

1 **DP₂ antagonism reduces airway smooth muscle mass in asthma by decreasing**
2 **eosinophilia and myofibroblast recruitment**

3

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21

22 **Overline:** Asthma

23

24 **One sentence summary:** Cellular and computational models and bronchial biopsies from
25 asthma patients show that a DP₂ antagonist reduces airway smooth muscle mass in asthma.

26 **Abstract**

27 Increased airway smooth muscle mass, a feature of airway remodeling in asthma, is the
28 strongest predictor of airflow limitation and contributes to asthma-associated morbidity and
29 mortality. No current drug therapy for asthma is known to affect airway smooth muscle mass.
30 Although there is increasing evidence that prostaglandin D₂ type 2 receptor (DP₂) is expressed
31 in airway structural and inflammatory cells, few studies have addressed the expression and
32 function of DP₂ in airway smooth muscle cells. We report that the DP₂ antagonist fevipiprant
33 reduced airway smooth muscle mass in bronchial biopsies from patients with asthma who had
34 participated in a previous randomized placebo-controlled trial. We developed a computational
35 model to capture airway remodeling. Our model predicted that a reduction in airway
36 eosinophilia alone was insufficient to explain the clinically observed decrease in airway smooth
37 muscle mass without a concomitant reduction in the recruitment of airway smooth muscle cells
38 or their precursors to airway smooth muscle bundles that comprise the airway smooth muscle
39 layer. We experimentally confirmed that airway smooth muscle migration could be inhibited
40 in vitro using DP₂-specific antagonists in an airway smooth muscle cell culture model. Our
41 analyses suggest that fevipiprant, through antagonism of DP₂, reduced airway smooth muscle
42 mass in patients with asthma by decreasing airway eosinophilia in concert with reduced
43 recruitment of myofibroblasts and fibrocytes to the airway smooth muscle bundle. Fevipiprant
44 may thus represent a potential therapy to ameliorate airway remodeling in asthma.

45 **Introduction**

46 Asthma affects over 300 million people worldwide and its prevalence is increasing (1) despite
47 currently available therapies (2). Asthma is characterised by variable airflow limitation that
48 becomes more persistent in severe disease. Increased airway smooth muscle (ASM) mass is an
49 important component of airway remodeling in asthma, contributing substantially to symptoms
50 and disordered airway physiology (3-5). To date, no drug has impacted upon the increased
51 ASM mass observed in asthma in randomized placebo-controlled trials (3, 4). However,
52 bronchial thermoplasty has demonstrated a potential reduction in ASM mass in asthma in
53 uncontrolled studies (6-7).

54

55 The prostaglandin (PG) D₂ type 2 receptor (DP₂, also known as chemoattractant receptor-
56 homologous molecule expressed on T helper [Th] 2 cells [CRTh2]) is expressed by
57 inflammatory cells critical in the immunopathogenesis of asthma, including eosinophils, Th2
58 lymphocytes, type 2 innate lymphoid cells, and mast cells. DP₂ activation promotes cellular
59 release of cytokines, inflammatory cell migration, and cell survival (8-10). Its archetypal ligand
60 PGD₂ is predominantly released by mast cells localized to the ASM-bundle (11). The DP₂
61 antagonist fevipiprant has been shown to improve asthma symptoms, lung function, airway
62 eosinophilia, and epithelial integrity (4). However, the role of the PGD₂/DP₂ axis in ASM
63 dysfunction in asthma has not been extensively studied. We hypothesized that the PGD₂/DP₂
64 axis may contribute to increased ASM mass in asthma, and that antagonism of DP₂ with
65 fevipiprant might result in a decrease in ASM mass.

66

67 Here, we analysed bronchial biopsies from asthma patients treated with the DP₂ antagonist
68 fevipiprant in a previous phase 2a randomized, placebo-controlled trial undertaken to
69 determine the impact of drug upon airway inflammation, remodeling and asthma control (4).

70 Using an agent-based computational model representing an asthmatic airway in human patients
71 and supported by in vitro ASM cell-based observations, we propose that the reduced ASM
72 mass observed in the bronchial biopsies after fevipiprant treatment may be a consequence of
73 inhibition of eosinophilic airway inflammation together with reduced recruitment of
74 myofibroblasts and fibrocytes to the ASM bundle.

75

76 **Results**

77 **Fevipiprant reduces ASM mass in subjects with asthma in a randomized placebo-** 78 **controlled trial**

79 We obtained bronchial biopsies from moderate-to-severe asthmatics with airway eosinophilic
80 inflammation, as evidenced by increased sputum eosinophil counts. These individuals had
81 participated in a 12-week single-centre (University of Leicester), randomized, double-blind,
82 parallel-group, placebo-controlled trial of the DP₂ antagonist fevipiprant (4). We then
83 performed an a priori quantification of ASM mass (percentage of total bronchial biopsy area)
84 (11). A representative photomicrograph of a bronchial biopsy from a subject showing
85 disrupted epithelium and increased ASM mass is shown in Fig. 1A. The absolute ASM mass
86 percentage (mean \pm standard error of the mean [SEM]) observed decreased significantly
87 following treatment with fevipiprant ($-13 \pm 5\%$; $p=0.022$, $n=14$) versus placebo ($4 \pm 5\%$;
88 $p=0.52$, $n=13$) (mean difference [95% confidence interval (CI)] -16.2 [-1.4 to -31.1] %;
89 $p=0.034$) (Fig. 1B). In view of the above data, we performed a post hoc quantification of ASM
90 mass (percentage of total biopsy area) in bronchial biopsies derived from a sub-group of
91 moderate-to-severe eosinophilic asthmatics who had participated in a 50-week single-centre
92 (University of Leicester), randomized, double-blind, parallel-group, placebo-controlled trial of
93 the anti-interleukin (IL)-5 neutralizing antibody mepolizumab (12). Although the sample size
94 was small, in contrast to fevipiprant, we observed no significant effect of mepolizumab on

95 ASM mass (absolute ASM mass percentage increase post-mepolizumab $2.9 \pm 4.0\%$, n=7 versus
96 placebo $1.5 \pm 2.2\%$, n=5) (mean difference [95% CI] 1.4 [-9.9 to 12.7] %; p=0.79). For these
97 and other data, see Data File S1.

98

99 **An agent-based computational model recapitulates the features of airway remodeling** 100 **observed in asthma**

101 To interrogate the mechanisms governing the pathogenesis of asthma, we developed an agent-
102 based computational model of airway remodeling comprising epithelial, mesenchymal, and
103 inflammatory parameters. In agent-based modeling, a system is divided into agents (here,
104 airway cells; table S1) capable of interacting with each other and their environment based on
105 defined rule-sets (13-15). The initial state of the model is illustrated in Fig. S1. Our model
106 considered interactions between epithelial (columnar and goblet cells), mesenchymal
107 (fibroblast, myofibroblast, and ASM cells), and inflammatory (eosinophil) cell types. The
108 various cell types, depending on their phenotype, displayed behaviours ranging from
109 proliferation, migration, (de)differentiation, apoptosis, and synthesis of extracellular matrix
110 (ECM) proteins and cytokines (table S1). These virtual cells were simulated within a Strahler
111 Order 3 virtual airway with a lumen diameter of 1.21 mm and wall area of 1.79 mm². The
112 number of each cell type within the model was based on geometrical constraints and published
113 data. The rule-set governing agent behaviours and interactions was derived from existing in
114 vitro, animal, and clinical studies (table 1). The underpinning agent interactions and rule-sets
115 attributed to the agents are summarized in table 1 and represented schematically in Fig. S2.

116

117 In the model, we initially damaged the epithelium to cause 50% epithelial denudation. We then
118 simulated the consequent normal injury repair and pathological airway remodeling over 180
119 days by introducing alterations to model parameters (tables S2 – S4). The following

120 pathological markers and value ranges were considered necessary in the model to reflect the
121 key hallmarks of severe asthma (1, 2): eosinophilic inflammation (eosinophils/mm² sub-
122 mucosa) >10; epithelial integrity <70%; and ASM mass ≥10% and ≤50%. We conducted
123 parametric testing by varying, both individually and collectively, parameters from all agent
124 categories and observing which conditions best captured the above hallmarks of asthma. We
125 defined the most parsimonious set of parameters to capture these three hallmarks (tables S2 –
126 S4). The response to epithelial injury in this model displayed significantly increased
127 eosinophilic inflammation (p<0.001), ASM mass (p=0.002) and persistent epithelial damage
128 (p<0.001) compared to the model of healthy control individuals over the 180-day time course
129 (Fig. 2A).

130

131 **Computational modeling predicts that a reduction in eosinophil recruitment is not**
132 **sufficient to decrease ASM mass**

133 In order to predict the impact of reducing eosinophil number in our model of airway
134 remodeling, we incorporated pro-apoptotic or anti-recruitment elements into the model. These
135 variables were chosen to represent the major respective effects of neutralizing IL-5 (12, 26),
136 an obligate cytokine for eosinophil survival and maturation, and of blocking activation of DP₂,
137 which promotes eosinophil recruitment (4). We tested an increasing range of intervention doses
138 and found they resulted in a progressive reduction in airway eosinophilia and ASM mass in our
139 model of airway remodeling (Fig. 2B, C).

140

141 We then used our computational model of a remodeled asthmatic airway to determine the
142 predicted percentage increase in eosinophil apoptosis and percentage reduction in eosinophil
143 recruitment required to reduce the number of bronchial wall eosinophils to that seen in vivo in
144 clinical trials of mepolizumab (27) and fevipiprant (4), which reduced the eosinophil count in

145 patients by 55% and 80%, respectively compared to placebo control. To attain the reduction in
146 airway eosinophil number clinically observed with mepolizumab, the model predicted that
147 15% of the eosinophil population must be induced to undergo apoptosis (reduction in airway
148 eosinophilia versus control of 54.1 ± 4.1 %; Fig. 2B, chequered bar). To attain the reduction in
149 airway eosinophil number clinically observed for fevipiprant, the model predicted that a 40%
150 reduction in eosinophil recruitment was required (reduction in airway eosinophilia versus
151 control of 81 ± 0.6 %; Fig. 2B, hatched bar).

152

153 We subsequently used the pro-apoptotic (15%) and anti-recruitment (40%) models resulting in
154 a reduction in eosinophil number equivalent to that seen in the mepolizumab and fevipiprant
155 clinical trials to predict the impact of each intervention on ASM mass. When assuming an
156 increase in eosinophil apoptosis of 15%, the pro-apoptosis model predicted a small mean \pm
157 SEM decrease in ASM mass (absolute reduction 4.0 ± 0.6 %; relative reduction 12 ± 2 % versus
158 control; Fig. 2C, chequered bar). This is consistent with the mepolizumab clinical trial (12) in
159 which no significant change in ASM mass was observed. When assuming a decrease in
160 eosinophil recruitment of 40%, the anti-recruitment model predicted a modest reduction in
161 ASM mass (absolute reduction 8.1 ± 0.5 %; relative reduction 25 ± 1 % versus control; Fig. 2C,
162 hatched bar), which was not sufficient to result in the observed response to fevipiprant (13%
163 absolute and 44% relative reduction in ASM mass). The model therefore suggested the
164 existence of additional mechanisms that, along with a reduction in airway eosinophilia,
165 mediated the reduction in ASM mass following treatment with fevipiprant.

166

167 **The ASM PGD₂/DP₂ axis mediates ASM migration**

168 To explore the mechanism by which DP₂ antagonism resulted in a decrease in ASM mass, we
169 assessed the expression and function of DP₂ in ASM. We found that DP₂ was expressed in the

170 ASM-bundle in bronchial biopsies from patients recruited for research bronchoscopies (Fig.
171 3A), in line with the previous finding that PGD₂ primes migration of ASM cells towards
172 platelet-derived growth factor via DP₂ (28). However, DP₂ expression was not significantly
173 different between subjects with severe asthma (60 ± 1 ; n=8) and healthy controls (57 ± 5 ; n=11)
174 (mean difference [95% CI] 2.6 [-9.9 to 15.0]; p=0.67). We also confirmed DP₂ expression in
175 primary human ASM cells at the mRNA (Fig. 3B) and protein levels (Fig. 3 C, D and Fig. S3).
176

177 PGD₂ can activate PGD₂ type 1 (DP₁), DP₂ and thromboxane (TP) receptors (9). Therefore, we
178 investigated the effect of the selective DP₂ agonist 13,14-Dihydro-15-keto-PGD₂ (DK-PGD₂)
179 and selective DP₂ antagonists (fevipiprant, CAY10471 and OC000459) on DP₂ receptor
180 activation, phenotype and behaviour of primary human ASM cells. DK-PGD₂ (10-100nM)
181 stimulated a small but significant increase in filamentous actin (F-actin) polymerisation and
182 intracellular calcium elevation (Fig. 3 E-F, area under curve of the dose response [AUC DR]
183 p=0.01 and p=0.002, respectively). Although this did not translate to an effect of DK-PGD₂ on
184 ASM cell migration in vitro (Fig. 4A), blocking activation of DP₂ by endogenous PGD₂ with
185 the DP₂ antagonist fevipiprant significantly inhibited ASM cell migration in vitro at the highest
186 drug concentrations (percentage reduction in cells migrating into the wound after 24h vs
187 vehicle control: 10 nM, 8.8 ± 7.8 , p=0.294; 50 nM, 7.7 ± 7.4 , p=0.332; 100 nM, 12.8 ± 4.9 ,
188 p=0.034, 500 nM, 17.4 ± 6.6 , p=0.034; Fig. 4A). We confirmed this effect using other DP₂
189 antagonists including CAY10471 (percentage reduction in cells migrating into the wound after
190 24h vs vehicle control: 10 nM, 11.6 ± 2.2 , p=0.010; 50 nM, 9.3 ± 3.7 , p=0.038; 100 nM, 13.6
191 ± 4.4 , p=0.027; Fig. 4A), and OC000459 (percentage reduction in cells migrating into the
192 wound after 24h vs vehicle control: 10 nM, 8.4 ± 3.3 , p=0.043; 50 nM, 6.7 ± 4.2 , p=0.157; 100
193 nM, 8.8 ± 1.9 , p=0.003, Fig. 4A). Representative photomicrographs of primary ASM
194 monolayer cultures wounded by scratching followed by incubation with different treatments

195 for 24h are shown in Fig. 4B. Thus, we hypothesized that PGD₂ was released into the
196 extracellular milieu by ASM cells to affect ASM behaviour in an autocrine manner. Indeed,
197 genes involved in PGD₂ biosynthesis and metabolism, including PGD₂ synthase, were
198 expressed by ASM cells from subjects with and without asthma (tables S5 and S6). Consistent
199 with previous reports (29), PGD₂ was released by ASM, albeit at a low concentration compared
200 with mast cells (30-31), and this PGD₂ release increased following wounding (129 ± 18 versus
201 176 ± 22 pg PGD₂/ml/ 10^5 ASM, mean difference [95% CI] 52.0 [4.8 to 99.2]; p=0.02, Fig.
202 4C). In addition to myofibroblasts, we demonstrated that the ASM progenitor fibrocytes
203 expressed DP₂ (Fig. 4D). The correlation between the change in ASM percentage observed in
204 those treated with fevipiprant or placebo and the change in lamina propria myofibroblast or
205 fibrocyte number supported the view that the effects of fevipiprant on ASM mass and lamina
206 propria mesenchymal cells may have occurred in parallel (Fig. 4E, F). These findings suggested
207 that anti-DP₂ might, in part, reduce ASM mass via a direct and concomitant effect upon ASM
208 and myofibroblast or fibrocyte recruitment to the ASM bundle.

209

210 The effects on ASM cell migration were not due to cytotoxic effects on the ASM cells as there
211 was no effect on cell number following treatment for 24h with DK-PGD₂ (100 nM), fevipiprant
212 (500 nM), CAY10471 (100 nM) or OC000459 (100 nM) (Fig. S4A). DK-PGD₂ (100 nM),
213 fevipiprant (500 nM) and CAY10471 (100 nM) had no effect on apoptosis or necrosis (Fig.
214 S4B). This was supported by a lack of effect of DK-PGD₂ (100 nM), fevipiprant (500 nM) or
215 CAY10471 (100 nM) on cell size or granularity, which are known to change during
216 apoptosis/necrosis (Fig. S4C-D). Furthermore, DK-PGD₂ (10 - 100 nM, Fig. S5A), CAY10471
217 (10 - 100 nM, Fig. S5B) and fevipiprant (10 - 500 nM, Fig. S5C) neither induced proliferation
218 of ASM in the presence of serum-free media nor inhibited the ASM cell proliferation induced
219 by fetal bovine serum (FBS) over 3 days, as assessed by the 3-(4,5-dimethylthiazol-2-yl)-5-(3-

220 carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H tetrazolium inner salt (MTS) assay and
221 carboxyfluorescein succinimidyl ester (CFSE) fluorescence (Fig. S5D, E). In the fevipiprant
222 clinical trial, there was no change in proliferating cell nuclear antigen (PCNA) staining in
223 bronchial biopsies pre- versus post- fevipiprant treatment or placebo after 12 weeks of
224 treatment. Additionally, DK-PGD₂ (10 – 100 nM), fevipiprant (10-500 nM) or CAY10471 (10-
225 100nM) had no effect on ASM α -smooth muscle actin (SMA) expression (Fig. S6A). This was
226 supported by a lack of effect of DK-PGD₂ (100 nM), fevipiprant (500 nM) or CAY10471 (100
227 nM) on basal or bradykinin (BK)-stimulated ASM contraction (Fig. S6B-C).

228

229 **Modeling predicts that reductions in myofibroblast and eosinophil recruitment are**
230 **required for fevipiprant to decrease ASM mass**

231 To support our in vitro findings, we reduced the myofibroblast recruitment (0-50%) in the
232 computational model together with the 40% reduction in eosinophil recruitment required to
233 reflect the observed reduction in bronchial biopsy eosinophils after fevipiprant treatment in
234 patients with asthma as described above. The resulting model predicted that a 50% reduction
235 in myofibroblast recruitment in concert with reduced eosinophil recruitment would result in a
236 decrease in ASM mass equivalent to that seen after fevipiprant treatment (cross hatched bars,
237 Fig. 4G). In contrast, a reduction in myofibroblast recruitment alone was predicted to result in
238 minimal effects on ASM mass ($1.8 \pm 1.2\%$ relative reduction). A comparison of the
239 computational model and fevipiprant trial findings is summarised in Fig. S7.

240

241 **Discussion**

242 We report that a drug intervention in asthma, namely fevipiprant (a DP₂ antagonist), reduced
243 ASM mass in bronchial biopsies from asthma patients who had participated in a previous
244 randomized placebo-controlled trial (4). This is in contrast to the lack of an effect on ASM

245 mass in response to mepolizumab that we report here, corticosteroids or the anti-IL-13
246 monoclonal antibody tralokinumab (3, 32, 33). Our computational model and in vitro work
247 supported the view that the reduction in ASM mass in response to fevipiprant was a
248 consequence of inhibiting eosinophilic inflammation in concert with a direct reduction in the
249 recruitment of myofibroblasts to the ASM-bundle. Thus, fevipiprant may be a potential therapy
250 to target airway remodeling in asthma and its clinical benefits observed previously could be in
251 part due to its effects upon ASM.

252

253 One limitation of our study is that the number of paired biopsies collected in the fevipiprant
254 trial included modest numbers of subjects despite the trial being one of the largest biopsy
255 studies undertaken in subjects with asthma. Therefore, it is important to extend and confirm
256 these findings in future studies. Likewise, it is possible that the lack of effect observed with
257 other anti-inflammatory interventions is due to lack of statistical power conferred by the small
258 sample sizes. However, our computational model data suggest that these anti-inflammatory
259 approaches are unlikely to be effective unless they have additional direct effects upon ASM.
260 Indeed, a small reduction in ASM mass was previously reported following treatment with the
261 calcium channel blocker gallopamil, which had been proposed to have direct effects upon ASM
262 activation, but the reduction in ASM mass was no different from placebo (34).

263

264 Another limitation of our study is that we cannot completely exclude the possibility that the
265 effect of fevipiprant upon ASM mass both in vivo and in vitro is an off-target effect. However,
266 we used 3 selective and specific DP₂ antagonists, including fevipiprant, for the in vitro
267 experiments, and therefore we consider it unlikely that the findings we report on ASM
268 activation and migration are due to off-target effects. Our in vitro findings also imply that the
269 major effect of DP₂ antagonism upon ASM function was the inhibition of migration of ASM

270 progenitors to the airway, either from the blood or via attenuation of epithelial-mesenchymal
271 transition, rather than through effects on proliferation or apoptosis. This is consistent with the
272 concept that mesenchymal cells exhibit plasticity in phenotype (35). In keeping with our in
273 vitro observations, we did not identify any changes in PCNA staining in the ASM bundle in
274 vivo, suggesting there was no active proliferation of ASM. Taken together, these results
275 suggest that neither proliferation nor apoptosis contribute to the effects of DP₂ antagonism
276 upon ASM mass, although we cannot completely exclude some contribution from these
277 processes.

278

279 A strength of our study is the integration of findings from in vivo clinical trials and in vitro and
280 computational models. We developed a comprehensive agent-based model of airway
281 remodeling during asthma. Previous computational approaches have been applied to uncover
282 mechanisms driving unresolved allergic inflammation and airway hyper-responsiveness in
283 asthma (15, 36), but not airway remodeling. Our agent-based model was created to represent
284 the airway in 3-dimensions. A possible limitation is that our model was utilized for one layer
285 of agents and simulated a distal airway to balance model resolution and computational
286 complexity. However, we believe our model is representative as it captures the features of the
287 normal and pathological workings of the entire airway. Specifically, our computational model
288 displayed features consistent with moderate-to-severe asthma including damaged bronchial
289 epithelium, eosinophilic inflammation and increased ASM mass. This model responded to
290 perturbations reflective of changes in eosinophil survival and trafficking and provided new
291 insights into possible mechanisms of action of DP₂ antagonists versus anti-IL5 upon airway
292 remodeling. This model has also given us insights into the effects of DP₂ antagonism, which
293 would not be possible in vitro due to the limitations of studying multiple cell-cell interactions
294 within a complex airway structure. Although our computational model is not patient-specific

295 it represents an average patient with asthma and airway remodeling. This ‘virtual patient’
296 represents a step towards patient-specific modeling in respiratory medicine. We anticipate our
297 integrated approach combining agent-based modeling with in vivo clinical data and in vitro
298 findings will provide further insights into asthma in future studies.

299 **Materials and methods**

300 **Study design**

301 The objective of the study was to use an integrated strategy encompassing samples from a
302 randomized placebo-controlled trial in asthma patients evaluating fevipiprant (DP₂ antagonist)
303 and mepolizumab (anti-interleukin-5 antibody), in vitro experiments, and predictive
304 computational agent-based models simulating asthma pathogenesis to investigate the impact of
305 DP₂ antagonism upon ASM mass and determine the mechanisms driving this effect.

306

307 Subjects with persistent moderate-to-severe asthma and an elevated sputum eosinophil count
308 (n=61) participated in a single-centre (University of Leicester) randomized placebo-controlled
309 trial of the DP₂ antagonist fevipiprant (225mg twice per day orally) in addition to standard of
310 care (4). In an independent study, subjects (n=61) who had refractory eosinophilic asthma
311 participated in a single-centre (University of Leicester), randomized placebo-controlled trial of
312 an anti-interleukin-5 neutralising antibody mepolizumab (750 mg intravenous infusions every
313 4 weeks over 50 weeks) in addition to standard of care (12). A subgroup of subjects underwent
314 bronchoscopy and bronchial biopsy in each independent study before and after administration
315 of drug or placebo. The studies were approved by the Leicester and Northamptonshire ethics
316 committee (05/Q2502/98 and 11/EM/0402, respectively) and registered with
317 ClinicalTrials.gov (ISRCTN75169762, NCT01545726 and with EudraCT, number 2011-
318 004966-13). The studies were carried out in accordance with CONSORT guidelines (4, 12).

319

320 The sample size for the fevipiprant and mepolizumab randomized controlled trials were
321 determined based on change in the sputum eosinophil count as the primary outcome as
322 described in Gonem et al (4) and on the number of exacerbations of asthma per subject as the
323 primary outcome as described in Haldar et al (12). Assessing change in airway smooth muscle

324 mass was in the pre-specified exploratory analysis plan for the fevipiprant clinical trial, and
325 was performed post-hoc for mepolizumab. The inclusion and exclusion criteria for the
326 fevipiprant and mepolizumab trials, randomisation and blinding procedures are described in
327 Gonem et al (4) and Haldar et al (12), respectively. For the in vitro experiments the observers
328 analysed the experiment blinded to conditions.

329

330 Additional asthmatic subjects and healthy controls were recruited from a single-centre
331 (University of Leicester) for research bronchoscopies from which tissue sections and primary
332 ASM cells could be derived. Those with asthma gave an appropriate history and had objective
333 evidence of variable airflow obstruction or airway hyper-responsiveness, as described
334 previously (37). Healthy controls had no history of asthma and possessed normal lung function.
335 The study was approved by the Leicestershire and Northamptonshire Ethics Committee
336 (08/H0406/189).

337

338 **Immunohistochemistry**

339 To determine DP₂ expression by ASM, bronchial biopsies from healthy controls (n=11 donors)
340 and asthmatic subjects (n=8 donors) were embedded in glycomethacrylate (GMA) (11). For
341 each subject, sequential 2 µm sections were cut and stained using polyclonal anti-DP₂ antibody
342 (Thermo-Fisher Scientific) or rabbit immunoglobulin (Ig) G isotype control (Immunostep), and
343 an α-SMA antibody (clone 1A4, Dako) or mouse IgG2a isotype control (clone DAK-GO5,
344 Dako). Antibody binding was detected using the EnVision FLEX kit (Dako). For determining
345 ASM mass pre- and post-treatment with fevipiprant (n=14) or placebo (n=13), and pre- and
346 post-treatment with mepolizumab (n=7) or placebo (n=5) bronchial biopsies from asthmatic
347 subjects were embedded in GMA and stained for α-SMA as above. ASM mass was determined
348 as the percentage of the total assessable biopsy area as previously described by a single

349 observer (RB). Repeatability of ASM mass assessment was tested and was excellent within
350 and between observers with intraclass correlations of 0.95 and 0.96 respectively.
351 Myofibroblasts were identified as α -SMA positive stained cells in the lamina propria that were
352 neither located as part of the ASM-bundle nor as vascular smooth muscle cells adjacent to
353 vessels per mm² of submucosa. To identify fibrocytes in bronchial biopsies pre- and post-
354 fevipiprant (n=12) or placebo (n=13), for each subject sequential 2 μ m sections were cut and
355 stained using an mouse monoclonal anti-cluster of differentiation (CD) 34 antibody (Dako) or
356 mouse IgG1 isotype control (Dako) and α -SMA as above. Fibrocytes were identified as the
357 subset of α -SMA positive cells/mm² lamina propria that also stained positive for CD34 in
358 sequential sections. The intensity of DP₂ stain was quantified as reciprocal intensity (38) on a
359 scale out of 250, assessed by a single observer. Assessors were blind to clinical characteristics,
360 treatment allocation and order of bronchial biopsy in the clinical trial.

361

362 **Cell culture**

363 ASM bundles were isolated from bronchial biopsies (n=27 asthmatic, 2 non-asthmatic) and
364 lung resection material (n=4, non-asthmatic). The clinical characteristics of subjects that
365 underwent bronchoscopy to provide primary ASM cultures are as shown (table S5). Primary
366 ASM cells were cultured in DMEM with Glutamax-1 supplemented with 10% FBS, 100U/mL
367 penicillin, 100 μ g/mL streptomycin, 0.25 μ g/mL amphotericin, 100 μ M non-essential amino-
368 acids, and 1 mM sodium pyruvate (Gibco). Cells were characterized for α -SMA expression
369 using a mouse monoclonal anti- α -SMA antibody (clone 1A4, Dako) or mouse IgG2a isotype
370 control (clone DAK-GO5, Dako) by flow cytometry and used between passage 2-6.

371

372 Fibrocytes (n=6) were isolated from peripheral blood mononuclear cells as described
373 previously (39). PBMCs were washed twice with HBSS and cultured in tissue culture flasks
374 coated with 40 µg/ml fibronectin for 5 -10 days prior to experimentation.

375

376 Prior to experimentation ASM cells from each individual donor were incubated in media in the
377 presence of a selective DP₂ agonist (DK-PGD₂, Cayman Chemical Company (40)) or selective
378 DP₂ antagonists (CAY10471, OC000459 and fevipiprant, Cayman Chemical Company and
379 Novartis (41-43) vs appropriate vehicle controls (Dimethyl sulfoxide (DMSO) for DK-PGD₂,
380 CAY10471 and OC000459, and 10% dH2O in DMSO for fevipiprant).

381

382 **Wound healing assay**

383 ASM cells from individual donors were seeded onto 6 well plates coated with 10 µg/ml
384 fibronectin at a density of 2×10⁵ cells and allowed to adhere and reach 90-100% confluence.
385 Cells were then serum deprived for 24h. Cells were wounded by scratching using a sterile 200
386 µl pipette tip in a predetermined grid pattern (44). Following wounding ASM cells were
387 washed x4 with serum free media prior to addition of serum free media with DK-PGD₂ (10-
388 100 nM), fevipiprant (10-500 nM), CAY10471 (10-100 nM) or OC000459 (10-100 nM) or
389 vehicle control for 24 h. Photographs of 4 different wounded areas per condition were then
390 photographed at baseline and after 24h using an EVOS xl core cell imaging system (Thermo
391 Fisher Scientific), and the outline of the wound at time zero transposed onto the corresponding
392 24h photograph. The number of cells that had moved into the wounds were analysed by a
393 blinded observer.

394

395 **Computational model approach and framework**

396 The computational model capturing airway remodeling was developed via the agent-oriented
397 approach (13), which charts the spatiotemporal evolution of a system as a result of flexible,
398 high-level interactions between agents as well as agents and their environment (14). The
399 *Flexible Large-scale Agent-based Modelling Environment* (www.flame.ac.uk), an agent-based
400 platform employing *stream communicating X-machines* (45) as agents, was utilized to develop
401 the model.

402

403 **The baseline model and computational iterations**

404 Based on the agents, set of rules, and initial conditions (table 1, table S1, Fig. S1, Fig. S2,
405 supplementary materials) a baseline model of airway remodeling, comprising epithelial,
406 mesenchymal, and inflammatory parameters, was developed that captures trends observed
407 during normal airway remodeling, and additionally following introduction of abnormal levels
408 of variation within model parameters leads to the emergence of patterns observed during
409 pathological remodeling and, as such, the key hallmarks of asthma – this approach is referred
410 to as *pattern-oriented modelling* (13). After review of clinical literature, the following clinical
411 markers were considered to appropriately reflect the key hallmarks of asthma: i) eosinophilic
412 inflammation (defined as eosinophils/mm² submucosal area) >10 (5, 11, 46), ii) epithelial
413 integrity <70% (4-5, 47-50) and iii) airway muscle mass/wall area ≥10% and ≤50% (4-5, 47,
414 49).

415

416 The model starts by assessing the epithelial integrity, the number and location of inflammatory
417 cells (both the universal inflammatory cells and eosinophils), and the status of muscle cells.
418 Remodeling is initiated in case of a compromised epithelium or increased inflammation within
419 the system, resulting in a cascade of events, which, depending on the relevant boundary

420 conditions, lead to further inflammation, fibrosis, goblet cell hyperplasia, recruitment of
421 muscle, and increased collagen deposition. Furthermore, remodeling, could be exacerbated or
422 prolonged by the nature of initial or secondary conditions assigned to the computation.

423

424 More specifically, a normal or ‘healthy’ set of conditions triggered remodeling in the absence
425 of an intact epithelium (or a challenge that resulted in epithelial denudation) by initiating
426 fibrosis and recruiting the universal inflammatory cell. The inflammatory cell further ‘released’
427 pro-inflammatory cytokines to recruit eosinophils and muscle – the latter was accounted for in
428 the model by the differentiation of fibroblasts into myofibroblasts. The eosinophils, moreover,
429 caused further damage by degranulating and releasing cytotoxic proteins, which, if close to the
430 epithelium, resulted in necrosis of the epithelial cells – thereby, prolonging remodeling. We
431 worked with the hypothesis that any set of conditions that perpetuate these interactions will
432 result in pathological remodeling, thereby capturing the hallmarks of asthma. The various
433 parameters and their quantitative values, derived from existing literature, have been, along with
434 the relevant references, listed in table 1, with a schematic interlinking the various elements of
435 the model shown in Fig. S2.

436

437 While the model does not explicitly consider cytokine activity, i.e. their release, diffusion, and
438 half-life, it implicitly accounts for it by requiring that those cells impacted by the cytokine
439 molecules share a localized region with the effector cell. For example, only ASM cells within
440 close proximity of the universal inflammatory cell will undergo hypertrophy or contraction,
441 refer to supplementary material for more details.

442

443 Finally, the simulations progress in a number of time steps, with each time step matching 1
444 hour of real time. Time intervals of 30 minutes and 2 hours were also tested on the baseline

445 case (Case I) and yielded results indistinguishable from simulations conducted with 1-hour
446 time steps. Thus, we opted for the 1-hour interval to strike a balance between computational
447 costs and ensuring adequate resolution regarding activities we wished to capture via the model.
448 The total simulated time for all simulations, including remodeling and intervention, was ~6
449 months (4350 iterations). This time period allowed investigation of both the short- and long-
450 term response following either a challenge or intervention. Each model was simulated five
451 times (n=5) to assess the sensitivity of the model to inherent stochastic elements (such as cell
452 cycle, new coordinates of the daughter cells and migration of the universal inflammatory cells).
453 The internal random elements accounted for intra- and inter-cellular biological stochasticity.
454 Testing model for insensitivity to these random elements also served to provide an indicator
455 for model precision.

456

457 A detailed description of the model, its development, and its validation is provided in the
458 supplementary materials.

459

460 **Statistical analysis**

461 Statistical analysis was performed using with SAS/STAT software and GraphPad Prism. Data
462 were tested for normality using the Shapiro-Wilk test. For normally distributed data, two-tailed
463 paired t-tests, one sample t-tests, or one-way ANOVA were used as appropriate. For non-
464 parametric data, Wilcoxon matched pairs sign ranked test or Kruskal-Wallis tests were used as
465 appropriate. Correlations were performed using Spearman's correlation. Details of statistical
466 tests used are provided in figure legends. $p < 0.05$ was considered statistically significant.

467 **List of Supplementary Materials**

468 **Materials and Methods**

469 **Fig. S1: The virtual airway at baseline.**

470 **Fig. S2: Model parameters and agent interactions.**

471 **Fig. S3: Flow cytometric analysis of ASM cells.**

472 **Fig. S4: DK-PGD₂, fevipirant, CAY10471, and OC000459 had no effect on ASM cell**
473 **number, apoptosis, or necrosis after 24h.**

474 **Fig. S5: DK-PGD₂, fevipirant, and CAY10471 had no effect on ASM proliferation after**
475 **72h.**

476 **Fig. S6: DK-PGD₂, fevipirant, and CAY10471 had no effect on basal or bradykinin-**
477 **induced ASM contraction.**

478 **Fig. S7: Conceptual summary.**

479 **Table S1. Description of agents used in computational model.**

480 **Table S2. Alterations made to epithelial parameters in the computational model.**

481 **Table S3. Alterations made to mesenchymal parameters in the computational model.**

482 **Table S4. Alterations made to inflammatory parameters in the computational model.**

483 **Table S5. Clinical characteristics of subjects that provided additional bronchial biopsies**
484 **for primary ASM cultures.**

485 **Table S6. Analysis of expression of genes involved in prostaglandin D₂ biosynthesis and**
486 **metabolism in ASM cells.**

487 **Table S7. Output of computations simulating pathological airway remodeling.**

488 **Data File S1. Data values for individual experiments.**

489 **References and notes**

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721

722 **Author contributions**

723 All authors contributed to the study concept and overall study design and read, edited and
724 approved the final manuscript. RS designed and conducted the in vitro experiments, analysed
725 data and wrote the draft manuscript. LC, RB, DK, AJS and MSB contributed to the design and
726 undertaking of experiments, analysed data and contributed to figures. HK participated in
727 computational modeling study design, developed the various agent-based models, conducted
728 the computational modeling, analysed the data and wrote the draft manuscript. RHS, CEB, SS
729 and BSB helped conceive the computational modeling. CEB, IDP, SS, AJW, RAK, RB, SG,

730 AS and MB contributed to the design and delivery of the clinical trials, recruitment and
731 characterisation of patients. CEB conceived the study, participated in experimental design and
732 wrote the draft manuscript.

733

734 **Conflicts of interest**

735 CEB serves on advisory boards for GlaxoSmithKline, AstraZeneca, Boehringer Ingelheim,
736 Chiesi, Roche, receives honoraria from Novartis, and receives research support from
737 GlaxoSmithKline, AstraZeneca, Chiesi, Novartis, Boehringer Ingelheim and Roche. AJW
738 serves on Advisory Boards for GSK, Astra Zeneca, Pulmocide, KNOPP Pharmaceuticals and
739 Anaxsys. In the last 5 years IDP has received speaker's honoraria for speaking at sponsored
740 meetings from Astra Zeneca, Boehringer Ingelheim, Aerocrine, Almirall, Novartis, Teva and
741 GSK and a payment for organising an educational event from AZ. IDP has received honoraria
742 for attending advisory panels with Almirall, Genentech, Regeneron, Astra Zeneca, Boehringer
743 Ingelheim, GSK, MSD, Schering-Plough, Novartis, Dey, Napp, Teva, Merck and Respivert.
744 IDP has received sponsorship to attend international scientific meetings from Boehringer
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746 conferences from GSK and Chiesi. At the time of this study RAK was an employee of Novartis
747 Pharmaceuticals AG. SS has performed advisory services for Mundipharma, GSK, Astra
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749

750 **Data and materials availability**

751 The agent-based model is available from figshare, doi: 10.25392/leicester.data.7610933 for
752 research purposes under the Creative Commons Attribution Non-Commercial 4.0 International
753 (CC BY-NC 4.0) license. Fevipiprant is in phase 3 trials and until licensed is not available to
754 other researchers to undertake clinical trials without permission from Novartis. Fevipiprant was

755 provided to the University of Leicester under a Material Transfer Agreement and is also
756 available from commercial suppliers. The gene array data have been deposited in the
757 ArrayExpress database at EMBL-EBI (www.ebi.ac.uk/arrayexpress) under accession number
758 E-MTAB-7346. All data are present in the main text or in the Supplementary Materials.

Category	Activity	Rules	Parameters	Baseline Value	Comments
Epithelial	Migration	Dedifferentiated epithelial cells migrate to repair the damaged epithelium, then undergo proliferation.	Migration rate	5 μm/h	Migration rate was consistent with in vitro studies (16-18).
			Migration delay	5h	Dedifferentiated cells migrate after 5h; doubled to 10 h to represent slowly recovering epithelium.
	Differentiation	Cells at the edge dedifferentiate into a flattened phenotype.	Dedifferentiation probability	50%	A 50% probability per iteration was applied to determine whether an epithelial cell dedifferentiates. This was altered to 5% per iteration for the defective epithelium.
			Delay in proliferation	2-8 h	Edge cells require 2-8h to flatten out (16); this was increased by 3X (6–24h) for slow epithelial recovery.
	Proliferation	Dedifferentiated epithelial cells proliferate following their migration to the opposite edge of a compromised epithelium.	Ciliated:Goblet ratio	0.7:0.3 & 0.1:0.9	The number of goblet cells increase by 2–3X in severe asthma (19-22) given the inflammation status in disease. The probability of differentiating to a ciliated: goblet cell fate was either 0.7:0.3 (less inflamed) or 0.1:0.9 (more inflamed).
Apoptosis	This feature was not included in the baseline model.	Auto-denudation	N/A	No apoptosis rate was applied to the baseline model. In 'mild' shedding every 25 h cells underwent apoptosis with 50% probability; 'moderate' apoptosis with the probability of 1% at each iteration; 'extreme' 10% at each iteration.	
Inflammatory	Cell migration and activation	Inflammatory cells migrate into the airway in response to epithelial denudation, and their activation promotes eosinophil recruitment.	Frequency of recruitment	120 h	Inflammatory cells were added every 120h to the model with recruitment frequency increased to 60h and 50h in disease.
			Inflammatory cells recruited	30	Inflammatory cell number was chosen to reflect previous reports (11) and, in disease, this was increased by 1.5-2X (23).
			Eosinophil recruitment	45	Eosinophil recruitment was triggered by increased inflammatory cell number; 45, based on previous reports (11) and in disease this threshold was halved.
	Degranulation	Inflammatory cell activation promotes cell recruitment and fibroblast differentiation	Inflammatory cytokine release	25/ 75/ 105 h	The 'universal' inflammatory cell was assigned 150h life; releasing cytokines for 25h (or 75 and 105h for epithelial integrity of <55% and 30% respectively). In disease, inflammatory cell life was reduced to 65, 40, and 25 h (releasing cytokines for 85, 110, and 125h, respectively).
Apoptosis	Inflammatory cells promote eosinophil survival	Eosinophil life in the airway	10/ 30/ 45h	Eosinophils survival is ~10h within a normal airway (24). This was increased to 30 and 45h for epithelial integrity of <55% and 30% respectively. In disease, the life of eosinophils was doubled to 20, 60, and 90 h.	
Mesenchymal	Differentiation	Inflammatory cells promote increased ASM mass	ASM activation	25 cells	The threshold number of inflammatory cells above which myofibroblast-ASM differentiation is induced (11) which was reduced by 50% in disease.
	Differentiation	Inflammatory cells promote fibroblast-myofibroblast differentiation	(Myo)fibroblast differentiation probability	30%	Increased fibroblast differentiation or myofibroblast recruitment in the presence of activated inflammatory cells increased to 50% in disease.
	Proliferation	Fibroblast proliferation increased by inflammatory and epithelial cells	Fibroblast growth rate	132 iterations	Animal models indicate that lung fibroblasts divide every 5.5 days (132 iterations in model), which reduces to 2 days (48 iterations in model) in the animal model of asthma (25).
	Apoptosis	Myofibroblast survival supported by activated inflammatory cells	Myofibroblast apoptosis	5 cells	The threshold number of inflammatory cells below which myofibroblast apoptosis was induced, which was reduced to 2 in disease.

759

760 **Table 1. Agents, Rules and Model.** The computational airway model rule-set, parameters, and
761 which parameters were altered to observe airway remodeling.

762 **Figure legends**

763

764 **Fig. 1. Increased ASM mass in asthma is reduced by fevipiprant.** **A.** Representative
765 photomicrograph of a bronchial biopsy from a participant with severe asthma in the fevipiprant
766 (DP₂ antagonist) trial, showing increased ASM (brown stained α -SMA), disrupted epithelium
767 and lamina propria. **B.** ASM mass, as measured by percentage α -SMA positive area, in
768 bronchial biopsies from asthmatic subjects pre- and 12 weeks post-treatment with fevipiprant
769 (n=14) or placebo (n=13). A two-tailed paired t-test was used for within group comparisons
770 (p=0.022 and p=0.522), and a two-tailed unpaired t-test was used to compare the difference in
771 ASM mass observed following treatment with fevipiprant to that seen in the placebo group
772 (p=0.034).

773

774 **Fig. 2. Computational model-based investigation of interactions between airway**
775 **inflammation and ASM mass.** **A.** The mean time course from 6 simulations of the response
776 to epithelial injury (50% denudation at time zero) over 180 days showing increased eosinophil
777 numbers, ASM mass and persistent epithelial damage in the model of airway remodelling in
778 asthma versus resolution of the epithelial injury, eosinophil numbers and persistently low ASM
779 mass in the healthy control model (p<0.01 for comparisons of each parameter over time
780 between the patient model versus healthy control model, two-tailed unpaired t-tests). **B.**
781 Predicted reduction in eosinophil number over 180 days following reduction in eosinophil
782 recruitment or increase in eosinophil apoptosis in the computational model (n=5 simulations).
783 **C.** Relative change in the ASM mass percentage at 180 days, predicted as a consequence of
784 results in panel B (n=5 simulations).

785

786 **Fig. 3. ASM cells express functional DP₂.** **A.** Representative photomicrograph of DP₂ staining
787 in bronchial biopsies from a subject with severe asthma (inset: isotype control). **B.** Quantitative
788 PCR cycle threshold values for expression of ASM DP₂ mRNA vs the 18S ribosomal RNA
789 housekeeping gene *RNA18S5*, mean DP₂ Ct (threshold cycle) [95% CI]: 27.9 [26.1 - 29.8],
790 n=7. **C.** Example histogram of DP₂ expression (black trace) in ASM cells by flow cytometry
791 versus isotype control antibody (grey trace); fold increase in geometric mean fluorescence
792 intensity (GMFI) of anti-DP₂ antibody/isotype control antibody [95% CI]: 1.3 [1.2 - 1.4], n=15
793 donors, p<0.001, two-tailed paired t-test against isotype control. **D.** Representative
794 photomicrographs (x20 magnification) showing ASM α -SMA expression (green, left hand
795 panel; isotype control antibody, inset) and ASM DP₂ expression (red, right hand panel; isotype
796 control antibody, inset) by immunofluorescence staining; nuclei are stained with 4',6-
797 diamidino-2-phenylindole (DAPI, blue). **E.** F-actin polymerisation in primary human ASM
798 cells (n=9 donors) in response to DK-PGD₂ treatment or Dulbecco's Modified Eagle's Medium
799 (DMEM) containing 50% FBS as a positive control; geometric mean AUC DK-PGD₂ DR [95%
800 CI]: 46 [25 - 104] x 10²; p=0.01, one sample t-test against a hypothetical value of zero. **F.**
801 Intracellular calcium (Ca²⁺_i) elevation in primary human ASM cells (n=6-9 donors) in response
802 to DK-PGD₂ treatment or ionomycin (1.5 μ g/ml) as a positive control; geometric mean AUC
803 DK-PGD₂ DR [95% CI]: 130 [78 - 230] x 10³; p=0.002, one sample t-test against a
804 hypothetical value of zero. Data are plotted as mean \pm sem. Two-tailed paired t-tests were
805 performed to compare each condition with its vehicle control; * p < 0.05, except FBS where
806 Wilcoxon matched pairs sign ranked test was used, denoted by ^ p < 0.05.

807

808 **Fig. 4. A DP₂ antagonist reduces ASM migration and recruitment of myofibroblasts and**
809 **fibrocytes.** All experiments were carried out in serum-free media. **A.** Shown are data for the
810 wound closure after 24h of ASM cells that had been grown in monolayers and then wounded

811 by scratching with a pipette tip followed by incubation with different treatments for 24h: DP₂
812 agonist DK-PGD₂ (n=4-5 donors), the DP₂ antagonists fevipiprant (n=8 donors), CAY10471
813 (n=6-8 donors) and OC000459 (n=7 donors), or DMEM culture medium containing 10% FBS
814 as a positive control. Two-tailed paired t-tests were performed to compare each condition with
815 its vehicle control; * p<0.05 vs vehicle control. Data are expressed as mean ± sem. **B.**
816 Representative photographs of ASM monolayers wounded by scratching with a pipette tip
817 after 24h (vehicle control for fevipiprant, 500 nM fevipiprant, DMEM containing 10% FBS
818 control (upper panel); vehicle control for CAY10471 and OC000459, 100 nM CAY10471 and
819 100 nM OC000459 (lower panel), black lines represent the wound edge at 0h, scale bar = 250
820 µm. **C.** PGD₂ release by unwounded and wounded ASM cells after 24h; p=0.02, Wilcoxon
821 matched pairs signed rank test, n=10 donors. Data are expressed as mean ± sem. **D.**
822 Representative flow cytometry traces of isotype control antibodies (grey traces) versus α-SMA
823 expression (left hand panel, black trace, mean percentage fibrocyte population positive for α-
824 SMA expression [95% CI]; 97 [93 – 100] %, n=4 donors) and DP₂ expression (right hand panel,
825 black trace, GMFI fold difference DP₂ antibody/isotype control antibody [95% CI]; 1.6 [1.3 –
826 2]; p=0.0064, two-tailed paired t-test against isotype control antibody, n=6 donors) by
827 fibrocytes. **E.** Correlation between change in myofibroblast number in the lamina propria and
828 absolute change in ASM mass as a percentage of the total biopsy area (fevipiprant: black circle,
829 n=14, placebo: black triangle, n=13), Spearman r [95% CI]: r=0.347 [-0.050-0.649]; p=0.076.
830 **F.** Correlation between change in fibrocyte number in the lamina propria and absolute change
831 in ASM mass as a percentage of the total biopsy area (fevipiprant: black circle, n=12, placebo:
832 black triangle, n=13), Spearman r [95% CI]: r=0.538 [0.169-0.774]; p=0.006. **G.** Predicted
833 relative reduction in percent ASM mass at 180 days in the computational model as a
834 consequence of reduced myofibroblast recruitment (30-50%) in combination with a 40%
835 reduction in eosinophil recruitment in the computational model (n=5 simulations).