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1 **Immune signatures distinguish frequent from non-frequent exacerbators among children with**
2 **severe asthma.**

3

4 **To the editor,**

5

6 Asthma is a heterogeneous condition with multiple phenotypes.^{1,2} Almost 5% of children with severe
7 asthma (SA) remain symptomatic despite high doses of inhaled corticosteroids (ICS) and other
8 controllers.³ Asthma has long been regarded as a type-2 (T2) disorder, but a dominant Th1 signature,
9 with Th17 and Th2 cells in a mixed cytokine milieu, was recently described in bronchoalveolar lavages
10 (BAL) from children with SA.⁴ Moreover, among children with SA, cellular components such as IL-17-
11 producing mucosal-associated invariant T cells may distinguish frequent (FE) from non-frequent
12 exacerbators (nFE).⁵ The inflammatory profiles of children with SA thus appear to be highly complex.
13 We aimed to provide preliminary results to identify immune signatures associated with clinical
14 phenotypes of SA.

15 Twenty children with SA were included (**supplementary material & table 1**) and their blood and BAL
16 collected. FE (n=13) were defined as children with at least three severe exacerbations (SE) in the
17 previous year and nFE (n=7) as those having one or two.⁵ The two groups did not differ, except for the
18 number of steroid bursts. Samples were also collected from control subjects with non-asthmatic (NA)
19 severe respiratory conditions (n=10). Preliminary analysis i) confirmed a mixed T1/T2-type cellular
20 profile in BAL (**figure 1A**), associated with blood eosinophilia (**table 1**), in children with SA relative to
21 NA, and ii) showed the immune profile of FE to differ from that of nFE (T2 *versus* T1 phenotype;
22 respectively, **figure 1B&C**). We then performed a comprehensive non-targeted analysis of cytokines
23 and cells in blood and BAL from children with SA (**supplementary material**) and then constructed a
24 model to distinguish FE from nFE through supervised analysis (PLS-DA) (**figure 2A**). The model classified
25 patients with a good predictive value ($R^2Y=0.799$), with both sensitivity and specificity of 100%.
26 Although all data were used to construct the model, we identified a set of constituents that mostly
27 supported the differences between the patient groups (**supplementary table 2**, VIP>1). In parallel, we
28 performed univariate comparisons of each constituent (**supplementary table 2**). Finally, we identified
29 11 immune constituents to be the most discriminative (PxVIP plotting, VIP>1 and $p<0.1$, **figure 2B**). A
30 higher frequency of ILC1 and Th1-associated chemokines in BAL (CCL2/8, CXCL9-11, **figure 2C&D**)
31 confirmed the more pronounced T1 phenotype in nFE. Conversely, the local T2 phenotype of FE was
32 associated with a higher frequency of activated Th17 (IL22⁺) cells in the blood (**figure 2C**) that tended
33 to correlate with the number of exacerbations ($\rho=0.41$, $p=0.08$). Previous studies found that the
34 number of circulating Th17 cells was higher in children with moderate-to-severe than mild asthma,⁶

35 that these cells may be steroid resistant,⁷ and that PBMC IL-17 secretion was induced by
36 dexamethasone.⁸ Th17 IL-22⁺ cells may therefore emerge after repeated systemic steroid
37 administration received to treat exacerbations, leading to a mixed T2/T17 phenotype. FE also exhibited
38 lower concentrations of total IgA and higher concentrations of TWEAK, TNFSF14, and TSLP in plasma
39 (**figure 2E**), and TSLP levels significantly correlated with the number of exacerbations ($\rho=0.45$,
40 $p=0.045$). This is consistent with previous studies showing the involvement of these individual
41 constituents in the pathogenesis and severity of asthma in children. Plasma constituents, such as
42 sTNFR1, CCL26, Pentraxin3, CXCL10, IL-32, and sIL16RB, were also highly discriminant, despite high p-
43 values. All these constituents thus contributed to characterize the FE phenotype and univariate
44 analysis alone would not have allowed their identification. For example, the T2 chemokine CCL26
45 tended to be higher in FE and significantly correlated with blood eosinophil counts ($\rho=0.432$, $p=0.025$).
46 CCL26 is a potent chemoattractant for eosinophils and elevated concentrations of CCL26 in plasma
47 have been shown to be related to mucosal eosinophilia and the severity of various eosinophilic
48 disorders (e.g.⁹), which may suggest tissue eosinophilia in FE.

49 In conclusion, despite a small sample size and ICS that may affect the immune response, our study
50 shows the potential interest of high-dimensional/non-targeted multivariate analysis to identify specific
51 biological signatures of children with different clinical phenotypes of SA. Although confirmation in an
52 independent cohort is needed, our study provides new leads for delineating asthma pathogenesis and
53 identifying new set of targets for diagnosis and personalized treatment.

54

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84 **Author contributions:**

85 GL, KAP, and MLM: designed the research.

86 KAP, MG, BG, CDi, TM, MB, and FM: performed the research.

87 GL, RAT, NG, HF, AN, and CD: were responsible for patient recruitment or establishing the patient
88 database.

89 KAP and GL: analyzed the data.

90 KAP, GL, and MLM: wrote the manuscript.

91

92 **Abbreviations:** BAL: bronchoalveolar lavage fluids, ICS: inhaled corticosteroids, NA: non-asthmatic,
93 PLS-DA: partial least squares-discriminant analysis, SA: severe asthma, FE: frequent exacerbators, nFE:
94 non-frequent exacerbators.

95

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103

104 **Conflict of interests**

105 The authors have no conflict of interests to declare.

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107

108 **Figure legends**

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110 **Figure 1. Complex immune profile of children with different SA phenotypes. A.** Higher frequency of
111 Th1 cells (trend for Th2) in BAL from children with SA (grey bars) than in that from non-asthmatic
112 children with severe respiratory disorders (NA, white bars). **B.** The higher frequency of Th1 cells in BAL
113 of children with SA relative to that in NA children (white bars) was significant only in non-frequent
114 exacerbators (nFE, n=7; light grey). Conversely, the higher number of Th2 cells in BAL (**B**) and
115 eosinophils in blood (**C**) was significant only in frequent exacerbators (FE, n=13; dark grey). Data are
116 shown as box and Tukey whisker plots. P values were obtained using the Kruskal-Wallis test comparing
117 all groups together.

118

119 **Figure 2. Identification of immune constituents that discriminate between SA children with frequent**
120 **(FE) and non-frequent (nFE) exacerbations. A.** Graph of the individuals provided by PLS-DA modelling.
121 **B.** VIP x p values plot of all measured immune constituents and selection of the most discriminating
122 and significant (red rectangle: VIP>1 and p<0.1; because of the small number of patients in each group,
123 we tolerated p<0.1 as a cut-off). Identified discriminant immune constituents within cellular (**C**) or
124 soluble constituents in BAL (**D**) or plasma (**E**), represented as box and Tukey whisker plots. Exact p
125 values (Mann Whitney test) are indicated.

126

127

128 **References**

129

- 130 1. Lezmi G, de Blic J. Assessment of airway inflammation and remodeling in children with severe
131 asthma: The next challenge. *Pediatric pulmonology*. 2018;53(9):1171-1173.
- 132 2. Kuruvilla ME, Lee FE, Lee GB. Understanding Asthma Phenotypes, Endotypes, and Mechanisms
133 of Disease. *Clinical reviews in allergy & immunology*. 2019;56(2):219-233.
- 134 3. Chung KF, Wenzel S. From the authors: International European Respiratory Society/American
135 Thoracic Society guidelines on severe asthma. *Eur Respir J*. 2014;44(5):1378-1379.
- 136 4. Wisniewski JA, Muehling LM, Eccles JD, et al. TH1 signatures are present in the lower airways
137 of children with severe asthma, regardless of allergic status. *J Allergy Clin Immunol*.
138 2018;141(6):2048-2060 e2013.
- 139 5. Lezmi G, Abou-Taam R, Garcelon N, et al. Evidence for a MAIT-17-high phenotype in children
140 with severe asthma. *J Allergy Clin Immunol*. 2019;144(6):1714-1716 e1716.
- 141 6. Chien JW, Lin CY, Yang KD, Lin CH, Kao JK, Tsai YG. Increased IL-17A secreting CD4+ T cells,
142 serum IL-17 levels and exhaled nitric oxide are correlated with childhood asthma severity. *Clin*
143 *Exp Allergy*. 2013;43(9):1018-1026.
- 144 7. Nagakumar P, Puttur F, Gregory LG, et al. Pulmonary type-2 innate lymphoid cells in paediatric
145 severe asthma: phenotype and response to steroids. *Eur Respir J*. 2019;54(2).
- 146 8. Gupta A, Dimeloe S, Richards DF, et al. Defective IL-10 expression and in vitro steroid-induced
147 IL-17A in paediatric severe therapy-resistant asthma. *Thorax*. 2014;69(6):508-515.
- 148 9. Yamada T, Miyabe Y, Ueki S, et al. Eotaxin-3 as a Plasma Biomarker for Mucosal Eosinophil
149 Infiltration in Chronic Rhinosinusitis. *Front Immunol*. 2019;10:74.
- 150

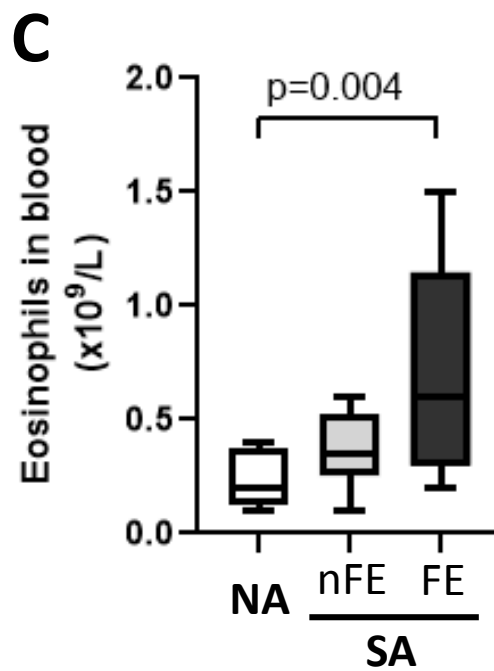
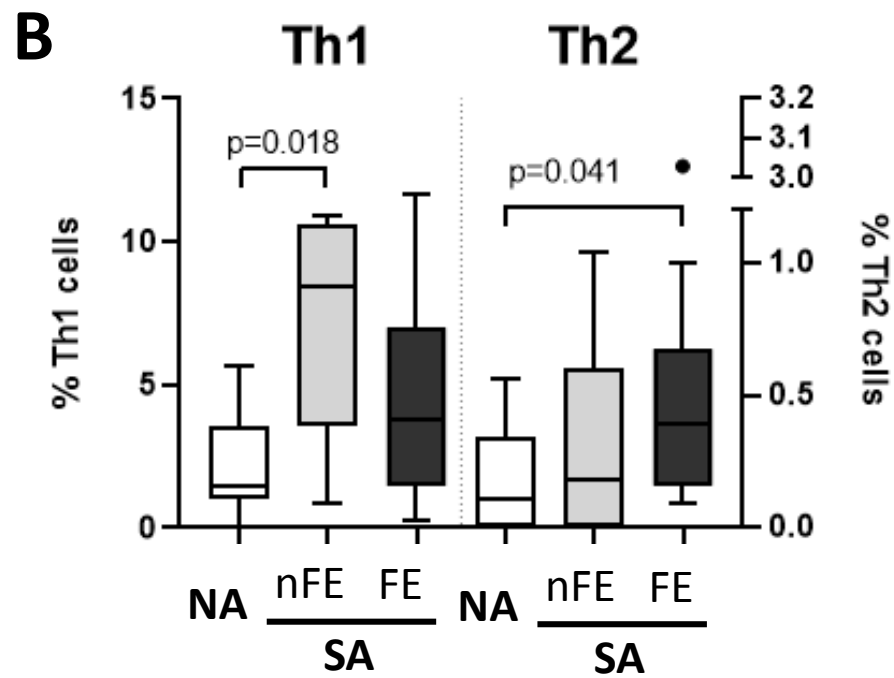
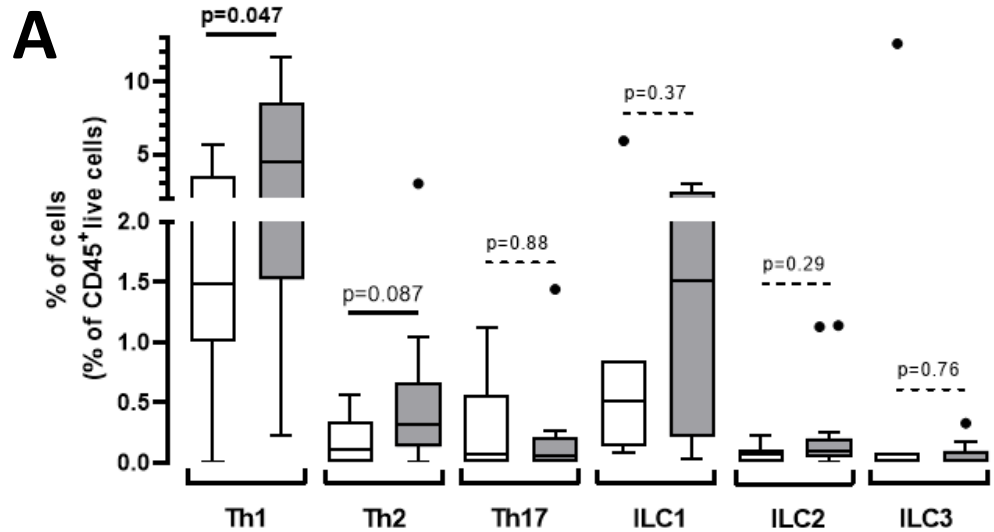


Figure 2

