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Allergic Diseases and Lifestyle Factors: Insights from Environmental and Microbial Interactions

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Abstract: Allergic diseases have emerged as global health concerns over the past decades. While immune mechanisms are relatively well-understood, the role of environmental factors and the gut microbiome have been gaining more attention in exploring the increasing prevalence and severity of allergies. This study, through a cross-sectional survey and statistical analyses, investigates how personal lifestyle choices impacting these factors contribute, providing potential avenues for mitigating allergic illnesses. Notably, findings regarding fermented food consumption, family allergy clustering, and environmental exposures emphasize certain connections over others. Understanding some of the many influences of lifestyle modifications on this public health issue can further help in the development of preventative approaches.

Keywords: Allergic diseases, Diet and immunity, Allergy prevention, Environmental exposures, Fermented foods

1. Introduction

Allergic diseases, including rhinitis, asthma, dermatitis, conjunctivitis, and food hypersensitivities, are evolving into some of the most common causes of chronic health concerns in the past decades [1]. The prevalence of allergic diseases is on a drastic rising trend, with projections suggesting that 4 billion people worldwide will be affected by 2050 [2]. The major immune and genetic mechanisms behind these conditions, some of which involving the Th2 polarization, production of type 2 cytokines, and mobilization of immunoglobin E (IgE), mast cells, basophils, and eosinophils are generally well-understood and central to the current understanding of allergies [3].

However, the growing occurrence of these conditions is not clearly attributed to one reason but known to be influenced by many different factors. Studies have demonstrated that microbial exposures, encompassing influences for immune maturation and development exerted by the gut microbiota through dietary changes, play a progressively substantial role in shaping the development of allergic diseases [4]. Similarly, more diversity in microbial environments, related to geographical areas or living conditions, have been found to inversely associate with the risk of allergic diseases [5]. A feature common to these lifestyle factors is that certain variations favor the formation of a more heterogeneous microbiota in an individual's gastrointestinal tract (GIT) and respiratory mucosa than others [6].

The GIT and respiratory mucosa play crucial roles in the development of immune tolerance to antigens by balancing Th1, Th2, Th17, and T regulatory cells. Gut and lung dysbiosis, or imbalances in the gut and lung microbiomes, are linked to the severity and risk of allergic diseases, such as asthma

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and food allergies, and IgE regulation. Thereby, the associations indicate that environment and dietary factors, that differ significantly in the extent of microbial exposure they provide, are able to create dysbiosis in the gut and lung, stimulating changes that directly affect the immunological mechanisms of allergies [4].

Current clinical guidelines of allergic diseases suggest a personalized combination of allergen avoidance, pharmacotherapy, and allergen immunotherapy. While these treatments have been shown to reduce symptoms and sensitivity in controlled trials, they either do not prevent disease progression or fail to address the potential long-term side effects [7]. Therefore, this study aims to examine the community-level strategies to improving the understanding of the complexity between modifiable lifestyle factors and allergies and to mitigating the public health issue in the long run.

2. Environmental and microbial factors

The environmental exposome, encompassing biological, physical, and chemical factors an individual encounters through ingestion, skin contact, or inhalation, demonstrates how lifestyle choices shape the human microbiota. The microbiome's composition can be impacted by nutrients, moisture, and pH at different body sites and harmfully affected by environmental substances, some of which are known to inhibit bacterial growth and damage the epithelia barrier [8]. The epithelia barrier constitutes the first immunological defense of the human body against environmental factors and can be compromised by disruptions in the microbiome. Thus, alterations to the microbiome caused by the environmental exposome suggest a potential increase in epithelial permeability and aggravated allergic inflammation. Specifically, impaired microbial DNA sequences as a result of certain environmental conditions are no longer able to restore epithelial barrier integrity and the hinder the influx of pathogens and toxins from heightening the induction of type 2 inflammation and the release of alarmins such as interlukin-25 and interleukin-23, exacerbating inflammatory responses [9].

Moreover, in allergic diseases, the composition and functionality of the gut microbiome are shown to have significant influence over the development of immune responses and the progression of immunological processes [8]. For instance, individuals in the United States with food allergies exhibit lower species diversity and imbalanced levels of certain orders of bacteria such as *Bacteroidales* and *Clostridiales* [10]. Early-life gut microbiota dysbiosis, or alterations of the composition or reduced diversity in the gut microbiome, can significantly impact immune cell maturation and pathogen resistance, influencing the development of allergic inflammation [11]. Factors such as Cesarean birth, antibiotic use, and airborne pollution have been known to shape the increasing trajectory of allergic disease development in children, attributed to the reduction of certain beneficial species of bacteria, like *Bifidobacteria* and *Lactobacilli,* that maintain the immune homeostasis and stimulation of regulatory T-cells and anti-inflammatory cytokines. Furthermore, specific diets also impact the composition of the gut microbiome to different extents and in distinct ways. Popular diets of Western, gluten-free, and vegetarian are linked to decreased beneficial microbes, specifically beneficial bacteria species *Bifidobacterium* and *Bacteroides* [12]. While certain sources and moderate amounts of protein, fat-soluble vitamin D, fermented foods, and dietary fibers are especially able to maintain the diversity of the gut microbiota, food additives, alcohol, and diets characterized by high fat/high sugar can negatively influence the growth and/or diversity of beneficial bacteria [13]. Dysbiosis leads to higher permeability of the intestinal barrier, promoting the entrance of allergens into the bloodstream and susceptibility to specific allergens [14].

Signals from the gut can also be indicated in a local cytokine environment in a distant area of the body, a mechanism facilitated by epithelial, structural, and immune cells that trigger pro-inflammatory processes through direct interactions with bacterial metabolites in gut bacteria [15]. For instance, short-chain fatty acids (SCFAs) from microbial fermentation are known to inhibit pro-inflammatory responses by acetylating histones in regulating the expression of genes involved in

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immune cell differentiation: most notably the expression of cytokines in regulatory T cells, or binding to G-protein-coupled receptors, leading to signaling cascades that deactivate transcription factors that promote the expression of pro-inflammatory cytokines [16].

3. Method

The study employed a cross-sectional survey to gather data on lifestyle, dietary, and environmental factors, as well as the presence and severity of different allergies among a sample of individuals recruited from a diverse array of community settings (e.g., schools, workplaces). The survey was designed to assess the participants' environmental and health choices and exposures to better understand its potential association with allergy severity.

The survey was administered to a total of 187 adult and adolescent individuals, aged 13 to 62 years. Participants were informed of the voluntary nature of their participation and consent was obtained in the questionnaire. The data was collected anonymously and through a secure online platform.

The survey questionnaire consisted of four primary sections: allergy history, lifestyle choices, environmental exposures, and dietary habits. Specifically, participants were asked to report or queried about factors such as overall adherence to specific dietary patterns, living environments, stress levels, as well as specific allergens causing sensitization, frequency and severity of allergic reactions and symptoms, and family history in allergic diseases.

All statistical analyses were conducted in Python (version 3.11) within a Jupyter Notebook environment to ensure an efficient and transparent workflow. For categorical data comparisons, Chi-square tests were utilized to determine whether the distribution of responses differed significantly between groups (e.g., presence versus absence of allergies). These tests allowed us to assess the independence of variables such as environment-related features and self-reported allergy status. For situations in which the data were ordinal or potentially non-normally distributed, we applied nonparametric approaches. Specifically, the Mann–Whitney U test was used to compare two independent groups (for instance, participants with and without a particular exposure or lifestyle habit), ranking the combined samples and evaluating whether the distributions of ranks differed significantly. When more than two groups needed to be compared on a numeric or ordinal measure (for example, frequency of antibiotic use categorized into three or more levels), the Kruskal–Wallis H-statistic was employed as a generalization of the Mann–Whitney U test to multiple independent samples. In each case, a threshold of $p < 0.05$ was adopted to declare statistical significance. Summaries included median and interquartile ranges for ordinal variables, alongside p-values or H-statistics when applicable, to provide a comprehensive overview of group differences.

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4. Results

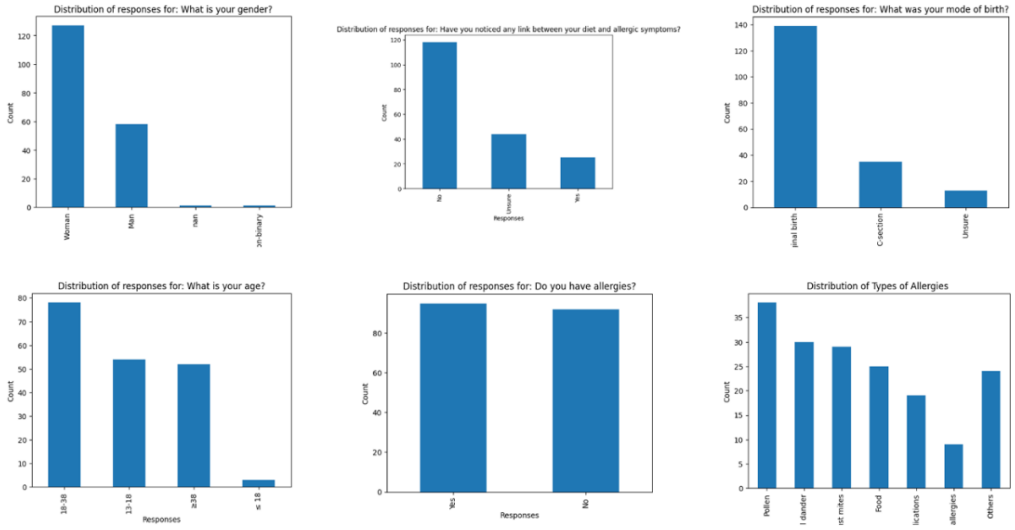

Figure 1: Overview of reported allergies, demographic characteristics, birth mode, and perceptions of allergy links

The majority of respondents identified as female (n>125), aged under 18-29 years, and reported being delivered via vaginal birth (n>100). Of the 187 individuals in this analysis, responses within those who reported having allergies, which were of higher prevalence in the population, indicate that the most common types of allergies included pollen, pet dander, and food. Among responses regarding whether a connection between diet and allergy symptoms is noticed, a small subset indicated “yes”, suggesting limited perceived awareness of diet-allergy correlations.

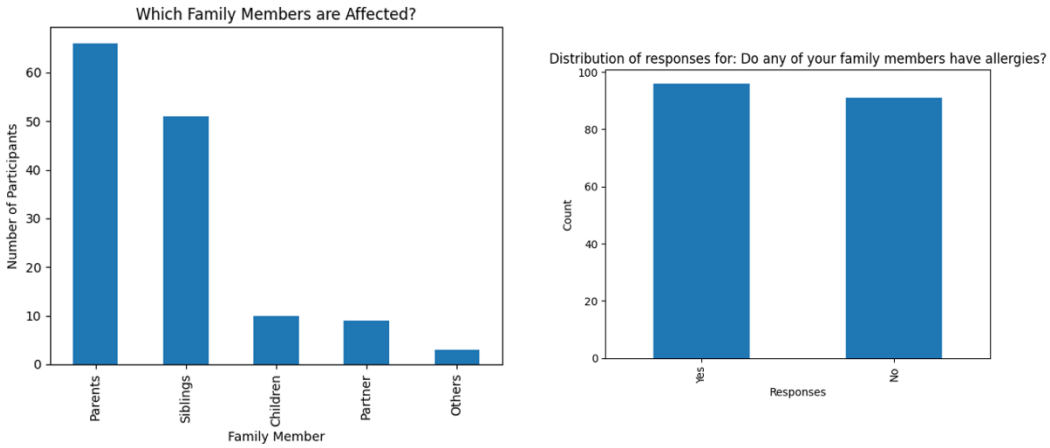

Figure 2: Survey findings on family allergy rates and which relatives are most affected

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A chi-square test showed a significant association between respondents having allergies and their family members also having allergies ($\chi^2(1) = 11.78$, $p < 0.001$). This suggests that individuals who have allergies are more likely to report that other members of their family also have allergies, compared to those without allergies.

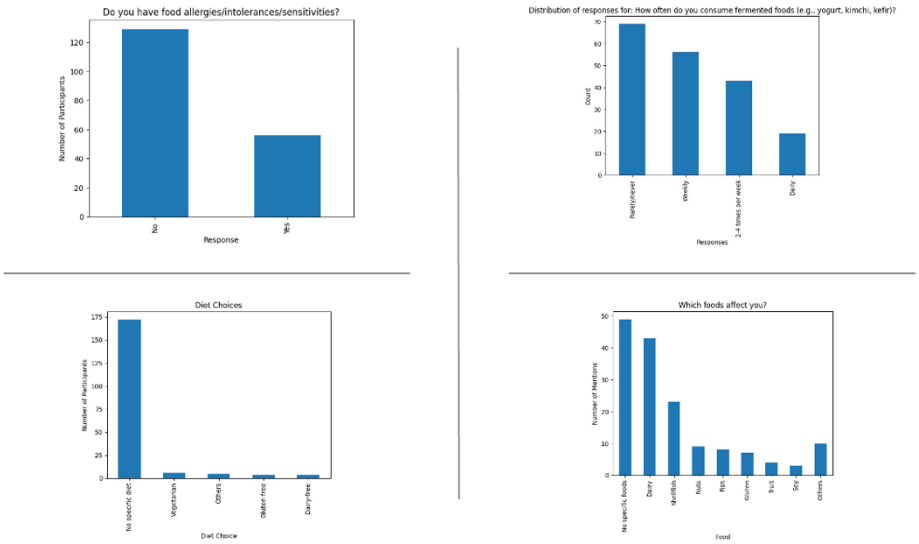

Figure 3: Survey insights on food allergies, fermented food consumption, dietary choice, and common trigger foods

Individuals of the sample who state that they have food sensitivities are significantly more likely to also say they have allergies. Mathematically, 55% of the allergy group has GI issues vs. 29% of the non-allergy group. This difference yields a p-value ~0.019, indicating a statistically significant association. A Kruskal–Wallis H-statistic of 7.599 with p-value = 0.022 (< 0.05) indicates a statistically significant difference in fermented-food consumption across the three allergy groups (e.g., "Food only," "Resp only," "Mixed/other"). In other words, at least one of these allergy groups differs in median fermented-food consumption from the others. There is also a statistically significant difference in fermented-food consumption between "Food only" allergy individuals and those with "Mixed" allergies. No other pairwise differences are significant at the 0.05 level. A significant Chi-square result, indicating an overall association between dietary restrictions and allergy type is presented, but the many categories and extremely low expected cell counts mean the standard Chi-square assumptions are violated.

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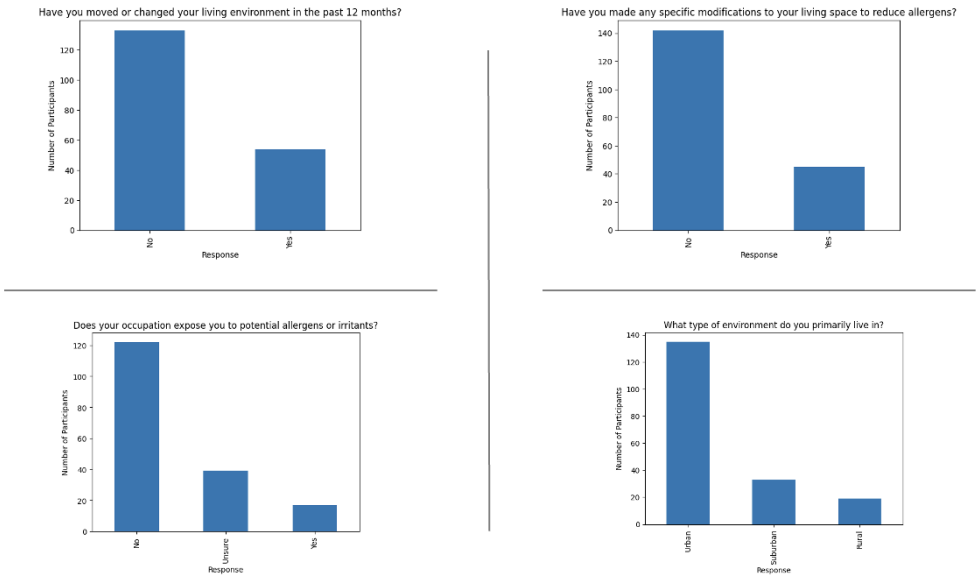

Figure 4: Survey results on housing changes, allergen control measures, occupational exposures, and environmental types

Suburban dwellers in this sample have the highest proportion of allergies (70%) compared to rural (42%) and urban (47%). However, because the Chi-square p-value was just above 0.05, it cannot be conclusively declared that environment and allergies are related based on this sample alone. Overall, no statistically significant link emerges between specific environmental exposures in the home/occupation and allergy presence/severity in this sample.

5. Discussion

The correlation between self-reported food sensitivities and allergies observed in the sample indicates that immune responses have significant connections to dietary habits. The likelihood of individuals with food sensitivities also reporting to have allergies suggests a shared proneness to certain immunological factors [17]. Moreover, the statistically significant association between allergies and gastrointestinal issues shown in the higher proportion of the allergy group experiencing gastrointestinal problems. The involvement of the gut in allergic reactions further indicates the essential role of the gut microbiota and intestinal barrier function in interacting with the immune system in responding to allergens, as observed in other studies [18].

Furthermore, the significant difference in fermented-food consumption patterns between individuals with “Food only” allergies and “Mixed” allergies implies that the gut microbiota composition may play a crucial role in the manifestation of different allergy subtypes. Fermented foods contain probiotics and a variety of bioactive compounds that are known to exert influence on the diversity of the gut microbiome [19]. Thus, this trend points to connections between the gut microbiome and allergy development. Among the numerous beneficial effects of probiotic supplements, containing beneficial bacteria known to reduce inflammation caused by allergens and regulate the immune system, through supporting the epithelial integrity, stimulating T and B cells of the immune system, and maintaining the intestinal homeostasis, can potentially play a role in alleviating allergies [20]. The study further corroborates with the effects of the usage of probiotics,

suggesting a potential benefit for increased commercial availability of probiotic supplements to combat allergies.

The finding that dwellers in metropolitan areas in this sample had the highest proportion of allergies highlight a potential influence of certain environmental factors on the prevalence of allergies. While the chi-square p-value was 0.02 above 0.05, preventing definitive significance, the observed trend calls for further investigation. Altered microbial exposures resulting from environmental factors such as increased allergen exposure and air pollution may contribute to increasing reports of allergies in urban settings compared to rural areas. Increasing and relatively higher incidence of allergic illnesses in developed and industrial nations may also be partly attributed to environmental pressures, such as exposure to fossil fuel emissions, aligning with the trends observed in this study [21].

A strong genetic or environmental component is suggested by the high proportion of respondents with allergies who also report affected family members. Genetic factors, such as IgE production and immune cell function, shape allergen responses, while shared family environments — including diet and living conditions — may also contribute to this trend [22]. Environmental exposures can further influence gene expression through epigenetic mechanisms; for example, air pollutants may alter DNA methylation in immune-regulating genes, raising asthma risk [23]. Further studies identifying specific exposures and conducting genetic analyses within families are needed to clarify these contributions.

6. Conclusion

This study highlights the intricate connections between certain factors, most notably the gut microbiome and environmental exposures, and the development and incidence of allergies. Significant associations observed in the trends elicited by the survey provided insights into how consumption of fermented foods, gastrointestinal issues, urban environments and living conditions, and family history play a potential role in the rising burden of allergies. The observations call for possible interventions or modifications of personal lifestyles to mitigate the prevalence of allergic illnesses and further research regarding a more profound and personalized analysis of the factors underscored in the findings of this study.

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