

GENE–ENVIRONMENT INTERACTION IN THE INTERGENERATIONAL TRANSMISSION OF ASTHMA

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SUMMARY

Researchers have found strong linkages between parent and child health, but the mechanisms underlying intergenerational health transmission are not well understood. This paper investigates how the importance of genetic health transmission mechanisms varies by environmental conditions in the case of pediatric asthma, the single most common chronic health condition among American children. Using a sample that includes approximately 2000 adoptees and a large number of similar biological families, I find that the relative importance of genetic transmission differs strongly by socioeconomic status (SES). In high SES families, parent–child asthma associations are approximately 75% weaker among adoptees than biological children, suggesting a dominant role for genetic transmission. In lower SES families, parent–child asthma associations are virtually identical across biological and adoptive children, suggesting a negligible role for genetic transmission. A potential interpretation of this difference is that as environmental conditions affecting asthma improve among higher SES children, an increasingly large share of asthma variation is due to genetics. Copyright © 2016 John Wiley & Sons, Ltd.

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1. INTRODUCTION

Social scientists have a longstanding interest in the extent to which individual outcomes are transmitted across generations.¹ While the extensive intergenerational mobility literature has focused primarily on income and education, a more recent strand of this literature explores linkages between parent and child health outcomes (for examples, Currie and Moretti (2007); Trannoy *et al.* (2010); Venkataramani (2011); and Bhalotra & Rawlings 2011, 2013). Such linkages are of interest to economists both because health is an important socioeconomic outcome in its own right and because health – particularly childhood health – is a well-established proximate cause of basic economic outcomes such as income and educational attainment (Currie, 2009).

One of the fundamental questions in the intergenerational mobility literature has been the extent to which observed parent–child associations are due to genetic as opposed to environmental transmission mechanisms, and this distinction is perhaps particularly germane when studying the transmission of health outcomes given that they are explicitly physiological in nature. However, while most serious health conditions are known to have significant genetic and environmental components, contemporary biomedical research has increasingly stressed the importance of interactions between genetic and environmental health determinants.

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¹ See Solon (1999) and Black & Devereux (2011) for reviews of the economic literature on intergenerational mobility.

In this framework, the relative importance of genetic traits is not a fixed proportion but rather varies with environmental circumstances. Two individuals who have identical genotypes but who experience different environmental conditions will in many cases have differential gene expression and ultimately disparate observable phenotypes as well. Such interactions would make the common practice of assigning fixed proportions of an outcome that are due to genes and environments conceptually incoherent. While intuitive and well supported empirically in most contexts, this conceptual framework has not been meaningfully incorporated into social scientific research on health transmission.

The primary contribution of the present paper is to apply the gene–environment interaction framework to better understand the intergenerational transmission of a specific health condition, asthma. Pediatric asthma is the single most common chronic condition among American children, impacting more than one in 10 children nationally, and family history is a strong risk factor (Akinbami, 2006). Asthma is a leading cause of missed school days and has been shown to have significant long-term impacts on health, human capital accumulation, and economic success (Case & Fertig *et al.*, 2005; Currie & Hanushek *et al.*, 2009; Fletcher & Green *et al.*, 2010).

It is generally well accepted that gene–environment interactions play a central role in asthma pathogenesis, and identifying specific susceptibility genes and investigating their interactions with various environmental triggers are an active area of medical and epidemiological research. For instance, Gilliland *et al.* (2002) found that *in utero* and early life exposure to tobacco smoke decreased lung function and increased asthma symptoms significantly more among children with one variant of the gene related to the processing of toxins than for children with another variant. Similarly, Lee *et al.* (2004) found that exposure to particulate matter increased asthma risk significantly more for children with a particular variant. Koppelman (2006) and Ober and Yao (2011) provide insightful reviews of this literature.²

While acknowledging the rigor and importance of this previous work using data containing genetic markers, the present paper implements an alternative approach. Rather than focus on specific genes, the aggregate importance of gene–environment interactions in asthma transmission is estimated by extending a well-established methodology based on comparisons of adoptive and biological children. This approach first compares the strength of intergenerational asthma transmission among adoptees relative to biological children with similar observable characteristics. Under imperfect but plausible assumptions discussed in detail next, these differences produce a credible estimate of the aggregate importance of genetics for asthma transmission.³ Next, the extent to which these estimates of genetic transmission vary by family socioeconomic status (SES) is measured.

The basic finding is that the importance of genetic transmission in asthma varies strongly by SES, with genetic mechanisms playing a much larger role in higher SES families. For instance, the results indicate that in families where the parent is a college graduate, asthma transmission is approximately 75% weaker for adoptees than for similar biological children, suggesting a dominant role for genetic transmission. In contrast, among the children of parents without a college degree, asthma transmission rates are virtually identical across biological and adoptive children, suggesting a modest or nonexistent role for genetic transmission.

The remainder of the paper proceeds in five sections. Section 2 describes the utilized data; Section 3 presents the main findings; Section 4 discusses possible interpretations and explanations for those findings; Section 5 presents additional results that address issues related to measurement and non-random adoptee placement; and Section 6 concludes.

2. DATA

The utilized data come from the National Health Interview Survey (NHIS). The NHIS is an annual, nationally representative survey conducted by the Centers for Disease Control. The survey's current design, which was

²For examples and discussions of genetic marker use in economic research, see Fletcher (2011); Beauchamp *et al.* (2011) and Benjamin *et al.* (2012).

³Several influential economic studies have used adoptees to isolate genetic transmission mechanisms for non-health related characteristics (see Plug 2004; Björklund & Lindahl *et al.*, 2006; and Sacerdote 2007, among others), but the approach has been only sparsely applied to intergenerational health transmission. Exceptions include Sorensen & Nielsen *et al.* (1988) and Thompson (2014).

first implemented in the 1998 wave, randomly selects approximately 40,000 households for participation and then within each household randomly selects one adult and one child (if present) to complete an extensive health-related survey instrument. The selected adult and child are often a parent and their child, and by pooling the 1998–2012 waves of the survey, it is possible to create a working data set that contains detailed information on asthma status for over 120,000 parent–child pairs. The primary asthma measure used in the following is an indicator of whether each parent and child has ever been formally diagnosed with asthma, which was collected in all of the utilized NHIS waves. Appendix S1 reports results using alternative asthma measures.

2.1. Adoptees in the National Health Interview Survey

While the NHIS did not intentionally seek out adopted children for participation, the large size of the combined annual samples led to the incidental inclusion of approximately 2000 adoptees. Adoptees are identified as cases where the selected adult listed their relationship to the selected child as ‘adopted parent’. Cases where the relationship between the selected adult and child is an extended family member, older sibling, stepparent or foster parent, as well as cases where the selected adult reports being the selected child’s adoptive parent but another parental figure in the household is listed as a blood relative of the child, are excluded from the adoptive sample. This rules out, for instance, situations where a biological parent’s partner or an extended family member formally adopts a child.⁴

An important shortcoming of the NHIS adoptee sample is that no institutional details of the adoption process are reported, including the method by which adopted children were assigned to families. This raises a concern that children may have been matched to adoptive families non-randomly on dimensions related to asthma outcomes, which could lead to genetic similarities between adoptive parents and children despite their lack of direct biological relatedness. This issue is discussed in greater detail in Section 5, and evidence presented there suggests minimal matching of adoptive parents and children on the basis of health.

The NHIS adoptee sample also has several desirable features. Most importantly, the sample is much larger than most previously used adoptee data sets, especially in the USA. For example, Das and Sjogren (2002) work with a sample of 126 adoptees; Plug (2004) uses information on 610 adoptees; and Sacerdote (2002) uses two samples of adoptees, one with a size of 300 and the other with a size of 120. Björklund *et al.* (2006) use exceptional administrative data from Sweden, but even their working sample is of comparable size with the NHIS data, with 2125 adoptees, while Sacerdote (2007) performed extensive original data collection to obtain a sample of 1650 Korean American adoptees. The relatively large size of the NHIS sample is critical for estimating interactive effects with acceptable precision. It is also noteworthy that the NHIS adoptees are derived from a national probability sample and therefore representative of the general adoptive population, whereas most existing US adoptee data sets are to varying degrees derived from convenience samples.

2.2. Matched biological sample construction

Families that include adopted children typically differ from those that include only biological children in terms of demographics, SES, and health-related characteristics such as access to health care. Because many of these factors could plausibly affect asthma transmission, unconditional comparisons of transmission among adoptive and biological parent–child pairs are potentially problematic. To account for this, the main analyses use a sample of biological children with observable characteristics that are similar to those of NHIS adoptees.

To construct a biological sample with observables similar to the adoptive sample, I estimate individual propensity scores with a probit specification that models the probability of adoptive status as a function of the age, race, and gender of both parents and children, the number of children in the household, parental education and marital status, child health insurance coverage status, and current region of residence. This propensity

⁴I drop 99 adoptees who had been diagnosed with autism, Down syndrome, mental retardation, muscular dystrophy, cerebral palsy, and cystic fibrosis both because the adoption process may be significantly different for children with these conditions and because they may affect the diagnosis and treatment of asthma.

Table I. Descriptive statistics by adoption status

	Adoptive sample		Full biological sample		Matched biological sample	
	Mean	SD	Mean	SD	Mean	SD
Parent high school or less	0.316	0.465	0.457	0.498	0.358	0.479
Parent some college	0.275	0.446	0.301	0.459	0.268	0.443
Parent college or beyond	0.409	0.492	0.242	0.428	0.374	0.484
Parent age	46.72	10.75	36.81	9.52	46.50	12.95
Parent white	0.802	0.398	0.764	0.424	0.786	0.410
Parent black	0.157	0.364	0.154	0.361	0.155	0.362
Parent Hispanic	0.098	0.297	0.266	0.442	0.132	0.339
Parent male	0.382	0.486	0.352	0.478	0.397	0.489
Parent married	0.706	0.456	0.664	0.473	0.689	0.463
Parent divorced	0.176	0.381	0.168	0.374	0.184	0.387
Parent never married	0.118	0.323	0.168	0.374	0.127	0.333
Child age	9.45	4.90	8.33	5.33	9.71	5.21
Child white	0.634	0.482	0.762	0.426	0.695	0.460
Child black	0.209	0.407	0.160	0.367	0.195	0.396
Child Hispanic	0.172	0.377	0.278	0.448	0.189	0.391
Child male	0.481	0.500	0.514	0.500	0.498	0.500
Child uninsured	0.048	0.215	0.103	0.304	0.056	0.229
Number of children	1.72	1.09	1.93	1.00	1.73	0.90
Region – Northeast	0.182	0.386	0.168	0.373	0.172	0.378
Region – Midwest	0.245	0.430	0.218	0.413	0.221	0.415
Region – South	0.343	0.475	0.357	0.479	0.351	0.477
Region – West	0.231	0.421	0.258	0.437	0.255	0.436
Parental asthma	0.128	0.335	0.103	0.304	0.105	0.307
Child asthma	0.168	0.374	0.127	0.333	0.141	0.348
Observations	1986		122,613		3470	

Data come from the 1998 to 2012 waves of the National Health Interview Survey; see Section 2 for sample descriptions.

score is used to match adoptive parent–child pairs to their two nearest neighbors in the biological sample (with replacement), and only these matched biological observations are used in the main analyses. Appendix S1 demonstrates that the paper’s central results are robust to various reasonable alternative methods of constructing this biological sample, as well as to using the full biological sample.⁵

Table I reports means and standard deviations for the adoptive sample, the full biological sample, and the matched biological sample. The table shows that relative to the full population of biological parents, adoptive parents tend to be better educated, older and whiter than biological parents. Adoptive parents are also more likely to be male and to be married, and adoptive children are older, less likely to be white, and much less likely to currently lack health insurance than their biological counterparts. Table I also indicates that, with the partial exception of race, the matched biological sample has observable characteristics that are very similar to the adoptive sample. Because the set of matching variables is not fully comprehensive, there could still remain important differences between the adoptive sample and the matched biological sample, but the close resemblance of the two groups is encouraging.

The bottom two rows of Table I report asthma prevalence rates for parents and children. Parental asthma is slightly more common in the adoptive sample than in the full biological sample (12.8% vs. 10.3%), and childhood asthma is substantially more prevalent among adoptive children than among children from the full biological sample (16.8% vs. 12.7%). The higher asthma prevalence rate among adoptive children is likely due

⁵While propensity scores are used to construct a sample of biological children with observable characteristics that are similar to those of NHIS adoptees, note that I do not implement a strategy in which each adoptive observation is compared only with matched biological observations. Rather, propensity scores are used only to identify a set of biological children with observables comparable with the adoptive sample.

to less favorable circumstances pre-adoption.⁶ While child asthma itself was not explicitly used as a matching variable, Table I also shows that the child asthma prevalence rate in the matched biological sample (14.1%) is closer to the prevalence rate in the adoptive sample, increasing the credibility of the adoptee–biological comparisons made subsequently.

3. BASELINE RESULTS

The paper's main empirical exercise is to estimate regression models of the following form:

$$Asthma_i^1 = \alpha + \beta_1 Asthma_i^0 + \beta_2 Adoptive_i + \beta_3 (Asthma_i^0 \times Adoptive_i) + \gamma X + \varepsilon_i \quad (1)$$

where $Asthma_i^1$ indicates whether the child from family i has ever been diagnosed with asthma, $Asthma_i^0$ indicates whether the parent from family i has ever been diagnosed with asthma, $Adoptive_i$ indicates whether the child is adopted, and X is a vector of controls containing the variables listed in Table I. The primary coefficient of interest is β_3 , which estimates the percentage point reduction in asthma transmission among adoptees relative to biological children with similar observable characteristics.

The first column in Table II reports ordinary least squares estimates of Equation 1 using the full sample of adoptive children and the matched sample of biological children described earlier.⁷ The coefficient on parental asthma is 0.204, indicating that having a parent who has been diagnosed with asthma increases the probability of a child being diagnosed by approximately 20.4 percentage points. The coefficient on the interaction of parental asthma and adoption status is estimated to be -0.064 and is statistically significant. This indicates that asthma transmission is approximately 6.4 percentage points weaker among adoptees than in biological children, a reduction of 32%. Subject to assumptions discussed in detail next, this can be interpreted as evidence that, on average, approximately one-third of the intergenerational transmission of asthma occurs via genetic mechanisms.⁸

However, if gene–environment interactions are an important component of asthma transmission, then this single point estimate may mask important heterogeneity in the strength of genetic transmission: More than 32% of transmission may occur via genetic mechanisms for populations facing particular sets of environmental circumstances, while less than 32% of transmission may be due to genes for populations facing other sets of environmental circumstances. Given this, the remaining columns in Table II reestimate the baseline specification separately for families in which the parent had a high school diploma or less, had attended some college but did not receive a 4-year degree, and where they were a college graduate or held a post-baccalaureate degree.⁹ These educational categories were chosen both because they are of practical significance and because they divided the adoptive sample into three roughly equal-sized groups, but in the following, it is demonstrated that using either a continuous education measure or a larger number of educational categories yields qualitatively similar results, as does using income-based SES measures.

Column 2 of Table II shows results for families where the parent had no more than a high school diploma. Parental asthma continues to be strongly associated with child asthma in this sub-population, but the coefficient on the interaction of parental asthma and adoptive status is statistically and substantively insignificant and is actually nominally positive at 0.018. Similarly, Column 3 shows results for families where the parent had some college training but did not graduate, and the interaction term is equal to -0.023 and is statistically insignificant.

⁶The possible effects of differences in child asthma prevalence by adoption status and SES are discussed in Section 5.

⁷The results are very similar if logit or probit models estimated via maximum likelihood are used instead of ordinary least squares. Because it is not conceptually clear what broader population the matched sample of biological children is intended to represent, sampling weights are not applied. Robust standard errors are reported in parenthesis.

⁸More precisely, reductions among adoptees can be interpreted as the proportion of transmission due to pre-adoption factors, which in addition to genetic composition include prenatal and early childhood environmental factors. The 32% reduction found in Column 1 of Table II is therefore an upper bound on the aggregate proportion of asthma transmission attributable to genetic mechanisms.

⁹These three educational attainment categories were constructed using NHIS questions on highest degree attained. Individuals with high school equivalency credentials ("GED" holders) are placed in the high school diploma or less category, while associates degree holders are placed in the some college category.

Table II. Asthma transmission by parental education and adoption status

	(1) All parental education levels	(2) Parent high school or less	(3) Parent some college	(4) Parent college or beyond	(5) All parental education levels
Parental Asthma	0.204*** (0.025)	0.190*** (0.042)	0.202*** (0.046)	0.210*** (0.041)	0.080 (0.101)
Adopted	0.032*** (0.010)	0.034* (0.019)	0.013 (0.021)	0.052*** (0.016)	0.037 (0.053)
Parental asthma × adopted	−0.064* (0.039)	0.018 (0.071)	−0.023 (0.074)	−0.152*** (0.058)	0.445** (0.194)
Parental education × parental Asthma × adopted					−0.036*** (0.013)
% Change in transmission among adoptees	−31.50%	9.60%	−11.20	−72.00%	
Observations	5461	1869	1477	2110	5456
R ²	0.051	0.062	0.057	0.056	0.055

Dependent variable is an indicator of whether the child has ever been diagnosed with asthma. All models control for the age, race and gender of both parents and children, parental marital status, child health insurance coverage status, number of children in the family, and the family's current region of residence. Specification reported in Column 5 additionally contains the main effect of parental education and its two-way interaction with adoption status and parental asthma. Robust standard errors in parentheses. *, **, and *** denote statistical significance at the 10%, 5%, and 1% levels, respectively.

These results suggest that genetic asthma transmission mechanisms are of minimal importance among families where the parent has less than a college education. Column 4 of Table II shows results for families where the parent was a college graduate or beyond. In strong contrast to the previous parental education groups, the coefficient on the interaction of parental asthma and adoption status is -0.152 and is highly statistically significant. This represents a reduction in the strength of asthma transmission of 72% among adoptive children relative to biological children and suggests that among higher SES families, shared genes are a critical asthma transmission mechanism.

The final column in Table II shows results from pooling all educational groups and estimating a regression of the following form:

$$\begin{aligned} Asthma_i^1 = & \alpha + \beta_1 Asthma_i^0 + \beta_2 Adoptive_i + \beta_3 Education_i \\ & + \beta_4 (Asthma_i^0 \times Adoptive_i) + \beta_5 (Asthma_i^0 \times Education_i) + \beta_6 (Education_i \times Adoptive_i) \quad (2) \\ & + \beta_7 (Asthma_i^0 \times Adoptive_i \times Education_i) + \gamma X + \varepsilon_i \end{aligned}$$

where $Education_i$ denotes the educational attainment of the parent from family i measured continuously in years.¹⁰ In this specification, the primary coefficient of interest is β_7 , which estimates how much an additional year of parental education changes the biological–adoptive asthma transmission *differential*. This specification is desirable in that it avoids creating semi-arbitrary parental education bins and also offers a convenient method of testing for the statistical significance of the identified gene–environment interaction.

The results in Column 5 in Table II mirror those of the split sample analysis. The coefficient on the triple interaction term is -0.036 and is highly statistically significant. The magnitude of the coefficient on the triple interaction term is in line with the split sample estimates. For example, the results predict that if a parent has 16 years of education, the size of the biological–adoptive asthma transmission differential would be 14.4 percentage points larger than if the parent had 12 years of education.¹¹

All of the models reported in Table II imposed functional form restrictions, because the biological–adoptive asthma transmission differential either was only allowed to vary across three broad educational categories (in Columns 2–4) or was restricted to be linear (in Column 5). Additionally, the estimation approach restricted the coefficients on the included covariates to be equal for adoptive and biological parent–child pairs. Both of these functional form restrictions can be relaxed by estimating models in which child asthma is regressed onto parental asthma and the vector of controls separately for biological and adoptive parent–child pairs and for each possible educational category. This approach allows both asthma transmission strength and the covariates to vary arbitrarily by educational attainment and adoption status.

The educational attainment questions in the NHIS allow for the construction of five distinct education categories: less than high school, high school graduate, some college, college graduate, and graduate degree recipient.¹² To assess the effects of relaxing the implicit functional forms restrictions imposed in Table II, asthma transmission regressions were estimated separately for biological and adoptive parent–child pairs within each of these five education categories (a total of 10 separate regressions), and the strength of asthma transmission within each of these subsamples is plotted in Figure 1.

Figure 1 estimates that among biological children (shown in the left-hand panel), the increase in the probability of child asthma that is associated with having an asthmatic parent is remarkably constant at approximately 20 percentage points across all parental education categories. In contrast, among adoptive children (shown in the left-hand panel), those from families where the parent dropped out of high school or was a high school

¹⁰This continuous education variable was constructed using a separate NHIS question in which parents reported their total years of schooling for 0–12 years and then assigned a value of 14 for those who reported ‘1 to 3 years’ of college, a value of 16 to those who reported ‘4 years of college’, and a value of 18 to those who reported ‘5 or more years of college’.

¹¹Because this is a difference of 4 years of education and $-0.036 \times 4 = -14.4$.

¹²While it is technically possible to further differentiate individuals who did not complete high school by their highest completed grade, these lower education categories are too sparsely populated in the working sample to produce meaningful results.

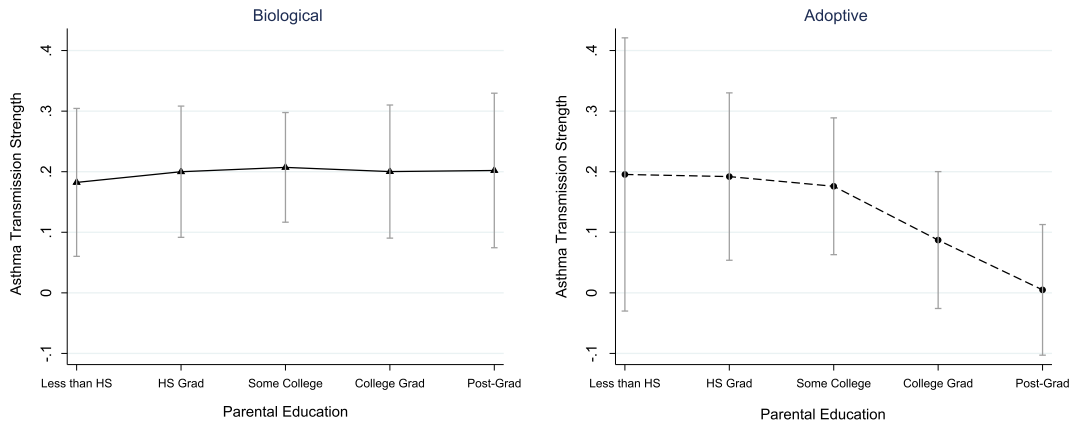


Figure 1. Asthma transmission by parental education and adoption status

graduate, asthma transmission is approximately 20 percentage points but then falls to around 17 percentage points in the some college category, 8 percentage points for college graduates, and zero percentage points for families where the parent has a graduate degree.

4. INTERPRETATION

Because asthma is a physiological condition, the most compelling interpretations of the results reported previously will likely come from biomedical research. However, a potentially insightful interpretation of the results can also be framed in terms of a simple economic model. Specifically, let the probability of child asthma be determined by a health production function with arguments corresponding to genetic and environmental asthma determinants:

$$P(\text{asthma}) = f(g, e) \quad (3).$$

Gene–environment interactions are present if the cross partial derivatives of this function are non-zero, or put differently, as long as genes and environments are not perfect substitutes in the production of asthma. While any specific form of the f function is necessarily ad-hoc for an output as specific as pediatric asthma, perfect substitution production functions are typically viewed as a special case in economics, and the presence of at least some physiological or institutional barriers to substituting genetic and environmental asthma determinants seems likely.

To gain some intuition into the types of health production functions that could generate the empirical findings reported earlier, it is useful to consider an extreme case. In particular, suppose there are just two asthma-relevant genotypes, g_1 and g_2 , and that children of genotype g_1 develop asthma with certainty irrespective of their environmental circumstances while for children of genotype g_2 the probability of developing asthma is a decreasing linear function of how favorable their environmental conditions are. In this case, the health production function is given by

$$P(\text{asthma}) = \begin{cases} 1 & \text{if genotype} = g_1 \\ 1 - \alpha e & \text{if genotype} = g_2 \end{cases} \quad (4)$$

There is strong evidence that higher SES children are less likely to be exposed to environmental asthma risk factors. For instance, Bell and Ebisu (2012) report that a 10% increase in census-tract level poverty rates is associated with a 2.16% increase in exposure to fine particulate matter ($PM_{2.5}$), a well-established asthma

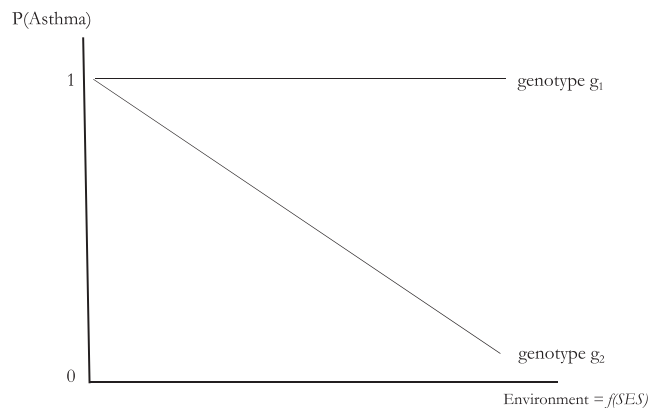


Figure 2. Hypothetical socioeconomic status (SES)–asthma gradients by genotype

determinant, with qualitatively similar associations for average education and income levels and for other air quality measures (see also Brooks & Sethi 1997 and Ash & Fetter 2004). Likewise, within the NHIS sample used in the present paper, children whose parent had a high school education or less had an uninsured rate of 9.7%, while the uninsured rate among children with a college-educated parent was just 1.8%. Similarly, 27.1% of lower education parents in the current NHIS sample reported being smokers, but only 8.1% of the college-educated parents reported smoking.¹³

Assuming that exposure to environmental asthma determinants does indeed fall with SES, Figure 2 displays hypothetical SES–asthma gradients by genotype based on Equation 4. The aggregate importance of genetic type is given by the distance between the two lines. Because this distance is negligible at the low end of the SES distribution then grows larger as SES increases, this production function generates a gene–environment interaction in line with the previous empirical findings. A heuristic interpretation of Figure 2 can be gained by initially imagining a population of very low SES children. These children are more likely to be from neighborhoods with high levels of particulate matter, have parents who are smokers, and are less likely to have regular access to primary medical care, and so on. Under these very unfavorable environmental circumstances, depicted in the far left-hand side of Figure 2, genotype is inconsequential because virtually all children have asthma. As SES and the relevant environmental conditions improve (moving from left to right in Figure 2), children of genotype g_2 respond with lower rates of asthma while children of genotype g_1 continue to experience asthma universally. Finally, in the context of highly favorable environmental conditions experienced by high SES children, depicted in the far right-hand side of Figure 2, differences between the two genotypes become very large. In a population of children that have minimal exposure to environmental triggers, regular access to high-quality preventative care, and so on, genes are ‘all that’s left’ to determine asthma status.

A conceptually similar interpretation of the results focuses on the extent to which the utilized parental asthma measures are more ‘genetically loaded’ at the higher end of the parent SES distribution. Specifically, if high SES parents experience more favorable average environmental circumstances themselves, then instances in which they still develop asthma despite those favorable conditions may signal strong genetic asthma predispositions. This would lead to stronger genetic asthma transmission within higher SES parent–child pairs, as found earlier. While this explanation focuses on the parent generation rather than the child generation, it is analogous to the child-focused explanation depicted in Figure 2 in that under more favorable environmental circumstances, genetic differences become increasingly more consequential until they account for virtually all of the variation in asthma outcomes.

¹³These rates are similar to those reported in other national analyses; for instance, see Kaiser Family Foundation (2012) on uninsured rates and Chahine *et al.* (2011) on smoking rates.

Many asthma production functions that are equally plausible to the one discussed earlier do not generate increased genetic transmission at higher SES levels. The example given in Equation 4 and Figure 2 is intended to simply illustrate one form of asthma technology that is consistent with this paper's empirical findings. Any credible attempt to specify a particular asthma production function would need to be based on a physiological model of pediatric asthma that is beyond the scope of the present study.

Still, these interpretations are in line with those of previous research producing qualitatively similar empirical findings for a varied set of characteristics. For instance, Turkheimer *et al.* (2003) use a twin-design to document that among families with poverty-level incomes, the genetic contribution to IQ scores is close to zero, while for affluent families, genetic factors explain almost all observed IQ variation. Likewise, Fogel (1994) and Floud *et al.* (2011) document that the heights of individuals from different geographic areas and ethnic groups varied substantially under historical conditions of food scarcity but largely converged when all of the populations had their basic nutritional needs met. These findings are consistent with the argument that under favorable environmental conditions, a relatively large share of variation in outcomes is due to genetic traits.

5. ROBUSTNESS AND ADDITIONAL RESULTS

5.1. Income-based socioeconomic status measure

In addition to parental educational attainment, family income is a commonly used SES measure, and the NHIS collects information on household income-to-needs ratios. An important advantage of using income-to-needs ratios over parental education is that they measure SES at the household level, whereas education is only reported for the parent who was randomly selected to complete the survey. The main disadvantage of using income-to-needs ratios is that because of refusals, they are missing for approximately 15% of the sample, and in addition, approximately 25% of the sample is assigned a top-coded ratio of 5. For these reasons, the education-based results in Table II are preferred, but for completeness results, using household income-to-needs ratios in place of parental education is presented in Table III.

Table III. Income-based socioeconomic status measure

	(1) All household incomes	(2) Income/needs < 2.5	(3) 2 ≤ Income/needs <5	(4) Income/needs ≥ 5	(5) All household incomes
Parental asthma	0.202*** (0.026)	0.184*** (0.040)	0.165*** (0.046)	0.262*** (0.054)	0.165*** (0.054)
Adopted	0.032*** (0.011)	0.036* (0.021)	0.047** (0.019)	0.031 (0.020)	0.044 (0.029)
Parental asthma × adopted	−0.092** (0.040)	−0.026 (0.066)	−0.057 (0.071)	−0.209*** (0.074)	0.029 (0.090)
Income/needs × parental Asthma × adopted					−0.039 (0.025)
% Change in transmission	−45.50%	−13.90%	−34.70%	−79.50%	
Among adoptees					
Observations	4736	1,694	1627	1415	4736
R ²	0.050	0.062	0.046	0.072	0.052

Dependent variable is an indicator of whether the child has ever been diagnosed with asthma. All models control for the age, race, and gender of both parents and children, parental marital status, child health insurance coverage status, number of children in the family, and the family's current region of residence. Specification reported in Column 5 additionally contains the main effect of the household income-to-needs ratio and its two-way interaction with adoption status and parental asthma. Robust standard errors in parentheses. *, **, and *** denote statistical significance at the 10%, 5%, and 1% levels, respectively.

The first column in Table III reports results from estimating Equation 1 on the full sample and shows that the reduction in asthma transmission among adoptees is equal to 9.2 percentage points or 45.5%.¹⁴ Columns 2–4 respectively report results from reestimating Equation 1 separately for families with income-to-needs ratios between 0 and 2.5, income-to-needs ratios of 2.5 or above but less than 5, and families who were assigned the top-coded income-to-needs ratio of 5 (and therefore had actual income-to-needs ratios of 5 or greater). The results are similar to those previously reported using parental education: The decline in asthma transmission among adoptees relative to biological children goes from 14% among low-income families, to 35% among middle-income families, and to 80% among high-income families.

The final column of Table III reports results from estimating a regression specification identical to the one given by Equation 2 but with income-to-needs ratios replacing parental education. The triple interaction term equals -0.039 , which for example predicts that the biological–adoptive asthma transmission differential is 15.6 percentage points larger for households at 500% of the federal poverty level than for households at 100% of the federal poverty level. This estimate is less precise than in the education-based estimates, possibly owing to the smaller sample size, and the triple interaction term narrowly fails to achieve statistical significance at conventional levels, with a t -statistic of 1.5 and a two tailed p -value of 0.134.

5.2. Non-random adoptee placement

As noted earlier, a major concern with all adoptee-based research designs is that adoptive children may be placed with parents in a non-random fashion. This could lead to genetic similarity between adoptive parents and children despite their lack of direct biological relatedness, and a major shortcoming of the NHIS data is that no details of the adoption process are available to directly assess this possibility.

While it is a significant concern, two factors mitigate the potential for bias from non-random adoptee placement. First, to threaten the current study's validity, matching would need to occur specifically with respect to asthma predispositions or correlates of asthma predispositions not controlled for in the presented regressions. Matching of adoptive parents and children on the relatively narrow characteristic of asthma predisposition is perhaps less likely than on more general demographic or socioeconomic traits. Second, because the present paper is primarily interested in how genetic transmission varies by SES, non-random placement is only problematic to the extent that its severity differs by parental SES. Such differentials in non-random placement are certainly plausible but represent a more narrow and perhaps less likely possibility than non-random placement in general.

These points notwithstanding, selective placement of adoptees remains a major threat to identification, and some empirical assessment of its potential presence is clearly desirable. One such possible assessment is to estimate the intergenerational transmission of health characteristics that are known to be transmitted primarily or exclusively through genetic channels. The logic of such a test is that if a condition is known to be overwhelmingly genetically determined, then it should be uncorrelated among adoptive parents and children unless some degree of adoptee matching along health-related dimensions occurred. On the other hand, a lack of intergenerational associations in genetically determined health characteristics among adoptees would be consistent with quasi-random placement of adoptees in terms of health predispositions.

To conduct such tests, I utilize data in the NHIS on height and heart disease. Height is widely believed to be primarily genetically determined in developed country contexts where basic nutritional needs are near-universally met.¹⁵ Likewise, heart disease among children is assumed to be primarily genetic because in developed countries, pediatric heart disease is typically due to congenital defects that have a very strong genetic

¹⁴The difference between these results and those in Column 1 of Table II are due to dropping observations with missing income-to-needs ratios.

¹⁵Heights are adjusted for gender and age and are standardized to have a mean of zero and a standard deviation of one. Unfortunately, the NHIS did not begin collecting height data for children until the 2008 version of the survey and then did so only for children ages 12–17, resulting in substantially reduced sample sizes for the height models.

Table IV. Transmission of placebo conditions by adoption status

	(1)	(2)	(3)	(4)
	Height		Heart condition	
	Biological	Adoptive	Biological	Adoptive
Parental height/heart condition	0.357*** (0.010)	−0.048 (0.068)	0.022*** (0.002)	−0.001 (0.011)
Observations	10,750	227	125,635	2043

Heights are adjusted for age and gender and measured in standard deviation units. Robust standard errors in parentheses. *, **, and *** denote statistical significance at the 10%, 5%, and 1% levels, respectively.

component.¹⁶ While maternal substance abuse or viral infection during pregnancy are also risk factors, in these cases, we would still expect no association between adoptive parents and children in the absence of selective placement.¹⁷

Transmission estimates for these ‘placebo’ conditions are reported in Table IV. To serve as a basis of comparison with adoptees, Columns 1 and 3 show results from regressing measures of child height and heart disease onto analogous measures among their biological parents. In both cases, strong intergenerational associations are present: A one standard deviation increase in parental height is associated with a statistically significant 0.357 standard deviation increase in child height, while having a parent with heart disease is associated with a statistically significant 2.2 percentage point increase in the probability that a child has a heart condition. Columns 2 and 4 in Table IV repeat this exercise using the sample of adoptive parent–child pairs. For both height and heart conditions, there are no statistically or substantively significant associations between adoptive parents and children, and indeed, both characteristics display a nominal negative association.

While these results are reassuringly consistent with the assumption of quasi-random adoptee placement with respect to health characteristics, it is acknowledged that selective placement still cannot be ruled out. The modest size of available samples and the relative rarity of heart disease among children may make it difficult to detect associations among adoptive parent–child pairs even if they exist, and the degree of selective adoptee placement with respect to asthma-related characteristics could very well differ from these other health conditions. The results in Table IV nonetheless provide some evidence that this paper’s main finding is not an artifact of matching adoptive children to families along health-related dimensions.

In addition to selective placement on the basis of health, a related issue is that adoptive children’s pre-adoption characteristics and experiences may vary by the SES of their adoptive parents. This could arise owing to the fact that multiple forms of adoption are practiced in the USA, including adoptions out of foster care, domestic adoptions through private agencies, and international adoptions. These different forms of adoption vary in terms of cost and complexity while also drawing upon different populations of children who may have different asthma risks. To the extent that these institutional features cause higher SES families to adopt children with different pre-adoption characteristics, it makes it difficult to distinguish whether the gene–SES interaction found earlier is due to differential transmission mechanisms as opposed to differential sample composition.

It should be noted that the direction of such selection is ambiguous. In terms of the characteristics of parents, higher SES parents may desire and have the resources to adopt younger children or children with more favorable pre-adoption circumstances, but at the same time, adopting a child with health needs requires resources that only higher SES parents may feel able to offer. There is similar ambiguity in terms of the populations of children adoptees are drawn from. For instance, international adoptions tend to be the most costly, and the pre-adoption circumstances of international adoptees may be more adverse than domestic US adoptions of all forms, leading

¹⁶In developing countries, rheumatic heart disease is a leading source of pediatric heart conditions but is rare in the contemporary USA.

¹⁷Parental heart disease is defined using an NHIS question on whether the parent had ever been diagnosed with a heart condition *other than* coronary heart disease, angina pectoris, or myocardial infarction (heart attack). This definition is intended to measure adult heart conditions that have a significant genetic component rather than being primarily due to lifestyle factors.

Table V. Tests of adoptive sample composition differences by socioeconomic status

	Parental education		Household income-to-needs ratio	
	Ever diagnosed	Recent attack	Ever diagnosed	Recent attack
Parent high school graduate	0.013	−0.022		
×Adopted	(0.037)	(0.026)		
Parent some college	−0.023	−0.010		
×adopted	(0.036)	(0.025)		
Parent college graduate	0.019	−0.014		
×adopted	(0.037)	(0.026)		
Parent post-graduate degree	−0.042	−0.021		
×adopted	(0.040)	(0.027)		
1 ≤ Income/needs <2			0.027	0.042
×Adopted			(0.043)	(0.029)
2 ≤ Income/needs <3			−0.005	−0.003
×Adopted			(0.043)	(0.029)
3 ≤ Income/needs <4			−0.007	−0.008
×Adopted			(0.044)	(0.030)
4 ≤ Income/needs <5			−0.015	0.013
×Adopted			(0.045)	(0.030)
Income/needs ≥ 5			−0.040	−0.023
×adopted			(0.038)	(0.026)
Observations	5504	5503	4779	4778
<i>F</i> -test for interactions jointly equal to zero	1.32 (0.26)	.24 (0.92)	0.32 (0.86)	1.14 (0.34)

Dependent variable is an indicator of whether the child has ever been diagnosed with asthma or had an asthma attack in the past years as indicated. All models additionally contain an indicator of adoption status and indicators for the main effects of the included parental education and household income-to-needs ratio categories. The omitted parental education category is less than high school, while the omitted household income-to-needs ratio category is less than 1. Value of *F*-test is reported with the associated *p*-value in parenthesis. *, **, and *** denote statistical significance at the 10%, 5%, and 1% levels, respectively.

to higher asthma prevalence among foreign-born children adopted by higher SES families. However, asthmatic children born in low-income foreign countries may also be less likely to survive to typical adoption ages, which would decrease asthma prevalence in the pool of international adoptees.

To gain some insight into these potential issues, Table V presents tests of whether the base asthma prevalence rates of adoptees relative to biological children vary by parental SES. Specifically, the table shows results from regressing a child asthma indicator onto adoption status and SES as well as interactions of adoption status and SES.¹⁸ This exercise is repeated using both parental education and income-to-needs ratios to measure SES and using both ever having been diagnosed with asthma and having had a recent asthma attack to measure child asthma. If higher SES parents are more likely to adopt children with lower (or higher) asthma risks, then we may expect to find significant interactions between adoptive status and parental SES. Table V shows that this is not the case. Across all asthma and SES measures, the interaction terms are individually and jointly insignificant, indicating that the relative asthma prevalence of adoptees does not vary by parental SES.

As was the case with health-based matching of adoptive parents and children discussed earlier, this evidence does not conclusively rule out the possibility of important sample composition effects but is consistent with the assumption that children adopted into higher SES families do not systematically vary in their asthma predispositions.

¹⁸The inclusion of biological children in the analysis sample for Table V is designed to account for the fact that children in higher SES families have lower asthma prevalence irrespective of whether they are biological or adoptive. The question of current relevance is whether the change in asthma prevalence associated with being adopted varies by SES, as this would suggest adoptee sample composition differences by SES.

6. CONCLUSION

The basic finding of this paper has been that the relative importance of genetic asthma transmission mechanisms is much larger in high SES families than in low SES families. For instance, among parent–child pairs where the parent is a college graduate, asthma transmission is approximately 73% weaker among adoptees than in biological children, implying a dominant role for genetic transmission, while no significant reductions are present in less educated families, implying a negligible role for genetic transmission.

Differences in the characteristics of families with adoptive and biological children were, to the extent possible, addressed through using a biological sample with observable characteristics similar to those of adoptees, and placebo tests using height and heart disease provided suggestive evidence that adoptees were not selectively placed with respect to health conditions. The empirical results are broadly consistent with health production functions in which some specific genotypes are more sensitive to environmental conditions than other genotypes, so that differences in asthma outcomes due to genes become more pronounced under favorable environmental conditions.

If the genetic transmission of important health traits does increase under more favorable environmental conditions, there are potential implications for public policy and for future research on equality of opportunity (EOP) in health.

With respect to policy design, it is often assumed that the potential for effective policy interventions is very limited when the outcome of interest has strong genetic determination. The present findings do not necessarily contradict this view but do suggest that it is perhaps overly simplistic. For instance, if policies were implemented that reduced exposure to environmental asthma determinants and improved access to preventative health care among lower SES children, asthma prevalence would likely be reduced, but the remaining variation in asthma would have a stronger genetic component. This suggests that while policy may be able to reduce health inequality, such reductions could become progressively more difficult or costly as environmental conditions improve and genetic health determinants become more predominant. This suggestion is made very cautiously, however, and more research is needed before any substantive policy implications can be reliably inferred.

With respect to equality of opportunity in health, the literature in this area distinguishes between health determinants outside the control of individuals on the one hand and health determinants for which individuals can be held personally accountable on the other (see Roemer & Trannoy 2015 for a recent comprehensive overview). The former have been termed *circumstances* and include both genetic health determinants and environmental circumstances that individuals did not choose, especially those occurring in childhood, while the latter have been termed *efforts* and include factors such as chosen diet, exercise, and smoking behavior. Health inequality due to *circumstances* is viewed as being ethically illegitimate in this literature, while health inequality due to *efforts* is viewed as ethically legitimate.

Because genes are not chosen by individuals, and are therefore a component of *circumstances*, the empirical results presented here indicate that more favorable overall environmental conditions could actually increase the role of ethically problematic *circumstances* in asthma determination. However, while genes are one component of *circumstances*, they are of course not the only component, and I caution that data limitations prevent the current study from directly measuring and quantifying the importance of the non-genetic aspects of *circumstances* or of any specific *efforts*.¹⁹ Because of these limitations, I cannot estimate the overall level of EOP in asthma or study directly how it varies with SES. For instance, in principle, both low SES and high SES children could have equal levels of EOP, but for higher SES children, *circumstances* could consist primarily of their genes, while for lower SES children, *circumstances* could consist primarily of their non-chosen early environmental conditions.

Although the present study has been unable to directly investigate *effort* and non-genetic aspects of *circumstances*, the possibility that genetic health determination varies greatly under different sets of

¹⁹Several recent studies do use data with credible measures of *efforts* and *circumstances*, in conjunction with structural or decomposition-based methodologies, to quantify equality of opportunity in health more rigorously (Jusot & Tubeuf *et al.*, 2013; Rosa Diaz 2009; Fleurbaey 2009). Jusot *et al.* (2013) in particular focus on the potential non-independence of *circumstances* (including genes) and *efforts*.

environmental conditions may be important for accurately measuring EOP in asthma and other health conditions in future work with richer data. This is especially true given that asthma specifically is strongly related to the smoking behavior of both individuals and their parents.

Gene–environment interactions remain an understudied aspect of both health transmission specifically and intergenerational mobility more generally. While the current study focused on a specific health condition and faced meaningful data limitations, additional work that expands our understanding of complex interactions between genetic and environmental determinants of physiological and socioeconomic well-being would be valuable.

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