

Realizing Personalized Medicine in Asthmatic Children Requires Large-Scale Collaboration

Susanne JH Vijverberg^{1*}, Steve W Turner², Colin NA Palmer³, Kelan G Tantisira⁴ and Anke Hilse Maitland-van der Zee¹

¹Division of Pharmacoepidemiology & Clinical Pharmacology, Utrecht University, Netherlands

²Department of Child Health, University of Aberdeen, UK

³Population Pharmacogenetics Group, University of Dundee, UK

⁴Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, USA

*Corresponding author: Anke Hilse Maitland van der Zee, Division of Pharmacoepidemiology & Clinical Pharmacology, Utrecht Institute for Pharmaceutical Sciences (UIPS), Faculty of Science, Utrecht University, Utrecht, Netherlands, Tel: 31 62 273 6715; Fax: 31 30 253 9166; E-mail: a.h.maitland@uu.nl

Rec date: Mar 20, 2015, Acc date: Mar 25, 2015, Pub date: Mar 27, 2015

Copyright: © 2015 Vijverberg SJ, et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Editorial

Although asthma treatment is effective in many children, there is large variability in the response as evidenced by improved symptom control, reduced exacerbations and lung function improvement. A study by the National Heart, Lung, and Blood Institute's Childhood Asthma Research and Education Network detailed the responses of 144 children with mild-to-moderate asthma to 8-weeks of treatment with inhaled corticosteroids (ICS) in a randomized cross-over design [1,2]. A large variation in lung function improvement from baseline was found [1]. Change in asthma-controlled days showed a similarly wide distribution, varying between an increase of seven asthma-controlled days per week to a decrease of four asthma-controlled days per week [2]. One mechanism for heterogeneity in treatment response seems likely to be due to genetic variations within the asthma population [3]. These genetic variants may be due to either innate differences in underlying disease subtype all manifesting clinically as asthma or to pharmacokinetic or pharmacodynamics influences on drug level or target. Candidate gene approaches and, to a lesser extent, whole-genome association studies have identified several genetic loci associated with poor treatment response or severe asthma, including FCER2 (coding for a low-affinity immunoglobulin E (IgE) receptor, also known as CD23) [4,5], the 17q21 locus [6-8], and GLCCI1 (encoding glucocorticoid-induced transcript 1 protein) [9]. This might have implications for the treatment of asthma and suggests that we should move to a personalized (or stratified) approach guided by both clinical and genetic cues (i.e. pharmacogenetics) to benefit children with asthma. The benefits would be in terms of improvement of both drug efficacy and also drug safety of existing drugs. The potential of pharmacogenomics for optimizing treatment in childhood asthma is reflected in the results of the recent small randomized clinical trial by Lipworth and colleagues [10]. The study showed that asthmatic children homozygous for the variant genotype of ADRB2 seem to benefit more from a leukotriene antagonist (LTRA) than from a long-acting beta (2)-agonist (LABA) as add on treatment to ICS.

Need of Large Meta-Analyses

Based on the inter-individual heterogeneity combined with intra-individual repeatability of asthma treatment responses, it was estimated that 60-80% of the observed variance in treatment responses might be due to genetic differences [3,11]. Current identified genetic variants comprise only a small portion of the estimated heritability of asthma treatment responses. This could mean that the current applied methods of studying genomic variations are inefficient (i.e. studies are

underpowered, searching methods are inadequate). Large scale meta-analyses can provide more insight on the current state of evidence for certain markers, but require collaboration. In addition, single biomarker approaches to phenotype asthma are increasingly regarded to be inaccurate and outdated. There is a need for large scale studies which combine multiple known biomarkers (genetic, but also non-genetic) in an integrated systems medicine approach to develop treatment algorithms [12].

Children are Not Small Adults

Most pharmacogenomics studies have focused on adults. We do have to realize that the biological factors influencing treatment response in children might differ from adults. It has been shown that inflammatory phenotypes differ between asthmatic children and adults [13]. These patterns may influence response to anti-inflammatory treatment. Furthermore, clinical trials in asthmatic adults could not demonstrate a modifying effect of ADRB2 Arg16 genotype on LABA treatment outcome [14,15], suggesting that the effect of ADRB2 might be restricted to LABA response in childhood-onset disease [16,17]. In addition, a recent GWAS analysis identified a SNP influencing FBXL7 expression to be associated with improvement in asthma symptoms in response to ICS [18]. This association was found in two independent pediatric asthma cohorts, but failed to be replicated in an adult asthmatic population. A large scale meta-analysis for the genetic markers identified in studies with asthmatic children is currently lacking.

Consensus on Outcome Definitions

The definition of response also needs to be taken into account. Poor response to treatment can be defined by various measurements, such as lack of improvement of lung function upon treatment, persistent airway hyperresponsiveness despite treatment, uncontrolled symptoms, or severe exacerbations despite treatment. The definition of response seems to influence the genetic profiles underlying that response phenotype [19]. Exacerbation-prone asthma is a different asthma phenotype compared to poorly controlled asthma [20], and children with limited symptoms can be prone to severe exacerbations [19]. Pharmacogenomics analyses should take into account different outcome phenotypes and consensus needs to be reached on uniform definition of response. Primary outcomes need to be patient focused (e.g. symptoms, exacerbations, quality of life), secondary outcomes can include health economic outcomes and physiological measures.

PiCA Consortium

In order to bring the field of personalized medicine in asthma further the Pharmacogenomics in Childhood Asthma (PiCA) consortium was initiated in 2014. This newly founded consortium has already brought together 20 studies (birth cohorts, asthma cohorts and clinical trials) with in total almost 15.000 asthmatic children. PiCA studies have genetic, medication exposure and treatment outcome data available (cross-sectional or longitudinally), or can obtain these data in asthmatic children in a short time-frame. The consortium covers the whole broad spectrum of asthmatics (from mild to severe) and aims to represent the global pediatric asthma population. First PiCA meta-analyses are in the startup phase and the active PiCA network welcomes new collaborators. If we want a future in which personalized medicine is part of clinical practice in childhood asthma, we need to collaborate.

References

1. Szeffler SJ, Phillips BR, Martinez FD, Chinchilli VM, Lemanske RF, et al. (2005) Characterization of within-subject responses to fluticasone and montelukast in childhood asthma. *J Allergy Clin Immunol* 115: 233-242.
2. Zeiger RS, Szeffler SJ, Phillips BR, Schatz M, Martinez FD, et al. (2006) Response profiles to fluticasone and montelukast in mild-to-moderate persistent childhood asthma. *J Allergy Clin Immunol* 117: 45-52.
3. Drazen JM, Silverman EK, Lee TH (2000) Heterogeneity of therapeutic responses in asthma. *Br Med Bull* 56: 1054-1070.
4. Tantisira KG, Silverman ES, Mariani TJ, Xu J, Richter BG, et al. (2007) FCER2: a pharmacogenetic basis for severe exacerbations in children with asthma. *J Allergy Clin Immunol* 120: 1285-1291.
5. Koster ES, Maitland-van der Zee AH, Tavendale R, Mukhopadhyay S, Vijverberg SJ, et al. (2011) FCER2 T2206C variant associated with chronic symptoms and exacerbations in steroid-treated asthmatic children. *Allergy* 66: 1546-1552.
6. Halapi E, Gudbjartsson DF, Jonsdottir GM, Bjornsdottir US, Thorleifsson G, et al. (2010) A sequence variant on 17q21 is associated with age at onset and severity of asthma. *Eur J Hum Genet* 18: 902-908.
7. Bisgaard H, Bønnelykke K, Sleiman PM, Brasholt M, Chawes B, et al. (2009) Chromosome 17q21 gene variants are associated with asthma and exacerbations but not atopy in early childhood. *Am J Respir Crit Care Med* 179: 179-185.
8. Tavendale R, Macgregor DF, Mukhopadhyay S, Palmer CN (2008) A polymorphism controlling ORMDL3 expression is associated with asthma that is poorly controlled by current medications. *J Allergy Clin Immunol* 121: 860-863.
9. Tantisira KG, Lasky-Su J, Harada M, Murphy A, Litonjua AA, et al. (2011) Genomewide association between GLCCI1 and response to glucocorticoid therapy in asthma. *N Engl J Med* 365: 1173-1183.
10. Lipworth BJ, Basu K, Donald HP, Tavendale R, Macgregor DF, et al. (2013) Tailored second-line therapy in asthmatic children with the Arg(16) genotype. *Clin Sci (Lond)* 124: 521-528.
11. Tantisira KG, Lake S, Silverman ES, Palmer LJ, Lazarus R, et al. (2004) Corticosteroid pharmacogenetics: association of sequence variants in CRHR1 with improved lung function in asthmatics treated with inhaled corticosteroids. *Hum Mol Genet* 13: 1353-1359.
12. Vijverberg SJ, Hilvering B, Raaijmakers JA, Lammers JW, Maitland-van der Zee AH, et al. (2013) Clinical utility of asthma biomarkers: from bench to bedside. *Biologics* 7: 199-210.
13. Wang F, He XY, Baines KJ, Gunawardhana LP, Simpson JL, et al. (2011) Different inflammatory phenotypes in adults and children with acute asthma. *Eur Respir J* 38: 567-574.
14. Bleecker ER, Postma DS, Lawrance RM, Meyers DA, Ambrose HJ, et al. (2007) Effect of ADRB2 polymorphisms on response to longacting beta2-agonist therapy: a pharmacogenetic analysis of two randomised studies. *Lancet* 370: 2118-2125.
15. Wechsler ME, Kunselman SJ, Chinchilli VM, Bleecker E, Boushey HA, et al. (2009) Effect of β 2-adrenergic receptor polymorphism on response to longacting β 2 agonist in asthma (LARGE trial): a genotype-stratified, randomised, placebo-controlled, crossover trial. *Lancet* 374: 1754-1764.
16. Palmer CN, Lipworth BJ, Lee S, Ismail T, Macgregor DF, et al. (2006) Arginine-16 beta2 adrenoceptor genotype predisposes to exacerbations in young asthmatics taking regular salmeterol. *Thorax* 61: 940-944.
17. Zuurhout MJ, Vijverberg SJ, Raaijmakers JA, Koenderman L, Postma DS, et al. (2013) Arg16 ADRB2 genotype increases the risk of asthma exacerbation in children with a reported use of long-acting β 2-agonists: results of the PACMAN cohort. *Pharmacogenomics* 14: 1965-1971.
18. Park HW, Dahlin A, Tse S, Duan QL, Schuemann B, et al. (2014) Genetic predictors associated with improvement of asthma symptoms in response to inhaled corticosteroids. *J Allergy Clin Immunol* 133: 664-669.
19. Wu AC, Tantisira K, Li L, Schuemann B, Weiss ST, et al. (2011) Predictors of symptoms are different from predictors of severe exacerbations from asthma in children. *Chest* 140: 100-107.
20. Carroll CL, Schramm CM, Zucker AR (2008) Severe exacerbations in children with mild asthma: characterizing a pediatric phenotype. *J Asthma* 45: 513-517.