Glucocorticoid receptor β and histone deacetylase 1 and 2 expression in the airways of severe asthma

Claire A Butler, Stephen McQuaid, Claire C Taggart, Sinead Weldon, Richard Carter, Grzegorz Skibinski, Timothy J Warke, David F Choy, Lorcan P McGarvey, Peter Bradding, Joe R Arron, Liam G Heaney

Abstract

Rationale Upregulation of glucocorticoid receptor β (GRβ) has been implicated in steroid resistance in severe asthma, although previous studies are conflicting. GRβ has been proposed as a dominant negative isoform of glucocorticoid receptor α (GRα) but it has also been suggested that GRβ can cause steroid resistance via reduced expression of histone deacetylase 2 (HDAC2), a key regulator of steroid responsiveness in the airway. Objectives To examine GRβ, GRα, HDAC1 and HDAC2 expression at transcript and protein levels in bronchial biopsies from a large series of patients with severe asthma, and to compare the findings with those of patients with mild to moderate asthma and healthy volunteers.

Methods Bronchoscopic study in two UK centres with real-time PCR and immunohistochemistry performed on biopsies, western blotting of bronchial epithelial cells and immunoprecipitation with anti-GRβ antibody.

Measurements and main results Protein and mRNA expression for GRα and HDAC2 did not differ between groups. GRβ mRNA was detected in only 13 of 73 samples (seven patients with severe asthma), however immunohistochemistry showed widespread epithelial staining in all groups. Western blotting of bronchial epithelial cells with GRβ antibody detected an additional ‘cross-reacting’ protein, identified as clathrin. HDAC1 expression was increased in patients with severe asthma compared with healthy volunteers.

Conclusions GRβ mRNA is expressed at low levels in a minority of patients with severe asthma. HDAC1 and HDAC2 expression was not downregulated in severe asthma. These data do not support upregulated GRβ and resultant reduced HDAC expression as the principal mechanism of steroid resistance in severe asthma. Conflicting GRβ literature may be explained in part by clathrin cross-reactivity with commercial antibodies.

Key messages

What is the key question?

• Increased glucocorticoid receptor β (GRβ) with resultant reduction in histone deacetylase 2 (HDAC2) expression has been implicated in the pathogenesis of severe steroid-resistant asthma, but previous data are conflicting.

What is the bottom line?

• GRβ mRNA was expressed at very low levels in the airways of a minority of patients with severe asthma. GRβ immunostaining was prominent in bronchial biopsies from all patients, but this was subsequently shown to be due to antibody cross-reactivity with heavy chain clathrin. No reduction in HDAC2 expression was identified in severe asthma.

Why read on?

• These data do not support altered GRβ/HDAC expression as the principal underlying mechanism of steroid resistance in severe asthma. Some of the discrepancies in the GRβ literature may be explained by clathrin cross-reactivity with commercial antibodies.

Introduction

Patients with severe asthma respond poorly to available therapies, which results in high healthcare costs due to unscheduled healthcare visits, treatment of co-morbidities and work absence.1 The cornerstone of asthma treatment is glucocorticoid therapy; however patients with severe asthma are relatively resistant to inhaled glucocorticoids, often resulting in a requirement for systemic steroids to maintain disease control.2 Proposed molecular mechanisms for glucocorticoid resistance include abnormalities of glucocorticoid binding,3–4 reduced glucocorticoid receptor nuclear translocation in response to steroids,5–6 increased expression of pro-inflammatory transcription factors (eg, activator protein-1 and nuclear factor-κB7,8) and altered expression of co-repressor proteins (eg, histone deacetylases).9 Two commonly proposed mechanisms for steroid resistance in severe asthma are increased expression of the dominant negative isoform of the glucocorticoid receptor, glucocorticoid receptor β (GRβ), and reduced expression and activity of histone deacetylase 2 (HDAC2).3,5 A recent study suggested the reduced HDAC2 in severe asthma may be regulated by GRβ overexpression.10 Existing data on GRβ expression in severe asthma have been variable. GRβ-immunoreactive peripheral blood mononuclear cells (PBMCs), CD5 T cells and bronchoalveolar lavage cells were increased in steroid-resistant asthma.3,11,12 Furthermore, Sousa et al reported increased GRβ-positive cells in steroid-resistant asthmatic tuberculin responses.13 In the lungs of patients who have died from asthma increased GRβ immunoreactivity has been reported,14 and in the only published
bronchial biopsy study, GRβ expression detected by immunohistochemistry was increased in the epithelium and submucosa of patients with severe asthma. However, other studies in PBMCs in severe asthma have been negative. Thus, it remains unclear if GRβ is elevated in the airways of severe asthma (and other ‘steroid resistant’ conditions) and why there is such variability in the published literature.

Our aims were to examine GRβ and GRα expression at transcript and protein levels in bronchial biopsies from a large series of patients with severe asthma, and to compare the findings with those for patients with mild to moderate asthma and healthy volunteers. We also studied HDAC1 and HDAC2 expression in matched biopsies.

**METHODS**

**Subjects**

This study was performed in two UK centres, Queen’s University Belfast and University of Leicester. Patients with severe asthma were recruited from the Belfast City Hospital and Glenfield Hospital, Leicester Difficult Asthma Services, where systematic evaluation protocols ensure patients have well characterised severe asthma as defined by current American Thoracic Society guidelines. All patients had symptoms persisting despite at step 4 or 5 of the Global Initiative for Asthma (GINA) guidelines. Patients with mild to moderate asthma and healthy volunteers were recruited from hospital clinics or by advertisement.

In total, 27 participants were recruited from Belfast (10 healthy volunteers (HV), 7 patients with mild to moderate asthma (MA) and 10 patients with severe asthma (SA)) and 56 participants from Leicester (12 HV, 25 MA and 21 SA) (table 1).

**Bronchoscopy**

Bronchoscopy was performed using standard techniques (see online supplement). Biopsies were either placed immediately in RNA preservative (RNeater, Ambion, Austin, Texas, USA) and submitted for real-time PCR (qPCR) or placed into dry acetone and methylsulfonyl fluoride and fixed overnight at –20°C for immunohistochemistry. Brushings were placed in Promocell medium containing penicillin/streptomycin and Primocin for immunohistochemistry. Brushings were placed in Promocell (Heidelberg, Germany).

**Gene expression analysis**

qPCR analysis was performed using RNA from homogenised bronchial biopsies (74 biopsies; 22 HV, 28 MA and 24 SA) using TaqMan® Gene Expression Assays (Applied Biosystems, Foster City, California, USA). RNA purification and qPCR quality control are detailed in the online supplement. Relative expression levels were determined by the 2(-DeltaDelta CT) method, as described in Applied Biosystems User Bulletin No. 2 (P/N 4303859).

**Bronchial biopsy immunohistochemistry and confocal microscopy**

For immunohistochemistry, biopsy samples were processed and stained using local protocols. Fifty-five biopsies (17 HV, 21 MA and 17 SA) were processed for immunohistochemistry. Infiltration and embedding with JB4 resin was performed. The immunohistochemical technique and confocal analysis are detailed in the online supplement.

Immunostained sections were evaluated by two independent assessors with consensus scoring for any conflicting results (scoring system given in the online supplement). Two polyclonal anti-GRβ antibodies were compared, ab5581 (Abcam, Cambridge, UK) and PAS-514 (Affinity Bioreagents, Golden, CO, USA via Pierce Biotechnology, Rockford, IL, USA) along with anti-GRα (sc-1002), HDAC1 (sc-7872) and HDAC2 (sc-7899) (Insight Biotechnology, Wembley, UK).

**RESULTS**

**GRβ, GRα, HDAC1 and HDAC2 mRNA expression**

In the samples available for qPCR (n=74), GRβ mRNA was detectable in only 15 of the 74 (18%) participants (seven SA—four of whom were on oral steroids, four with moderate persistent asthma on inhaled steroids, one with steroid-naïve asthma and one HV) (figure 1A). There was a similar rate of detection in the SA group (p=0.10, Fisher’s exact test). Despite the use of different specific primer-probe sets for GRβ, GRβ mRNA was not detected in any of the other samples. GRα mRNA was detectable in 70 of the biopsy samples (figure 1B, median (IQR) relative fold expression of GRα mRNA expression was 345.7 (137.4–928.2), 498.4 (200.4–1459) and 463.1 (186.3–1549) in HV, MA and SA groups respectively, p=0.62,
Kruskal–Wallis). HDAC1 mRNA was significantly upregulated in the SA group compared with the HV group (figure 1C, HDAC1—median (IQR) relative fold expression was 0.08 (0.04, 0.21), 0.22 (0.09, 0.49) and 0.27 (0.10, 0.94) in the HV, MA and SA groups respectively (p=0.02, Kruskal–Wallis, post hoc analysis p<0.05 between HV and SA). HDAC2 expression did not differ between participant subgroups (figure 1D, HDAC2—median (IQR) relative fold expression was 0.52 (0.14–0.97), 0.65 (0.53–4.29) and 0.76 (0.56–1.97) in the HV, MA and SA groups respectively (p=0.25, Kruskal–Wallis). There was a significant correlation between HDAC2 mRNA and GRα mRNA (figure 3D, Spearman r=0.75, p<0.001).

**Table 1** Demographic characteristics of patients with asthma and healthy volunteers (Belfast and Leicester cohorts combined)

<table>
<thead>
<tr>
<th></th>
<th>Healthy volunteers (n=22)</th>
<th>Patients with mild to moderate asthma (n=30)</th>
<th>Patients with severe asthma (n=31)</th>
<th>p Value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years), median (IQR)</td>
<td>30 (22–45)</td>
<td>29 (24–39)</td>
<td>48 (38–54)†</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Sex, men/women (n)</td>
<td>10/12</td>
<td>14/16</td>
<td>22/9</td>
<td>0.09</td>
</tr>
<tr>
<td>Duration of asthma (years), mean±SD</td>
<td>N/A</td>
<td>12±10</td>
<td>22±15‡</td>
<td>0.007</td>
</tr>
<tr>
<td>Atopy (n)</td>
<td>11</td>
<td>21</td>
<td>23</td>
<td>0.16</td>
</tr>
<tr>
<td>FEV1 (litre/min), mean±SD</td>
<td>3.67±0.78</td>
<td>3.32±0.77</td>
<td>2.48±0.57§</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>FEV1 (% predicted), mean±SD</td>
<td>102.8±11.9</td>
<td>93.5±16.0</td>
<td>75.9±16.9¶</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>FEV1/FVC, mean±SD</td>
<td>82.1±9.8</td>
<td>75.9±10.6</td>
<td>64.6±11.1**</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Inhaled steroid (n)</td>
<td>0</td>
<td>19</td>
<td>31</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>BDP equivalent (µg), median (IQR)</td>
<td>0</td>
<td>400 (0–800)</td>
<td>1600 (1200–1600)††</td>
<td></td>
</tr>
<tr>
<td>Maintenance systemic steroids (n)</td>
<td>0</td>
<td>0</td>
<td>15 (median dose prednisolone 5 mg (0–10 mg) plus 1 subject maintenance intramuscular triamcinolone)</td>
<td></td>
</tr>
<tr>
<td>Theophylline (n)</td>
<td>0</td>
<td>1</td>
<td>17</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Long-acting β2-agonists (n)</td>
<td>0</td>
<td>14</td>
<td>31</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Prior smoking history (pack years), median (IQR)</td>
<td>1 (4)</td>
<td>5 (1, 1–10)</td>
<td>13 (2.5, 1–20)</td>
<td>0.004</td>
</tr>
<tr>
<td>Eosinophils (10⁶/litre), median (IQR)</td>
<td>0.1 (0.07–0.21)</td>
<td>0.26 (0.14–0.45)‡‡</td>
<td>0.49 (0.25–0.74)§§</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>lgE (kU/litre), geometric mean (95% confidence interval)</td>
<td>24.6 (13.3 to 45.8)</td>
<td>159.8 (89.8 to 284.6)¶¶</td>
<td>238.1 (136.2 to 471.5)***</td>
<td>&lt;0.0001</td>
</tr>
</tbody>
</table>

Comparison with the healthy volunteer group: *p<0.001, §p<0.001, ¤p<0.001, **p<0.001, §§p<0.001, §§§p<0.001, ¶¶p<0.001. Comparison with patients with mild to moderate asthma: ¡p<0.001, ¡¡p<0.001, ¡¡¡p<0.001, ¡¡¡¡p<0.001, ¡¡¡¡¡p<0.001, ¡¡¡¡¡¡p<0.001, ¡¡¡¡¡¡¡p<0.001. Comparison with patients with severe asthma: ¡¡¡¡¡¡¡¡p<0.001. Comparison with patients with mild to moderate asthma: *p<0.001, *p<0.007, §p<0.001, §p<0.001, §§p<0.001, §§p<0.001, §§p<0.001, §§p<0.001. *Calculated by analysis of variance (ANOVA) with Bonferroni’s multiple comparison test (parametric) or Kruskal–Wallis with Dunn’s multiple comparison test (non-parametric) or t-test when only asthma groups compared or χ² for categorical variables (sex, atopy, theophylline, long-acting β2 agonists, smoking history).

BDP, beclometasone dipropionate; FEV1, forced expiratory volume in 1 s; FVC, forced vital capacity.
Glucocorticoid receptor β (GRβ) expression in bronchial biopsies; representative immunohistochemistry shown at ×400 magnification. (A) Biopsy from a patient with severe asthma, demonstrating the pattern and anatomical localisation of GRβ expression to be identical in both clinical centres. (B) GRβ expression in individual patient groups. (C) Quantitative immunohistochemical epithelial expression for GRβ in bronchial biopsies. There was no significant difference between groups (p=0.18, Kruskal–Wallis). (D) Immunostaining with GRβ antibody (ab3581) using confocal microscopy in bronchial biopsy from a patient with severe asthma, demonstrating diffuse epithelial staining with scattered submucosal reactivity (×400 magnification).
significant correlation between glucocorticoid receptor (GR) and ulcerative colitis and rheumatoid arthritis, GR expression in severe asthma reported in Bronchial biopsy samples. The only other bronchial biopsy studies examined GR expression in healthy volunteers and patients with asthma, but that group was also unable to detect any GR expression in bronchial biopsies from patients with severe asthma.15 Their pattern of staining was similar to that reported here but tissue expression of GR at the mRNA level was not examined. Other studies examining GR expression in severe asthma using these antibodies have reported variable associations. GR immunoreactivity was increased in PBMCs and bronchoalveolar lavage (BAL) cells from patients with severe asthma.3 12 25 However, another PBMC study was unable to identify any GR immunoreactivity in healthy volunteers and patients with asthma that is steroid sensitive or resistant.15 Of note, that study was unable to identify GR mRNA in the first round of PCR, though it did on the second cycle of nested PCR.16 A further PBMC study by Torrego et al reported 600-fold lower GR mRNA expression than GRα, but that group was also unable to detect any GR expression on bronchial biopsy.17 Coleva et al demonstrated readily appreciable GR expression using immunohistochemistry in BAL macrophages but demonstrated only femtograms of GR mRNA.22

In other inflammatory disease states, such as glaucoma, ulcerative colitis, and rheumatoid arthritis, GR expression has been reported to be upregulated in glucocorticoid-unresponsive disease, although again there is controversy.26–30 Some of these studies have looked at mRNA expression from PBMCs rather than immunohistochemistry. For example, GR mRNA was detected in PBMCs from patients with glucocorticoid-resistant ulcerative colitis compared with low detection in glucocorticoid-responsive disease and healthy volunteers.27 This same group also demonstrated elevated PBMC GR mRNA in patients with active ulcerative colitis compared with inactive disease or Crohn’s disease, though this was disputed by Hausmann et al, who did not find elevated PBMC GR mRNA in relation to steroid resistance.26 29 PBMC GR mRNA and GRα-positive PBMCs were increased in steroid-resistant rheumatoid arthritis.28 Zhang et al were able to confirm that glaucomatous trabecular meshwork cells expressed lower levels of GR protein by western blotting and these cells were more sensitive to the effects of steroids compared with normal trabecular meshwork cells.30 A recent immunohistochemistry study by Ishida et al reported increased GR expression in patients with severe allergic rhinitis compared with healthy controls, and of note, GR mRNA was not assessed in this study.31

Our data suggest that tissue immunohistochemistry with these GR antibodies is unreliable due to concomitant clathrin staining. This illustrates the problems associated with using antibodies for immunohistochemistry in the absence of validation with other methods, for example, mRNA expression and target protein specificity using western blots. If multiple bands are seen on western blot from the target tissue, we would suggest that this antibody may be inappropriate for use in immunofluorescence, immunocytochemistry or immunohistochemistry. These techniques have been widely used in the GR literature and this study questions the validity of previous immunohistochemical and immunocytochemical data utilising

Figure 3  Immunohistochemical epithelial expression for histone deacetylase 1 (HDAC1) and HDAC2 in bronchial biopsies. (A) HDAC1: there was no significant difference between groups (p=0.55, Kruskal–Wallis); (B) HDAC2: there was no significant difference between groups (p=0.89, Kruskal–Wallis). (C) HDAC2 expression in individual patient groups—representative immunohistochemistry shown at ×400 magnification. (D) Highly significant correlation between glucocorticoid receptor α (GRα) and HDAC2 mRNA.
these antibodies and supports the need for western blotting techniques. In view of the low mRNA signal compared with that for GRα, we would further conclude that GRβ is not highly expressed in the airways of patients with severe asthma. Given the substantially higher expression of GRα, GRβ is unlikely to function as a dominant-negative isoform of GRα and this mechanism has little to do with the relative steroid resistance seen in this group.

Another proposed mechanism for the induction of steroid resistance by GRβ is reduced tissue expression of HDAC2 mRNA and recent data suggested reduced HDAC2 in severe asthma may be regulated by GRβ overexpression. If this mechanism of HDAC2 regulation is correct, then our data provide no support that it is relevant in severe asthma because, consistent with the low levels of GRβ expression in severe asthma biopsies, we identified no reduction in HDAC2 expression in matched biopsies from the same patients when compared with normal controls and patients with mild to moderate asthma. Reduced HDAC2 tissue expression has been described in patients with chronic obstructive pulmonary disease (COPD) and those who smoke and is associated with reduced HDAC function, but the data in asthmatic airway samples are conflicting. One study suggested decreased expression of HDAC1 and HDAC2 in mild asthma which increased with steroid treatment. In more severe asthma, Bergeron et al reported similar HDAC2 expression between patients with asthma that is steroid resistant and steroid responsive, whereas another study reported reduced HDAC2 mRNA expression in BAL cells. Importantly, in previous studies in which HDAC mRNA data have been presented along with functional HDAC activity, when there has been a reduction in HDAC activity, there has been a concomitant reduction in HDAC mRNA. Thus, there has been no suggestion that reduced HDAC function in asthma or COPD disease is due to any specific alteration in HDAC function, but rather reduced activity is due to reduced tissue expression. Therefore, we believe it is reasonable to conclude that an absence of reduction of HDAC1 and HDAC2 in this large cohort of patients with refractory asthma argues against this being the mechanism of steroid resistance in this patient group.

At a transcriptional level, we found HDAC1 was increased in patients with severe asthma on higher dose steroid treatment compared with healthy volunteers but not those with mild to moderate asthma, which is consistent with the previously described steroid effect of upregulating HDAC1. However, this difference appeared small compared with milder disease and no difference was identified in HDAC1 protein expression. Thus, even if HDAC1 is upregulated by steroid treatment, the fact that many patients with severe asthma remain dependent on oral steroids suggests that this upregulation does not enhance steroid efficacy in this group. There was no association between HDAC2 and theophylline treatment, suggesting that the normal HDAC2 levels in severe asthma are not due to theophylline treatment, as has previously been suggested. The close correlation of HDAC2 with GRα expression at the transcriptional level suggests that these molecules are co-regulated, with increased expression of both molecules tending to increase steroid responsiveness. We did not specifically examine bronchoalveolar macrophages in the present study and thus a reduction in HDAC2 activity in macrophages contributing to steroid resistance cannot be completely excluded. However, other

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**Figure 4**  
(A) Immunocytochemical analysis of primary bronchial epithelial cells from a healthy volunteer showing predominantly cytoplasmic glucocorticoid receptor β (GRβ) expression with occasional cells demonstrating nuclear expression (arrowed). (B) Typical western blot showing GRβ band (at around 90 kDa) and higher molecular weight band (band 2) at 180 kDa in primary bronchial epithelial cells. (C) Recombinant clathrin (250–2500 ng) was immunoblotted with (i) anti-clathrin antibody (1:1000 in 5% milk) and (ii) anti-GRβ antibody (1:500 in 3% bovine serum albumin (BSA)). Similar bands were noted in the anti-GRβ and anti-clathrin probed gels at 180 kDa. (D) Gene expression for clathrin in bronchial biopsies. There was no significant difference between patient groups noted.
important and relevant immunological mechanisms in asthma pathogenesis have been identified in proximal airway samples obtained at bronchoscopy.

In conclusion, we have demonstrated that commercially available GRβ antibodies cross-react with clathrin and are unreliable for the analysis of GRβ expression in situ. GRβ mRNA was expressed at low levels in the airways with no difference between steroid-sensitive and severe disease. Our findings may explain the discrepant reports for the role of GRβ in steroid-resistant states in a variety of diseases, and do not support the view that GRβ plays a role in severe asthma. In addition, our data suggest that downregulation of HDAC1 or HDAC2 does not occur in severe asthma, and so the mechanism of relative steroid resistance in severe asthma remains unclear.

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**Competing interests** None.

**Contributors** CB and SMcQ performed immunostaining in the Belfast cohort, analysed the data and contributed to the writing of the manuscript. DC and JA performed and analysed the gene expression data, analysed the data and contributed to the writing of the manuscript. CB and LH recruited subjects, performed bronchoscopy and acquired the demographic data for the Belfast cohort and PB recruited subjects, performed bronchoscopy and acquired the demographic data for the Leicester cohort. TJW and LMcG assisted with bronchoscopy in the Belfast cohort. RC undertook immunohistochemistry for the Leicester cohort and assisted with data analysis under the supervision of PB. CT and SW performed the clathrin western blots and immunostaining. LH and GS conceived and designed the research, with data analysis under the supervision of PB. CB and SMcQ performed immunostaining in the Belfast cohort, performed and analysed the gene expression data, analysed the data and contributed to data analysis and interpretation, drafted the original manuscript and supervised CB. All authors approved the final manuscript.

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