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Loss of the homeostatic protein BPIFA1, leads to exacerbation of otitis media severity in the Junbo mouse model

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Otitis Media (OM), or middle ear (ME) inflammation, is characterized by epithelial abnormalities and defects in innate immunity in the middle ear (ME). Although, BPIFA1, a member of the BPI fold containing family of putative innate defence proteins is abundantly expressed by the ME epithelium and SNPs in Bpifa1 have been associated with OM susceptibility, its role in the ME is not well characterized. We investigated the role of BPIFA1 in protection of the ME and the development of OM using murine models. Loss of Bpifa1 did not lead to OM development. However, deletion of Bpifa1 in Evi1abo+ mice, a model of chronic OM, caused significant exacerbation of OM severity, thickening of the ME mucosa and increased collagen deposition, without a significant increase in pro-inflammatory gene expression. Our data suggests that BPIFA1 is involved in maintaining homeostasis within the ME under steady state conditions and its loss in the presence of inflammation, exacerbates epithelial remodelling leading to more severe OM.

Otitis Media (OM), or middle ear (ME) inflammation, is the most prevalent paediatric disease and the leading cause of paediatric surgery, antibiotic prescription and conductive hearing impairment1. Acute OM is primarily caused by the normally commensal bacteria non-typeable Haemophilus influenzae (NTHi), Streptococcus pneumoniae and Moraxella catarrhalis2 while chronic forms of OM show a genetic component of 45–75%3. The large numbers of OM susceptibility genes that have been identified emphasize the importance of innate immunity in protection against OM development4–7. More than 20 mouse genetic models of chronic OM have been characterised in recent years and these have proven to be a powerful tool in understanding the pathobiology of OM (For review, see 8) One such model is the N-ethyl-N-nitrosourea (ENU) mutant mouse, Junbo, that spontaneously develops chronic suppurative Otitis media (CSOM) under specific pathogen free (SPF) conditions, characterised by development of cellular fluid and hypoxia in the ME and inflammatory thickening of the mucoperiosteum. The causative mutation is a SNP in the gene encoding the transcription factor EVI1, also known as MECOM8,9. EVI1 is an inducible negative regulator of NFkB10 and a repressor of the TGFβ signalling pathway11. The heterozygous mutant Evi1abo+/− mouse has increased responsiveness to microorganisms and inflammatory stimuli12. The ME is an anatomical extension of the upper respiratory tract (URT) and demonstrates similar physiological and immune mechanisms. The epithelium of the URT and its secretions play a key role in protection against environmental insults and infections. BPIFA1, a member of the bacterial permeability-increasing (BPI) fold containing family of putative innate defence proteins, is one of the most abundant secretory proteins in the URT. Its expression is restricted to the nasal passages, oropharynx, trachea and bronchi13,14, where it localises to a non-goblet, non-ciliated population of secretory cells15, minor glands and mucous cells of the sub-mucosal glands16–18. Secreted BPIFA1 is found in nasal lavage, saliva, sputum and bronchoalveolar lavage (BAL)19 and in the apical surface lining (ASL) fluid from air liquid interface cultures of differentiated tracheobronchial epithelial cells16,17.
Alterations of BPIFA1 levels are associated with multiple URT diseases such as cystic fibrosis and chronic rhinosinusitis. Despite the lack of compelling mechanistic evidence to identify the precise biological function of BPIFA1, an increasing number of studies suggest that it plays a multifunctional host defence role in the conductive airways. In line with the structural similarity to BPI, BPIFA1 exhibits antimicrobial activity against a variety of respiratory pathogens and deletion of Bpifa1 in mice is associated with increased susceptibility to pulmonary infections. Other proposed functions of BPIFA1, include a surfactant-like activity, dispersal of bacterial biofilms, and regulation of ASL volume by modulation of epithelial sodium channel (ENaC) function.

Recently, evidence of BPIFA1 expression in the ME and its involvement in OM pathogenesis has started to emerge. Knocking down Bpifa1 expression in vivo using siRNA in chinchillas led to impaired mucociliary clearance and BPIFA1 protein was present in the effusions of patients with chronic OM and BPIFA1 was also identified as one of the top hits in a Genome Wide Association Study of genes associated with OM susceptibility. We recently showed production of BPIFA1 in the murine ME, in vivo and in vitro and it has been reported that Bpifa1−/− mice greater than 10 months-of-age show increased susceptibility to spontaneous development of chronic OM. Together this data suggests that BPIFA1 may be a determinant for predisposition to OM.

In this study, we have studied the role that BPIFA1 plays in protection of the ME and its association with OM development. Our data shows that although the loss of BPIFA1 did not lead to the development of spontaneous OM in mice up to 6 months-of-age, it significantly exacerbates the inflammatory phenotype in the Junbo model of chronic OM. Our data suggests that BPIFA1 is involved in maintaining homeostasis within the ME under steady state conditions. This is the first study to report the use of compound Bpifa1 mutants and it underlines the importance of investigating the additive effect of multiple genetic defects in order to better understand the aetiology of multifactorial diseases such as OM.

Results

BPIFA1 is localised to the middle ear epithelium from birth but loss of the protein is not associated with spontaneous or bacteria induced development of OM. We have previously reported significant production of BPIFA1 in the respiratory epithelium of the nasal passages and ME. In order to evaluate the onset of BPIFA1 production during the post-natal development of the bulla, immunohistochemistry (IHC) was performed from the day of birth (P0) to P30 at intervals of 5 days. BPIFA1 was detected in the ME throughout this period. As described previously, between P0 to P10, the ME space is occupied by mesenchyme and BPIFA1 was detected in the non-ciliated epithelium enclosing this mesenchyme mass, in the region where it retracted from the opposing epithelial surface. Regression of the mesenchyme began at P5, until an air filled cavity was formed by P15. BPIFA1 was localised to the non-ciliated cells throughout the ME epithelium from P15 to P30 (Fig. 1C,D,E,G). The epithelium that lines the internal surface of the tympanic membrane (Tm) also stained positively for BPIFA1 (Fig. 1F).

Having established that BPIFA1 is present in the ME epithelium during the process of bulla cavitation, we went on to determine whether loss of the protein caused OM. Hearing thresholds, measured using broad-spectrum Auditory Brainstem Response (ABR) (which is indicative of conductive hearing loss), did not differ significantly in Bpifa1−/− and Bpifa1+/+ mice compared to WT mice at 8 (data not shown) or 12 weeks of age (Fig. 2A). Histological assessment of WT and Bpifa1−/− mice did not show signs of OM development, such as middle ear mucosal thickening or fluid build-up, at 12 weeks (Fig. 2B,C) or 6 months of age (Fig. 2D) (Sup Fig. 1). No morphological differences were noted in the nasal passages, trachea or lung, (the primary sites of BPIFA1 expression) between WT and Bpifa1−/− mice up to 6 months of age (Sup Fig. 2) and no evidence of inflammatory disease was detected following a comprehensive screen of 42 tissues of Bpifa1−/− mice at 6 months of age (data not shown).

As the development of OM is often associated with bacterial infection, we investigated whether the loss of BPIFA1 modulated the ability of mice to respond to the intranasally (IN) inoculated ototopathogen NTHi. The majority of ME bullae examined after culling the mice at day 3 post inoculation, were healthy, air-filled and had intact tympanic membranes. Only a small proportion of Bpifa1−/− (2/12) and Bpifa1+/+ (2/8) bullae contained NTHi culture positive. WT bullae (n = 16 ears) did not have fluids and all were NTHi culture negative. Although this data was suggestive of an effect of Bpifa1 on infection these differences did not achieve statistical significance. A similar outcome was achieved when we challenged WT, Bpifa1+/+ and Bpifa1−/− mice with NTHi using baroinoculation and sampled bulla fluids at day 3 post-inoculation (data not shown).

Taken together, the data suggested that deletion of Bpifa1 does not lead to spontaneous development of OM and does not lead to an increased ME infection or overt induction of OM following NTHi inoculation.

Evi1−/− mice show alterations of BPIFA1. As the loss of BPIFA1 did not result in spontaneous OM or increased susceptibility to ME infection following intranasal bacterial challenge we investigated how the protein might influence OM disease progression in an established model of OM, the Evi1−/− mouse. OM initiates spontaneously in Evi1−/− mice from P21 onwards and is characterised by significant remodelling of the middle ear epithelium. At P28, HIC staining for BPIFA1 appeared to be reduced in the ME epithelium of Evi1−/− mice compared to their age matched WT littermate controls (Fig. 3A,B) and continued to reduce with OM progression up to P56 (Sup Fig. 3). In WT mice there was strong staining throughout the middle ear epithelium whereas staining in the Evi1−/− mice was seen in fewer cells and on the epithelial surface (Fig. 3B). To confirm whether the reduction in the epithelial staining intensity of BPIFA1 in Evi1−/− bullae was a result of a difference in epithelial gene expression, we compared expression of Bpifa1 in freshly isolated ME mucosal cells (mMMCs) from WT and Evi1−/− mice using RT-qPCR. This analysis showed that there was a significant down-regulation of Bpifa1 mRNA in Evi1−/− mMMCs when compared to WT (Fig. 3C). However, BPIFA1 was clearly seen in the inflammatory exudates in histology sections of Evi1−/− mice by IHC (Fig. 3B) and by western blotting of Evi1−/− bulla fluid (Fig. 3D). The lack of middle ear fluid in WT mice precluded analysis of the secreted protein in these animals.
Loss of Bpifa1 leads to an exacerbation of OM severity in P28 Evi1<sup>Jbo/+</sup> mice. Next we tested if loss of BPIFA1 altered the prevalence or severity of OM in the Evi1<sup>Jbo/+</sup> mouse. To do this we backcrossed the Bpifa1<sup>−/−</sup> mice onto the same background as the Evi1<sup>Jbo/+</sup> mice, C3H/HeH. Analysis of the ME of P28 mice showed that histological OM was highly prevalent in both Evi1<sup>Jbo/+</sup> and Bpifa1<sup>−/−</sup>-Evi1<sup>Jbo/+</sup> mice as evidenced by microscopic thickening of ME mucosa and variable presence of bulla fluids and their cellularity (Fig. 4A–H). However, the proportion of Bpifa1<sup>−/−</sup>-Evi1<sup>Jbo/+</sup> ears that had grossly evident bulla fluids was significantly higher.

**Figure 1.** BPIFA1 is localised to the middle ear epithelium from birth. Low and high magnification images, representative of n = 3 mice showing IHC for BPIFA1 localisation in the non-ciliated epithelial cells of the developing ME cavity at P5 (A,B), P15 (C,D,E) and P30 (F,G). The mesenchyme which fills the post-natal ME cavity (A,B) is resorbed by P15 to form a fully air filled adult ME cavity (C).
Figure 2. Loss of the BPIFA1 is not associated with hearing deficits or development of OM. Auditory brain stem thresholds for Bpifa1−/− (n = 13) and Bpifa1+/− (n = 18) mice do not differ significantly from those of WT mice (n = 9) at 12 weeks of age (A). p > 0.05 for One-way ANOVA with Tukey’s posthoc test. Representative High power images of H&E sections of the ME of n = 8 WT (B), and Bpifa1−/− (C) at 12 weeks age and n = 13 Bpifa1−/− (D) mice at 6 months of age show no histological abnormalities. Scale bar 50 µm for 60x objective images.

Exacerbation of OM in Bpifa1−/− Evi1Bos−/− mice is not due to an enhanced proinflammatory response, differentiation or proliferative response. As BPIFA1 has been suggested to exhibit an anti-inflammatory role we evaluated whether exacerbation of OM severity in Bpifa1−/− Evi1Bos−/− mice resulted in an enhanced cytokine response. In order to test this, gene expression analysis for a selected panel of inflammatory markers was performed on RNA from freshly isolated mouse middle ear mucosal cells (mMMCs) from 7 to 10 week old Bpifa1−/− Evi1Bos−/−, Evi1Bos+/−, Bpifa1−/− and WT mice. Although mMMCs of Evi1Bos+/− and Bpifa1−/− Evi1Bos−/− mice had significantly elevated levels of the pro-inflammatory cytokines Cxc2, Il1β, Tnfa, and the profibrotic mediator, Tgfβ3, compared to WT mMMCs, there was no significant difference in the expression levels for any of these genes between WT and Bpifa1−/− mMMCs or between Evi1Bos−/− and Bpifa1−/− Evi1Bos−/− mMMCs (Sup Fig. 3A–D), suggesting that the loss of Bpifa1 did not modulate the cytokine response.

To evaluate if Bpifa1 loss on the Evi1Bos+/− background led to an alteration in other epithelial cell types, we investigated expression of the secretory cell marker, Muc5ac, and the ciliated cell marker, Foxj1, in Bpifa1−/− Evi1Bos−/−, Evi1Bos+/−, Bpifa1−/− and WT mMMCs. Foxj1 was significantly down regulated in Evi1Bos+/− and Bpifa1−/− Evi1Bos−/− mMMCs compared to WT mMMCs (Sup Fig. 5E). The difference in the level of expression of these markers between WT and Bpifa1−/− mMMCs and between Evi1Bos−/− and Bpifa1−/− Evi1Bos−/− mice did not reach statistical significance (Sup Fig. 5E,F). This suggests that Evi1Bos+/− mice show epithelial cellular alterations marked by down-regulation of Bpifa1 and Foxj1, but there is no significant additive effect of Bpifa1 deletion on expression of these epithelial cell type marker genes at this point. Muc5ac was significantly downregulated in Bpifa1−/− Evi1Bos−/− mice compared to WT mice, but not in Evi1Bos+/− mice, and there was also no significant difference between the levels of Muc5ac between Bpifa1−/− Evi1Bos+/− and Evi1Bos+/− mice (Sup Fig. 5F). Further evaluation using a larger number of mice may be necessary to unmask the potential effect of deletion of Bpifa1 on Muc5ac levels on the Evi1Bos−/− background.
In order to investigate if the OM phenotype of the hyper-proliferative mucosa in Evi1\textsuperscript{Jbo/+} and Bpifa1\textsuperscript{−/−} Evi1\textsuperscript{Jbo/+} mice resulted in a cell-autonomous defect in the ME epithelium, we compared in vitro growth characteristics of mouse middle ear epithelial cells (mMECs) and ibroblasts isolated from the bullae of Bpifa1\textsuperscript{−/−} Evi1\textsuperscript{Jbo/+}, Evi1\textsuperscript{Jbo/+}, Bpifa1\textsuperscript{−/−} and WT mice. No significant differences in doubling times were seen in either mMECs (Sup Fig. 5G) or ibroblasts (Sup Fig. 5H) cultured from the 4 genotypes, indicating that the cells proliferated at similar rates in vitro. Thus, our data suggests that there is no cell-autonomous proliferative or differentiation defect in the Bpifa1\textsuperscript{−/−} Evi1\textsuperscript{Jbo/+} cells that explains the differences observed in the ME in vivo.

Discussion

In this study we have explored the role of BPIFA1 in the context of ME host defence and OM. BPIFA1 is one of the most highly expressed proteins in the URT of humans and mice\textsuperscript{12,13}, and forms a major component of secretions from these sites\textsuperscript{12,13}. We have shown that the protein is present in the murine ME epithelium from birth. Bpifa1 is expressed in the mouse nasal passages from e14.5\textsuperscript{35,36} whereas expression in the mouse trachea begins around the time of birth\textsuperscript{36}. Previous reports have shown presence of BPIFA1 in the ME of mice aged 10–18 months\textsuperscript{30}. The abundant expression of BPIFA1 in the murine ME throughout the life span suggests a homeostatic role in protection of the ME epithelium and that its loss may play a role in the progression of OM.

However, our data shows that loss of Bpifa1 alone does not lead to the development of spontaneous OM in the mouse, up to 6 months of age. Although BPIFA1 is highly expressed in the nasal passages and trachea of WT mice, Bpifa1\textsuperscript{−/−} mice did not exhibit any overt phenotypes in these regions either. In contrast an ENU Bpifa1\textsuperscript{−/−} mutant, on a C3HeB/FeJ background, has been shown to develop low penetrance OM (30%) by 10–18 months of age\textsuperscript{30}. This apparent difference could be due to strain differences (as we have studied mice on C57BL/6J and C3H/HeJ backgrounds) and could be further examined by studying our Bpifa1\textsuperscript{−/−} model at a comparable age. However, OM is typically studied in young mice as this better represents the timing of the paediatric disease in humans\textsuperscript{9,28} and the relevance of any late development of the disease is unclear. As mice over expressing BPIFA1 showed reduced levels of lung fibrosis when exposed to a sterile irritant\textsuperscript{37}, it is possible that extended exposure to...
Figure 4. Exacerbation of otitis media severity in Bpifa1<sup>−/−</sup> Evi1<sup>bo/c+</sup> mice. Dorsal plane H&E sections from MEs of P28 WT (n = 28) (A,B) and Bpifa1<sup>−/−</sup> (n = 12) (C,D) mice show no otitis media development. Representative H&E sections from ME of P28 Evi1<sup>bo/c+</sup> (n = 34) (E,F) and Bpifa1<sup>−/−</sup> Evi1<sup>bo/c+</sup> (n = 32) (G,H) mice demonstrate presence of an OM phenotype characterised by mucosal thickening and the presence of inflammatory ear fluids (marked by star). Mucosa of Bpifa1<sup>−/−</sup> Evi1<sup>bo/c+</sup> (G,H) appears thicker than Evi1<sup>bo/c+</sup> mice (E,F). Scale bar 500 µm for low magnification images and 100 µm for high magnification images. High power images show overlays used to quantitate epithelial thickness. The percentage of MEs with grossly evident fluids (Fishers exact test) (I) and the mean mucosal thickness (One-way ANOVA with Tukeys post hoc test) (J) for Bpifa1<sup>−/−</sup> Evi1<sup>bo/c+</sup> was significantly higher compared to Evi1<sup>bo/c+</sup>, WT and Bpifa1<sup>−/−</sup> mice; *p < 0.05; **p < 0.01; ****p < 0.0001.
respiratory irritants or previous episodes of bacterial infection may be contributory to the low penetrance OM in aged Bpifa1−/− mice.

The loss of bpfia1 has previously been shown to predispose mice more severe respiratory infections following an experimental challenge and yet we found that IN challenge of Bpifa1−/− mice with the major otopathogen NTHi, did not result in significant ME infection, although our data did appear to suggest that Bpifa1−/− mice infection prevalence was marginally higher. NTHi is a significant causative pathogen isolated from a majority of AOM and COME patients and the potential role that BPIFA1 plays in defence against this organism requires further studies.

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**Figure 5.** Sub-epithelial fibrosis in Bpifa1−/− Evi1+/+ and Evi1−/+ middle ears. Picrosirius red staining showing collagen fibres in the sub-epithelial connective tissue of WT (A) and Bpifa1−/− (B) ME. Staining intensity increases in the inflamed and expanded mesenchyme of Evi1+/+ (C) and Bpifa1−/− Evi1+/+ (D) ME indicating increased deposition of collagen fibres. IHC analysis of ME sections shows no α-SMA staining in the thin sub-epithelial mesenchyme of WT (E) and Bpifa1−/− (F) ME epithelium but intense α-SMA staining in the lower half of the expanded mesenchyme of Evi1−/+ (G) and Bpifa1−/− Evi1−/+ (H) ME. Arrowheads indicate positive staining. Data is representative of n = 3 mice for all genotypes. Scale bar: 500 µm for 4x objective images and 50 µm for 60x objective images (insets).
Given the high levels of BPIFA1 seen in the ME, but the absence of spontaneous OM or lack of significantly increased susceptibility to ME infection by NTHi in our Bpifa1−/− mice, we investigated the contribution of the protein to OM disease progression by studying compound mutant Bpifa1−/−Evi1Bocc−/− mice. Evi1Bocc−/− mice represent an established model of OM and develop hallmarks of the disease soon after middle ear cavitation occurs. Our analysis suggests that BPIFA1 protein staining was reduced in the remodelled epithelium in Evi1Bocc−/− mice compared to WT. It seems possible that this loss of staining may be due to an alteration of cell populations in the mucosa, with a reduction in the number of BPIFA1 producing cells being present. However we could still readily detect the protein in the ME exudates from Evi1Bocc−/− mice. This is consistent with proteomic data from human ME exudates and our own data from the apical secretions of differentiated mMECs.

The most striking observation from these studies is that Bpifa1−/−Evi1Bocc−/− bullae demonstrated an exacerbation of OM severity compared to Evi1Bocc−/− mice. This suggests that removal of BPIFA1 from the middle ear environment allows for a more significant remodelling response. This further suggests a shifting of the time required to produce the OM phenotype. Indeed analysis of compound mutant mice at day 21 also revealed an exacerbation of OM severity (results not shown). It seems likely that the loss of BPIFA1 from the middle ear mucosa during the process of cavitation directly exacerbates the development of OM. Previous studies of Evi1Bocc−/− bullae demonstrated elevated inflammatory gene networks and hypoxia signalling genes compared to venous blood as a baseline control. We have shown up-regulation of the pro-inflammatory mediators Cxcl2, Tnfa, Il1β and Tgfb in the ME mucosa of Evi1Bocc−/− and Bpifa1−/−Evi1Bocc−/− mice. Evi1Bocc−/− and Bpifa1−/−Evi1Bocc−/− bullae also appeared to demonstrate epithelial cellular alterations characterised by down regulation of the ciliated cell marker, Fosj1, and the secretory cell marker, Mac3ac, and Evi1Bocc−/− mice demonstrated reduced levels of Bpifa1 expression. However, despite the exacerbated OM phenotype in Bpifa1−/−Evi1Bocc−/− mice, there was no significant additive effect of the loss of Bpifa1 on the expression of these inflammatory and epithelial markers. This may be a consequence of comparison based on the already inflamed Evi1Bocc−/− epithelium that has high basal expression levels of these inflammatory genes. At this time we are unable to identify exactly which cell type(s) express these pro-inflammatory markers but our mucosal cell isolation procedure generates a population of structural (epithelial and mesenchymal) cells without a significant inflammatory cell component.

The differences in the mucosal thickening of Evi1Bocc−/+ and Bpifa1−/−Evi1Bocc−/+ mice do not appear to be explained by proliferation rates of the epithelial cells and fibroblasts measured ex-vivo. It seems likely that inflammatory changes such as connective tissue oedema, dilation of lymphatics and blood vessels, infiltration of inflammatory cells and fibrosis are responsible for the mucosal thickening seen in the ME. An interesting feature observed in the inflamed Evi1Bocc−/+ and Bpifa1−/−Evi1Bocc−/+ MEs was fibrosis of the sub-epithelial connective tissue, indicated by collagen deposition and accumulation of myofibroblasts. These features are characteristic of fibrotic pulmonary diseases such as asthma and idiopathic pulmonary fibrosis, and indicative of epithelial remodelling due to an over-active wound repair response following inflammation. In turn this is suggestive of over-activation of the TGFβ signalling pathway (a target for EVI1)10. The enhanced thickness of the Bpifa1−/−Evi1Bocc−/+ mucosa compared to that of Evi1Bocc−/+ mice suggests greater fibrosis due to loss of BPIFA1. BPIFA1 has been previously associated with an allergen-induced asthma-like phenotype in mice and overexpression of BPIFA1 has been shown to protect against pulmonary fibrosis. A recent report suggesting a role for BPIFA1 as an epithelial derived smooth muscle relaxing factor is supportive of a potential role for this epithelial protein in mediating crosstalk with the underlying connective tissue.

Another important observation in this study was the downregulation of epithelial Bpifa1 in the inflamed microenvironment of the Evi1Bocc−/+ ears. This reduction in BPIFA1 may represent transcriptional down regulation of Bpifa1 or perhaps more likely is a consequence of phenotypic changes in the epithelial cell populations. Previous work with BPIFA1 has largely focused on evaluation of a role for the protein in bacterial and viral pathogen challenge studies or in the presence of pre-existing chronic allergic and inflammatory pulmonary disease (for review see46). Importantly, we did not observe any phenotypic abnormalities or signs of organ inflammation in the non-challenged Bpifa1−/− mice. Thus, the presence of an infectious or inflammatory stimulus seems to be a pre-requisite to uncover functional roles of BPIFA1. This may also explain why Bpifa1 deletion alone does not lead to the spontaneous development of OM in Bpifa1−/− mice. Consistent with this hypothesis we have recently shown that Bpifa1−/− mice are more susceptible to influenza A infection through a mechanism that allows Bpifa1 deficient cells to be more readily infected by the virus44.

This work provides new insights into the function of BPIFA1 in the ME. From birth onwards BPIFA1 is secreted at high levels into a film that overlies the epithelium lining the ME, but its absence does not predispose to spontaneous OM or increase the susceptibility to bacterial infection. This indicates that, within normal limits, BPIFA1 is a functionally redundant innate immune protein that plays a homeostatic role in mucosal protection in a manner described for multiple respiratory proteins47,48. Further studies are required to address this point and whether the mechanism(s) are via alteration in surfactant function, epithelial permeability, and/or impaired antimicrobial action.

We have explored the role of BPIFA1 in mouse hearing an OM predisposing Evil1 mutation, and shown an upregulation of ME epithelial cytokine expression and down-regulation of epithelial markers, with dispersal of BPIFA1 from this surface layer into bulla fluid. Deficiency of BPIFA1 on an Evil1 mutant background does not markedly alter epithelial cytokine and cell marker expression probably via perturbation of epithelial cell populations, and consequently exacerbates inflammatory thickening of the submucosal connective tissues.

Together this suggests that BPIFA1 aids homeostasis in the ME by contributing to the epithelial barrier function, and its role is revealed only under significant epithelial insult. Future time course studies are needed to defne whether the deletion of Bpifa1 on an OM prone background results in the earlier initiation of OM and whether, once initiated, the progression of disease is significantly altered. It is also important to study if loss of BPIFA1 exacerbates the OM phenotype in other OM mutant mouse lines. Given that features such as mucosal...
fibrosis have been noted in chronic OM in Tlr4 and Evi1 mutant mice, early fibrosis, and mucosal thickening may suggest accelerated disease in the absence of BPIFA1 rather than substantially altered pathogenesis.

Materials and Methods

Ethics statement. Mice were bred and maintained by the Mary Lyon Centre, MRC Harwell and were housed in specific-pathogen free conditions. All animal experimentation was approved by the Animal Welfare and Ethical Review Body at MRC Harwell. The humane care and use of mice in this study was under the authority of the appropriate UK Home Office Project License.

Mice and husbandry. Bpifa1−/− mice on a C57BL/6 background were obtained from Professor Ralph Shohet at the University of Hawaii. The generation of these mice in which exons 2 and 3 of the Bpifa1 gene have been deleted have been described in detail elsewhere. C57BL/6 Bpifa1−/− mice were re-derived at MRC Harwell Institute, UK and backcrossed 5 times to C3H/HeH mice to produce a congenic background. Junbo heterozygote (Evi1Homo) mice were maintained on the C3H/HeH background. Compound Bpifa1−/− Evi1Homo mutants and their littermate controls were generated by intercrossing Bpifa1−/− and Evi1Homo mice and mice were examined at P28 and at 6 months of age. P0-P30 WT C3H/HeH mice, used for IHC of BPIFA1, were obtained from MRC Harwell Institute. For comparative purposes Bpifa1−/− mice on the original C57BL/6 background and a mixed C3H/HeH-C57BL/6 background were used in some infection studies. Husbandry of SPF mice and microbiological surveillance is described elsewhere.

Auditory Brainstem Response (ABR) measurement. The hearing thresholds of 8 and 12 week-old mice were assessed using ABR measurements as previously described.

Tympanic membrane assessment. Mice were euthanized by intraperitoneal overdose of sodium pentobarbital (Pentoject Animalcare, UK). The mouse was decapitated and head skin removed. The tympanic membrane was examined under 10× binocular magnification to establish whether there was evidence of opacity which is indicative of macroscopic bulla fluid accumulation.

Histology. Tissue samples were fixed in 10% formaldehyde (Surgipath Europe) for 48 hours at room temperature and the skulls decalcified in Kristenson D.F.B agent (Pioneer Scientific) for 72 hours before wax embedding. Four μm H&E stained sections of the bullae and nasal passages were scanned using the NanoZoomer Digital Pathology system and morphometric measurements made with NanoZoomer software (Hamamatsu). Thickness of the ME mucosa was measured in a defined 1 mm area in the promontory region opposite the tympanic membrane. Average mucosal thickness was calculated using 5 measurements taken at a distance of 250 μm within this region. Both male and female mice were analysed and no sex-related differences were seen in the development of OM. H&E slides for sections of a total of 42 target tissues from Bpifa1−/− mice at 6 months of age were analysed for morphological abnormalities.

Immunohistochemistry. Four μm wax sections were used for IHC. Endogenous peroxidase activity was blocked using 0.3% hydrogen peroxide in methanol (Fischer Scientific, UK). Non-specific binding was blocked by incubating the sections in 100% goat serum for 30 minutes at room temperature. Sections were washed and incubated in rabbit anti-Bpifa1 (1:750) or rabbit anti-αSMA (1:200) (Abcam 5694) antibodies overnight in a humidified chamber at 4 °C then washed twice in PBS, incubated in 0.5% biotinylated polyclonal goat anti-rabbit secondary antibody (Vector Elite ABC kit, Cat No- SK-6101) for 30 minutes at room temperature, followed by incubation for 30 minutes with the ABC reagent for signal amplification before colour detection using a NovaRed system (Vector, Cat No- SK 4800). Images were captured with an Olympus BX61 light microscope and Olympus colour view digital camera.

Preparation of NTHI bacterial inoculum and intranasal inoculation. Intranasal bacterial challenge experiments, using genomically sequenced, streptomycin resistant strain NTHi #375 (NTHi37558), was performed as previously described.

Intranasal inoculation of mice using a barochamber. The baroinoculation protocol was adapted from previously published studies in mice and rats. For baroinoculation, mice were first anaesthetised with isoflurane then intranasally inoculated with 5 μl of 1 × 1010 CFU/ml NTHi into each nostril and placed in a pressure chamber (Scientific workshop, MRC Harwell Institute). The pressure was raised to approximately 1.4 pounds per square inch (Psi) by compressed air through an inlet port. Thereafter, the pressure was increased by approximately 0.7 Psi every 15 secs to achieve a maximum pressure of 5.8 Psi, then after 2 minutes was decreased by venting air via an outlet port at 30 seconds intervals to return the chamber to atmospheric pressure.

Middle ear cell isolation and culture. The isolation of mMECs was performed as previously described. Fibroblasts were isolated using a differential adherence method described in the same paper. Adherent fibroblasts were cultured by adding 5 ml of mMEC basic 10% FBS media to the tissue culture dish and incubating at 37 ºC in a 5% CO2 incubator till confluent. Upon confluence, cells were washed with warm HBSS and sub-cultured twice to obtain a pure fibroblast population. For the third passage, 3mls of Trypsin-EDTA solution (Sigma) was added to the dish and incubated as above for a minute to dislodge the cells. Trypsin was neutralised by adding of 3 ml neutralising medium (mMEC basic plus 10% FBS) and cells were centrifuged at 500 × g for 5 minutes. Cell pellets were resuspended in 5 ml of fresh mMEC basic 10% FBS and split into five T25 flasks for expansion of the fibroblast cultures. 4ml of media was added to each flask and cells were cultured at 37 ºC in 5% CO2 till confluence. When calculating population doubling time (PD), the purified fibroblasts were seeded at 5 × 104 cells/well
in mMEC basic 10% FBS media in 6 well tissue culture plates (Falcon). Similarly, fresh mMECs were seeded at 5 x 10^4 cells/well in mMEC-Plus media in submersed culture. Media was changed every 48 hours. Fibroblasts were harvested every 24 hours from day 1 to day 3 whereas mMECs were harvested every 48 hours by trypsinisation and quantified using a haemocytometer from day 2 to day 10. Population doubling time was calculated using the formula:

\[ PD = \frac{T \times \log 2}{\log C2 - \log C1} \]  

(1)

where, PD = Population doubling, T = time (24 hours for fibroblasts and 48 hours for mMECs), Log = Log_{10}, C1 = initial cell count, C2 = final cell count.

**Western Blotting.** Bulla fluids were sampled by pipetting as previously described, these were then mixed with an equal volume of 2XSDS lysis buffer. Samples were denatured at 95 °C for 5 minutes and resolved on a 12% polyacrylamide gel, transferred to a PVDF membrane using a semi dry blotting system (Biorad Trans-blot turbo) then probed with rabbit anti-Bpifa1 primary antibody (1:200), overnight at 4 °C. The primary antibody was detected using a polyclonal goat anti-rabbit secondary antibody (Dako P0448) conjugated with HRP (1:2000) and bound antibody was visualised using the EZ-Chemiluminescence detection system (Geneflow, Cat No-30500500B) and manual development. Images were scanned as a whole with no modification.

**Real time quantitative PCR (RT-qPCR).** For comparison of gene expression between WT, Bpifa1−/−, Evil−/− and Bpifa1−/− Evil−/− MEs, mouse mucosal epithelial cells (mMMEs), i.e. ME epithelial cells before undergoing the differential fibroblast separation, were used. Total RNA was extracted, cleaned from residual genomic DNA contamination, quantified and reverse transcribed into cDNA as previously described. RT-qPCR was performed using Applied Biosystems’ TaqMan gene expression assays for Cxcl2 (Mm00436450_m1), Tnfα (Mm99999068_m1), TGFβ3 (Mm01178820_m1), Bpifa1 (Mm00465064_m1), FoxJ1 (Mm01267279_m1) and Muc5ac (Mm01276718_m1) on a 7500 Fast Real Time PCR system (Applied Biosystems), with 2 × Taqman Fast Universal Master Mix (Applied Biosystems, Cat No-432574). 10 ng cDNA was added to each reaction and three technical replicates were performed for each assay in each batch. Target gene expression levels were normalized to three endogenous controls: Atp5b, Cxcl1 and Canx (Primerdesign geNorm™ Reference Gene Selection Kit) and analysed using ABI 7500 software v2.1. Using the 2−ΔΔCt method. Data is presented as mean Relative quantification (RQ) and error bars represent standard error of the mean.

**Statistics.** The normality of experimental data was determined by performing Levene’s test prior to the statistical analysis. GraphPad Prism (version 6.0) was used to perform all statistical tests. 2 tailed students t-test was used to compare two groups of data. One way or two-way analysis of variance (ANOVA) with Tukey’s post hoc test was used to compare more than two groups, for parametric data. Fisher’s exact test was used for analysing frequency data such as presence or absence of bulla fluids or genotype ratios (Chi squared analysis was used if there were more than 3 groups). Significance threshold was set at p < 0.05. Data are presented as the mean ±/− standard error of the mean (SEM) unless otherwise stated. Significance levels represented on graphs are as follows: ns = not significant; *p ≤ 0.05; **p ≤ 0.01; ***p ≤ 0.001; ****p ≤ 0.0001.

**References**

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Author Contributions
A.M., M.C. and C.D.B. conceived and designed the experiments and interpreted results. A.M. performed the majority of the experiments and analysed data. A.M. and C.D.B. wrote the paper. M.C., S.D.M.B. and L.B. assisted critical evaluation of results and drafting of the manuscript. D.W. helped with design and analysis of qPCR experiments. C.R. performed IHC for α-SMA. L.B. oversaw the IHC work. C.D.B. and L.B. generated the BPIFA1 antibodies. D.H. provided the NTHi strain and helped perform the intranasal infection experiments.

Additional Information
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