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HSD3B1 genotype identifies glucocorticoid responsiveness in severe asthma


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Asthma resistance to glucocorticoid treatment is a major health problem with unclear etiology. Glucocorticoids inhibit adrenal androgen production. However, androgens have potential benefits in asthma. HSD3B1 encodes for 3α-hydroxysteroid dehydrogenase-1 (3α-HSD1), which catalyzes peripheral conversion from adrenal dehydroepiandrosterone (DHEA) to potent androgens and has a germ-line missense-encoding polymorphism. The adrenal restrictive HSD3B1(1245A) allele limits conversion, whereas the adrenal permissive HSD3B1(1245C) allele increases DHEA metabolism to potent androgens. In the Severe Asthma Research Program (SARP) III cohort, we determined the association between DHEA-sulfate and percentage predicted forced expiratory volume in 1 s (FEV1-PP) for homozygous adrenal restrictive genotype and adrenal permissive genotype, it is 66.7 vs. 67.7 (P = 0.92).

Since their discovery and introduction into clinical medicine about 70 y ago, glucocorticoids (GCs) have been recognized as eliciting a systemic anti-inflammatory response, and currently play a major role in the treatment of severe asthma and other inflammatory disease processes (1). However, unresponsiveness to GC treatment is a major barrier to treatment of inflammatory disease processes, and the underlying mechanisms of this clinical entity have yet to be clearly elucidated (2). Management of GC-unresponsive disease represents a significant challenge for the treatment of asthma. Indeed, severe asthma is generally defined as asthma that remains symptomatic despite high-dose inhaled GC and/or systemic GC therapy (3).

Suppression of endogenous adrenal androgens and cortisol is a known consequence of systemic GC treatment. Substantial evidence suggests that stimulation of the androgen receptor (AR) expressed in the lung could be beneficial in asthma. Androgens inhibit human airway smooth muscle and fibroblast proliferation (4–6), promote airway smooth muscle relaxation (7), and inhibit both Th2 and Th1 inflammation in animal models of asthma (8, 9). Androgens are associated with better lung function in large healthy cohorts (10, 11) and in asthma (12). Increasing circulating androgens | glucocorticoids | inflammation | androgens | HSD3B1

Significance

Although resistance to glucocorticoids is a major clinical problem, the underlying mechanisms are unknown. It is known that glucocorticoid use can suppress adrenal androgen production. In population studies, animal models, and cell culture experiments, androgens are associated with several benefits in asthma, but neither androgen use in glucocorticoid-resistant asthma nor the genetic determinants of androgen responsiveness have been studied in humans. A missense-encoding variant in HSD3B1 is known to regulate conversion from adrenal precursors to potent androgens and clinical outcomes in prostate cancer. This is the first genetic evidence to our knowledge that implicates an androgen synthesis variant in resistance to glucocorticoids for asthma or any other inflammatory disease. Furthermore, this study demonstrates an adverse consequence of adrenal androgen suppression with glucocorticoid therapy.


Competing interest statement: Cleveland Clinic has applied for patents on HSD3B1. This article is a PNAS Direct Submission. This open access article is distributed under Creative Commons Attribution-NonCommercial-NoDerivatives License 4.0 (CC BY-NC-ND).

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levels of adrenal and gonadal androgens in males and females during adolescence are associated with improving asthma during adolescence (12). However, the role of GC-induced androgen suppression in the pathophysiology of severe, GC-resistant human asthma is not established.

The androgen dehydroepiandrosterone (DHEA) and its sulfate (DHEA-S) are secreted from the adrenal glands (13, 14), and together are the most abundant steroid in circulation. However, its function is not known. DHEA-S may have an immunomodulatory effect, but clinical results have been inconsistent, possibly because variations in DHEA-S metabolism are generally not taken into account (15). In peripheral tissues, DHEA is metabolized by the enzyme 3β-hydroxysteroid dehydrogenase-1 (3β-HSD1; encoded by HSD3B1) to potent downstream androgens (e.g., testosterone and dihydrotestosterone). A common missense-encoding variant in HSD3B1, rs1047303 (c.1245C > A, p.T367N), regulates biochemical function and clinical phenotypes. The HSD3B1 (1245A) allele encodes for an adrenal permissive enzyme that limits conversion from DHEA to downstream androgens, whereas the HSD3B1 (1245C) allele encodes for an adrenal permissive enzyme that results in increased metabolic flux from DHEA to more potent androgens (16). Multiple studies from the United States, Japan, and Spain, now further confirmed in a phase 3 clinical trial, clearly show that men with advanced prostate cancer treated with castration who inherit the adrenal permissive 3β-HSD1 enzyme, which confers more rapid conversion from DHEA to androgens, have more rapid onset of androgen-driven disease progression (17–22). These studies establish that clear clinical phenotypes are associated with HSD3B1 genotypes that biochemically confer fast and slow metabolic flux to potent androgens. We hypothesized that the restrictive HSD3B1 genotype that disables DHEA-S conversion to potent androgens impairs FEV1 PP specifically when GC treatment suppresses adrenal DHEA-S production, limiting substrate availability for 3β-HSD1 and possibly providing a mechanistic explanation for GC-resistant severe asthma in patients with this genotype.

Severe Asthma Research Program (SARP) is a comprehensive network supported by the National Institutes of Health/National Heart, Lung, and Blood Institute that aimed to characterize and understand the pathobiology of severe asthma. Here, we determined FEV1 PP in the SARP III cohort for patients with asthma treated with (GC) and without (noGC) daily GCs (i.e., systemic). The remaining 40% of patients with asthma were adults (aged > 35 y of age), or < 5 pack-years if < 30 y of age) and were required to have evidence of bronchial hyperresponsiveness (defined as a PC20 methacholine value < 16 mg/mL or reversible airflow obstruction, as evidenced by an increase in FEV1 of 12% or greater after albuterol inhalation, ipratropium bromide inhalation, or both. Spirometry was performed according to the American Thoracic Society/European Respiratory Society guidelines (23, 24). The 2012 Global Lung Initiative standard reference equations were used to predict spirometric reference values (25). DHEA-S levels were analyzed at the University of Virginia Center for Research in Reproduction Lindag Core Laboratory, using the Siemens Immulite 2000 immunoassay system, which has a lower limit of detection for DHEA-S of 15 μg/dL. Information on SARP III network, protocol, and characterization procedures have been published previously (26–28). All participants provided written informed consent. The institutional review board at each center approved the study. The study is listed on ClinicalTrials.gov.

To replicate primary findings, 184 Caucasian participants (from a total of 263 of all races) with severe asthma were selected from the SARP I&II cohorts. Similarly, SARP I&II is a National Institutes of Health/National Heart, Lung, and Blood Institute-sponsored multicenter study that recruited patients with asthma between 2001 and 2012 from 9 sites in the United States and 1 in the United Kingdom. However, as compared with SARP III, patients with asthma enrolled in SARP I&II were less likely to have severe asthma (40% vs. 60%) (28–30). In contrast to SARP III, severe asthma was defined in SARP I&II according to the initial ATS workshop definition of severe asthma (31).

### Statistical Analysis.
Whole-genome sequence of 1,888 patients enrolled in SARP I, II, and III was released by the Trans-Omics for Precision Medicine (TOPMed) program (https://www.nhlbiwgs.org/) in its genotype call sets freeze 6a version. Whole-genome sequence with a read depth of 38x was performed on blood DNA, using Illumina HiSeq X technology. The TOPMed freeze 6a genotype call set includes 107,047 samples and 642M high-quality variants genomewide, > 7.5M coding variants, and > 350,000 loss-of-function variants. Genotype calling and quality control were performed by the AmTryne quality control algorithm. Genotype data were released by the Informatics Research Center, led by the University of Michigan.

Genotypes for variant rs1047303 (position chr1:119514623 [build GRCh38.p12]) in SARP I, II, and III were extracted with PLINK2 (32, 33) (https://www.cog-genomics.org/plink2). HSD3B1 genotypes were directly confirmed in 28 patients, using a method previously validated with 100% match (17).

Student’s t test was used for 2 group comparisons of continuous normally distributed variables. The means of the 3 different genotype groups were compared using the ANOVA test. Pairwise comparisons were performed using the Tukey–Kramer Honest Significant Differences (HSD) test. Otherwise, Wilcoxon’s rank sum test or Kruskal–Wallis one-way ANOVA were used when normality assumptions were not met. Categorical variables were compared using a χ2 test. We assumed an additive model of inheritance, in which minor or major variables were an additive effect for the rs1047303 genotype (coded as the number of C alleles). Interaction terms were included between rs1047303 genetic variants and daily oral GC as the dependent variables of the prebronchodilator FEV1, PP (pre-FEV1, PP) post-FEV1, PP. Models were fit under the assumption of a normal distribution for FEV1, PP. All statistical analyses were conducted using R, version 3.5.3 (R Project for Statistical Computing, Vienna, Austria). A P value < 0.05 was considered statistically significant because only one position was tested.

### Data Availability.
**Baseline DHEA-S and FEV\textsubscript{PP}.** FEV\textsubscript{PP} was weakly associated with serum DHEA-S in both men and women. In the SARP III cohort, the \(R^2\) (proportion of FEV\textsubscript{PP} variability explained by DHEA-S) was 0.04 for all races (\(n = 314; \ P < 0.001\)) and 0.04 (\(n = 203; \ P < 0.001\)) for Caucasians. Similarly, for severe asthma in SARP I&II, the \(R^2\) was 0.13 (\(n = 271; \ P < 0.001\)) for all races and 0.20 (\(n = 178; \ P < 0.001\)) in Caucasians (Fig. 1 and SI Appendix, Table S1). This association appears to be driven by patients with low DHEA-S (i.e., first quartile; SI Appendix, Fig. S1). Strikingly, no women and very few men with DHEA-S levels over 200 \(\mu\text{g/dL}\) in either cohort had a baseline FEV\textsubscript{PP} of less than 75% in SARP III.

**DHEA-S Suppression Is Associated with Oral GC Use.** Daily oral GC therapy was commonly used in SARP III with median dose and duration that did not differ among the 3 \(HSD3B1\) genotypes. The median duration was 12 mo for each of the 3 genotypes (\(P = 0.18\) by Kruskal–Wallis test), and the median dose was 10 mg prednisone (\(P = 0.74\) by Kruskal–Wallis test). Overall, 22.6% (29% of Caucasians) of adults with severe asthma enrolled in SARP III were treated with daily oral GC therapy (26) (SI Appendix, Table S2). Endogenous circulating cortisol declined significantly (\(P < 0.001\)) in patients receiving oral GCs, confirming both patient compliance and adrenal suppression (SI Appendix, Fig. S2).

As expected, our analysis of DHEA-S from 314 adult participants with asthma enrolled in SARP III showed significantly lower plasma DHEA-S levels in patients treated with daily oral GC therapy, as opposed to those not receiving daily oral GCs for both men and women. Not surprisingly, DHEA-S decline occurs more rapidly in men and women (Fig. 1B), irrespective of \(HSD3B1(1245)\) genotype (SI Appendix, Fig. S3), and there is no association between genotype and circulating testosterone (SI Appendix, Fig. S4). Overall, daily GC therapy was associated with a 70% decrease in DHEA-S compared with no GC use in SARP III and SARPII (\(P < 0.001\)) (SI Appendix, Table S3). Circulating DHEA also decreased by about 70% with GC therapy (SI Appendix, Fig. S5).

**\(HSD3B1(1245)\) Genotype and GC Resistance.** To test our hypothesis that the \(HSD3B1(1245A)\) adrenal restrictive allele is specifically associated with impaired lung function with GC treatment-mediated adrenal suppression, lung function was compared in 318 GC and noGC Caucasian patients enrolled in SARP III for whom \(HSD3B1(1245)\) genotype data were available. Statistical comparisons of GC and noGC FEV\textsubscript{PP} by \(HSD3B1(1245)\) genotype, before and after bronchodilation (BD), are summarized.

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**Table 1. Baseline characteristics comparing the 2 SARP cohorts, SARP III vs. SARP I&II, stratified by \(HSD3B1(1245)\) genotypes*\**

<table>
<thead>
<tr>
<th></th>
<th>AA</th>
<th>AC</th>
<th>CC</th>
<th>P value</th>
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<tbody>
<tr>
<td>SARP III</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N</td>
<td>146</td>
<td>131</td>
<td>41</td>
<td></td>
</tr>
<tr>
<td>Age, y</td>
<td>49.5 ± 14.5</td>
<td>48.7 ± 13.8</td>
<td>47.8 ± 14.2</td>
<td>0.762</td>
</tr>
<tr>
<td>Female sex, n (%)</td>
<td>92 (63.0)</td>
<td>80 (61.1)</td>
<td>31 (75.6)</td>
<td>0.230</td>
</tr>
<tr>
<td>BMI</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td></td>
<td>30.2 ± 6.2</td>
<td>31.8 ± 8.6</td>
<td>33.4 ± 9.8</td>
<td>0.038</td>
</tr>
<tr>
<td>Daily oral GC therapy, n (%)</td>
<td>23 (15.8)</td>
<td>24 (18.3)</td>
<td>8 (19.5)</td>
<td>0.787</td>
</tr>
<tr>
<td>Severe asthma, n (%)(^\dagger)</td>
<td>82 (56.2)</td>
<td>77 (58.8)</td>
<td>20 (48.8)</td>
<td>0.530</td>
</tr>
<tr>
<td>FEV1/FVC ratio</td>
<td>0.84 ± 0.12</td>
<td>0.84 ± 0.12</td>
<td>0.90 ± 0.10</td>
<td>0.011</td>
</tr>
<tr>
<td>Pre-FEV1, % of predicted value</td>
<td>71.8 ± 19.3</td>
<td>72.6 ± 21.8</td>
<td>77.9 ± 16.3</td>
<td>0.224</td>
</tr>
<tr>
<td>Post-FEV1, % of predicted value</td>
<td>80.8 ± 20.2</td>
<td>80.3 ± 20.8</td>
<td>88.0 ± 16.5</td>
<td>0.083</td>
</tr>
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</table>

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<th>AC</th>
<th>CC</th>
<th>P value</th>
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<td>SARP I&amp;II</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N</td>
<td>80</td>
<td>79</td>
<td>25</td>
<td></td>
</tr>
<tr>
<td>Age, y</td>
<td>43.3 ± 11.2</td>
<td>46.3 ± 13.6</td>
<td>42.7 ± 13.7</td>
<td>0.26</td>
</tr>
<tr>
<td>Female sex, n (%)</td>
<td>46 (57.5)</td>
<td>47 (59.5)</td>
<td>20 (80.0)</td>
<td>0.11</td>
</tr>
<tr>
<td>BMI</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>30.3 ± 7.2</td>
<td>30.5 ± 7.5</td>
<td>29.9 ± 6.9</td>
<td>0.93</td>
</tr>
<tr>
<td>Daily oral GC therapy, n (%)</td>
<td>35 (43.8)</td>
<td>30 (38.0)</td>
<td>10 (40.0)</td>
<td>0.76</td>
</tr>
<tr>
<td>Severe asthma, n (%)(^\dagger)</td>
<td>80 (100)</td>
<td>79 (100)</td>
<td>25 (100)</td>
<td></td>
</tr>
<tr>
<td>Pre-FEV1, % of predicted value</td>
<td>57.4 ± 19.2</td>
<td>61.1 ± 21.6</td>
<td>67.3 ± 23.7</td>
<td>0.09</td>
</tr>
<tr>
<td>Post-FEV1, % of predicted value</td>
<td>73.5 ± 19.2</td>
<td>76.3 ± 20.7</td>
<td>79.3 ± 24.8</td>
<td>0.43</td>
</tr>
</tbody>
</table>

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*GC, daily oral glucocorticoid therapy; FVC, forced vital capacity; Post-, postbronchodilator; Pre-, prebronchodilator.

\(^\ast\)Plus–minus values are means ± SD.

\(^\dagger\)The BMI is the weight in kilograms divided by the square of the height in meters.

* Analyzed SARP I&II cohort includes patients with severe asthma.

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**Fig. 1.** DHEA-S concentration is associated with FEV\textsubscript{PP} and suppressed with daily systemic GC use. (A) In subjects with asthma, FEV\textsubscript{PP} correlates significantly with DHEA-S levels in both Caucasian men (blue circles; \(R^2 = 0.15; \ P < 0.001\)) and women (open red circles; \(R^2 = 0.03; \ P = 0.047\)). (B) Chronic daily GC use is associated with DHEA-S suppression in SARP III in men and women.
The mechanisms by which androgens can benefit asthma have been described in detail in animal models. In particular, androgens directly inhibit airway inflammation (4, 8, 9, 15), airway smooth muscle, and fibroblast proliferation (4–7). Consistent with these data, we have recently shown that DHEA therapy improves lung function in low-DHEA-S women (34). Moreover, our additional analysis shows that all women in our study whose serum DHEA-S increased by more than 300 μg/dL had an increase in FEV1 (n = 8) compared with those who had less of an increase in DHEA-S (P = 0.018 by Fisher’s exact test). Furthermore, the plausibility of DHEA/DHEA-S benefit in asthma is further supported by 3β-HSD1 expression in the human lung (SI Appendix, Fig. S10). A model that summarizes the effect of the association between HSD3B1(1245) genotype, DHEA-S suppression with GC treatment and FEV1PP is shown in Fig. 3.

Discussion

Severe asthma is defined as asthma that remains symptomatic and exacerbation-prone despite controlled high-dose inhaled ICS or systemic steroid treatment in conjunction with a second controller medication (3). Causes underlying severe asthma are heterogeneous (28, 30, 35, 36), and many patients are refractory, even to recently developed biological therapies (36). An aspect of severe asthma that is not commonly considered is that systemic GC therapy increases risk for low circulating levels of androgens, particularly DHEA-S (37).

Our study supports a model in which HSD3B1(1245) genotypes that confer less active conversion from adrenal precursors to potent androgens in peripheral tissues leads to a physiologic state of relative androgen deficiency that occurs specifically with DHEA-S suppression that is a consequence of systemic GC treatment. Strikingly, an HSD3B1(1245) allele-dose dependent effect appears to be clear and occurs for pre-BD-FEV1PP and post-BD-FEV1PP in both SARP III and SARP I&II.

In general, androgens require the AR to mediate much of their physiologic effects. Potent AR stimulation from adrenal DHEA/DHEA-S, which is available in circulation, requires enzymatic conversion by 3β-HSD1 to testosterone and dihydrotestosterone, which occurs in peripheral tissues. Given the variety of tissues in which AR is expressed, the association observed in our study may be attributable to androgen stimulation in several different cell types. Androgens have many effects that could be beneficial for the asthmatic airway. For example, DHEA-S inhibits human airway smooth muscle and fibroblast proliferation and may benefit airway epithelial to mesenchymal transition (4–6). Both DHEA-S

Table 2. Comparison of maximum post-BD-FEV1% between patients treated with and without daily oral GCs among the HSD3B1(1245) AA, AC, and CC genotypes*

<table>
<thead>
<tr>
<th>HSD3B1(1245) Genotype</th>
<th>SARP III</th>
<th>SARP I &amp; II</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Not on GC</td>
<td>On GC</td>
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<tr>
<td>AA</td>
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<td></td>
</tr>
<tr>
<td>n</td>
<td>123</td>
<td>23</td>
</tr>
<tr>
<td>Pre-FEV1, % of predicted value</td>
<td>75.1 ± 18.3</td>
<td>54.3 ± 15.3</td>
</tr>
<tr>
<td>Post-FEV1, % of predicted value</td>
<td>83.9 ± 18.8</td>
<td>64.2 ± 19.6</td>
</tr>
<tr>
<td>AC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>n</td>
<td>107</td>
<td>24</td>
</tr>
<tr>
<td>Pre-FEV1, % of predicted value</td>
<td>75.6 ± 21.2</td>
<td>59.4 ± 19.8</td>
</tr>
<tr>
<td>Post-FEV1, % of predicted value</td>
<td>83.2 ± 20.5</td>
<td>67.7 ± 17.9</td>
</tr>
<tr>
<td>CC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>n</td>
<td>33</td>
<td>8</td>
</tr>
<tr>
<td>Pre-FEV1, % of predicted value</td>
<td>78.9 ± 16.3</td>
<td>73.4 ± 16.6</td>
</tr>
<tr>
<td>Post-FEV1, % of predicted value</td>
<td>89.2 ± 17.0</td>
<td>83.1 ± 14.4</td>
</tr>
</tbody>
</table>

*Data are presented as mean ± SD for continuous variables and proportions or percentages for categorical variables.

1P value comparing daily oral GC vs. no GC in each genotype group AA, AC, and CC.
and testosterone promote airway smooth muscle relaxation (7). Testosterone is associated with decreased Th2 and Th1 inflammation in animal models of asthma (8, 9). Epidemiologically, androgens are associated with better lung function in large healthy cohorts (10, 11) and in disease (12). Increasing circulating levels of adrenal and gonadal androgens in males and females during adolescence are believed to be associated with improving asthma during adolescence (12), and gonadal androgens in particular may be associated with gender-based differences in asthma incidence and severity in adulthood (12, 38–40). Notably, steroid metabolites downstream of DHEA-S are generated at the level of the target peripheral tissue and are generally not appreciable in circulation (41, 42).

These data suggest that androgen depletion, whether circulating and/or at the tissue level, could contribute to the pathophysiology

![Diagram](image)

**Fig. 2.** The adrenal restrictive HSD3B1(1245A) allele is specifically associated with poor pulmonary function in GC-treated patients with severe asthma. In Caucasian AA genotype patients with asthma enrolled in SARP III, baseline prebronchodilator FEV1 (Pre-BD FEV1) (A) and postbronchodilator FEV1 (Post-BD FEV1) (B) is lower for those in the GC vs. no GC treatment groups. In contrast, for the CC genotype, there is no difference between GC and no GC treatment groups. Lower Pre-BD FEV1 (C) and Post-BD FEV1 (D) for AA genotype patients receiving GC also occurs in Caucasian patients with severe asthma enrolled in SARP I&II. Error bars indicate SEs.

**Fig. 3.** A model that explains physiologic effects of HSD3B1 inheritance on FEV1 in patients with severe asthma. GC treatment suppresses adrenal DHEA, which may become a limiting substrate for 3β-HSD1, depending on HSD3B1 genotype. Adrenal permissive and adrenal restrictive alleles enable and limit metabolic flux through 3β-HSD1 and recovery of airflow.
of severe asthma and resistance to oral GC therapy. Our data confirm that low DHEA-S levels in asthma are associated with low lung function. However, we do not know whether this is a causal relationship, whether low androgen levels are simply a marker associated with patients with low lung function on more GCs, or both. We recently published a pilot study suggesting that DHEA supplementation in women with low DHEA-S improves FEV₁ (34).

An important study of prostate cancer has shown that the adrenal restrictive HSD3B1(1245A) allele limits conversion of DHEA to more potent androgens, whereas the adrenal permissive HSD3B1(1245C) allele increases tissue production of potent androgens (16, 17). The SARP studies provided an opportunity to study androgen metabolism effects in severe asthma. We therefore hypothesized that the restrictive allele, which impedes conversion from adrenal DHEA-S to testosterone and dihydrotestosterone, would be associated with lower lung function in severe asthma when systemic GCs are used and suppress substrate availability for 3β-HSD1. Data were analyzed in the SARP III cohort, enriched for severe asthma, and then validated in the patients with severe asthma in the SARP I&II cohort and are strikingly consistent with our hypothesis across both cohorts.

Limitations of this study include that it is restricted to Caucasian patients with asthma and the sample size, particularly for patients with non-permissive HSD3B1(1245C) genotypes. The low frequency of the adrenal permissive HSD3B1(1245C) allele in African-American subjects combined with the limited number of subjects did not allow for a sufficiently powered analysis in non-Caucasians. For example, only 1 African American participant with CC genotype was enrolled in SARP III, and 2 others in SARP I&II. The lower prevalence of the adrenal permissive C allele in African Americans could contribute to higher severity and risk from asthma, as well as GC resistance, in this patient population. Similarly, none of the 27 adult Hispanic participants with asthma enrolled in SARP III, and only 1 of the 34 adult Hispanics enrolled in SARP I&II, respectively, carried the CC genotype. Of note, the adrenal permissive allele frequency (i.e., the C allele) was 36% and 37% in adult Caucasian participants

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