al., 2024). They are similar in clinical manifestations, so it is difficult to determine typing by signs. Currently, there are no diagnostic methods or biomarkers for endotyping. Treatment of hypersensitivity is aimed at controlling and eliminating symptoms (Oktarina et al., 2018). To date, despite a wide range of studies, there are no ways to prevent asthma or allergic dermatitis, and severe forms can develop rapidly, with the inability to control symptoms. Despite comprehensive research on the molecular mechanisms of allergy disorders, a substantial gap remains in the development of preventive measures and personalised treatment techniques. Contemporary methods predominantly emphasise symptom management instead of targeting the underlying biological causes. This study investigates the regulatory function of microRNAs to connect molecular mechanisms with therapeutic interventions, offering insights into personalised treatments that can either activate or inhibit specific molecular pathways implicated in the pathogenesis of these diseases.

The role of microRNAs (miRs) in allergology has been studied for more than 10 years. This type of nucleic acid determines the intensity of the inflammatory process in the affected areas (Rebane, 2015). Depending on the type of pathological process, the concentration of miR varies in different tissues. Therefore, miR is a diagnostic marker of obesity, chronic inflammation, cardiovascular disease, cancer transformation, viral infections, and hypersensitivity (Hussain & Grayson, 2022; Sharma & Tiwari, McGeachie, 2022; Elpianora et al., 2024; Miharja et al., 2024; Castro, 2025). miR is involved in the pathogenesis of many allergic diseases: eosinophilic esophagitis, eczema, allergic rhinitis, and asthma (Lu & Rothenberg, 2018). Studying the mechanism of their action as inhibitors of a number of global transcription factors will help to identify prognostic targets for therapy.

Specjalski et al. (2022) proved the overexpression of certain miR molecules (miR-138, miR-190, miR-208) in the blood of patients with allergic rhinitis. In particular, after 6 months of subcutaneous immunotherapy, there was a decrease in the titre of pro-inflammatory microRNAs and an increase in the titre of those miRs that determine the balance between T helper cells 1 and 2. This proves the regulatory role of miR in activating immunotolerance. Langwiński et al. (2022) identified 9 tissue-specific miRs that were expressed differently in the lungs and nasal epithelium of rats under conditions of generating an allergic reaction. A higher concentration of transcripts was recorded for miR-223-3p and miR-184. Inhibition of mIR-223-3p resulted in an increase in the level of phosphorylated NF-kB protein synthesis, and a greater copy of mucin MUC5AC, cytokine CCL24 and lymphopoietin TSLP genes. Adamczyk et al. (2021) tracked a decrease in miR-320e synthesis in children with otitis media in allergic reactions. Duan et al. (2023) demonstrated the pro-inflammatory role of miR-146a-3p in model objects, which transmits a signal through MBD2 and promotes T helper 17 maturation. The term “model objects” refers to experimental organisms, such as Mus musculus and Rattus norvegicus, used in laboratory-based studies to simulate human allergic responses and test the effects of microRNAs in the pathogenesis of allergic diseases. The latter synthesise interleukins 17 and 17F, which cause an acute immune response in asthma. According to the researchers, miR-135b acts via a ligand to the G-protein Cxcl12 and attenuates airway inflammation in asthma. Wardzyńska et al. (2023) found overexpression of miR-146a and miR-126a in older patients with acute asthma.

This study aims to elucidate the regulatory function of microRNAs in allergy disorders by methodically organising and explaining contradictory findings from prior research. Numerous researchers have investigated the impact of individual miRNAs; however, their findings frequently conflict, resulting in a lack of clarity regarding the specific processes by which microRNAs affect the aetiology of allergic diseases. This work seeks to address this gap by delivering a thorough analysis of the processes via which miRNAs operate in these diseases, thereby improving our comprehension and aiding the formulation of more targeted and successful treatment methods.

THEORETICAL OVERVIEW

The miRs are short RNA molecules with a length of 19-25 nucleotides that regulate post–transcriptional silencing of coding sequences (Lu & Rothenberg, 2018). They bind complementarily to the 3'-end of messenger RNA (mRNA), causing the matrix molecule to either be destroyed or become unfit for translation (Sharma, Tiwari and McGeachie, 2022). The targets of a single miR can be hundreds of different transcripts (mRNAs). Thus, miR affects the expression of many genes (Lu & Rothenberg, 2018). In addition, miR can epigenetically regulate expression at the DNA level, mainly through methylation. Intracellular miR affects the synthesis of a pool of proteins within the cell. Circulating miRs (in exosomes, macrovesicles, and apoptotic bodies) provide intercellular regulation as messengers (Sharma, Tiwari and McGeachie, 2022). miR-146a, miR-21, and miR-155 are the best studied. Of the entire pool of microRNAs, they are most associated with the immune system, involved in the development of allergies and the appearance of inflammation (Figure 1).

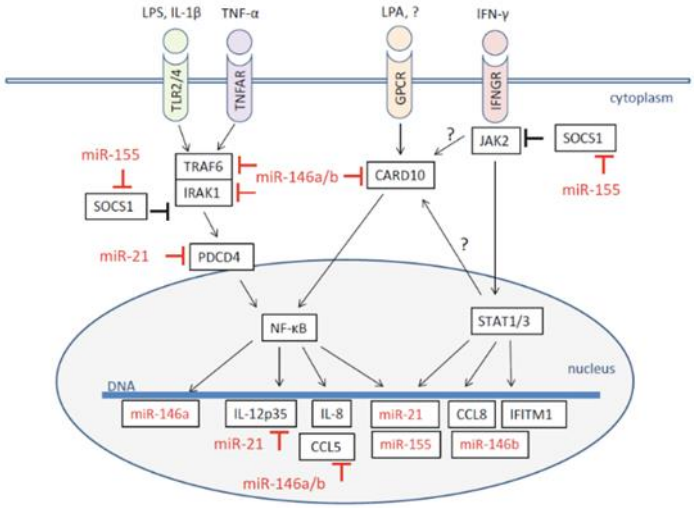

Figure 1. Regulatory cascade involving miR

Source: (Rebane, 2015).

As can be seen from Figure 1, miR-21 expression is positively regulated by Kappa nuclear factor (NF-kB) in the B-lymphocyte nucleus, and STAT1/3 (signal transducers and activators 1/3)-enhancers in the nuclei of other cells. In turn, NF-kB enhances the expression of *IL-8* and *IL-12P35*, which cause chemotaxis of immune cells in the area of inflammation, and differentiation of T-lymphocytes, B-lymphocytes, natural killers, and the synthesis of gamma interferon (Dmitrova et al., 2021; Rubins et al., 1992). However, *IL-12P35* promotes polarisation of type 2 T-helper cells. miR-21 is an expression inhibitor of *IL-12P35* and *PDCD4* (pro-inflammatory protein) and activators of the synthesis of immunosuppressive interleukin 10. Due to this mechanism, miR-21 inhibits the inflammatory process. miR-155 is an inflammatory activator. They are synthesised in macrophages in the presence of the vesicular stomatitis virus; their synthesis is triggered by transcription factors STAT3 and NF-kB and they are inhibitors of SOCS1 (suppressor of cytokine signalling type 1) (Martins et al., 2024). The product of the SOCS1 gene stops the "pro-inflammatory" regulatory cascades triggered by tumour necrosis factor-alpha (TNF-α), interleukin-1-beta (IL-1β), lysophosphatidic acid (LP) and interferon-gamma (IFN-γ) (Hartmane et al., 2021). Signalling in these cascades is carried out by phosphorylation chains involving Janus kinase 2 (*JAK2*), interleukin-I-associated kinase 1 (*IRAK1*), and caspase recruitment domain-containing protein 10 (*CARD10*). In addition, miR-155 is involved in the activation of adaptive immune cells of the T-effector population (Potaczek, Alashkar Alhamwe, Miethe and Garn 2022; Zeng, Liu, Luo and Lu, 2019).

It is evident that environmental factors, including allergens, air pollutants, and climate variations, exert a substantial influence on microRNA (miRNA) expression, thereby modulating immune responses and contributing to the development of allergic diseases (Febriansyah et al., 2024; Komilova et al., 2024). Exposure to diverse environmental triggers has been demonstrated to alter the transcriptional profiles of miRNAs, which function as pivotal regulators of immune system functions. Pollutants, microorganisms, tobacco smoke and certain dietary components are known to drive

epigenetic changes essential for immune regulation, including shifts toward T helper 2 (Th2) cell polarization and decreased regulatory T-cell (Treg) differentiation (Komilova et al., 2021; Mijač et al., 2024).

Specific microRNAs, such as miR-21, miR-146a, and miR-155, have been intensively studied for their roles in regulating immune responses and tissue inflammation in allergic diseases (Syamsurizal et al., 2024). These microRNAs have been found to be involved in inflammatory pathways, and their altered expression has been linked to the exacerbation of conditions such as asthma and allergic rhinitis. For instance, miR-146a has been associated with the regulation of inflammatory cascades through its interaction with the NF-kB pathway, and its expression is influenced by both genetic predispositions and environmental factors like pollutants (Melnychaiko and Andreychyn, 2023).

Mature miR-146a and b molecules differ structurally only by two nucleotides, so their targets are the same genes or similar in the composition of their sequence. Synthesis of 146a mediated by transcriptional activator NF-kB, and 146b – STAT1/3 miR-146a/b are anti-inflammatory biomolecules because they inhibit inflammatory cascades through direct repression *IRAK1*, TNF-associated factor 6 (*TRAF6*), *CARD10* and chemokine ligand *5CCL5*). In mice with gene knockout miR-155 over time, autoimmune processes develop due to loss of immunosuppression function by the T helper 1 (Th1) line (Zhu et al., 2023; Zou, Zhou and Zhang, 2021). Other microRNAs are involved in the regulation of innate and acquired immune responses. Among them, miR-9, miR-125a, miR-147b, miR-301a are activators of the NF-kB pathway. Differentiation of T-lymphocytes is affected by miR-10a, miR-29a/b, miR-117-92, miR-181A, miR-182; miR-34a, miR-17-92, miR-125b, miR-150, miR-181b, miR-217 are involved in the regulation of B-lymphocyte maturation. In terms of allergies, attention should be paid to how miR affects the polarisation of type 2 T helper cells, the suppressive properties of Treg cells, and changes in the immunoglobulin profile of B-lymphocytes (Rebane, 2015; Asniwita et al., 2024).

RESEARCH METHOD

Understanding the epigenetic mechanisms described above, it is possible to make assumptions about the effect of certain micromolecules on the body during the manifestation of allergic symptoms. The research follows a systematic review methodology, where primary studies, systematic reviews, and meta-analyses have been collected, assessed, and synthesized. The primary objective is to establish the molecular mechanisms by which miRNAs regulate immune responses, with particular focus on their impact on allergic reactions.

The sample for this study consists of 61 research papers published between 2017 and 2024. These papers were chosen based on strict inclusion and exclusion criteria, ensuring that only studies addressing the involvement of miRNAs in allergic diseases, such as asthma, dermatitis, rhinitis, and urticaria, were selected. The inclusion criteria were studies focused specifically on microRNAs, allergic asthma, atopic dermatitis, allergic rhinitis, and urticaria. A total of 61 research papers were analysed, of which 51 were included in the analysis. The text of 45 sources has been fully developed; 6 – revised briefly. During the analysis, 10 sources were selected, 3 of which were duplicated, and 7 did not fall under the inclusion criteria (6 were excluded from thoroughly studied sources, and 1 was briefly revised). Scientific and clinical experiments were conducted in the USA, Spain, Portugal, China, India, Great Britain, Germany on samples of biomaterial obtained from patients or on model objects Mus musculus and Rattus norvegicus. The materials used for the experiments were swabs from the nasal mucosa, smooth muscles and bronchial epithelium, skin samples, whole blood, and serum. The researchers identified and quantified transcriptome titres in normal and allergic conditions using real-time quantitative polymerase chain reaction with reverse transcription (RT-qRT-PCR). The data for this study was collected through an extensive electronic search of leading scientific databases: PubMed, Elsevier, MEDLINE, Scopus, and Web of Science. The keywords used for the search were “miRNA”, “microRNA”, “allergic asthma”, “atopic dermatitis”, “allergic rhinitis”, “urticaria”. The initial selection of articles was based on reading the titles and abstracts to assess relevance, followed by a full-text review of studies meeting the inclusion criteria. A data collection instrument grid was established to capture detailed information from each study, including the first author and year of publication, study design and methodology, miRNAs investigated and their targets, molecular mechanisms of action, phenotypic manifestations of allergic reactions, types of biomaterial used (such as serum, blood, skin samples), and whether the study involved human subjects or animal models.

Statistical analysis was performed utilising meta-analysis methods and software, including R and comprehensive meta-analysis. Effect sizes were computed for each miRNA’s correlation with

allergic disorders, and heterogeneity among studies was evaluated using the I^2 statistic. Subgroup analyses were conducted according to research design, geographic region, and the specific type of allergy illness examined. Only high-quality studies, including randomised controlled trials, cohort studies, and meticulously conducted case-control studies, were incorporated to uphold the rigour of the review.

However, it is important to acknowledge the potential geographical and ethnic variations in microRNA expression, which can influence study outcomes. MicroRNA profiles are known to differ based on factors such as genetic background, environmental exposures, and lifestyle, meaning that findings from one population may not be entirely applicable to others. Additionally, while animal models like Mus musculus and Rattus norvegicus have been crucial for understanding the regulatory mechanisms of microRNAs, there are limitations in extrapolating these results to humans. Differences in immune responses, microRNA regulation, and metabolic processes between species necessitate careful evaluation of the applicability of animal model findings to human conditions. Therefore, further studies involving diverse human populations and validation in human clinical trials are needed to fully understand the implications of these variations for allergic diseases and microRNA-based therapies.

To form summary tables of results, the name of the microRNA under study, the target of its action, the molecular mechanism of action, and its phenotypic manifestation, the type of biomaterial, the object of study, the author's last name and the year of publication were included. To determine the mechanism of action, attention is focused on pathway-specific and pleiotropic transcription regulators, the metabolic cascades in which they are involved, the effect of microRNAs on these regulators, and the terminal link of regulation. There were also a number of regulatory non-coding RNAs that were biomarkers of a particular allergic disease.

RESULTS AND DISCUSSION

In the material of mastocytes from patients with atopic dermatitis, allergic asthma, and allergic rhinitis, 18 miRs (26A2, 29B2, 33B, 142, 590, 614, 638, 645, 1276, 1304, 2355, 3175, 3064, 4308, 4434, 4523, 4673, 4785), which were differently expressed in eosinophils, depending on the type of disease and IgE titre, and also differed from the expression level in healthy individuals (3). miR polymorphisms are associated with pathologies. Specifically, rs3746444 (replacing C with T) in miR-499 is associated with asthma susceptibility, and rs2910164 (replacing C with G) is associated with insensitivity to allergic asthma (Dong, Sun, Lu, 2021). These polymorphisms play a crucial role in modulating immune responses, influencing both the susceptibility to and progression of allergic diseases. For example, the miR-146a polymorphism, particularly the rs2910164 (G>C) variant, has been linked to changes in the regulation of inflammation, which may increase susceptibility to asthma. Similarly, the miR-499 rs3746444 (T>C) polymorphism has been implicated in the pathogenesis of asthma, influencing the immune response and exacerbating allergic symptoms.

Overexpression of miR-133 and miR-126 mitigated asthmatic symptoms (Rahbarghazi et al., 2021). These polymorphisms affect the expression of key immune modulators such as IL-12, IL-13, and TGF-β, altering the differentiation of T-helper cells (Th1 and Th2) and the balance between pro-inflammatory and anti-inflammatory cytokines. This imbalance can facilitate the progression of allergic diseases by enhancing the production of IgE and inflammatory cytokines, which are central to the allergic response. Understanding how these miRNA polymorphisms influence immune cell differentiation and cytokine production can lead to the development of targeted therapies that modulate miRNA activity, offering a potential avenue for preventing or treating allergies. miR-139 is known for its ability to suppress the inflammatory response of type 2 T helper cells (Tx2) by blocking the Notch metabolic cascade. This regulatory molecule stimulated the differentiation of mesenchymal stem cells (Wang et al., 2021). Table 1 illustrates the significance of some miRs in the development and course of an allergic reaction in asthma.

Table 1. Role of miR in the pathogenesis of allergic asthma

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
miR-21	n/a	Provokes inflammation and oxidative stress through the DDAH1-Wnt-beta-catenin signalling cascade	Airway smooth muscles	*Mus musculus*	-	Zou et al. (2021)
miR-21	*SMAD7, TGF-β*	SMAD7, TGF-β-cascade stimulates ovalbumin-mediated chronic asthma	Airway smooth muscles	*Homo sapiens*	-	Hur et al. (2021)
miR-21	n/a	Activates M2 alveolar macrophages in ovalbumin-mediated asthma	Airway smooth muscles	*Mus musculus*	-	Lee et al. (2021)
miR-21	n/a	Circulatory disorders of the lungs	n/a	*Mus musculus*	-	Weinder et al. (2021)
miR-21	*CSF1R, IRF5, IL-12P3*	M2 macrophage polarisation, impaired T helper response	n/a	*Homo sapiens*	-	Cañas et al. (2021)
miR-21	*IL-12P35*	Activation of proinflammatory cells	Blood serum	*Homo sapiens*	-	Paul et al. (2021)
miR-21-5p	*SMAD7*	It accumulates in macrophage exosomes, improves airway patency via the *SMAD7* gene	Airway smooth muscles	*Mus musculus*	+	Li et al. (2021)
miR-21-5p	*IL-12*	Disruption of T helper 1, 2 maturation processes	Bronchial epithelium	*Homo sapiens*	-	Paul et al. (2021)
miR-21	*IL-13*	Increased expression of miRs in asthma and positive correlation with *IL-13*	Bronchial epithelium	*Homo sapiens*	Considering the migration of eosinophils to the inflammatory zone under the influence of *IL-13*	Ghafouri-Fard et al. (2020)
miR-21, miR-155	n/a	Biomarkers of bronchial asthma	Blood serum	*Homo sapiens*	n/a	Lu et al. (2023)

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
miR-146a	*EGFR*	Inhibits proliferation and triggers apoptosis of airway smooth muscle cells	n/a	*Homo sapiens*	-	Ghafouri-Fard et al. (2020)
miR-146a, miR-206, miR-720	n/a	Potential markers of asthma	Whole blood	*Homo sapiens*	n/a	Weinder et al. (2021)
miR-146a	*IRAK1*	Negatively regulated in asthma, inhibits expression *CXCL1* and *IL-8* and slows down neutrophil migration	Bronchial epithelium	*Homo sapiens*	-	Weinder et al. (2021)
miR-146a	n/a	Correlation of expression with intensity of symptom expression and systemic inflammation	Blood serum	*Homo sapiens*	-	Wardzyńska et al. (2023)
miR-146a, miR-499	n/a	Association of asthma polymorphisms *rs2910164* (replacement of C with G) and *rs3746444* (replacement of C with T); markers	n/a	*Homo sapiens*	n/a	Dong et al. (2021)
miR-146a-5p	*TRAF6*	Inhibits the inflammatory process and damage to the airway epithelium due to factor 6 associated with tumour necrosis factor	Airway epithelium	*Homo sapiens*	+	Zhu et al. (2023)
miR-146b, miR-206, miR-720	n/a	Involved in NF-kB-GSK3/AKT Cascades, prognostic markers of asthma	Blood serum	*Homo sapiens*	n/a	Benincasa et al. (2021)

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
		exacerbation				
miR-146a, miR-155	n/a	Correlation of expression with intensity of symptom expression	Blood serum	*Homo sapiens*	-	Weinder et al. (2021)
miR-155	n/a	Biomarker of impaired pulmonary function	Blood	*Homo sapiens*	n/a	Cañas et al. (2021)
miR-155	n/a	Reduced expression during the allergy season	Lymphocytes	*Homo sapiens*	n/a	Weinder et al. (2021)
miR-155	n/a	Welding inductor	Cell lines	*Mus musculus, Homo sapiens*	-	Kim et al. (2022)
miR-155	n/a	Flame inducer, activates the synthesis of pro-inflammatory *IL-4, IL-5, IL-13*	Bronchoalveolar lavage, lung tissue	*Mus musculus*	-	H. Chen et al. (2017)
miR-155-5p	*CCL11, CCL26, IL-13*	Inhibition of eosinophil synthesis	Bronchial epithelium	*Homo sapiens*	+	Paul et al. (2021)
miR-126, miR-133	n/a	Inhibition of asthma-related pathological processes by increasing the titre of these miRs	C-kit+-bone marrow cells	*Homo sapiens*	+	Rahbarghazi et al. (2021)
miR-126	n/a	Higher expression in asthma; biomarker	Blood serum	*Homo sapiens*	n/a	Alhamwe et al. (2021)
miR-126	*DNMT1*	Promotes disease progression	Blood serum	*Homo sapiens*	-	Farmanzadeh et al. (2022)
miR-139	n/a	Inhibition of inflammation at the level of T helper 2 via the Notch cascade	Lung tissue	*Homo sapiens*	+	Quan et al. (2022)
miR-133a, miR-155	n/a	Reduced expression in asthma; biomarkers	Condensate of exhaled air	*Homo sapiens*	n/a	Weinder et al. (2021)
miR-133b	n/a	Specific marker of asthma	Blood plasma	*Homo sapiens*	n/a	Weinder et al. (2021)
miR-221	*SPRED*	Regulation of mast cell	Whole blood	*Homo sapiens*	n/a	S. Paul et al. (2021)

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
		functions				
miR-221	*SIRTI*	Overexpression of these miRs and inhibition SIRTI triggers apoptosis processes and inhibits the division of bronchial epithelial cells	Cell culture	*Homo sapiens*	-	Ghafouri-Fard et al. (2020)
miR-221	n/a	Reduced expression levels in the bronchial epithelium correlate with eosinophilic inflammation	Epithelium and sputum	*Homo sapiens*	+	Weinder et al. (2021)
miR-221	n/a	Overexpression attenuates airway inflammation in mice	Airway epithelium	*Mus musculus*	+	Ghafouri-Fard et al. (2020)
miR-221-3p	*CXCL17*	Regulation of the number of eosinophils and the synthesis of reactive oxygen species	n/a	*Homo sapiens*	+	Cañas et al. (2021)
miR-221-3p	*CXCL17*	Repression of a target gene whose product is an anti-inflammatory cytokine and protects the lungs from eosinophilic expansion	n/a	*Homo sapiens*	+, since miR 221-3p transcription is inhibited in asthma	Ghafouri-Fard et al. (2020)
miR-140-3p	*IL-13*	Decreased miR expression leads to RhoA over-synthesis via *IL-13* regulation	Airway smooth muscles	*Homo sapiens*	-, since RhoA overexpression is associated with carcinogenesis	Chiba et al. (2022)
miR-140-3p	*CD38*	Reduced miR expression leads to *CD38* protein supersynthesis	Airway smooth muscles	*Homo sapiens*	-, since *CD38* via Ca^{2+}-signalling can cause muscle spasms	Gautam et al. (2022)
miR-143-3p	*CDK4, Cyclin D1, TGF-β 1*	Overexpression of miRs inhibits airway remodelling by inhibiting Ecm	Airway smooth muscles	*Homo sapiens*	+	Akbari Dilmaghnai et al. (2021)

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
miR-143-3p	*HMGB1*	protein synthesis and promoting cell proliferation Increases the inflammatory allergic reaction in response to dust	Bronchial epithelium	*Homo sapiens*	-	Cay et al. (2022)
miR-375	*KLF4*	Synthesis of pro-inflammatory cytokines via the IL-13 link and stimulation of mucus secretion	Nasal cavity epithelium	*Homo sapiens*	-	Wang et al. (2021)
miR-590-5p	*FGF1*	Binds to the target transcript and blocks the start of the process of bronchial lumen reduction	Bronchial epithelium and smooth muscles	*Homo sapiens*	+	Ghafouri-Fard et al. (2020)
miR-223-3p	*NF-kB, CCL24, TSLP, MUC5AC*	miR inhibitors enhance target gene expression	Lung tissue	*Rattus norvegicus*	+	Langwiński et al. (2022)
miR-320e	*PTEM*	“Switching” the synthesis of immunoglobulins of different classes; wound healing	Ear fluid for otitis media	*Homo sapiens*	+	Adamczyk et al. (2021)
miR-146a-3p	*MBD2*	Maturation of T helper 17 cells, synthesis of proinflammatory *IL-17, IL-17F*, mucus accumulation, acute immune response	Whole blood	*Mus musculus*	-	Duan et al. (2023)
miR-135b	*CXCL12*	Reduces the synthesis of the pro-inflammatory cytokine *CXCL12*	Whole blood	*Homo sapiens, Mus musculus*	+	Liu et al. (2023)
miR-19, miR-146a, miR-126a	n/a	Increased expression levels correlate with the severity of the disease	Blood serum	*Homo sapiens*	-	Wardzyńska et al. (2023)

Based on the data summarised above, and data from other sources (Potaczek, Alashkar Alhamwe, Miethe, Garn 2022; Flajnik, Singh, Holland, 2022), it is possible to present a general scheme of regulation of biochemical processes in allergic asthma involving microRNAs (Figure 2). The key regulator of the cascade is *GATA3*. It is a transcription factor responsible for the differentiation of Th2 and the balance between Th1 (type 1 T helper cells) and Th2. It binds to gene promoters *IL-5, IL-4, IL-13*, the products of which mediate the release of pro-inflammatory molecules by mastocytes and, as a result, epithelial destruction (Flajnik, Singh, Holland, 2022). Another cause of damage to the airway epithelium is inhibition of the transcription factor *SIRT1* by miR-221 molecules. Mucus secretion is generated due to blocking of the transcription factor *KLF4*, which is responsible for the normal barrier function of the skin. MiR-375, miR-141-3p, and miR-181b are involved in this regulation. miR-146a/b triggers type 2 macrophage polarisation, which activates Th2, B lymphocytes, IgE synthesis, and mast cells. These elements are responsible for the inflammatory process and clinical signs of allergic asthma. Moreover, miR-146 is a shuttle regulator of inflammation, since it acts through factors *TRAF6, NOTCH5, PTGS2* and the cytokine *IL-1b*, prevent the destruction of the airway epithelium.

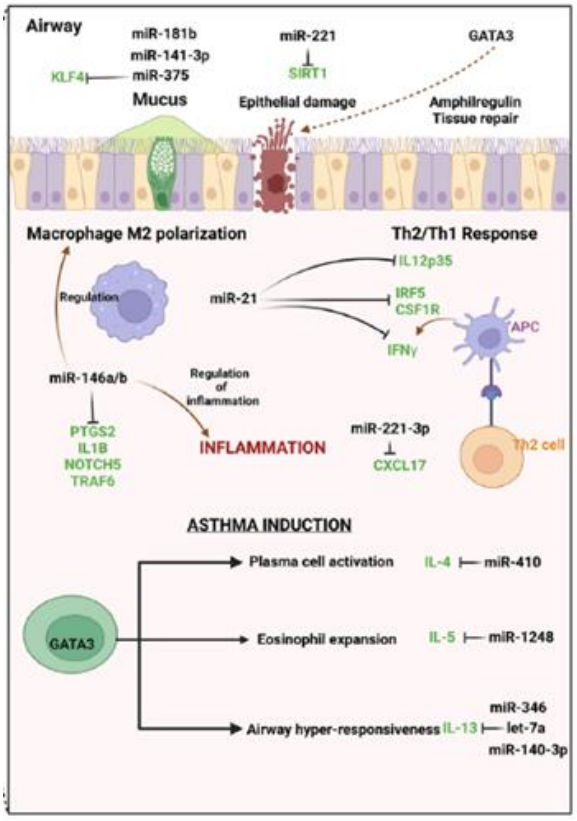

Figure 2. Allergic reaction in asthma after contact with an irritant

Source: (Sharma, Tiwari and McGeachie, 2022).

IL-12 is an inhibitor of hypersensitivity because it inhibits IgE synthesis and Th2 activity.. Together with interferon gamma (IFN), *IL-12* triggers the process of differentiation of macrophages by type 1, which are not involved in the development of allergies. miR-21 is a repressor of "anti-allergic genes" – *IL-12b, γ-IFN, IRF5, CSF1R*, because it binds to mRNA and blocks translation. Therefore, super-synthesis of this type of microRNA enhances the inflammatory response at the final stage of interaction between antigen-presenting cells (APC) and Th2. miR-221-3p acts through the anti-inflammatory chemokine *Cxcl17*, which is a protector of eosinophilic airway inflammation. This microRNA blocks the expression of this factor. Instead, miR-221-3p transcription is suppressed in allergic asthma (Ghafouri-Fard, Shoorei, Taheri and Sanak, 2020). Therefore, in a particular case, miR-221-3p becomes an indirect suppressor of the inflammatory process. *GATA3* and Th2 cytokines *IL-4, IL-5,* and *IL-13* positively regulate T/B lymphocyte activation, eosinophil overproduction, lung transport, and IgE secretion (Ghafouri-Fard, Shoorei, Taheri and Sanak, 2020; Flajnik, Singh and Holland, 2022). miR-410, miR-1248, miR-346, miR-140-3p, and let-7A are repressors of the interleukin

genes listed above. Therefore, in the conditions of their constitutive expression during allergies, symptoms should be less pronounced. Table 2 illustrates the miR involved in regulating the immune response in atopic dermatitis.

Table 2. Role of miR in the pathogenesis of atopic dermatitis

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
miR-10a-5p	n/a	Regulation of keratinocyte proliferation and differentiation	Skin	*Homo sapiens*	n/a	Khosrojerdi et al. (2024)
miR-29b	*BCL2L2*	Involved in the progression of pathogenesis due to exposure to the target	Skin	*Homo sapiens*	-	Gu et al. (2017)
miR-29b	n/a	Regulation of keratinocyte apoptosis and skin barrier function	Skin	*Homo sapiens*	n/a	Khosrojerdi et al. (2024)
miR-124	*NF-kB*	Anti-inflammatory effect through regulation *NF-kB*-signalling cascade	n/a	*Homo sapiens*	+	Khosrojerdi et al. (2024)
miR-143	*IL-13*	Modulates the *IL-13* signalling cascade, counteracts inflammation	n/a	*Homo sapiens*	+	Khosrojerdi et al. (2024)
*miR-146a, *miR-146b-5p, *miR-155, *miR-342	n/a	Predictive marker for risk diagnosis and prevention	Blood serum	*Homo sapiens*	0	Hicks et al. (2022)
miR-146a	*SUMO1*	Involved in the progression of pathogenesis due to exposure to the target	n/a	*Homo sapiens*	-	Yan et al. (2019)
miR-146a	*UBD, CCL5, CCL8*	Inhibition of inflammation due to suppression of target gene transcripts	n/a	*Homo sapiens*	+	Ghafouri-Fard et al. (2020)
miR-146a, miR-146a-5p, miR-155-5p	*CCL5, NF-kB*	Inhibits *NF-kB*-mediated inflammatory response	n/a	*Mus musculus*	+	Ueta et al. (2023)
miR-146a-5p	n/a	Regulates immune response and correlates	n/a	*Homo sapiens*	-	Khosrojerdi et al. (2024)

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
miR-151A	*IL-12RB2*	with IgE titre Involved in the progression of pathogenesis due to exposure to the target	White blood cells	*Homo sapiens*	-	Ueta et al. (2023)
miR-151A	IL-12 β2 receptor	Diagnostic marker	n/a	*Homo sapiens*	n/a	Khosrojerdi et al. (2024)
miR-155	*SOCS1*	Represses *SOCS1* of T-helper 17 cells, which contributes to their differentiation; diagnostic and therapeutic potential	Blood serum	*Homo sapiens*	-, since T-helper 17 cells are the initiators of inflammation and tissue destruction	Khosrojerdi et al. (2024)
miR-155	*CTLA4*	Represses *CTLA4,* activates T-lymphocyte proliferation	Skin	*Homo sapiens*	n/a	El-Korashi (2024)
miR-203, miR-205	n/a	Predictive marker for risk diagnosis and prevention	Skin	*Homo sapiens*	0	Hicks et al. (2022)
miR-677-3p, miR-770a-5p	n/a	Predictive therapeutic target	Skin	*Homo sapiens*	0	Wangyang et al. (2018)
miR-184	n/a	Overexpression after contact with an allergen	Nasal cavity epithelium	*Rattus norvegicus*	n/a	Langwiński et al.(2022)
miR-190, miR-208, miR-138	n/a	Inhibition of expression after immunotherapy; pro-inflammatory molecules	Whole blood	*Homo sapiens*	-	Specjalski et al. (2022)
miR-320e	*PTEM*	“Switching” the synthesis of immunoglobulins of different classes; wound healing	Ear fluid for otitis media	*Homo sapiens*	+	Adamczyk et al. (2021)

*Note: * – miR suppression.*

Overall, model objects have altered expression of about 200 miR in response to atopic dermatitis, and transcription of 23 molecules remains disrupted during remission (Ghafouri-Fard, Shoorei, Taheri and Sanak, 2020). As can be seen from Table 2, the miR series are diagnostic markers. Thus, atopic dermatitis can be distinguished from T-cell lymphoma and fungal mycosis by their level of expression. It should be noted that upregulation of a particular miR does not always determine pathogenesis. MiR-146a and miR-155 are most often involved in the regulation of atopic dermatitis (Hartmane, 2024). In particular, miR-146a can have mixed effects. Acting through the transcription factor *SUMO1*, microRNA causes inflammation. In other regulatory cascades due to mediated suppression of pro-inflammatory cytokine gene transcripts UBD (ubiquitin D) *CCL5* and *CCL8*, and

also in the NF-kB signalling pathway, the inflammatory process is suppressed. The regulatory function of miR in allergic rhinitis is summarised in Table 3.

Table 3. Role of miR in the pathogenesis of allergic rhinitis

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
miR-19a	*IL-10*	*IL-10* transcript suppressor	Whole blood	*Homo sapiens*	+, because *IL-10* causes inflammation	Yu et al. (2017)
miR-19A-5p, miR-26a-5p, miR-126-5p	n/a	Biomarker of risks in allergic rhinitis	n/a	*Homo sapiens*	0	Jia et al. (2018)
*miR-21	*IL-12A, TGFBR2, HMGB2, IRF3*	With a reduced miR titre, *TGFBR2* is overexpressed, a lot of IgE is produced and an allergic reaction develops	Umbilical cord blood	*Homo sapiens*	-	Mao et al. (2024)
miR-133b	*Nlrp3*	miR overexpression inhibits IgE synthesis and symptom manifestation by inhibiting *Nlrp3*	n/a	*Mus musculus*	+	Xiao et al. (2017)
miR-142-3p, miR-221	n/a	Biomarker of risks in allergic rhinitis	Nasal mucosa	*Homo sapiens*	0	He et al. (2017)
miR-143	*IL13Ra1*	Acting on the target, it blocks the synthesis of *IL-13*-mediated pro-inflammatory cytokines and reduces the generation of mucus in the nasal cavity	Nasal mucosa	*Homo sapiens*	+	Tunçer et al. (2022)
miR-146a	*FOXP3, TRAF6, IL-10, STAT5B*	Biomarker; activator of Treg cell differentiation	Nasal mucosa	*Homo sapiens*	+	Zhang et al. (2022)
miR-155	*IL-4, IL-5, IL-9, IL-13,*	Regulates the inflammatory process in *ILC2* lymphoid undifferentiated cells	Nasal mucosa	*Homo sapiens*	-	Zhong et al. (2023)
*miR-155, *miR-181a	*SOCS1, IL-10, TGF-β, SIRT1, PI3K/Akt*	Reduced miR titre correlates with reduced Treg cell titre	n/a	*Homo sapiens*	n/a	Zeng et al. (2019)
miR-	*MATN2*	Regulation of	Whole	*Homo*	n/a	Wang et

miR	Target gene for miR	Mechanism of action	Type of biomaterial	Object of research	Positive (+) /neutral (0)/negative (-) health effects	Research source
202-5p		differentiation and function of T-lymphocytes	blood	*sapiens*		al. (2019)
miR-202-5p	*MATN2*	Activates M2 polarisation of macrophages	Nasal mucosa	*Homo sapiens*	-	Wang et al. (2019)
miR-375	*JAK/STAT*	Inhibits *JAK/STAT*-cascade that prevents epithelial apoptosis and eases the course of allergies	n/a	*Mus musculus*	+	Yang et al. (2018)
miR-375	*IL-4, IL-13, TSLP*	Regulator of allergic rhinitis development	n/a	*Homo sapiens*	n/a	Jin et al. (2022)
miR-487b	*IL-33, ST2*	Inhibits *IL-33 / ST2*, a signalling cascade that eases allergy symptoms	Nasal mucosa	*Homo sapiens*	+	Liu et al. (2018)
miR-320e	*PTEM*	"Switching" the synthesis of immunoglobulins of different classes; wound healing	Ear fluid for otitis media	*Homo sapiens*	+	Adamczyk et al. (2021)

*Note: * – miR suppression.*

In the nasal mucosa in allergic rhinitis, the expression of about 85 miR changes (Ghafouri-Fard, Shoorei, Taheri and Sanak, 2020). As can be seen from Table 3, transcripts of pro-inflammatory cytokines *IL-4, IL-5, IL-10, IL-13*, less often – anti-inflammatory cytokines (*IL-12A*), and a number of pleiotropic regulators become targets for suppression: *JAK/STAT, SOCS1, SIRT1, TGFBR2, HMGB2, MATN2, FOXP3*. Urticaria is a type of hypersensitivity in which oedema is formed due to vasodilation, increased permeability of their walls and fluid leakage under the skin. The pathogenesis is mainly due to the activation of mast cells and their release of granules with pro-inflammatory compounds. Changes in the expression of 16 miRs were detected during the course of the disease. In particular, the titre of miR-29c-5p, miR-125a-5p, miR-155, miR-221, miR-361-3p, miR-2355-3p, miR-2355-5p, and miR-4264 transcripts was increased. They are involved in the regulation of metabolic cascades of the glucocorticoid receptor, *TGF-β* (transforming growth factor), regulator p53, and cytokine *CCL17*. The over-synthesis of these regulatory molecules correlated with the activation of the inflammatory process. In particular, simultaneous overexpression of miR-155 and IgE were observed; the miR-221 titre increased simultaneously with the C-reactive protein content. Urticaria-specific overexpressed miR-125a-5p can serve as a diagnostic marker, since its serum titre increases significantly in the acute phase and decreases during remission (Karstarli Bakay et al., 2023). Consequently, the hypersensitivity reaction is accompanied by a change in the expression of short-chain RNAs, among which the main regulators are miR-21, miR-146a/b, miR-155, miR-221, miR-221-3p, miR-375.

The meta-analysis has demonstrated that around one hundred microRNAs (miRs) are significantly involved in the regulatory pathways related to allergic responses. These microRNAs function predominantly at the epigenetic level, regulating the translation of mRNA molecules that govern several pleiotropic regulators. This regulation can either enhance hypersensitivity under certain conditions or alleviate it in others, contingent upon the miR's interaction with particular mRNA targets. Among the most thoroughly investigated microRNA molecules related to allergic asthma are miR-21, miR-146a, miR-155, miR-221, and miR-143-3p, each demonstrating a unique function in the regulation of inflammatory processes and immunological responses. MiR-21 and miR-146a are identified as significant pro-inflammatory agents that facilitate the activation of M2-type macrophages, whilst miR-155 is a crucial biomarker for inflammation, participating in the production of pro-inflammatory cytokines including IL-4, IL-5, and IL-13 (Melnychaiko & Andreychyn, 2023). miR-221 plays a complex role in immune control by influencing mast cell activities and apoptosis. The findings

substantiate the concept that microRNAs can either intensify or mitigate allergic reactions, contingent upon their concentration and regulatory targets. A comparative analysis with other studies (Pokryshko and Dutchak, 2024) emphasises the originality of our research and emphasises the necessity for specific therapeutic strategies that regulate miR activity to mitigate allergy disorders.

Habib et al. (2022) found three critical prognostic indicators of allergic asthma: miR-25, miR-203, and miR-509. The levels of miR-203 and miR-509 were observed to be diminished in asthma, indicating a possible involvement in the regulation of two critical protein kinases, c-Abl and Plk1. These kinases are recognised for inducing impulsive contractions, proliferation, and migration of bronchial smooth muscle cells. It is significant that miR-25 overexpression is associated with the pathological remodelling of myocytes, indicating that although miR-25 may contribute to asthma exacerbations, its impact is intricate and context-dependent. This conclusion contradicts previous findings (Wang et al., 2022), which indicated that miR-25 may alleviate asthma symptoms by decreasing inflammatory markers. These disparities underscore the necessity for additional study to elucidate the therapeutic potential and constraints of miR modification in asthma treatment. Thus, microRNAs can be used for therapeutic purposes in the future. The current meta-analysis also reported that a number of other microRNAs may be attenuators of asthma symptoms, in particular, miR-21-5p (improvement of airway patency), miR-146a-5p (suppression of the inflammatory process due to a factor of TRAF6), miR-155-5p (inhibition of eosinophil proliferation), miR-133, miR-139 (weakening of the inflammatory process at the level of T-helper type 2), miR-590-5p (prevents remodelling of the bronchial epithelium, blocking fibroblast growth factor FGF1) (Mialiuk et al., 2021; Tazhibayeva et al., 2020).

In atopic dermatitis, the most studied regulators from the class of microRNA biomolecules are miR-146a, miR-151A, miR-155, and miR-29b. miR-146A, as in asthma, can be a stimulant of the pathological process, inhibiting the pleiotropic transcription factor SUMO1 (ubiquitin-like modifier). It is involved in coordinating the processes of apoptosis, nuclear transport, and maintaining the stability of protein molecules (Takamura et al., 2022). However, unlike the type of regulation in asthma, miR-146a can inhibit inflammation. miR-151a apparently suppresses the translation of the interleukin receptor beta subunit IL-12RB2 (according to Table 2 above). Since IL-12 triggers type 1 T helper differentiation, in this case, IL-12 signalling is blocked, and a population of type 2 T helper cells is generated, which is one of the links in the inflammatory pathway (Flajnik, Singh, and Holland, 2022). miR-155, as in the case of allergic asthma, directs the immune response towards the progression of hypersensitivity. In addition to the mechanisms mentioned above, this microRNA can also stimulate the synthesis of cyclooxygenase Cox2 and pro-inflammatory cytokines IL-6, IL-13 in mastocytes by acting through the factor FCεR1 (Mohammed et al., 2022). miR-29b inhibits the transcript BCL2L2 (a regulator of apoptosis) and also exhibits pro-inflammatory properties. According to a study by Beheshti et al. (Beheshti, Halstead, McKeone, Hicks, 2022), the severity of atopic dermatitis was positively correlated with the miR-375-3p titre and negatively correlated with miR-21-5p. When summarising the data, these molecules were assigned to regulators in asthma with a similar effect. Given targeted transcripts – KLF4 and SMAD7 – these regulators can be generalised through IL-13 and growth factors, and therefore, the localisation of inflammation rather depends on the nature of the stimulus.

Among the best-studied epigenetic regulators of the pathological process in allergic rhinitis are miR-146a, miR-375, miR-202-5p, miR-155. miR-146a and miR-375 act through global factors TRAF6, FOXP3, STAT5B, IL-10, JAK/STAT as a result, the titre of differentiated Treg lymphocytes increases, the immune response to the allergen is weakened, and apoptotic processes of the nasal epithelium are inhibited. Thus, the course of allergies is facilitated. Instead, miR-155 and miR-202-5p provoke inflammation by activating M2 macrophage polarisation, type 2 lymphocyte differentiation, and production of inflammatory molecules. Data on pro-inflammatory miR-155 are consistent with data from experiments conducted in 2024. In particular, Zeng et al. (2024) confirmed the negative role of miR-155 in pathogenesis in allergic rhinitis, but found a biochemical association with other anti-inflammatory agents. Namely, overexpression of miR-155 caused over-synthesis of pro-inflammatory cytokines (IL-5, IL-13) in the type 2 lymphocyte population. The administration of apolipoprotein Apo-A-I blocked the expression of this microRNA and thus attenuated inflammatory events. Apo-A-I, in one context, is involved in the synthesis of high-density lipids, and in another context, it has anti-inflammatory effects on eosinophils, neutrophils, macrophages and monocytes. Thus, by combining anti-inflammatory microRNAs with other signalling compounds, hypersensitivity can be reduced.

In allergies, there is usually a change in the balance between the titre of T-helper type 1 and type 2. A detailed understanding of the mechanisms of regulation of T-cell activity and differentiation by microRNAs facilitates the recognition of marker molecules in a specific pathological process. Their titre differs at different stages of the disease, and during periods of exacerbation and remission. In addition, the transcriptional pool changes in response to specific immunotherapy (as shown by Ghafouri-Fard et al. (2020) on mucosal samples of model objects Mus musculus after administration of the drug for allergic rhinitis) (Koniah et al., 2021). Comparative assessment of the qualitative composition and level of microRNA expression in the biomaterial of healthy individuals and allergy sufferers can serve as a biomarker of the disease. Given the sensitivity of the real-time PCR method, quantification can be performed quickly and efficiently using native biosamples. Since regulatory molecules are concentrated both at the sites of inflammation and circulate in the blood, smears from damaged areas of the skin, epithelium, and mucus of the respiratory tract, whole blood, serum or a fraction of shaped elements can be used to analyse biological markers. In particular, specific markers of bronchial asthma are miR-133b, miR-155 (reduced expression compared to healthy people), miR-133a (reduced expression), miR-21, miR-126 (increased expression) (Smiyan et al., 2015). Specific markers for atopic dermatitis are miR-203 and miR-205, while miR-677-3p and miR-770a-5p are potential therapeutic targets. Regarding allergic rhinitis, risk biomarkers can be considered miR-142-3p, miR-221, miR-19A-5p, miR-26a-5p, miR-126-5p.

Existing treatment modalities for asthma, rhinitis, and dermatitis are inadequate, with around 10% of patients suffering from uncontrolled severe manifestations of allergic asthma and eczema (Rebane, 2015). The extensive data provided here serve as a crucial basis for the design of forthcoming scientific studies and clinical trials focused on investigating the potential of microRNA-based therapeutics. These methods seek to suppress the expression of critical pro-inflammatory transcription factors by targeting specific microRNAs, presenting a promising strategy for diminishing the inflammatory response and alleviating the severity of allergic disorders. This approach's innovation resides in its capacity to selectively alter miRs that govern immune responses, potentially offering more precise and effective treatments for individuals with severe manifestations of these conditions.

This study enhances the existing knowledge of the involvement of microRNAs in allergy disorders by elucidating their dual regulatory function. This research illustrates that miRs can function as both inducers and inhibitors of inflammation, contingent upon the unique molecular context, in contrast to other studies that predominantly concentrated on pro-inflammatory miRs. The results have considerable implications for the future of precision medicine in allergy treatment, as microRNA regulation may function as a tailored intervention to either amplify or inhibit specific immune pathways. Additional clinical validation is required to substantiate these findings and evaluate the prospective therapeutic advantages and constraints of miR-based therapeutics in human subjects.

CONCLUSION

Data on the role of various microRNA molecules in the pathogenesis of allergic asthma, atopic dermatitis, allergic rhinitis, and urticaria are systematised. In general, allergies can change the transcription level of about 200 different microRNA molecules. The best-studied regulators of the immune response in asthma are miR-21, miR-146a, miR-155, miR-221. The first three are triggers of inflammation. They act through the Wnt-beta-catenin cascade, transcription factors SMAD7, TGF-β, CSFIR, IRF5, IL-12P3, IL-13, EGFR, IRAK1. Phenotypically, regulation is manifested by M2-type macrophage polarisation, activation of pro-inflammatory lymphocytes, and synthesis of pro-inflammatory molecules (IL-4, IL-5, IL-13), and stimulation of apoptosis, miR-221 has a mixed impact. In atopic dermatitis, transcriptional inhibition is mainly mediated by miR-29b, miR-146a, miR-151A, and miR-155. They bind to mRNA BCL2L2, SUMO1, UBD, CCL, NF-kB, IL-12RB2, SOCS1, CTLA4. Regulatory cascades in most cases provoke inflammation, and miR-146a acts as an anti-inflammatory agent in inhibiting signal transmission through NF-kB. The inflammatory process of allergic rhinitis is mainly coordinated by miR-146a, miR-155, miR-202-5p, miR-375. Their targets are FOXP3, TRAF6, IL-4, IL-5, IL-9, IL-10, IL-13, SOCS1, SIRT1, TGF-β, MATN2, TSLP, JAK/STAT. miR-146A and miR-375 promote Treg lymphocyte differentiation and block JAK/STAT-mediated apoptosis of the epithelium, which facilitates the course of allergies. miR-155 and miR-202-5p cause maturation of "inflammatory" T-lymphocytes and M2 polarisation of macrophages, so they exhibit pro-inflammatory properties. Overexpression of miR-221 and miR-155 in urticaria leads to increased production of C-reactive protein and pro-allergic IgE, and a specific marker of the acute phase of the

disease is miR-125a-5p. The signalling markers of asthma biomolecules are miR-133a, miR-133b (reduced transcriptome titre), and miR-126 (increased transcriptome titre). Risk markers for atopic dermatitis should be distinguished miR-203 and miR-205; for allergic rhinitis – miR-19A-5p, miR-26a-5p, miR-126-5p, miR-142-3p. The research prospects include the search for microRNAs as potential therapeutic targets and ways to block them to suppress the inflammatory process in response to allergens. This study not only consolidates the role of microRNAs in allergic diseases but also suggests a paradigm shift in allergy treatment toward miRNA-targeted therapies. Future research should focus on the feasibility of using miRNA inhibitors or mimics to regulate immune responses and develop precision medicine approaches for allergic disorders.

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M.Z.L. is asingle author of the article.

CONFLICTS OF INTEREST

The author(s) declare no conflict of interest.

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