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Effects of inhaled corticosteroids on DNA methylation in peripheral blood cells in children with asthma

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Effects of inhaled corticosteroids on DNA methylation in peripheral blood cells in children with asthma

Running title:

Childhood asthma, corticosteroids and DNA methylation

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Abbreviations:

AP-1: Activating Protein 1

NF- κ B: Nuclear Factor Kappa B

CpGs: Cytosine-phosphate-Guanine (CpG) sites

DNA: deoxyribonucleic acid

COPD: Chronic Obstructive Pulmonary Disease

EWAS: Epigenome-Wide Association Study

FDR: False Discovery Rate

QQ plot: Quantile-Quantile plot

35 **To the Editor,**

36

37 Asthma is a chronic heterogeneous inflammatory airway disease. Its treatment includes
38 bronchodilators and anti-inflammatory medication such as corticosteroids. Corticosteroids reduce
39 transcription of AP-1 and NF- κ B and hence may affect DNA methylation. Epigenetics refers to
40 changes in DNA that can affect transcription, such as methylation of a cytosine nucleotide beside a
41 guanine nucleotide (CpGs).

42

43 Asthma is associated with differentially methylated CpGs in specific genes [1, 2]. In the largest
44 study to date, asthmatic children had significantly lower blood methylation levels at 14 CpGs
45 compared to controls [3]. One previous study found 19 CpGs that were differentially methylated in
46 blood during systemic corticosteroid exposure in patients with COPD [4]. Possible effects of
47 inhaled asthma medication on peripheral blood methylation profiles are currently unknown.

48

49 Our aim was to study the association between inhaled corticosteroids and DNA methylation in
50 peripheral blood cells in children with asthma. First, we performed an epigenome-wide association
51 study (EWAS) investigating the effects of variable inhaled corticosteroid exposure on DNA
52 methylation in 8-year-olds with diagnosed asthma in the BAMSE (Barn/Child, Allergy, Milieu,
53 Stockholm, Epidemiology) cohort followed by replication attempts. Second, using a candidate gene
54 approach, we evaluated if identified CpGs from the systemic steroid study [4] and the largest
55 asthma study to date [3], in total 33 CpGs, were differentially methylated in relation to inhaled
56 asthma treatment.

57

58 BAMSE is a Swedish prospective birth cohort study [5]. A total of 4089 children born 1994-1996
59 enrolled and information was collected in repeated questionnaires. Blood samples were taken at the
60 8- and 16-year follow-ups (n=2480; 61 % and n=2547; 62 %, respectively) [6]. For the present
61 study, we included all subjects with a doctor's diagnosis of asthma ever up to 8 years and with
62 DNA methylation data available for analyses (n=215) [3]. Subjects were grouped based on
63 exposure established in the questionnaires: any medication for breathing difficulties (n=130), any
64 inhaled corticosteroids or combination medication for any period of time (n=107), and inhaled
65 corticosteroids continuously (at least 2 consecutive months) (n=39), all in the last 12 months.
66 STOPPA (Swedish Twin Study on Prediction and Prevention of Asthma), a cohort study of twins
67 aged 9-14 years [7] was used for replication analyses, and a subset of BAMSE 16-year cohort

68 (n=96 cases) was used for additional look-up (Tables E1-2). The regional ethics committee in
 69 Stockholm approved the studies, and written consent was obtained from all parents.

70

71 Robust linear regression was used for the analysis. The reference group comprised subjects
 72 diagnosed with asthma without any asthma medication in the last 12 months (n=85). We applied the
 73 Benjamini-Hochberg method to control the false discovery rate (FDR) at 5 %. P values below FDR
 74 were considered statistically significant in EWAS. Analyses were performed separately in BAMSE
 75 and STOPPA followed by fixed-effects meta-analysis using METAL.

76

77 Beta value was a dependent variable and each mode of asthma medication was a binary independent
 78 variable. Each model was adjusted for sex, age, sensitization to airborne allergens at 8 years,
 79 wheezing in the last 12 months, mother's smoking at least 1 cigarette per day at baseline and/or
 80 during pregnancy, bisulfite treatment date, and estimated cell types according to the Houseman
 81 method [6] (Table 1). Similar subject groupings and identical models were applied in STOPPA and
 82 BAMSE 16-year analyses.

83

84 **Table 1.** Distribution of background characteristics of BAMSE subjects with DNA methylation data
 85 measured at 8 years of age in relation to type of asthma treatment. Results shown as n (%), compared to the
 86 total number of subjects in each group.

	Diagnosed asthma (n=215)		Asthma treatment					
			Any medication for diagnosed asthma (n=130)		Any inhaled corticosteroid treatment (n=107)		Continuous inhaled corticosteroid treatment (n=39)	
Male	134 (62 %)		83 (64 %)		68 (64 %)		28 (72 %)	
Age in years (mean, SD)	8.1, 0.4		8.1, 0.4		8.1, 0.4		8.1, 0.4	
Sensitization [†]	106 (49 %)		79 (61 %)		66 (62 %)		28 (72 %)	
At least 1 episode of wheezing in the past 12 months	104 (48 %)		96 (74 %)		83 (78 %)		31 (79 %)	
Either parent smoked at the time of the 8-year questionnaire	46 (21 %)		22 (17 %)		20 (19 %)		6 (15 %)	
Mother's smoking [‡]	34 (16 %)		14 (11 %)		12 (11 %)		3 (8 %)	
Socioeconomic status at baseline, § blue collar worker compared to white collar worker	35 (16 %)	180 (84 %)	23 (18 %)	107 (82 %)	20 (19 %)	87 (81 %)	9 (23 %)	30 (77 %)

One or both parents' asthma/hay fever/ allergy [¶]	101 (47 %)	65 (50 %)	55 (51 %)	21 (54 %)
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87 † Sensitization is defined as an IgE antibody level of 0.35 kUA/L or greater against any inhalant allergen at age 8.

88 ‡ The child's mother smoked at least 1 cigarette per day at any point of time during the pregnancy and/or at the time of
89 questionnaire 0 (median age of 2 months).

90 § Socioeconomic status for the household at the time of questionnaire 0, according to dominance order in two classes.

91 ¶ Mother and/or father with doctor's diagnosis of asthma and asthma medication and/or doctor's diagnosis of hay fever
92 in combination with furred pets- and/or pollen allergy at the time of questionnaire 0.

93

94 In total, methylation at 24 individual CpGs was significantly associated at FDR level with asthma
95 treatment in BAMSE (Table 2; Figures E1-3). However, none of these EWAS hits was nominally
96 significant in the replication study STOPPA or in BAMSE 16-year-olds, and in the meta-analysis,
97 none of the CpGs reached genome-wide significance (FDR). As a sensitivity analysis, we repeated
98 regression analyses in BAMSE 8-year-olds, not adjusting for cell types, and found overall very
99 consistent results comparing the regression coefficients in the models with and without cell type
100 adjustment (Table 2).

101

102 **Table 2.** Statistically significant CpGs (defined as p value below respective FDR) from epigenome-wide
103 association study analyses of **any asthma medication, any corticosteroid medication, and continuous**
104 **corticosteroid medication exposure** in the last 12 months and DNA methylation change in peripheral blood
105 cells from Swedish 8-year-olds. Total sum of subjects included in each group is stated after the exposure type
106 (n). FDR for all is 2,2E-06. “-“ indicates missing value as these CpGs were not included in the STOPPA
107 DNA methylation data after normalization. See appendix for further description.

108

CpG site	Gene [†]	Distance (bp) [‡]	Coefficient, BAMSE 8 [§]	p value, BAMSE 8	p value, STOPPA	p value, Meta analysis*	p value, BAMSE 16	Coefficient BAMSE 8: no cell adjustment [¶]	p value, BAMSE 8: no cell adjustment
<i>Any asthma medication exposure, n=130</i>									
cg25214924	<i>AK058177</i>	-42380	-0.016	2.5E-08	0.29	2.6E-03	0.62	-0.013	1.0E-05
cg03877376	<i>TBX5</i>	85	0.008	2.0E-07	-	-	0.64	0.007	7.3E-06
cg20423602	<i>ADARB2-AS1</i>	-8232	-0.014	5.5E-07	0.13	1.5E-06	0.21	-0.012	1.2E-05
cg15954046	<i>LMNA</i>	303	-0.012	5.5E-07	0.60	1.9E-04	0.51	-0.006	6.8E-02
cg23966329	<i>UBE2G1</i>	-162	-0.003	1.3E-06	0.34	7.4E-03	0.89	-0.003	1.1E-06
cg14063914	<i>SERAC1</i>	349	-0.007	1.7E-06	0.45	4.3E-04	0.72	-0.008	7.3E-08
cg21731304	<i>NMNA T3</i>	-212	-0.021	2.0E-06	0.49	3.3E-05	0.15	-0.021	4.3E-06
<i>Any corticosteroid exposure, n=107</i>									

cg16048421	<i>LOC338579</i>	0	0.014	3.9E-07	0.80	7.2E-04	0.29	0,015	7,2E-07
cg15115986	<i>C1orf112</i>	-20	-0.004	4.9E-07	-	-	0.48	-0,004	2,7E-07
cg03877376	<i>TBX5</i>	85	0.008	5.5E-07	-	-	0.68	0,007	1,2E-05
cg03146079	<i>ADD1</i>	0	-0.005	5.9E-07	0.32	1.6E-06	0.99	-0,005	7,4E-07
cg17629264	<i>MAPK8IP2</i>	-390	-0.021	6.1E-07	0.34	1.5E-05	0.18	-0,014	4,3E-03
cg24144651	<i>BC043227</i>	-560	-0.009	8.8E-07	-	-	0.18	-0,006	2,8E-03
cg00025044	<i>ERCC6</i>	-1952	-0.011	1.0E-06	0.19	3.7E-05	0.42	-0,015	1,2E-08
cg25745861	<i>TMEM54</i>	-2782	0.012	1.1E-06	0.46	1.5E-05	0.85	0,016	5,8E-08
cg14136328	<i>SYT1</i>	-69884	-0.013	1.1E-06	0.32	1.4E-03	0.43	-0,010	5,8E-05
cg18046087	<i>KLC2</i>	0	-0.006	1.1E-06	0.76	4.9E-05	0.87	-0,007	3,9E-08
cg03043078	<i>MMP17</i>	2420	-0.006	2.0E-06	0.99	4.0E-05	0.23	-0,006	1,3E-06
<i>Continuous corticosteroid exposure, n=39</i>									
cg07665222	<i>ACRV1</i>	-1393	-0.022	3.3E-07	0.28	3.8E-06	0.75	-0,018	2,3E-04
cg03877376	<i>TBX5</i>	85	0.010	9.4E-07	-	-	0.94	0,009	2,2E-05
cg22997262	<i>LOC100128531</i>	-2329	0.017	1.1E-06	0.43	9.5E-03	0.54	0,018	9,2E-09
cg15074789	<i>EPHA2</i>	0	-0.008	1.2E-06	-	-	0.96	-0,008	9,4E-06
cg13688889	<i>FOXE1</i>	-6829	-0.048	1.4E-06	0.72	3.1E-04	0.20	-0,049	1,6E-06
cg00947413	<i>MIR3679</i>	-99303	-0.044	1.8E-06	0.22	1.4E-05	0.26	-0,046	1,0E-07
cg26281051	<i>DEFB129</i>	-95	-0.018	2.0E-06	0.46	2.9E-04	0.30	-0,017	1,3E-04
cg25745861	<i>TMEM54</i>	-2782	0.016	2.6E-06	0.71	1.4E-03	0.54	0,018	9,8E-06
cg13492223	<i>FUT6</i>	-159	0.017	2.9E-06	0.81	6.0E-04	0.98	0,019	4,6E-04

109 †, ‡ Gene annotation according to Illumina450K. CpGs were annotated using the IlluminaHumanMethylation450k.db R
110 package, with enhanced annotation for nearest genes within 10Mb of each site, as previously described [8].

111 § Regression coefficient, adjusted for sex, age, sensitization to airborne allergens at 8 years, wheezing in the last 12
112 months, mother's smoking at least 1 cigarette per day at baseline and/or during pregnancy, bisulfite treatment date, and
113 estimated cell types. Reference group includes subjects without any asthma medication.

114 *Meta-analysis of results in BAMSE 8-year-old cohort and STOPPA using a fixed-effects model weighted by the
115 inverse of the variance using METAL. BAMSE 16-year-olds were not included in the meta-analysis due to overlap with
116 BAMSE 8 data.

117 ¶ Regression coefficient, adjusted for sex, age, sensitization to airborne allergens at 8 years, wheezing in the last 12
118 months, mother's smoking at least 1 cigarette per day at baseline and/or during pregnancy, and bisulfite treatment date.
119 Reference group includes subjects without any asthma medication.

120

121 Next, we investigated possible DNA methylation changes in the 33 selected CpGs from the
122 literature [3], [4]. Three CpGs were nominally significant in BAMSE 8-year-olds when comparing
123 any corticosteroid exposure to no medication and six CpGs showed nominally significant

124 methylation increases in relation to continuous corticosteroid exposure with three CpGs increasing
125 $\geq 1\%$. However, none of the CpGs survived multiple testing adjustment (Tables E3-5). We
126 investigated the 33 candidate CpGs in a subset of BAMSE 16-year-olds with an asthma diagnosis
127 through identical analyses and congruently found no FDR-significant associations with asthma
128 treatment.

129

130 In summary, several CpGs in EWAS were found differentially methylated in BAMSE at the FDR
131 genome-wide significance level and results were very similar in models with and without cell-type
132 adjustment. However, none of these CpGs replicated even at a nominal significance level in
133 STOPPA or BAMSE 16-year cohort, and after meta-analyses, none of the CpGs survived multiple
134 test adjustment. Thus, our study does not find evidence for DNA methylation changes in relation to
135 inhaled asthma treatment, although changes through other epigenetic mechanisms cannot be ruled
136 out. Our results are based on an observational study and hence do not produce intention-to-treat
137 results. There are some limitations: firstly, we could not completely adjust for severity of asthma as
138 the severity is reflected in the medication mode itself. Secondly, in the 8-year follow-up we did not
139 enquire about systemic steroid use and hence there may be subjects that have used systemic
140 corticosteroids in the “any medication” group. Thirdly, heterogeneity between the BAMSE and
141 STOPPA cohorts unlikely explains the lack of replication as both cohorts are from areas with
142 similar lifestyle factors, ethnic background and sensitization patterns, although more mothers
143 smoked during pregnancy in BAMSE and more parents in STOPPA had asthma, hay fever or
144 allergies.

145

146 Furthermore, we explored potential treatment–methylation associations using a candidate gene
147 approach. We selected CpGs that were found robustly associated with asthma (per se) in the large
148 study by Xu et al [3], where the authors did not specifically investigate potential influence from
149 medication. We found a handful nominally associated CpGs with increased methylation in
150 peripheral blood cells, whereas for asthma, Xu et al reported consistently lower methylation levels.
151 However, none survived multiple test adjustment in our study.

152

153 There are well-known side effects from long-term systemic corticosteroid treatment, and the study
154 by Wan et al found DNA methylation differences in COPD patients associated with systemic
155 steroid use [4]. By exploring the top CpGs from Wan et al, we found no significant methylation
156 differences in children and adolescents with asthma associated with inhaled corticosteroid

157 treatment. However, it should be noted that Wan et al studied adult COPD patients and we included
158 children and adolescents with asthma in our study.

159

160 In conclusion, we found no evidence that inhaled corticosteroids or other asthma medications affect
161 peripheral blood cell DNA methylation levels to any major extent, although smaller effects cannot
162 be excluded.

163

164 **References**

165

- 166 1. Yang, I.V., et al., *DNA methylation and childhood asthma in the inner city*. J Allergy Clin
167 Immunol, 2015. **136**(1): p. 69-80.
- 168 2. Reese, S.E., et al., *Epigenome-wide Meta-analysis of DNA Methylation and Childhood*
169 *Asthma*. J Allergy Clin Immunol, 2018.
- 170 3. Xu, C.J., et al., *DNA methylation in childhood asthma: an epigenome-wide meta-analysis*.
171 Lancet Respir Med, 2018. **6**(5): p. 379-388.
- 172 4. Wan, E.S., et al., *Systemic steroid exposure is associated with differential methylation in*
173 *chronic obstructive pulmonary disease*. Am J Respir Crit Care Med, 2012. **186**(12): p. 1248-
174 55.
- 175 5. Hallberg, J., et al., *Asthma phenotypes and lung function up to 16 years of age-the BAMSE*
176 *cohort*. Allergy, 2015. **70**(6): p. 667-73.
- 177 6. Gref, A., et al., *Genome-Wide Interaction Analysis of Air Pollution Exposure and Childhood*
178 *Asthma with Functional Follow-up*. Am J Respir Crit Care Med, 2017. **195**(10): p. 1373-
179 1383.
- 180 7. Almqvist, C., et al., *Cohort Profile: Swedish Twin Study on Prediction and Prevention of*
181 *Asthma (STOPPA)*. Twin Res Hum Genet, 2015. **18**(3): p. 273-80.
- 182 8. Joubert, B.R., et al., *DNA Methylation in Newborns and Maternal Smoking in Pregnancy:*
183 *Genome-wide Consortium Meta-analysis*. Am J Hum Genet, 2016. **98**(4): p. 680-96.

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211 **Conflicts of interest**

212 EM reports personal fees from Novartis (advisory board reimbursement) during the conduct of the
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