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Asthma heterogeneity and severity



Tara F. Carr^{1*} and Eugene Bleecker²

Abstract

REVIEW

Asthma is a common, chronic inflammatory airways disease characterized by a clinical syndrome of bronchial hyperresponsiveness, inflammation, and reversible airflow obstruction. Individuals with asthma can vary widely in clinical presentation, severity, and pathobiology. The incident factors, pathogenesis, prognosis, and treatment of asthma remain incompletely understood. Utilizing measurable characteristics of asthmatic patients, including demographic, physiologic, and biologic markers, can however identify meaningful phenotypic categories in asthma. Identification of these phenotypes may help improve precision therapeutics targeted toward an individual's' disease, and may identify strategies for preventing progression of disease severity.

Keywords: Severe asthma, Phenotype, Heterogeneity

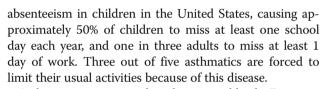
Background

Asthma is a chronic inflammatory disease of the airways. Individuals with asthma may experience recurrent wheezing, dyspnea, chest tightness, and cough. These symptoms reflect episodes of reversible airflow obstruction, which may remit spontaneously or with treatment. Over time, many asthmatics experience progressive airway remodeling, leading to an incompletely reversible, or fixed, airflow obstruction. Further, inflammation in the asthmatic airway induces airway bronchial hyper-responsiveness to a variety of allergic, infectious, or irritant stimuli.

Public health impact of asthma

Asthma is a very common chronic disorder. Asthma severity can range from intermittent to severe; more severe asthma is associated with significant morbidity and mortality. Further, asthma prevalence is increasing with time [1], perhaps due to better recognition and phenotyping. It is estimated that, in the United States in 2013, asthma affected 16.5 million adults and 6.1 million children, reflecting 8.3% and 7.0% of the population, respectively [2]. Approximately half of those individuals experienced an asthma attack, which is defined as sudden worsening of asthma symptoms due to bronchoconstriction, and when severe, hyperinflation and "air trapping" [3]. Asthma is the leading cause of

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Asthma remains a prevalent disease worldwide. Estimates from worldwide analyses such as the Global Burden of Disease Study from the Forum of International Respiratory Societies suggest that asthma affects at least 235-334 million individuals [4, 5]. Using data from the International Study of Asthma and Allergies in Childhood surveys, approximately 14% of the world's children suffer from asthma in any given year. Latin American and English-speaking countries of Australiasia, Europe, North America, and South America have the highest prevalence of childhood asthma, estimated at over 20% [6]. Reported asthma symptoms in children increased from 1993 to 2003 in low- and middle-income countries. Estimates of asthma prevalence in adults are more difficult to obtain. Approximately 8.6% of adults worldwide between the ages of 18-45 have asthma symptoms. The morbidity and mortality burden of disease, however, disproportionately affects older adults [5].

Global measures of disability rank asthma 14th in number of years lost to asthma-associated morbidity and mortality [7]. This most significantly affects individuals in some countries of Europe, Central and South America, Africa, and Austrailasia. Annually in the United States, asthma accounts for approximately 15.5 million outpatient health care visits, 1.8 million emergency department visits,



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and 439,000 hospitalizations, costing the US \$56 billion each year, or roughly \$3259 per person [8]. In a European study from 2011, the estimated total cost of asthma in adolescents and adults was €19.3 billion [9]. In the Asia-Pacific region, the estimated direct and indirect cost of asthma per person range from \$184 to 1189. In the United States in 2013, 3630 individuals died from asthma, or nine people per day [1, 8]. These data suggest asthma is often poorly controlled, despite the availability of pharmacologic therapies that are recommended in National and International Asthma Guidelines [10–12].

Development of asthma

An individual's susceptibility to the development of asthma, or to severity of asthma, are likely determined by an interaction of host or genetic characteristics that interact with environmental exposures. For example, specific genotypes can confer susceptibility to developing wheezing with rhinovirus exposure [13], atopy, or responsiveness to bronchodilator therapy [14, 15]. Currently, there are a number of genes that are associated with asthma susceptibility [16]. An important question in whether these or different genes influence asthma progression and severity. Environmental exposures, including prenatal influences [17], allergens [18, 19], respiratory infections [20-22], cigarette smoke [23], and air pollution [24] are implicated in the development of asthma. Cumulative environmental exposures may lead to persistent, progressive disease with potentially irreversible changes in lung structure and function. These concepts are illustrated in Fig. 1 which describes the interaction between genetics and environment in the development and progression of asthma. Because of differences in the influence of genes and environment, there is a wide range of disease heterogeneity and severity in asthma.

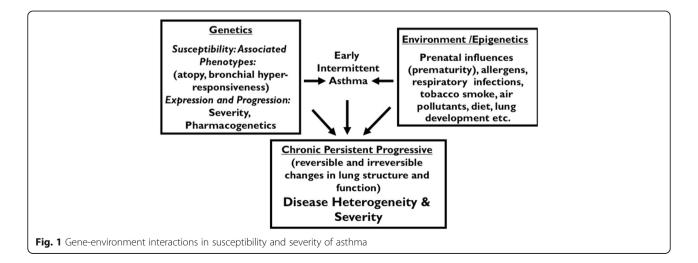
Assessment of asthma

All that wheezes is not asthma, and all asthma does not wheeze. Accurate diagnosis of asthma is important, as treatment will benefit both morbidity and mortality from this disorder. As many non-asthmatic diseases have overlapping clinical findings with asthma, accuracy of clinical diagnosis is critical for planning appropriate treatment strategies. The Global Strategy for Asthma Management and Prevention 2015 report update [12] and the National Institutes of Health Guidelines for the Diagnosis and Management of Asthma Expert Panel Report-3 [10] provide recommendations for the diagnosis of asthma. In addition to obtaining a detailed history of symptoms and physical exam, these guidelines suggest obtaining studies of lung function such as spirometry to measure forced expiratory volume in 1 s (FEV1) and forced vital capacity (FVC) measurement, as the FEV1/FVC ratio objectively measures airflow obstruction. Additional pulmonary function testing such as diffusing capacity, lung volumes, or bronchoprovocation studies to support or refute the asthma diagnosis. Comorbidities and alternate diagnoses should be evaluated when symptoms are atypical or not responding to therapy.

Treatment of non-severe asthma

Goals of asthma treatment are multifaceted. A combination of controller and rescue therapy for asthma usually allows an individual to achieve and maintain control of asthma symptoms. Control of asthma should confer a normal dayto-day activity level, including exercise capacity. Treatment of asthma may prevent the development of irreversible airflow limitation and allow maintenance of best possible pulmonary function. Adequate control of asthma, by definition, should prevent exacerbations and limit mortality due to asthma [10, 12]. Importantly, treatment should also identify and minimize medication side effects.

The Global Strategy for Asthma Management and Prevention 2015 report update [12] and the National Institutes



of Health Guidelines for the Diagnosis and Management of Asthma Expert Panel Report-3 [10] also provide a framework for the treatment of asthma. These guidelines emphasize evaluation of impairment and risk, with ongoing assessment of control. The domains of impairment and control focus on assessment of symptom frequency, frequency of use of rescue medications, impact on activity levels, and lung function. The risk domain identifies risk of exacerbations and adverse outcomes utilizing an individuals' history of exacerbations and lung function, with a goal of prevention of future exacerbations or fixed airflow limitation. The severity of asthma as measured through these domains is then used to guide treatment.

A stepwise approach to therapy is recommended, which highlights use of controller medications, particularly inhaled corticosteroids, then titrating doses or adding additional therapies as needed to achieve the necessary level of symptom control. At every level, assessment of proper inhaler device techniques, adherence to therapy, environmental control, and use of rescue inhalers for quick relief of sudden symptoms are recommended. Well recognized, however, is the inter-individual variability in response to each treatment [25, 26], reflecting the heterogeneity of disease which exists across severity groups.

Severe asthma

Task force definitions of severe asthma

The American Thoracic Society and European Respiratory Society released a Task Force document in 2014 entitled "International ERS/ATS Guidelines on Definition, Evaluation and Treatment of Severe Asthma [11]." The purposes of this document include defining severe asthma and treatment-resistant asthma; discussing phenotypes of severe asthma with respect to genetics, natural history, pathobiology, and physiology; outlining evaluation of a patient with severe asthma; and providing recommendations for treatment of severe asthma in children and adults. Assuming asthma diagnosis is accurate and comorbidities are being addressed, severe asthma is defined as asthma that requires treatment with guidelines-suggested medications such as high dose inhaled corticosteroids and a second controller for the previous year, and/or systemic corticosteroids for at least half of the previous year, to prevent it from becoming 'uncontrolled' or which remains 'uncontrolled' despite this therapy. Uncontrolled asthma is defined as the presence at least one of the following characteristics: persistently poor symptom control, two or more exacerbations requiring bursts of systemic corticosteroids in the preceding year, at least one serious exacerbation requiring hospitalization in the previous year, or chronic airflow limitation of FEV1 < 80% predicted with FEV1/FVC ratio less than the lower limit of normal [11].

Evaluation of patients with severe asthma

Individuals with severe asthma should undergo a careful systematic assessment to confirm this diagnosis. Lung function testing is utilized to confirm airflow obstruction and to measure reversibility or variability of airflow obstruction. Bronchoprovocation testing, such as with methacholine inhalation or exercise, may also be utilized. Medication noncompliance or poor inhaler technique can be identified in many severe asthmatics [27, 28]. Atopy and unregulated allergic exposures, such as ongoing house dust mite or cockroach exposure in an individual with sensitization to these antigens, may contribute to severe asthma, particularly in children [29]. Chronic rhinosinusitis is a very common comorbidity of asthma and contributes to disease severity [30, 31]. Obesity, obstructive sleep apnea, and psychological factors may contribute to asthma severity or perception [11, 32]. Symptomatic gastro-esophageal reflux disease is common in asthmatics, but the effect of treatment on asthma control or severity is currently unclear. The contribution of tobacco smoke exposure, hormones, and medication use should be carefully considered, as avoidance of the offending agent can confer major benefits on asthma control [11].

Treatment of patients with severe asthma

Inhaled corticosteroids remain the mainstay of asthma treatment, particularly in mild to moderate disease. By definition, those individuals with severe asthma require high doses of corticosteroid to control disease, and often remain symptomatic despite this therapy. Further, a subset of severe asthmatics is relatively corticosteroid insensitive, with relative or complete lack of clinical improvement from treatment with inhaled or systemic corticosteroids. While corticosteroid insensitivity seems more common in those with vitamin D deficiency or obesity, eosinophilic or type-2 inflammation-high asthma may have a relative benefit from steroids when compared to those with non-eosinophilic, non-type-2 inflammation [33].

Other controller therapies may benefit some individuals with severe asthma. Beta-agonists provide smooth muscle relaxation and bronchodilation through beta-adrenergic receptors. While short acting and long acting beta-agonists are used in asthma, concern that these drugs may contribute to asthma treatment failure, particularly in individuals with genetic differences in the beta-adrenergic receptor, may impact use [15]. However, recent results of United States Food and Drug Administration-mandated safety studies with inhaled corticosteroid-long acting beta agonist combination therapy do not show evidence of adverse effects [34, 35]. Leukotriene modifiers may benefit severe asthmatics with aspirin exacerbated respiratory disease. Anticholinergics block smooth muscle contraction through inhibition of the muscarinic receptor-3. The long-acting muscarinic antagonist Tiotriopum bromide has shown

benefit some individuals with severe asthma [36, 37]. These treatments, as well as potential future approaches, are highlighted in Fig. 2.

Biological therapeutics, those with a specific pathobiological target, have been and continue to be developed for use in severe asthma with particular phenotypes. Three are available currently in the United States for clinical use. Omalizumab, a monoclonal anti-Immunoglobulin E antibody, may be beneficial for some allergic asthmatics uncontrolled on therapy [38]. Mepolizumab and Reslizumab, both monoclonal anti-IL5 antibodies, reduce asthma exacerbations in those with severe eosinophilic asthma [39, 40], Different treatments, particularly for those with both-type 2 and non-Th2 inflammatory asthma, are under active development [41–43].

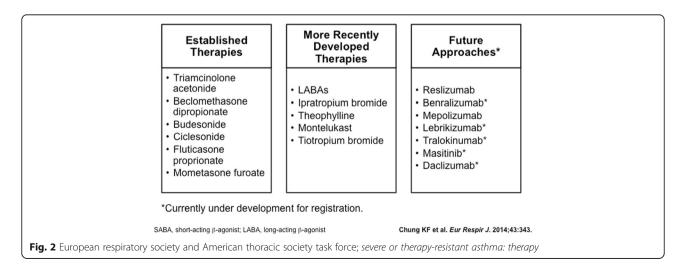
Asthma heterogeneity

With a developing understanding of the marked heterogeneity within the disease of asthma, we hypothesize, and expect to confirm, that the heterogeneity of asthma is attributable largely to individuals' genetic and epigenetic variability, mediated by certain environmental exposures. Environmental exposures are highly dependent on regional characteristics with varying climatic conditions, geography and population distributions. This variability in turn drives the immunologic mechanisms, or endotype, that confer the pathobiological and physiologic characteristics of asthma, the phenotype, as measured in the clinical setting. Importantly, our understanding of this variability and the mechanisms causing this disease may facilitate the development of interventions for primary prevention, disease modification, and precision therapeutics.

Hypothesis-driven univariate approaches to phenotyping have been utilized to clarify differences among groups of asthmatics. This type of approach defines groups based on the presence or quality of one variable, which is chosen to support testing a specific hypothesis. Disease severity may be the most straightforward, if not oversimplified, way of delineating disease phenotype. As anticipated, and likely as a result of the definitions of severe asthma, groups with severe asthma can be distinguished from non-severe asthmatics in terms of disease duration, symptomatology, health care utilization, lung function, and comorbidities [44–47]. However, it is well recognized that disease heterogeneity is present and vitally important among these severity classes, particularly among the more severe asthmatics [48] wherein cellular characteristics and airway remodeling have been long shown to confer different physiologic subtypes. Phenotypic characterization solely by disease severity therefore lacks the granularity to understand and delineate subtypes of asthma.

Other clinical characteristics have been assessed using hypothesis-driven univariate approaches. Reduction in mid forced expiratory flow rates (FEF25-75), as well as in FEV1, have been shown to be independently associated with markers of asthma severity, including ICU admissions, persistent or nocturnal symptoms, peripheral blood eosinophilia, and bronchial hyperreactivity [49]. A striking relationship between age and the probability of severe asthma was identified, particularly in men, increasing with duration of disease and from ages 18 to 45 [47, 50]. Airway mast cell phenotype and activation may contribute to phenotype and clinical characteristics. Indeed, mast cells containing both tryptase and chymase have been identified as the predominant phenotype in patients with severe asthma, whereas mast cells containing only tryptase are identified in biopsies from individuals with mild disease [51].

Inflammatory mediators within the airway may also be used for disease phenotyping. These inflammatory markers, present in sputum supernatant or bronchoalveolar lavage, may be related to cellular patterns that then relate to clinical phenotypes [52], or to disease characteristics such as eosinophilia, neutrophilia, airway bronchial



hyperresponsiveness, and bronchodilator response [53]. Interestingly, when examining broncoalveolar lavage of children with asthma, while markers such as IL-13 and IL-6 can differentiate asthmatics from controls, and other cytokines can distinguish moderate from severe asthma, severe asthma itself does not have a clearly TH1 or TH2 inflammatory pattern [54]. This further underscores the heterogeneity of severe asthma.

Finally, technology to measure gene expression such as microarray and RNA-seq can provide insight into abnormally expressed pathways. Bronchial airway epithelial gene expression patterns were assessed in relationship to the clinical biomarker fractional exhaled nitric oxide (FeNO). Using a subset of genes that correlated with FeNO, subject clusters can be identified as having distinct clinical and molecular characteristics [55].

Model-free multivariate (Unbiased Cluster) approaches

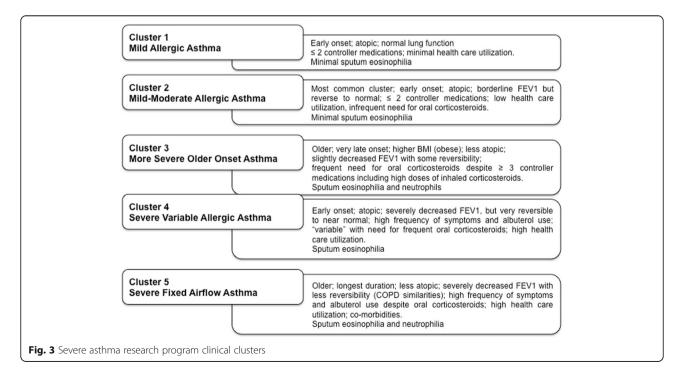
Unbiased approaches to phenotyping utilize computer algorithms to evaluate hypothesis-free relationships among many clinical and biological characteristics. The resultant clusters, because they were created in an unbiased manner, can provide novel insights into asthma phenotypes.

The National Institutes of Health-sponsored Severe Asthma Research Program (SARP) enrolled and carefully assessed large cross-sectional cohorts of mild, moderate, and severe asthmatic adults and children. Unsupervised hierarchical cluster analysis performed on clinical and physiologic data from ~700 adult asthmatics in the SARP cohort identified five clusters of asthmatic subjects (Fig. 3) [47, 56]. Clinical clusters 1, 2, and 4 contain early onset, atopic asthmatics of increasing disease severity and worsening lung function. Cluster 3 is characterized by older, obese women with late-onset non-atopic asthma, with moderate lung function deficits and frequent exacerbations. Cluster 5 is characterized by later onset non-atopic asthma with more severe, irreversible airflow obstruction and high health care utilization. The most influential variables in forming these clusters include gender, age of asthma onset, asthma duration, use of inhaled betaagonists and corticosteroids, and lung function preand post-bronchodilator administration [57].

With an unrelated cohort, investigators from Leicester likewise examined adult asthmatics through cluster analysis, revealing similar phenotypes of benign (mild) asthma, early onset atopic asthma, early onset symptom predominant asthma, obese non-eosinophilic asthma, and late onset inflammation predominant asthma [58]. The reproducible findings of these and other unrelated cohorts support these phenotypes as relevant [44, 59, 60].

Unsupervised cluster analyses were also performed on 161 subjects in the pediatric asthmatic cohort from SARP [61]. Four clusters were identified. Cluster 1 consists mainly of mild, later onset, less atopic asthma with normal lung function. Clusters 2, and 3 represent the spectrum of early onset, atopic asthma with increasing severity and worsening lung function. Cluster 4 identified a subset with more severe, fixed airflow obstruction and the highest health care utilization. These clusters have similarities to those seen in the adult SARP analyses.

Unsupervised cluster analysis was similarly utilized by researchers from the Trousseau Asthma Program in Paris,



France [62] to identify phenotypic clusters in a pediatric severe asthma cohort of 315 subjects. Clinical and inflammatory markers were included in these analyses. Three clusters were identified: one of mild asthma, one of highly atopic asthma with eosinophilia and severe exacerbations, and one of higher body mass index, neutrophilia and more severe airflow obstruction. Despite the differences between the SARP and Trousseau cohorts, the clusters have features that generally overlap: SARP cluster 1 similar to the "mild" cluster, SARP cluster 4 to the "airflow obstruction" cluster.

Sputum cellular characteristics can identify patterns of airway inflammation and may have clinical utility. For example, individuals with sputum eosinophilia are likely to derive benefit from use of inhaled corticosteroids [63]. Phenotyping by cellular characteristics also can identify groups with differences in clinical and inflammatory markers. Airway neutrophilia has been associated with severe asthma defined by low lung function and use of high dose inhaled or oral corticosteroids [64]. Similarly in the SARP cohort, when using pre-defined normal and elevated cell counts, in the absence of cluster analysis, cellular asthmatics with elevated sputum eosinophilia ($\geq 2\%$) and neutrophilia ($\geq 40\%$) tended to have lower lung function, increased symptoms and health care utilization when compared with others [52].

A further examination of the adult SARP data integrated inflammatory cellular measures with the clinical variables in an unsupervised cluster analysis. Four phenotypic clusters were identified, which represented a severity spectrum from those with mild-to-moderate allergic disease (SARP clusters 1,2), having predominantly paucigranulocytic or eosinophilic sputum, to those with moderate-to-severe asthma or impaired lung function, most of whom had significant sputum neutrophilia with or without significant eosinophilia (SARP clinical clusters 3, 4, and 5) [65]. Importantly, the more inflammatory and severe clusters had markedly increased asthma medication use and health care utilization, including bursts of systemic corticosteroids and hospitalizations [57, 65].

Data collected from longitudinal cohorts can also be used for unsupervised cluster analyses, leveraging the power of the longitudinal design to provide insight into the variable patterns of disease over time. Analyses of pediatric birth cohorts have identified clusters of wheeze, atopy, or other characteristics that are associated with risk for asthma-related outcomes into the teenaged years. For example, the Avon Longitudinal Study of Parents And Children (ALSPAC) study collected data on wheezing at multiple time points from birth to age 7 years, for 6265 children in the United Kingdom [66]. The authors utilized wheeze data in latent class analysis to describe patterns of early wheeze, then examined clinical characteristics of individuals in these classes. Associations with atopy, airway hyper-responsiveness, and lung function abnormalities were seen in intermediate and late onset wheezing. These findings were similar to those from analyses of the Dutch Prevention and Incidence of Asthma and Mite Allergy (PIAMA) study, a multicenter birth cohort that enrolled 4146 pregnant women [67]. A latent class analysis of the PIAMA data identified 5 phenotypes of childhood wheeze, similar to those seen in ALSPAC [68]. The ALSPAC cohort was again assessed after age 16; latent class analysis identified early onset persistent wheeze to confer risk of lung function abnormalities.

The Manchester Asthma and Allergy Study is an unselected birth cohort of over 1000 children with periodic lung function and assessments of atopy and other clinical characteristics. Principal component analysis was performed using twenty one variables available at up to 5 years of age; patterns of wheeze and cough components were significant contributing components to the groups [69]. With the availability of 8-year old data for this cohort, a latent class analysis was performed, which identified differences in lung function trajectories over time among the classes, as well as more severe asthmatics with exacerbation risk in the persistent troublesome wheezing group [70].

In a population-based longitudinal cohort that enrolled 1,650 preschool children in Leicestershire, United Kingdom, early life wheeze and atopy data were used for latent class analysis [71]. The three wheeze and two cough phenotypes identified from early life data were assessed for associations with school age respiratory outcomes. The atopic persistent wheezers from early life had highest rates of current or frequent wheeze at ages 8-13. These authors identified a validation cohort of 6970 children born in a different county of the United Kingdom, for whom atopy and respiratory assessments were available at ages 8–13 in approximately 900. Latent class analyses revealed five groups with very similar characteristics to the groups seen in the original cohort [72].

Unbiased analyses from longitudinal cohorts indeed complement those of the cross-sectional cohorts. Despite slight differences among the clusters in each cohort, these unsupervised analyses ultimately identify clearly that asthma phenotypes vary by atopy, age of wheeze onset, clinical and physiologic characteristics. The stability of these clusters into adulthood is not well known, however, and the potential for progression from milder asthma to more severe disease, or vice versa, needs further elucidation.

Conclusion

We can easily recognize the clinical syndrome of asthma, presenting as symptoms of reversible airflow obstruction with airway hyper-reactivity and inflammation. More severe asthma is associated with exacerbations that cause a significant degree of morbidity and even mortality. However, the incident factors, pathogenesis, prognosis, and treatment of asthma remain incompletely understood. Utilizing measurable characteristics of asthmatic patients, including demographic, physiologic, and biologic markers, can identify meaningful phenotypic categories of asthma. These phenotypes, while providing a helpful albeit partial understanding of disease state, can be further leveraged toward endotypic characterization, with the ultimate goals of identifying preventative strategies and improving precision therapeutics targeted toward an individual's disease.

Abbreviations

ALSPAC: Avon longitudinal study of parents and children; FeNO: Fractional exhaled nitric oxide; FEV1: Forced expiratory volume in 1 s; FVC: Forced vital capacity; PIAMA: Prevention and incidence of asthma and mite allergy; SARP: Severe asthma research program

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TFC and EB drafted, edited, and approved this manuscript.

Competing interests

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Consent for publication

Not applicable.

Ethics approval and consent to participate

Not applicable.

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References

- Akinbami LJ, Moorman JE, Bailey C, et al. Trends in asthma prevalence, health care use, and mortality in the United States, 2001-2010. NCHS Data Brief. 2012;94:1–8.
- National Health Interview Survey (NHIS) Data. 2013; http://www.cdc.gov/ asthma/nhis/2013/data.htm.
- Moorman JE, Person CJ, Zahran HS. Asthma attacks among persons with current asthma - United States, 2001–2010. MMWR Surveill Summ. 2013;62 Suppl 3:93–8.
- Ferkol T, Schraufnagel D. The global burden of respiratory disease. Ann Am Thorac Soc. 2014;11(3):404–6.
- The Global Asthma Report 2014. http://www.globalasthmareport.org/. Accessed 15 Oct 2016.

- Lai CK, Beasley R, Crane J, Foliaki S, Shah J, Weiland S. Global variation in the prevalence and severity of asthma symptoms: phase three of the International Study of Asthma and Allergies in Childhood (ISAAC). Thorax. 2009;64(6):476–83.
- Walter H, Sadeque-Iqbal F, Ulysse R, Castillo D, Fitzpatrick A, Singleton J. The effectiveness of school-based family asthma educational programs on the quality of life and number of asthma exacerbations of children aged 5 to 18 years diagnosed with asthma: a systematic review protocol. JBI Database System Rev Implement Rep. 2015;13(10):69–81.
- Asthma's Impact on the Nation Data from the CDC National Asthma Control Program. http://www.cdc.gov/asthma/impacts_nation/ asthmafactsheet.pdf. Accessed 19 Feb 2016.
- World Health Organization. The Global Asthma Report. 2014. 2015; http:// www.globalasthmareport.org/burden/burden.php. Accessed 12 Nov 2016.
- Expert Panel Report 3 (EPR-3). Guidelines for the Diagnosis and Management of Asthma-Summary Report 2007. J Allergy Clin Immunol. 2007;120(1):S94–S138.
- Chung KF, Wenzel SE, Brozek JL, et al. International ERS/ATS guidelines on definition, evaluation and treatment of severe asthma. Eur Respir J. 2014;43(2): 343–73.
- 12. From the Global Strategy for Asthma Management and Prevention, Global Initiative for Asthma (GINA) 2015. Available from http://ginasthma.org/.
- Bochkov YA, Watters K, Ashraf S, et al. Cadherin-related family member 3, a childhood asthma susceptibility gene product, mediates rhinovirus C binding and replication. Proc Natl Acad Sci U S A. 2015;112(17):5485–90.
- 14. Turner S, Francis B, Vijverberg S, et al. Childhood asthma exacerbations and the Arg16 β 2-receptor polymorphism: A meta-analysis stratified by treatment. J Allergy Clin Immunol. 2016.
- 15. Ortega VE, Hawkins GA, Moore WC, et al. Effect of rare variants in ADRB2 on risk of severe exacerbations and symptom control during longacting β agonist treatment in a multiethnic asthma population: a genetic study. Lancet Respir Med. 2014;2(3):204–13.
- Meyers DA, Bleecker ER, Holloway JW, Holgate ST. Asthma genetics and personalised medicine. Lancet Respir Med. 2014;2(5):405–15.
- 17. DeVries A, Vercelli D. Early predictors of asthma and allergy in children: the role of epigenetics. Curr Opin Allergy Clin Immunol. 2015;15(5):435–9.
- Stern DA, Morgan WJ, Halonen M, Wright AL, Martinez FD. Wheezing and bronchial hyper-responsiveness in early childhood as predictors of newly diagnosed asthma in early adulthood: a longitudinal birth-cohort study. Lancet. 2008;372(9643):1058–64.
- Guilbert TW, Morgan WJ, Zeiger RS, et al. Atopic characteristics of children with recurrent wheezing at high risk for the development of childhood asthma. J Allergy Clin Immunol. 2004;114(6):1282–7.
- 20. Voraphani N, Stern DA, Wright AL, Guerra S, Morgan WJ, Martinez FD. Risk of current asthma among adult smokers with respiratory syncytial virus illnesses in early life. Am J Respir Crit Care Med. 2014;190(4):392–8.
- 21. Stein RT, Sherrill D, Morgan WJ, et al. Respiratory syncytial virus in early life and risk of wheeze and allergy by age 13 years. Lancet. 1999;354(9178):541–5.
- Jackson DJ, Gangnon RE, Evans MD, et al. Wheezing rhinovirus illnesses in early life predict asthma development in high-risk children. Am J Respir Crit Care Med. 2008;178(7):667–72.
- Stein RT, Holberg CJ, Sherrill D, et al. Influence of parental smoking on respiratory symptoms during the first decade of life: the Tucson Children's Respiratory Study. Am J Epidemiol. 1999;149(11):1030–7.
- 24. lerodiakonou D, Zanobetti A, Coull BA, et al. Ambient air pollution, lung function, and airway responsiveness in asthmatic children. J Allergy Clin Immunol. 2016;137(2):390–9.
- Jarjour NN, Erzurum SC, Bleecker ER, et al. Severe asthma: lessons learned from the National Heart, Lung, and Blood Institute Severe Asthma Research Program. Am J Respir Crit Care Med. 2012;185(4):356–62.
- Moore WC, Pascual RM. Update in asthma 2009. Am J Respir Crit Care Med. 2010;181(11):1181–7.
- 27. Robinson DS, Campbell DA, Durham SR, Pfeffer J, Barnes PJ, Chung KF. Systematic assessment of difficult-to-treat asthma. Eur Respir J. 2003;22(3):478–83.
- Gamble J, Stevenson M, Heaney LG. A study of a multi-level intervention to improve non-adherence in difficult to control asthma. Respir Med. 2011; 105(9):1308–15.
- Morgan WJ, Crain EF, Gruchalla RS, et al. Results of a home-based environmental intervention among urban children with asthma. N Engl J Med. 2004;351(11): 1068–80.

- Peters AT, Spector S, Hsu J, et al. Diagnosis and management of rhinosinusitis: a practice parameter update. Ann Allergy Asthma Immunol. 2014;113(4):347–85.
- Fokkens WJ, Lund VJ, Mullol J, et al. European Position Paper on Rhinosinusitis and Nasal Polyps 2012. Rhinol Suppl. 2012;23(3):1–298.
 Gerald JK, Carr TE, Wei CY, Holbrook JT, Gerald J B, Albuterol Overuse: A Ma
- Gerald JK, Carr TF, Wei CY, Holbrook JT, Gerald LB. Albuterol Overuse: A Marker of Psychological Distress? J Allergy Clin Immunol Pract. 2015;3(6):957–62.
- Woodruff PG, Boushey HA, Dolganov GM, et al. Genome-wide profiling identifies epithelial cell genes associated with asthma and with treatment response to corticosteroids. Proc Natl Acad Sci U S A. 2007;104(40):15858–63.
- 34. Stempel DA, Szefler SJ, Pedersen S, et al. Safety of Adding Salmeterol to Fluticasone Propionate in Children with Asthma. N Engl J Med. 2016;375(9):840–9.
- Peters SP, Bleecker ER, Canonica GW, et al. Serious Asthma Events with Budesonide plus Formoterol vs. Budesonide Alone. N Engl J Med. 2016; 375(9):850–60.
- Kerstjens HA, Engel M, Dahl R, et al. Tiotropium in asthma poorly controlled with standard combination therapy. N Engl J Med. 2012;367(13):1198–207.
- Peters SP, Kunselman SJ, Icitovic N, et al. Tiotropium bromide step-up therapy for adults with uncontrolled asthma. N Engl J Med. 2010;363(18): 1715–26.
- 38. Normansell R, Walker S, Milan SJ, Walters EH, Nair P. Omalizumab for asthma in adults and children. Cochrane Database Syst Rev. 2014;1:Cd003559.
- Bel EH, Wenzel SE, Thompson PJ, et al. Oral glucocorticoid-sparing effect of mepolizumab in eosinophilic asthma. N Engl J Med. 2014;371(13):1189–97.
- 40. Ortega HG, Liu MC, Pavord ID, et al. Mepolizumab treatment in patients with severe eosinophilic asthma. N Engl J Med. 2014;371(13):1198–207.
- Wenzel S, Castro M, Corren J, et al. Dupilumab efficacy and safety in adults with uncontrolled persistent asthma despite use of medium-to-high-dose inhaled corticosteroids plus a long-acting beta2 agonist: a randomised double-blind placebo-controlled pivotal phase 2b dose-ranging trial. Lancet. 2016;388(10039):31–44.
- 42. Bleecker ER, FitzGerald JM, Chanez P, et al. Efficacy and safety of benralizumab for patients with severe asthma uncontrolled with highdosage inhaled corticosteroids and long-acting beta2-agonists (SIROCCO): a randomised, multicentre, placebo-controlled phase 3 trial. Lancet. 2016.
- O'Byrne PM, Metev H, Puu M, et al. Efficacy and safety of a CXCR2 antagonist, AZD5069, in patients with uncontrolled persistent asthma: a randomised, double-blind, placebo-controlled trial. Lancet Respir Med. 2016; 4(10):797–806.
- Bourdin A, Molinari N, Vachier I, et al. Prognostic value of cluster analysis of severe asthma phenotypes. J Allergy Clin Immunol. 2014;134(5):1043–50.
- Denlinger LC, Phillips BR, Ramratnam S, et al. Inflammatory and Co-Morbid Features of Patients with Severe Asthma and Frequent Exacerbations. Am J Respir Crit Care Med. 2016.
- Hekking PP, Wener RR, Amelink M, Zwinderman AH, Bouvy ML, Bel EH. The prevalence of severe refractory asthma. J Allergy Clin Immunol. 2014;35: 896–902.
- Moore WC, Bleecker ER, Curran-Everett D, et al. Characterization of the severe asthma phenotype by the National Heart, Lung, and Blood Institute's Severe Asthma Research Program. J Allergy Clin Immunol. 2007;119(2):405–13.
- Wenzel SE, Schwartz LB, Langmack EL, et al. Evidence that severe asthma can be divided pathologically into two inflammatory subtypes with distinct physiologic and clinical characteristics. Am J Respir Crit Care Med. 1999;160(3):1001–8.
- Riley CM, Wenzel SE, Castro M, et al. Clinical Implications of Having Reduced Mid Forced Expiratory Flow Rates (FEF25-75), Independently of FEV1, in Adult Patients with Asthma. PLoS ONE. 2015;10(12), e0145476.
- Zein JG, Dweik RA, Comhair SA, et al. Asthma Is More Severe in Older Adults. PLoS ONE. 2015;10(7), e0133490.
- Balzar S, Fajt ML, Comhair SA, et al. Mast cell phenotype, location, and activation in severe asthma. Data from the Severe Asthma Research Program. Am J Respir Crit Care Med. 2011;183(3):299–309.
- Hastie AT, Moore WC, Meyers DA, et al. Analyses of asthma severity phenotypes and inflammatory proteins in subjects stratified by sputum granulocytes. J Allergy Clin Immunol. 2010;125(5):1028–1036.e1013.
- Brasier AR, Victor S, Ju H, et al. Predicting intermediate phenotypes in asthma using bronchoalveolar lavage-derived cytokines. Clin Transl Sci. 2010;3(4):147–57.
- Fitzpatrick AM, Higgins M, Holguin F, Brown LA, Teague WG. The molecular phenotype of severe asthma in children. J Allergy Clin Immunol. 2010; 125(4):851–857.e818.

- Modena BD, Tedrow JR, Milosevic J, et al. Gene expression in relation to exhaled nitric oxide identifies novel asthma phenotypes with unique biomolecular pathways. Am J Respir Crit Care Med. 2014;190(12):1363–72.
- Moore WC, Meyers DA, Wenzel SE, et al. Identification of asthma phenotypes using cluster analysis in the Severe Asthma Research Program. Am J Respir Crit Care Med. 2010;181(4):315–23.
- 57. Moore WC, Fitzpatrick AM, Li X, et al. Clinical heterogeneity in the severe asthma research program. Ann Am Thorac Soc. 2013;10(Suppl):S118–24.
- Haldar P, Pavord ID, Shaw DE, et al. Cluster analysis and clinical asthma phenotypes. Am J Respir Crit Care Med. 2008;178(3):218–24.
- Kuhlen Jr JL, Wahlquist AE, Nietert PJ, Bains SN. Identification of asthma phenotypes in a tertiary care medical center. Am J Med Sci. 2014;348(6):480–5.
- 60. Patrawalla P, Kazeros A, Rogers L, et al. Application of the asthma phenotype algorithm from the Severe Asthma Research Program to an urban population. PLoS ONE. 2012;7(9), e44540.
- Fitzpatrick AM, Teague WG, Meyers DA, et al. Heterogeneity of severe asthma in childhood: confirmation by cluster analysis of children in the National Institutes of Health/National Heart, Lung, and Blood Institute Severe Asthma Research Program. J Allergy Clin Immunol. 2011;127(2):382–389.e381-313.
- Just J, Gouvis-Echraghi R, Rouve S, Wanin S, Moreau D, Annesi-Maesano I. Two novel, severe asthma phenotypes identified during childhood using a clustering approach. Eur Respir J. 2012;40(1):55–60.
- 63. Cowan DC, Taylor DR, Peterson LE, et al. Biomarker-based asthma phenotypes of corticosteroid response. J Allergy Clin Immunol. 2014.
- Jatakanon A, Uasuf C, Maziak W, Lim S, Chung KF, Barnes PJ. Neutrophilic inflammation in severe persistent asthma. Am J Respir Crit Care Med. 1999; 160(5 Pt 1):1532–9.
- Moore WC, Hastie AT, Li X, et al. Sputum neutrophil counts are associated with more severe asthma phenotypes using cluster analysis. J Allergy Clin Immunol. 2014;133(6):1557–1563.e1555.
- Henderson J, Granell R, Heron J, et al. Associations of wheezing phenotypes in the first 6 years of life with atopy, lung function and airway responsiveness in mid-childhood. Thorax. 2008;63(11):974–80.
- Brunekreef B, Smit J, De Jongste J, et al. The prevention and incidence of asthma and mite allergy (PIAMA) birth cohort study: design and first results. Pediatr Allergy Immunol. 2002;13 Suppl 15:55–60.
- Savenije OE, Granell R, Caudri D, et al. Comparison of childhood wheezing phenotypes in 2 birth cohorts: ALSPAC and PIAMA. J Allergy Clin Immunol. 2011;127(6):1505–1512.e1514.
- Smith JA, Drake R, Simpson A, Woodcock A, Pickles A, Custovic A. Dimensions of respiratory symptoms in preschool children: populationbased birth cohort study. Am J Respir Crit Care Med. 2008;177(12):1358–63.
- Belgrave DC, Simpson A, Semic-Jusufagic A, et al. Joint modeling of parentally reported and physician-confirmed wheeze identifies children with persistent troublesome wheezing. J Allergy Clin Immunol. 2013;132(3):575–583.e512.
- Spycher BD, Silverman M, Brooke AM, Minder CE, Kuehni CE. Distinguishing phenotypes of childhood wheeze and cough using latent class analysis. Eur Respir J. 2008;31(5):974–81.
- Spycher BD, Silverman M, Pescatore AM, Beardsmore CS, Kuehni CE. Comparison of phenotypes of childhood wheeze and cough in 2 independent cohorts. J Allergy Clin Immunol. 2013;132(5):1058–67.

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