A multi-omics approach to delineate sputum microbiome-associated asthma inflammatory phenotypes

To the Editor:

Asthma is a heterogeneous disease with multiple clinical presentations (phenotypes) [1]. Neutrophilic asthma is characterised by increased sputum neutrophils and generally has a poor response to corticosteroids and limited other therapeutic options. Neutrophilia originates from different factors, including the defective resolution of inflammation or bacterial infections [2]. An association between airway bacterial imbalance (disturbance) and the neutrophilic phenotype has been reported [3], suggesting that airway microbiota composition is involved in neutrophilic asthma. Rather than being a separate entity [4], neutrophilic asthma may be in part, an alliance between innate immunity and microbiota composition that prompts protective mechanisms against invading pathogens [2].

In the Unbiased BIOmarkers in PREDiction of respiratory disease outcomes (U-BIOPRED) study, adults with severe asthma were classified into two clusters (phenotypes) based on the sputum microbiome [3]. The microbiome-driven cluster 2 (C2) showed relatively worse asthma outcomes, sputum neutrophilia and microbial imbalance (reduced microbial diversity and commensals and enrichment of pathogenic bacteria, particularly *Haemophilus influenzae* and *Moraxella catarrhalis*) compared with cluster 1 (C1). We investigated the underlying molecular mechanisms of microbiome-driven phenotypes by investigating differences in sputum eicosanoids, transcriptomics, and proteomics to reveal potential targets for diagnosis and treatment.

Sputum omics, including eicosanoids, transcriptomics, and SomaScan® proteomics, were assayed as described previously [3, 5, 6]. C2 was compared with C1 patients, mild–moderate asthma patients (MM), and healthy controls (H) according to a panel of 11-eicosanoids and Shannon metagenomics α-diversity using Kruskal–Wallis H test. C2 and C1 were compared by sputum transcriptomics and proteomics using linear models for microarray data (limma) analysis after adjusting for age, sex and oral corticosteroid intake. Pathway enrichment analysis for the sputum differential transcriptome was performed by gene set enrichment analysis (Gage R package) using two databases for *Homo sapiens*; the Kyoto Encyclopedia of Genes and Genomes (KEGG) database and the Molecular Signatures Database (MSigDB) Hallmark gene sets. A similar analysis was also performed comparing C2 against MM and H groups. Multiple testing was adjusted for using Benjamini Hochberg false discovery rate correction and an α (q-value) <0.05 was considered significant.

The sputum 11-dehydrothromboxane B2 and prostaglandin (PG) E2 (but not leukotriene (LT) B4) levels were significantly elevated in C2 compared to C1 subjects (q<0.05) (figure 1a), consistent with sputum PTGS2 gene upregulation in C2 ($\log_2$ fold change (FC) 1.1; q<0.05). Furthermore, the levels of 15-hydroxyeicosatetraenoic acid (HETE), LTE4 and PGD2 were elevated in C2 compared with MM and/or H groups. These findings were associated with decreased Shannon alpha-diversity in C2 compared to other groups (p<0.001) (figure 1b), consistent with the increase in the inflammatory signal with the increased severity level in the groups.

A total of 2578 differentially expressed genes (DEGs; q<0.05) were found to be different between C2 and C1, of which 194 genes had a least a two-FC (figure 1c). Several upregulated DEGs were related to immune regulation and inflammation, particularly tumour necrosis factor (TNF)-α and related regulatory

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A multi-omics approach revealed the underlying biological pathways in the microbiome-driven severe asthma phenotypes. This may help to elucidate new leads for treatment development, particularly for the therapeutically challenging neutrophilic asthma. https://bit.ly/3FWuJqS
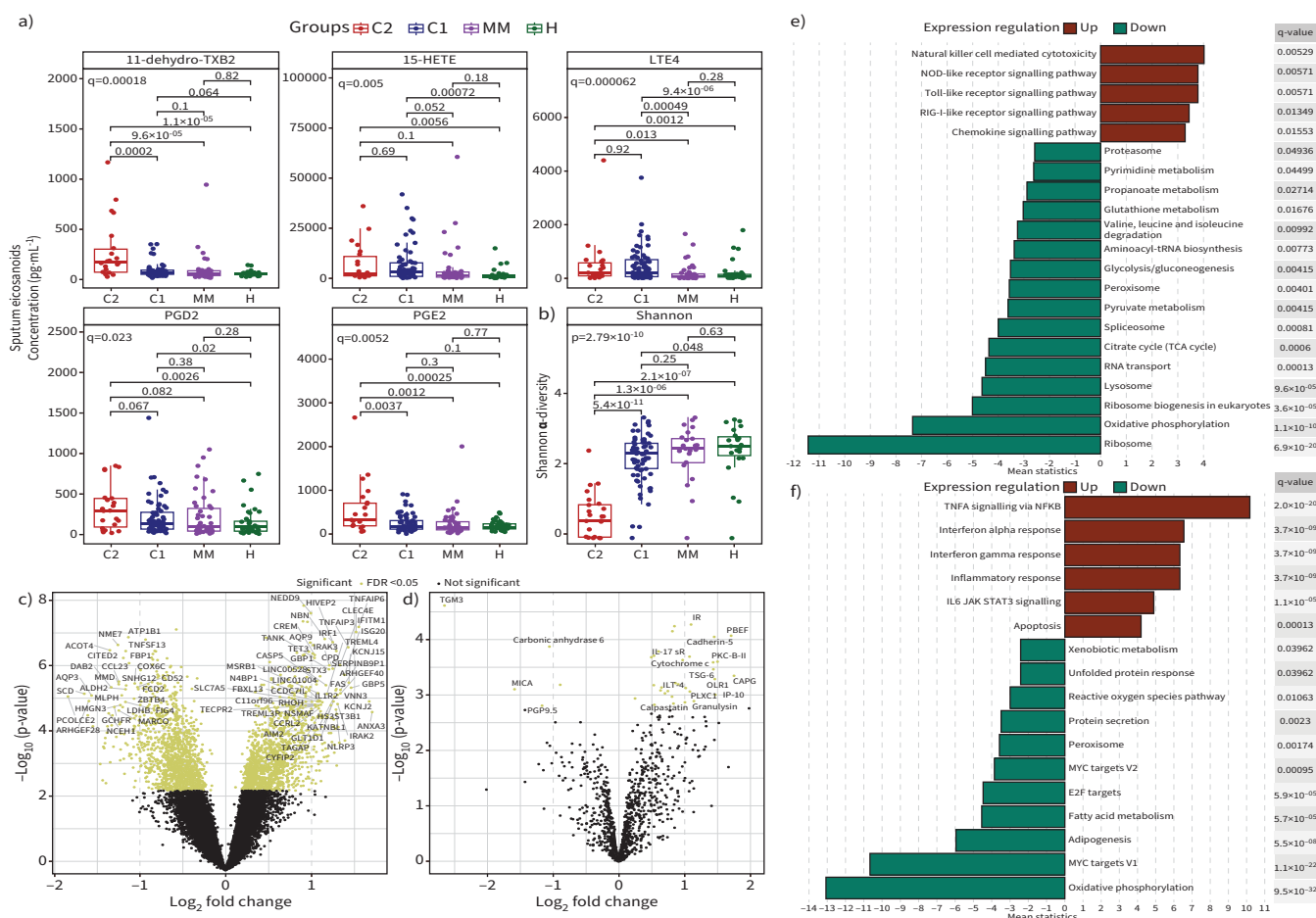
FIGURE 1 a) Box and whisker plots showing differences in sputum eicosanoids lipidomics between severe asthma microbiome-driven cluster 2 (C2; n=22), severe asthma microbiome-driven cluster 1 (C1; n=75), mild–moderate asthma (MM; n=46) and healthy controls (H; n=47). A panel of 11-eicosanoids was tested (namely; 11-dehydro thromboxane (TX) B2, 12-hydroxyeicosatetraenoic acid (12-HETE), 15-HETE, 5-HETE, 6-keto prostaglandin (PG) F1α, leukotriene (LT) B4, LTE4, PGD2, PGE2, and tetranor PGDM and PGEM). q-values were computed using the Kruskal–Wallis H-test followed by Benjamini Hochberg false discovery rate (FDR) correction, and only eicosanoids with q-values <0.05 were shown. Pairwise differences between the groups (p-values) were computed using the Mann–Whitney U-test. b) Box and whisker plot showing differences in metagenomics Shannon α-diversity between C2 (n=25), C1 (n=75), MM (n=24) and H (n=23) groups. Overall p-value was computed using the Kruskal–Wallis H-test and pairwise differences between the groups (p-values) were computed using the Mann–Whitney U-test. c) Differentially expressed genes (DEGs) between C2 (n=23) and C1 (n=61). Positive $\log_2$ fold change represents over-expressed sputum genes in C2 patients relative to C1, while negative $\log_2$ fold change represents down-expression in C2. DEGs with a q-value <0.05 are highlighted. Only the top 75 DEGs, with at least two-fold change, were labelled. Similar DEGs (q-values<0.05) were observed when C2 was compared independently to MM (n=20), and H (n=16) groups (not shown). d) Differentially abundant proteins (DAPs) between C2 (n=13) and C1 (n=61). Positive $\log_2$ fold change represents over-abundant sputum proteins in C2 patients relative to C1, while negative $\log_2$ fold change represents down-abundance in C2. DAPs with a q-value <0.05 are highlighted. Only the top DAPs, with at least two-fold change, were labelled. Similar DAPs (q-values <0.05) were observed when C2 was compared independently to MM (n=20), and H (n=21) groups (not shown). e) Up- and down-regulated KEGG (Kyoto Encyclopedia of Genes and Genomes) gene expression pathways in C2 relative to C1 based on sputum gene differential expression. Mean statistics: mean individual statistics from multiple single array-based gene set tests calculated using the gage R package, where its absolute value estimates the magnitude changes of gene-set level, and its sign indicates the direction of the changes. The figure only depicts the statistically significant pathways, in which the ones that passed the multiple testing correction (q-values <0.05) are depicted. f) Up- and down-regulated Hallmark gene expression pathways in C2 relative to C1 based on sputum gene differential expression. The figure only depicts the statistically significant pathways, in which the ones that passed the multiple testing correction (q-values <0.05) are depicted.

genes (*TNFAIP-6*, *TNFAIP3*, *TNFSF10*, *TNFRSF10* and *TNFSF14*); interleukins (ILs) and related regulatory genes (*IL18R1*, *IL18RAP*, *IL1R1*, *IL1R2*, *IL1B*, *IRAK2*, *IRAK3*, *IL6* and *IL6R*); Toll-like receptors (TLRs; *e.g. TLR2*, *TLR4* and *TLR10*); and inflammasomes (*e.g. NLRP3*, *NLRP12* and *NLRC5*) in C2 relative to C1. Similar DEGs were significantly upregulated in C2 compared to MM and H groups.

Upregulated KEGG pathways in C2 mainly related to pathogen fighting, inflammation and innate immune-regulation mechanisms such as natural killer cell-mediated cytotoxicity, chemokine, NOD-, Toll-, and RIG-I-like receptor signalling pathways (q<0.05) (figure 1e). Downregulated KEGG pathways in C2 were related to cell proliferation and growth, including ribosome biogenesis, DNA replication and repair; fatty acid, amino acid, nucleotide and carbohydrate metabolism; and cellular degradation and catabolism (lysosome, peroxisome and proteasome). The Hallmark gene sets supporting KEGG analysis including up-regulation of immuno- and inflammatory pathways in C2, such as TNF-α signalling *via* nuclear factor (NF)κB, interferon (IFN)-α, IFN-γ, inflammatory response, IL-6 JAK-STAT3 (Janus kinase-signal transducer and activator of transcription) signalling, and apoptosis (figure 1f). Downregulated pathways included oxidative phosphorylation (OXPHOS), reactive oxygen species (ROS), DNA repair, cell cycle, proliferation and growth, peroxisome, and metabolism. Similar upregulated and downregulated pathways were significant in C2 compared to MM and H groups. Additional KEGG/Hallmark upregulated pathways in C2 relative to MM and H groups were hypoxia, JAK-STAT, MAPK (mitogen-activated protein kinase), T-cell, KRAS and IL2 STAT5 signalling (data not shown).

36 differentially abundant proteins (DAPs) were significant (q<0.05) between C2 and C1, of whom 14 proteins had at least a two-FC (figure 1d). Upregulated DAPs in C2 (TSG-6, IL-17RA, IP-10, granulysin, ILT-4, PBEF, TLR4:MD-2 complex, MMP-10, NKp46, and IGFIR) were related to neutrophilia, inflammation, and/or Th17 and Th1 mediated pathways. Similar DAPs were significant when C2 patients were compared to MM and H groups. Additional enriched (pro)inflammatory DAPs were found in C2 relative to MM and/or H groups (q<0.05), including CRP, light, protein-S, azurocidin, PGRP-S, TIMP-2, IL-8, Notch1, MMP1, MMP2 and C5a.

The bacterial imbalance in C2 was associated with sputum neutrophilia, suggesting an immune-modulatory response to fight clinical/subclinical infections, potentially resulting in more inflamed/obstructed airways [7] with worse lung function parameters, as observed in C2 patients. Interestingly, sputum macrophages were significantly decreased in C2 compared to C1, consistent with a defective immune capacity to adequately eliminate pathogenic micro-organisms [8]. Most of the elevated signalling eicosanoids molecules in C2 are proinflammatory and/or induce bronchoconstriction [9], which may partly explain the reduced lung function in the relatively more severe C2 cluster. In addition, sputum PGE2 and PGD2 regulate neutrophils and/or Th17 and Th1 pathways [10], suggesting that their elevated levels in C2 patients might be driving these clinical features. PGE2 suppresses phagocytosis by airway macrophages in asthma [11], consistent with our sputum pathway enrichment analysis showing that C2 patients had down-regulated lysosome and ROS pathways, which are critical in pathogen fighting [12], relative to C1.

Many of the observed DEGs, DAPs, and pathways are implicated in immune regulation and/or are characteristic of the neutrophilic asthma signature [7] distinguishing C2 patients. TNF-α was markedly upregulated in C2, consistent with what was found in the *Haemophilus*-enriched cluster in patients with asthma and COPD [13]. Upregulation of the interferon pathways was observed in patients with C2, and IFN-γ has been shown to decrease epithelial barrier function and enhance neutrophil transmigration [14]. Impaired barrier function could render the airway mucosa of C2 subjects vulnerable to pathogenic bacterial infections. Our metagenomics analysis did not detect key RNA viruses, such as RV16, whose presence at a subclinical level could enhance RIG-I and IFN-γ pathways.

In contrast, downregulated pathways showed defective cell growth, proliferation, metabolism and DNA repair, suggesting an impaired capacity to repair inflamed cells and maintain homeostasis. Moreover, C2 exhibited downregulation of OXPHOS, tricarboxylic acid cycle, and ROS pathways suggesting mitochondrial dysfunction [15]. These results support previous data where neutrophilic inflammation was associated with reduced OXPHOS gene expression and mitochondrial dysfunction in bronchial epithelial cells [16].

These findings reveal potential targets for the C2 microbiome-driven asthma phenotype, which might constitute a selected subtype within corticosteroid-resistant asthmatics. Therapeutic options for this cluster might be antibiotics (*e.g.* macrolides) or phage therapy. In addition, the dysregulated neutrophilic and cytokines/chemokines might be diagnostic/therapeutic targets in C2 patients [7]. Differing biological pathways and mediators involved in these patients suggest that pharmacotherapies targeting multiple mechanisms might be required. This also suggests neutrophilic asthma is not a single phenotype [4] and underlying mechanisms should be considered to optimise treatment.

Mahmoud I. Abdel-Aziz [1,2], Susanne J.H. Vijverberg[1], Anne H. Neerincx [1], Paul Brinkman [1], Ariane H. Wagener[1], John H. Riley[3], Ana R. Sousa[3], Stewart Bates[3], Scott S. Wagers[4], Bertrand De Meulder[5], Charles Auffray[5], Åsa M. Wheelock[6,7], Aruna T. Bansal[8], Massimo Caruso [9], Pascal Chanez[10], Mohib Uddin[11], Julie Corfield[12,13], Ildiko Horvath[14], Norbert Krug[15], Jacek Musial[16], Kai Sun[17], Dominick E. Shaw [18], Thomas Sandström[19], Paolo Montuschi[20], Stephen J. Fowler [21], René Lutter [1,22], Ratko Djukanovic[23], Peter Howarth[23], Paul Skipp[24], Marek Sanak[25], Ian M. Adcock [26], Kian Fan Chung[26], Peter J. Sterk[1], Aletta D. Kraneveld[27] and Anke H. Maitland-van der Zee[1,28], on behalf of the U-BIOPRED Study Group

[1]Dept of Respiratory Medicine, Amsterdam UMC, University of Amsterdam, Amsterdam, The Netherlands. [2]Dept of Clinical Pharmacy, Faculty of Pharmacy, Assiut University, Assiut, Egypt. [3]Respiratory Therapeutic Unit, GlaxoSmithKline, Stockley Park, UK. [4]BioSci Consulting, Maasmechelen, Belgium. [5]European Institute for Systems Biology and Medicine, CIRI UMR5308, CNRS-ENS-UCBL-INSERM, Lyon, France. [6]Respiratory Medicine Unit, Dept of Medicine and Center for Molecular Medicine, Karolinska Institutet, Stockholm, Sweden. [7]Dept of Respiratory Medicine and Allergy, Karolinska University Hospital, Stockholm, Sweden. [8]Acclarogen Ltd, St John's Innovation Centre, Cambridge, UK. [9]Dept of Biomedical and Biotechnological Sciences, University of Catania, Catania, Italy. [10]Département des Maladies Respiratoires APHM, U1067 INSERM, Aix Marseille Université Marseille, Marseille, France. [11]AstraZeneca BioPharmaceuticals R&D, Gothenburg, Sweden. [12]AstraZeneca R&D, Mölndal, Sweden. [13]Areteva R&D, Nottingham, UK. [14]Dept of Public Health, Semmelweis University; National Koranyi Institute for Pulmonology, Budapest, Hungary. [15]Fraunhofer Institute for Toxicology and Experimental Medicine Hannover, Hannover, Germany. [16]Dept of Medicine, Jagiellonian University Medical College, Krakow, Poland. [17]Data Science Institute, South Kensington Campus, Imperial College London, London, UK. [18]Respiratory Research Unit, University of Nottingham, Nottingham, UK. [19]Dept of Public Health and Clinical Medicine, Dept of Medicine, Respiratory Medicine Unit, Umeå University, Umeå, Sweden. [20]Pharmacology, Faculty of Medicine, Catholic University of the Sacred Heart, Rome, Italy. [21]Division of Infection, Immunity and Respiratory Medicine, School of Biological Sciences, Faculty of Biology, Medicine and Health, University of Manchester, and Manchester Academic Health Science Centre and NIHR Biomedical Research Centre, Manchester University Hospitals NHS Foundation Trust, Manchester, UK. [22]Dept of Experimental Immunology, Amsterdam UMC, University of Amsterdam, Amsterdam, The Netherlands. [23]NIHR Southampton Respiratory Biomedical Research Unit, Clinical and Experimental Sciences, and Human Development and Health, University of Southampton, Southampton, UK. [24]Centre for Proteomic Research, Biological Sciences, University of Southampton, Southampton, UK. [25]Dept of Internal Medicine, Jagiellonian University Medical College, Krakow, Poland. [26]National Heart and Lung Institute, Imperial College London, and Royal Brompton and Harefield NHS Trust, London, UK. [27]Division of Pharmacology, Utrecht Institute for Pharmaceutical Sciences, Faculty of Science, Utrecht University, Utrecht, The Netherlands. [28]Dept of Pediatric Respiratory Medicine, Emma Children's Hospital, Amsterdam UMC, Amsterdam, The Netherlands.

Corresponding author: Anke H. Maitland-van der Zee (a.h.maitland@amsterdamumc.nl)

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