

1 **Title: The effects of growing up on a farm on adult lung function and allergic phenotypes:**
2 **An international population based study.**

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31 **What is the key question?**

32 What is the relative impact of early life farm exposure and other biodiversity proxies on adult
33 lung function and BHR?

34

35 **What is the bottom line?**

36 This is the first study to report beneficial effects of growing up on a farm on adult FEV₁ and
37 compare biodiversity proxy exposures for inner city participants to confirm the beneficial effects
38 of early farm life on sensitization, asthma, rhinitis, and BHR.

39

40 **Why read on?**

41 This study describes the associations between early life farm or microbial proxy exposures and
42 adult measures of clinical lung function, BHR, and allergic disease to help define the role of
43 microbial biodiversity and farm exposure on adult lung function outcomes.

44

45

46 **Abstract**

47 **Rationale:** Evidence has suggested that exposure to environmental or microbial biodiversity in
48 early-life may impact subsequent lung function and allergic disease risk.

49 **Objectives:** To investigate the influence of childhood living environment and biodiversity
50 indicators on atopy, asthma and lung function in adulthood.

51 **Methods & Measurements:** The European Community Respiratory Health Survey II
52 investigated ~10,201 26-54 year old participants from 14 countries, including participants' place
53 of upbringing (farm, rural environment or inner city) before age 5 years. A "biodiversity score"
54 was created based on childhood exposure to cats, dogs, day care, bedroom sharing and older
55 siblings. Associations with lung function, bronchial hyper responsiveness (BHR), allergic
56 sensitization, asthma and rhinitis were analysed.

57 **Main Results:** As compared to a city upbringing, those with early-life farm exposure had less
58 atopic sensitization (aOR 0.46, 95% CI=0.37-0.58), atopic BHR (0.54[0.35-0.83]), atopic asthma
59 (0.47[0.28-0.81]), and atopic rhinitis (0.43[0.32-0.57]), but not non-atopic outcomes. Less
60 pronounced protective effects were observed for rural environment exposures. Women with a
61 farm upbringing had higher FEV₁ (adjusted difference 110 mL [64-157]), independent of
62 sensitization and asthma. In an inner city environment, a higher biodiversity score was related to
63 less allergic sensitization.

64 **Conclusions:** This is the first study to report beneficial effects of growing up on a farm on adult
65 FEV₁. Our study confirmed the beneficial effects of early farm life on sensitization, asthma,
66 rhinitis, and found a similar association for BHR. In persons with an urban upbringing, a higher
67 biodiversity score predicted less allergic sensitisation, but to a lesser magnitude than a childhood
68 farm environment.

69

70 **Introduction**

71 A dramatic rise in asthma and allergic disease over recent decades has motivated extensive
72 research into the aetiological factors responsible for these conditions. Various hypotheses have
73 been put forth to explain this rise in allergic disease with respect to early-life exposures. Recent
74 evidence has indicated that the level of exposure to environmental or microbial biodiversity in
75 early-life may impact the subsequent risk of allergic outcomes. This hypothesis was initially
76 generated by the observation of an inverse association between family size and hay fever, and has
77 since been coined the “hygiene hypothesis”. (1) This work has been subsequently expanded as
78 the microbial hypothesis by observations on the links between exposure to farming environments
79 and a reduction in allergic diseases. The ‘farm effect’ has been observed by a number of studies,
80 the majority of which have focussed on childhood farm exposure and disease onset in childhood,
81 while fewer studies have investigated the impact of early life exposures on adult disease
82 phenotypes. (2,3) Exposure to increased loads of microbes such as viral, bacterial, and parasitic
83 agents associated with farming environments have been proposed as contributing factors in this
84 link and previous studies have explored various routes of exposure associated with farm life
85 more thoroughly to investigate their relative contributions to this ‘farm effect’. (2) Supporting
86 this hypothesis, studies have also shown that endotoxin and fungal loads in farming homes are
87 significantly higher than those in non-farming homes. (4–8).

88 Following the interest in early life as a critical window for exposures that determine lifelong
89 health and disease status, numerous studies have investigated associations between childhood
90 farm exposure and childhood allergic diseases. Systematics reviews synthesizing considerable
91 evidence from studies on early life farm exposure and childhood disease outcomes have shown a
92 decreased risk of asthma, wheeze and allergic disease associated with the ‘farm effect’. (3,9)

93 However, fewer studies have analysed the impact of these childhood exposures on well-defined

94 allergic adulthood outcomes or the potential persistence of the ‘farm effect’ into adult life. (2,3,9)
95 While the majority of existing research has investigated allergic outcomes including asthma, little
96 work has been conducted on the association between early life farm exposure and clinical
97 measures of lung function in childhood, adolescence or adulthood. (10–14) Findings in younger
98 cohorts have been conflicting, with one study finding no improvements in spirometric measures
99 related to the ‘farm effect’ (12), another study showing only higher FVC in children born on a
100 farm (14), and a third study finding a lower prevalence of BHR in adolescents raised on a farm- a
101 finding that was more distinct in girls (13) . Although few manuscripts have completely stratified
102 this association by atopy to investigate this association among atopic and non-atopic groups, in a
103 study on farming environments childhood health outcomes, Fuchs et al. found that farm exposure
104 reduced risk of wheeze independent of atopic status and observed a statistically significant
105 interaction between atopy and fractional exhaled nitric oxide, but not lung function or BHR.(12)
106 In this under-researched area, only one study has investigated the association between early life
107 farm exposure and adult lung function, finding no statistically significant results.(11) This study
108 also found no association between a farm upbringing and risk of BHR. The only other study on
109 this topic found decreased odds of adult BHR with being “born and raised” on a farm. (10)
110 Additionally, many studies on farming exposures and allergic disease outcomes rely on
111 comparisons between categorized “farming” and “non-farming” communities, which may
112 overlook the significance of intermediary rural exposures. This is an important distinction in the
113 context that increasing urbanization is linked to a higher prevalence of allergic disease. (15)
114 Moreover, the strength of the ‘farming effect’ is not often compared to the other associated early-
115 life exposures related to environmental biodiversity such as pet keeping, older siblings, bedroom
116 sharing, and interactions with other children through day care or nursery school attendance.(16–
117 18) As such, it is currently unclear if exposures to an increased microbial load in an urban setting

118 might approximate the effect of early-life farming exposure on allergic and respiratory disease
119 outcomes.

120
121 In this manuscript, we aim to add knowledge to these gaps in this field of research using the
122 European Community Respiratory Health Survey (ECRHS), the largest international multi-
123 country study of adult asthma, collected information on early childhood exposure to farming and
124 place of upbringing. In addition, information was collected on other environmental exposures
125 related to biodiversity and microbial load along with objective outcome measures of IgE
126 mediated sensitization and lung function in adult life. Using these data we aimed to investigate
127 whether exposure to farming is related to adult allergic outcomes and lung function, and if so,
128 whether any associations can be explained by microbial proxy markers.

129

130 **Methods**

131 *Study design and data collection tools*

132 The methods of the European Community Respiratory Health Study (ECRHS) I survey have
133 been fully described elsewhere. (19,20) Briefly, in the ECRHS I, participating centres randomly
134 selected samples of 20-44 year olds, from a total of 48 centres in 22 countries during 1991-1993.
135 A sampling frame randomly selected 1500 men and women from pre-existing administrative
136 boundaries with a population of at least 150,000 people, who were mailed a short postal
137 questionnaire about asthma and asthma-like symptoms (Stage 1). During Stage 2, a random
138 subsample, made up of roughly 20% of Stage 1 respondents were invited to attend a local testing
139 centre to complete a more detailed questionnaire administered by an interviewer and undergo
140 skin prick and blood tests, assessment of lung function by spirometry, and methacholine
141 challenge testing. In addition, participants who were not in the random sample, but who reported

142 current use of treatment for asthma, an asthma diagnosis, or that they had been woken with
143 shortness of breath in the previous 12 months (symptomatic sample) were also invited to
144 participate in Stage 2.

145
146 The ECRHS II, conducted between 1998 and 2002, was a follow-up of the clinical participants
147 included in the ECRHS I. Twenty-nine centres participated in this follow-up, where participants
148 underwent a self-completed screening questionnaire, an administered clinical interview, lung
149 function testing and serum IgE analysis. Clinical measures used in this analysis were collected
150 during the ECRHS II follow-up. The data on early-life farm exposure and current respiratory
151 symptoms that were used in this analysis were also collected in this survey. The detailed protocol
152 can be found at www.ecrhs.org.

153
154 ***IgE measurements***
155 Using the Pharmacia CAP System (Pharmacia Diagnostics AB, Uppsala, Sweden), total serum
156 IgE and specific IgE levels to cat, house dust mite (*D. pteronyssinus*), mold *Cladosporium* and
157 timothy grass were measured. Each sample was handled in a similar manner, with centrifugation
158 and subsequent storage at -20°C until IgE analysis. The serum level measurement range for total
159 IgE was 2–2000 kU/L and 0.35–100 kUA/L for specific IgE.

160
161 ***Lung Function***
162 Lung function was assessed by spirometry, and the maximum forced expiratory volume in one
163 second (FEV₁) and forced vital capacity (FVC) were measured through a maximum of five
164 acceptable tests.

165
166 Bronchial Hyperresponsiveness (BHR) was measured by methacholine challenge testing.
167 Methacholine was released via a Mefar dosimeter (Mefar, Bovezzo, Italy). Two minutes after
168 each inhalation FEV₁ was recorded, and the test was stopped when either a 20% fall in FEV₁ was
169 achieved or the final methacholine dose had been given.

170

171 **Definitions**

172 *Outcomes*

173 Bronchial Hyperresponsiveness (BHR) was defined by a fall of at least 20% in FEV₁ after the
174 methacholine challenge test (accumulated dose 1 mg), and allergic sensitization was
175 characterized by at least one positive test to any specific allergen (≥ 0.35 kUA/L). Nasal allergies
176 were determined by questionnaire with response to “Do you have any nasal allergies including
177 ‘hayfever’?”. Current asthma was defined as BHR AND current wheeze OR the use of asthma
178 medications in the last 12 months. (21) Participants were classified as having current wheeze if
179 they answered yes to the question “Have you had wheezing or whistling at any time during the
180 last 12 months?”. Continuous measures of FEV₁, FVC, and FEV₁/FVC were used in this analysis.
181 The outcomes of asthma, rhinitis and BHR were stratified into allergic and non-allergic
182 phenotypes based on the presence or absence of allergic sensitization as defined above.

183

184 *Primary exposure*

185 For this analysis, participants were grouped by place of upbringing before the age of five years as
186 reported in the ECRHS II follow-up survey. The question that collected the participant’s
187 childhood living environment was “What term describes the place you lived most of the time
188 when you were under the age of five years? a) farm b) village in a rural area c) small town d)

189 suburb of a city e) inner city”. A three level variable was used in the analysis with inner city,
190 farm, and a combined intermediary category of village, town, or suburb. Similar findings and no
191 statistically significant differences in outcomes were observed between the three intermediary
192 groups when investigated individually. A small, but insignificant, difference was observed
193 between suburb and village with suburbs having a lower benefit than village.

194

195 *Other exposures*

196 The “proxy microbial load score” was calculated from answers to the following survey questions
197 from the ECRHS II: (a) “At what age did you first attend a school, play school, day care or
198 nursery?” (=1 if attended before age 5); (b) “Was there a dog/cat in your home during your first
199 year of life OR when you were aged 1 to 4 years OR when you were aged 5-15 years?” (=1 for
200 each affirmative answer) (c) “How many *other* children regularly slept in your bedroom before
201 *you were five years old?*” (=1 if >0) and; (d) “How many older brothers (or sisters) [do you
202 have]?” (=1 if >0). The combined effect of daycare, pets, bedroom sharing, and siblings in early
203 life was examined together as the cumulative “proxy microbial load score”. Individuals were
204 given a score for the number of factors (0, 1, 2, 3, 4, 5 exposures).]”.

205

206 *Analytical methods*

207 The significance of variation in baseline demographics by early life residence was assessed with
208 chi-squared tests or ANOVA methods. Multiple and multinomial logistic regression analyses
209 were performed to estimate adjusted odds ratios for the associations between childhood
210 environment and clinical phenotypes while adjusting for relevant confounders. Multiple linear
211 regression was performed to estimate mean differences in lung function by differing early-life
212 home environments while adjusting for possible confounders. A potential interaction between sex

213 and childhood environment was investigated, and a stratified analysis was presented in the
214 presence of a significant interaction. Sensitivity analyses were performed with adjustment for
215 random and symptomatic sample membership and were consistent with the presented findings.

216

217 For all analyses, the following *a priori* confounders were included: age, sex, study centre,
218 smoking status, and family history of allergic disease. In addition, height² was determined to be
219 an *a priori* confounder in the analysis of lung function data. A set of potential confounders were
220 also explored during the analyses and were only included in the final model if the point estimate
221 changed by more than 10 percent; these variables included maternal/paternal smoking, older
222 siblings or bedroom sharing, early day care or nursery school attendance, early-life cat/dog
223 ownership, socioeconomic status and weight in lung function analyses. Potential heterogeneity
224 of associations was studied across countries. A fixed effect model was used to meta-analyse risk
225 estimates when there was no significant heterogeneity based on the I^2 value (<50%) in order to
226 compare risk estimates across participating countries.

227

228 A subgroup analysis, limited to those with inner city upbringing in the first five years, was
229 performed using a score of microbial load and diversity exposures to evaluate whether potential
230 risk reduction in the outcomes are similar to any risk reduction related to exposure to farming.

231

232 All analyses were carried out using Stata 12 (StataCorp, College Station Texas).

233

234

235 **Results**

236 Of the 10,201 participants with survey data for the question on childhood living environment, the
237 majority reported living in a village in a rural area, small town, or suburb of a city before the age
238 of five years (63.9%). The percentage of inner city participants was 26.9% and the smallest group
239 was those living on farms at 9.2%. Farm-exposed participants were significantly older at follow-
240 up than those born in rural or inner city environments (Table 1). The prevalence of exposure to
241 dogs or cats during childhood, older siblings, or bedroom sharing with older children was also
242 higher in those who reported living on a farm environment before the age of five years. In
243 addition, a family history of allergic disease was less prevalent in this group.

244

245 ***Allergic phenotypes***

246 A lower prevalence of any allergic sensitization ($p<0.001$), nasal symptoms ($p<0.001$) or BHR
247 (0.002) was observed in participants reporting farm exposure before the age of five (Table 2).
248 Those who lived on a farm before the age of five years had a reduced risk (OR=0.46 95%
249 CI=0.37-0.58) of adult atopy compared to those living in the inner city (Table 2). Only a
250 moderate reduction was observed in adults from a village/town/suburb. Stratification of nasal
251 symptoms by sensitization showed that the protective effect of the farming environment was
252 limited to those with allergic nasal symptoms (OR= 0.43, 95%CI=0.32-0.57). Participants with
253 early-life village, town or suburb, exposure did not have reduced risk of allergic nasal symptoms
254 when compared to the inner city reference group. A similar pattern was observed for current
255 allergic/non-allergic asthma in reference to place of upbringing, in which farm children
256 experienced a significant reduction in the risk of allergic asthma by approximately 50%. On the
257 other hand, the risk of current allergic asthma for those participants from a village, town, or
258 suburb was not-significantly reduced when compared to the inner city reference group. A very

259 similar pattern was also observed in the analysis of allergic/non-allergic BHR in relation to
260 childhood environment.

261

262 ***Lung function***

263 An interaction ($p=0.03$) was observed between gender and early-life home environment for FEV₁
264 (Table 3), but not FEV₁/FVC ratio. After adjustment for *a priori* confounders and weight,
265 females from a childhood farming environment experienced a significantly higher FEV₁ of
266 approximately 110 mL (95% CI 64-157). Slightly higher FEV₁/FVC values were observed for
267 those who lived on a farm before the age of five years (0.60 $p=0.036$, Table 2). However this
268 increase was found to be only modest after adjustment for maternal/paternal smoking and serious
269 respiratory infections before the age of five years ($p=0.115$). No significant associations were
270 observed with FEV₁/FVC categorized above and below 70%. Also, a higher FEV₁/FVC was not
271 observed for village/town/suburb participants as compared to the inner city reference group.

272

273 ***Meta-analysis of the effects***

274 No heterogeneity was seen between the associations of place of upbringing between countries for
275 the outcome of allergic sensitisation (Figure 1; $I^2=0\%$) while some heterogeneity was observed
276 for the outcome of FEV₁ (Figure 2; $I^2=44.8\%$). The pooled risk estimate for any sensitization in
277 the farming subgroup indicates a 53% (95%CI=0.36-0.59) reduction in the risk of sensitization,
278 while the village group had only 26% (95%CI=0.74-0.96) reduction when compared to
279 individuals exposed to an inner city environment in early life. Higher FEV₁ levels were observed
280 in females with a farm upbringing when compared to those from an inner city (pooled mean =
281 0.13 L, 95% CI = 0.09-0.18).

282

283 ***Sub group analyses***

284 Descriptive statistics for each biodiversity score subgroup are displayed in Table 4. Among those
285 who lived in an inner city in the first five years of life, a reduction in risk of any sensitization was
286 observed with increasing proxy microbial load score (trend $p=0.05$) (Table 5). Similarly, for most
287 outcomes, decreased odds of all allergic phenotypes were observed with increasing proxy
288 microbial load score. However, as seen in Table 5, early life farming exposure was associated
289 with a stronger reduction in the risk of sensitization and allergic disease phenotypes than any
290 level of proxy microbial exposure in the inner city.

291 **Discussion**

292 In this international study, interestingly, a higher FEV₁ was observed only in females exposed to
293 farming in the first five years of life independent of asthma and sensitization, which to our
294 knowledge has never been reported before. Furthermore, a protective effect of early-life farming
295 exposure was observed on allergic sensitization and, allergic phenotypes of nasal symptoms,
296 asthma, and BHR in adults, and while those raised on a rural setting had some reduction in the
297 risk of sensitisation, this was not as strong as seen for those raised on a farm. The association
298 between farm exposure and sensitization was consistent across all countries participating in this
299 study while the effect on FEV₁ varied slightly across centres. Our findings on atopic sensitization
300 are consistent with an earlier ECRHS I analysis, conducted by Leynaert et al, comparing farm vs.
301 non-farm participants, which found a reduced risk of atopic sensitization in adulthood (ORc 0.68,
302 CI 95% 0.55–0.86) with living on a farm in childhood, but no associations were observed for risk
303 of asthma (ORc 0.82; CI 95% 0.53–1.27) or wheeze (ORc 1.09; CI 95% 0.82–1.46). (22) While
304 early life exposures in the inner city related to increasing proxies of microbial diversity were also
305 shown to be associated with a decreased risk of sensitization, this reduction of risk was not as
306 large as with farm exposure alone.

307
308 Our analysis of proxy markers of increasing microbial exposures indicated that within an urban
309 environment increased exposure to microbial load may reduce risk of atopic disease but the
310 magnitude of this effect does not match that observed with farm exposure. It is possible that
311 prolonged contact with unique farm exposures such as livestock with extensive microbial
312 diversity are unmatched by any exposure in the inner city. These findings further support the role
313 of both load and diversity in environmental exposures in the development of allergic diseases, as
314 proposed by the “microbial diversity hypothesis”. (23–27) It is also relevant to consider the
315 possibility that proxy measures such as pet, daycare and crowding exposure can represent
316 alternate factors or mechanisms that influence disease risk in addition to microbial biodiversity,
317 which could potentially influence the estimates related to our biodiversity score. Additionally,
318 selective avoidance of pets due to asthma or allergy could also influence inner city biodiversity
319 scores, but would likely only play a small role in our estimates.(28) However, the overall
320 findings from our analysis indicate that diversity of early life microbial exposures impact disease
321 outcomes later in adult life.

322
323 To date, the majority of work done on farm exposures has focused on the association between
324 early life farm contact and childhood allergic and respiratory disease outcomes, while very few
325 studies have investigated the impact of early farm contact on adult disease, and especially adult
326 lung function. (9). Our findings on the impact of farm exposure on lung function in women are
327 novel. Differential response to a range of environmental exposures, such as microbial diversity,
328 indoor environment and air pollution, might possibly contribute to this gender difference.
329 Further, the actual exposures related to urban and rural environment might differ between men
330 and women. It is possible that men work in different roles or for longer periods on a farm than

331 females, to a point where their exposure levels become harmful instead of protective. (29) The
332 social differences around standards of cleanliness for males and females could also impact the
333 function of the hygiene hypothesis in relation to sex.(30) A sex-dependent functioning of the
334 'farm-effect' has been observed in children or adolescents in relation to cumulative incidence of
335 asthma and in adults with early life farm exposure in relation to asthma, hay fever and atopy.
336 (29,31,32) In addition, gender differences have already been explored in relation to other
337 environmental exposures and lung health and allergic disease outcomes. In a recent study by
338 Mészáros et al., exposure to home environmental tobacco smoke was found to increase the odds
339 of current asthma only in males. (33) Although the findings have been inconsistent, gender
340 differences in response to air pollution have also been reported. (34,35)

341
342 Gene-environment interactions have also been reported to play a crucial role in the association
343 between farming and allergic/respiratory disease outcomes. (36,37). It is suggested that those
344 genetically susceptible may be at a higher risk of allergies and respiratory outcomes when
345 exposed to farming and such groups may select themselves out of farming populations.
346 Interestingly, we observed those with farming exposure to have a lower prevalence of family
347 history of allergies supporting this hypothesis.

348
349 Our recent review consolidated published literature showing significant interactions between
350 CD14 gene polymorphisms and environmental microbial exposures with evidence of a protective
351 effect on atopic disease in childhood.(37) Additional evidence has also shown that the expression
352 of toll like receptor 2 (TLR2) genes may differ between farm and non-farm children, and it is
353 believed that some TLRs may act through various pathways to modify risk of allergic or
354 respiratory diseases.(38,39) It has also been hypothesized that polymorphisms in oxidative stress

355 genes may play a role in gene-environmental pollutant interactions that impact allergic and
356 respiratory disease. However, investigations into the modification of respiratory disease risk
357 through an altered oxidative stress response related to genetic variants of NAD(P)H:quinone
358 acceptor oxidoreductase 1 (NQO1) and glutathione S-transferase (GST) genes, have shown
359 mixed results. (40) The above discussion highlights that multiple genes may modify the role in
360 the observed ‘farm effect’, and that future research into this field needs to take into account a
361 number of potential environmental and genetic modifiers.

362
363 The strengths of our study is that it is a well-powered multinational study on adult asthma and
364 atopy, which collected various exposure data and objective clinical measures of atopic
365 sensitization and lung function by a standardized protocol. The potential limitations of this study
366 are survey data on early-life exposures were collected retrospectively and no objective measures
367 of microbial diversity were available for comparison. Residual confounding, stemming from a
368 wide variety of exposures associated with different living environments as mentioned above may
369 also be present in this analysis. These uncontrolled confounders may all contribute to the
370 observed “farm effect” in a unique way, that should be teased out in future investigations.
371 Finally, self-selection out of farm life for those with a family history of allergic disease can
372 present bias. Although we have adjusted for a family history of allergic disease in our analyses,
373 an amount of residual confounding may remain based on the severity of allergic disease
374 symptoms. Without further exploration into early life clinical outcomes such as lung function or
375 age at disease onset we are unable to completely determine whether effects on adult lung function
376 or disease are arising as a result of the direct effect of childhood farm exposure on adult health or
377 mediated through distinct effects on childhood disease. It is also possible that adult exposures,
378 such as occupational or home environment, may modify the effect of early life exposures on adult

379 disease, however no significant interactions were observed between early life home environment
380 and adult cleaning or agriculture occupations in these analyses.

381

382 **Conclusions**

383 Consistently across 14 countries, this analysis shows that early-life exposure to farm
384 environments is protective against subsequent adult allergic diseases. The consistency of the
385 findings across multi-country settings suggests that farming effects may be due to biological
386 mechanisms rather than socio-cultural effects that would differ between countries. A novel
387 finding was that women who grew up on a farm had higher lung function, and only mild
388 heterogeneity was observed across 14 countries. Further work is necessary to explain gender
389 differences. Our analysis further showed protective effects of markers of microbial diversity
390 (pets, siblings, day care etc) in persons with an inner city background, however, not as strong as
391 protective effects related to farm upbringing. Future studies should aim to discern critical farm
392 exposures that drive the association with sensitization by exploring the microbial components of
393 farm environments through molecular studies.

394

395

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659 **Tables & Figures**

660
661 **Table 1:** Characteristics and demographic data for the study population, according to childhood
662 living environment.
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	Inner City mean [SD]	Village/Town/Suburb mean [SD]	Farm mean [SD]	P-value
Mean Age (years)	41.9 [7.2]	42.6 [7.2]	45.1 [6.4]	p<0.001
	% (n)	% (n)	% (n)	
Gender				
Male	45.5 (1201)	48.0 (2991)	46.8 (432)	
Female	54.5 (1441)	52.0 (3239)	53.3 (492)	p=0.083
Ever smoker	57.4 (1512)	56.3 (3505)	54.3 (501)	p=0.2674
Paternal Smoking	66.5 (1705)	65.3 (3932)	61.0 (541)	p=0.019
Maternal smoking	27.8 (726)	23.1 (1415)	14.0 (128)	p<0.001
Cat in childhood	32.2 (717)	44.3 (2772)	84.0 (743)	p<0.001
Dog in childhood	30.1 (677)	42.8 (2707)	73.2 (655)	p<0.001
Older siblings	53.4 (702)	54.2 (2065)	61.7 (409)	p=0.001
Bedroom sharing	65.3 (1774)	66.9 (4332)	71.2 (666)	p=0.005
Family history of allergic disease	37.9 (883)	31.5 (1714)	26.4 (218)	p<0.001
Serious respiratory infection <5yrs	12.2 (319)	10.7 (649)	12.1 (108)	p=0.088
School attendance <5yrs	50.3 (1124)	36.2 (2288)	18.4 (163)	p<0.001

691 *Statistical significance determined by Chi² or ANOVA

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706 **Table 2:** Associations between lung function measures and allergic disease outcomes with
 707 childhood home environment (Inner city reference group)

	Inner city % (n)	Village/town/ suburb % (n)	Farm % (n)	Village/town/ suburb <i>OR [95%CI];or Mean Difference (SD)</i>	Farm <i>OR [95%CI I];or Mean Difference (SD)</i>
BHR	18 (306)	16 (625)	12 (78)		
+BHR -Atopy				1.05 (0.81-1.36)	0.92 (0.61-1.39)
-BHR +Atopy				0.82 (0.69-0.96)	0.46 (0.34-0.61)
+BHR + Atopy				0.88 (0.69-1.11)	0.54 (0.35-0.83)
Mean FEV₁/FVC (SD)*	80.2 (6.8)	80.0 (6.7)	80.6 (6.8)	-0.06 (-0.41-0.29) p=0.746	0.60 (0.04-1.16) p=0.036
Any atopic sensitization	38 (771)	31 (1564)	18 (143)	0.83 (0.73-0.94)	0.46 (0.37-0.58)
Nasal Symptoms	36 (950)	32 (1992)	25 (230)		
+Nasal Symptoms -Atopy				1.04 (0.87-1.24)	0.96 (0.73-1.26)
-Nasal Symptoms + Atopy				0.76 (0.64-0.91)	0.51 (0.37-0.69)
+Nasal Symptoms +Atopy				0.90 (0.77-1.05)	0.43 (0.32-0.57)
Current Asthma	6.1 (168)	5.5 (361)	4.4 (41)		
+Current Asthma -Atopy				1.08 (0.72-1.61)	1.09 (0.60-1.99)
-Current Asthma + Atopy				0.82 (0.72-0.93)	0.47 (0.37-0.59)
+Current Asthma +Atopy				0.92 (0.70-1.21)	0.47 (0.28-0.81)

708 Statistically significant associations in **bold**

709 Adjustment for: age, sex, study center, smoking, family history of allergic disease

710 Additional adjustment*: height², weight

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Table 3: Lung function outcomes in relation to childhood living environment

	MEN ♂		WOMEN ♀	
	<i>Mean FEV₁, L (SD)</i>	<i>Adjusted difference in FEV₁, mL*</i>	<i>Mean FEV₁, L (SD)</i>	<i>Adjusted difference in FEV₁, mL*</i>
Inner city	4.03 (0.59)	(reference)	2.97 (0.40)	(reference)
Village/town /suburb	4.06 (0.73)	41 (-5, 86) p=0.080	2.99 (0.40)	22 (-7, 51) p=0.142
Farm	4.08 (0.59)	52 (-20, 124) p=0.158	3.08 (0.40)	110 (64, 157) p<0.001

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*Adjusted for age, height², weight, study center, smoking, family history of allergic disease

739 **Table 4:** Characteristics and demographic data for the inner city study population, according to biodiversity score.

	Score 0 mean [SD]	Score 1 mean [SD]	Score 2 mean [SD]	Score 3 mean [SD]	Score 4 mean [SD]	Score 5 mean [SD]	P-value*
Mean Age (years)	43.6 [7.3]	43.7 [7.3]	42.3 [7.3]	42.2 [7.3]	41.9 [7.0]	39.9 [7.4]	p<0.001
	% (n)	% (n)	% (n)	% (n)	% (n)	% (n)	
Gender							
Male	53.6 (30)	50.1 (137)	45.7 (313)	45.1 (296)	41.9(142)	40.8 (44)	
Female	46.4 (26)	49.8 (136)	54.3 (372)	54.9 (361)	58.1 (197)	59.3 (64)	p=0.243
Ever smoker	48.2 (27)	61.3 (166)	55.8 (381)	58.0 (380)	64.3 (218)	62.0 (67)	p=0.058
Paternal Smoking	70.9 (34)	62.8 (165)	64.4 (428)	68.4 (437)	73.4 (240)	78.9 (82)	p=0.004
Maternal smoking	27.3 (15)	23.3 (62)	25.1 (169)	24.8 (161)	32.9 (110)	34.3 (37)	p=0.020
Cat childhood	0	3.9 (11)	12.9 (95)	36.0 (247)	72 (249)	100 (108)	p<0.001
Dog childhood	0	5.6 (16)	9.8 (72)	31.6 (217)	71.4 (247)	100 (108)	p<0.001
Older siblings	0	48.6 (139)	82.4 (605)	91.8 (630)	97.4 (337)	100 (108)	p<0.001
Bedroom sharing	0	23.1 (66)	58.0 (426)	78.1 (536)	90.2 (312)	100 (108)	p=0.005
School attendance <5yrs	0	18.9 (54)	36.8 (270)	62.4 (428)	69.1 (239)	100 (108)	p<0.001
Family history of allergic disease	31.9 (15)	33.8 (78)	32 (191)	35.4 (204)	31.8 (93)	33.3 (31)	p=0.849
Serious respiratory infection <5yrs	9.4 (5)	11.9 (32)	10.6 (74)	8.9 (58)	11.1 (37)	11.3 (11)	p=0.754

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742 *Statistical significance determined by Chi² or ANOVA

743 **Table 5:** Associations between lung function measures and allergic disease outcomes across
 744 varied biodiversity levels in an inner city childhood living environment (grouped by biodiversity
 745 score) and farm.

	Biodiversity score 0/1 Inner city Reference	Biodiversity score 2 Inner city	Biodiversity score 3 Inner city	Biodiversity score 4/5 Inner city	Farm
FEV1* ♂ mL	-	-16 (-133, 101)	-56 (-179, 67)	-91 (-229, 46)	32 (-90, 153)
FEV1* ♀ mL	-	11 (-73, 95)	-9 (-96, 77)	51 (-41, 143)	116 (29, 202) P=0.009
FEV₁/FVC*	-	-0.22 (-1.17, 0.72)	-0.44 (-1.42, 0.54)	-0.43 (-1.5, 0.64)	0.30 (-0.67, 1.28) P=0.545
+BHR -Atopy	-	0.99 (0.51-1.91)	0.64 (0.31-1.32)	0.78 (0.36-1.68)	0.77 (0.39-1.51)
-BHR +Atopy	-	0.66 (0.43-1.01)	0.72 (0.47-1.12)	0.54 (0.29-0.88)	0.31 (0.19-0.49)
+BHR + Atopy	-	0.83 (0.43-1.60)	0.80 (0.41-1.57)	0.96 (0.47-1.96)	0.46 (0.23-0.95)
Any atopic sensitization	-	0.81 (0.58-1.12)	0.76 (0.54-1.07)	0.70 (0.49-1.02)	0.36 (0.25-0.52)
+Nasal Symptoms -Atopy	-	1.23 (0.78-1.96)	0.94 (0.58-1.51)	0.87 (0.52-1.46)	0.85 (0.55-1.32)
-Nasal Symptoms + Atopy	-	0.76 (0.49-1.18)	0.81 (0.53-1.26)	0.83 (0.52-1.33)	0.42 (0.28-0.66)
+Nasal Symptoms +Atopy	-	0.96 (0.65-1.42)	0.88 (0.59-1.31)	0.85 (0.55-1.31)	0.38 (0.25-0.56)
+Current Asthma -Atopy	-	0.80 (0.32-2.00)	0.48 (0.17-1.34)	0.31 (0.08-1.11)	0.55 (0.21-1.41)
-Current Asthma + Atopy	-	0.77 (0.55-1.09)	0.70 (0.49-1.00)	0.61 (0.41-0.90)	0.34 (0.23-0.50)
+Current Asthma +Atopy	-	1.16 (0.47-2.88)	1.26 (0.50-3.13)	1.57 (0.60-4.10)	0.56 (0.21-1.50)

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 747 Statistically significant associations in **bold**
 748 Adjustment for: age, sex, study center, smoking, family history of allergic disease
 749 Additional adjustment* : height² and weight
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