Development Given Geography, Climate, and Genes[1]

Robert Klitgaard

Claremont Graduate University, 150 East Tenth St., Claremont, CA 91711

USA robert.klitgaard@cgu.edu

Johannes W. Fedderke

Pennsylvania State University, State College, PA USA

Valerio Napolioni

Stanford University, Stanford, CA USA

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[1] We dedicate this paper to our late friend and colleague James MacMurray, whose words and inspiration appear throughout. Thanks to Kevin Grier, Robbert Maseland, Lant Pritchett, and Peter Richerson for helpful comments and criticisms; alas, not all of their valuable suggestions could be incorporated here, and the usual caveat applies.

ABSTRACT

Recent research examines some “deep roots” of world development, such as geography, climate, pathogen burden, and genetic diversity. This paper extends the literature in several ways. First, we focus on adaptations to particular climatic driver (ultraviolet exposure) and supply new data about the country-level frequencies of a particular genetic polymorphism that responds to climate and disease and in turn affects human traits and values. This gene and others have been studied at the level of individuals; we connect the country-level frequencies to outcomes such as per capita income, governance, disability-adjusted life years, fertility, and self-reported happiness. Second, we employ a novel identification strategy, and our results are robust to a variety of econometric challenges. Third, we explore the uses and misuses of findings about genes and other deep roots of development.

INTRODUCTION

Over centuries and millennia, geography, climate, and human genetic characteristics have interacted in ways that have implications for development outcomes today. Many infectious diseases, for example, breed more readily in hot, humid climates. These diseases affect human populations through migration and adaptation (both genetic and environmental). The evolution of geography-climate-gene complexes can modify physiological traits, such as skin pigmentation or the ability to breathe easily at high altitudes. They also modify behavioral suites that influence psychological traits, social interactions, and cultural repertoires; and these in turn may affect development outcomes.

These possibilities are difficult to specify and estimate. "Although the promise of genomics and related high-throughput techniques to study human evolution is high, human biology, evolutionary history, and extant population structure are all intimidatingly complex," note Richerson *et al.* (2010). "Not every problem will be quickly solved, and many analytical improvements are needed." Theories of international development do not provide accepted models for how various outcomes vary with geographic, climatic, and genetic variables (Liu *et al.* 2012; Spolaore & Wacziarg 2013). From economic well-being to governance to good health, the mapping of measures onto concepts is contentious; and across the many variables that plausibly matter, longitudinal data range from weak to absent. Even if we had excellent data, estimating dynamic relationships across times and places would confront challenges ranging from heterogeneity to nonstationarity (Eberhardt & Teal 2011; Teal *et al.* 2014).

As a result of these problems, estimating a full causal model is impossible. At best we can mark out some empirical patterns and apparent exceptions to them. We are fortunate to have new

data on a particular genetic adaptation to climate and disease, which enables us to build a web of associations that culminate in testable and perhaps actionable links to development outcomes.

This paper presents new results about genetic variables that may account for cross-country variation in various measures of world development. One of us (Napolioni) assembled existing studies of the *ACP1* genetic polymorphism to create an incomplete but path-breaking country-level dataset. *ACP1* is one of many genes that adapt to ultraviolet radiation and to pathogen burdens, and these adaptations in turn have behavioral consequences. To our surprise, we find that *ACP1* frequencies are significantly related to national outcomes ranging from GDP per capita to type and quality of governance to measures of national "competitiveness" to health to fertility to measures of satisfaction with life—in other words, *ACP1* frequencies are related to many dimensions of "development."

As with all econometric studies of development, two questions arise. Are the correlations a sign of causation or simply an artifact? We use exposure to ultraviolet radiation as an instrument in assessing the relationship between *ACP1* frequencies and development outcomes. We carry out a variety of tests of the satisfaction of the exclusion restriction, with positive results. The effects of the ACP1 variable are not explainable by reverse causation or the influence of some of the usual variables in studies of long-run development. But as we will explain, *ACP1* frequencies are no doubt proxies for other genes that also respond to climate and disease—and possibly for social and cultural adaptations as well. No one is stating that a particular gene has a direct effect on development. Understanding what "significant genetic effects" mean and do not mean is a key point of this paper.

A second question is what it implies (and does not imply) to find that one or another development outcome is "significantly explained" by deep roots such as climate, geography,

disease burdens, and genes. Since these deep roots are not under a country's control, such findings may invite a degree of fatalism. As more and more genetic information becomes available, we expect an increasing need to understand what statistical regularities imply and do not imply. In particular, understanding these deep roots of development can be helpful for designing adaptive policies and for finding exceptions and learning from them.

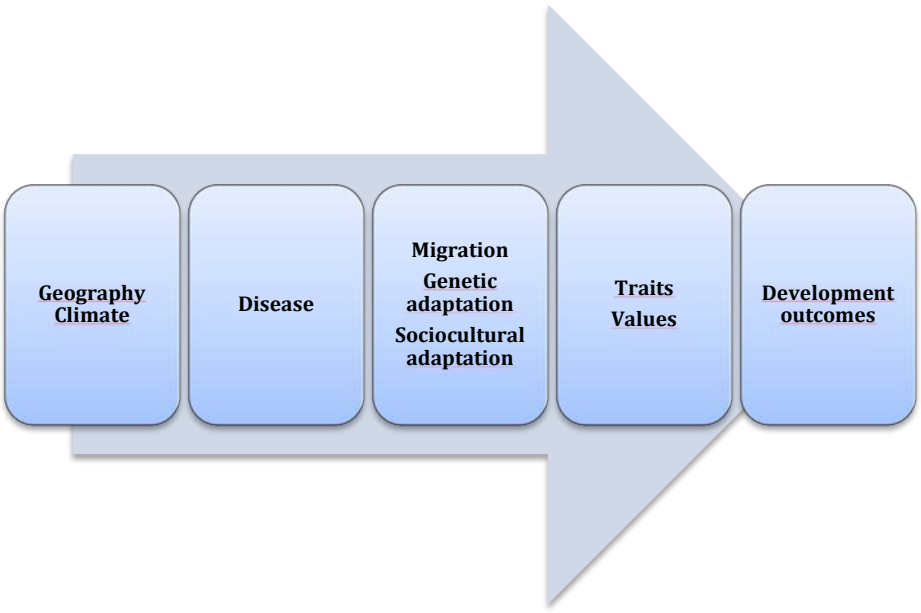
A Schematic Model

Recent work in international development examines deep roots such as geography, climate, parasite stress, and genetic endowments (Spolaore & Wacziarg 2013). What Galor (2011) calls "unified growth theory" goes beyond analyzing standard economic and institutional variables in models of growth covering years and decades. These scholars and others also consider factors that operate over centuries and millennia—factors that, their research suggests, are powerful predictors today as well. Thornhill & Fincher (2014) review a fast-moving, multidisciplinary literature showing how long-term genetic and cultural adaptations to pathogen burdens predict a variety of current outcomes from health to education to politics.

Recent theories investigate some of these links:

Figure 1

How Deep Roots May Affect Development Outcomes



① Geography and Climate to Pathogens and Disease

Geography and climatic conditions create differences in disease environments (for a thorough review, see Thornhill & Fincher 2014).

In this paper we focus on a particular driver, exposure to ultraviolet radiation. UVR exposure lowers folate, increases oxidative stress, and increases immune suppression (switch from pro- to anti-inflammatory immune responses). The "faster evolution" hypothesis (Wright *et al.* 2003) argues that higher UVR near the equator increases evolutionary rates and species production through shorter generation times and faster mutation rates. One consequence: more and more rapidly evolving pathogens (Keesing *et al.* 2010).

② FROM DISEASE ENVIRONMENTS TO HUMAN ADAPTATIONS

Different disease environments lead to three responses: migration; genetic adaptation (Fumagalli *et al.* 2011); and what Thornhill and Fincher (2015), following Schaller (2006), call "behavioral immune systems" in the form of cultural values and behaviors.

In this paper we take advantage of new data we have assembled on the country-level frequencies of several genetic polymorphisms that respond to the effects of lower folate, higher oxidative stress, increased immunosuppression, and more pathogens. We focus on Acid phosphatase controlled by locus 1 (*ACP1*), an enzyme found in the cytoplasm of many tissues. *ACP1* seems to adapt to UVR exposure in order to reduce oxidative stress (Apelt *et al.* 2009). *ACP1* mediates the shift from pro-inflammatory to anti-inflammatory bias, and carriers of *ACP1*B* are less susceptible to heat stress and tropical diseases (Bottini *et al.* 2009).

These adaptations of *ACP1* have side effects in terms of various physical ailments, personality characteristics, and mental illnesses that differentially affect people carrying different *ACP1* genotypes (Willour *et al.* 2012; Bottini *et al.* 2002d; Napolioni *et al.* 2014).

We hypothesize that *ACP1* allele frequencies also capture the effects of other genes that adapt to UVR and disease. Annex 1 provides more details about UVR, *ACP1*, and two pro- and anti-inflammatory cytokines, interleukin-6 (*IL6*) and interleukin-10 (*IL10*).

We also analyze Ashraf and Galor's (2013) measure of genetic diversity within countries. Ancestry-adjusted genetic diversity gauges the expected heterozygosity between two randomly selected people in a country using allelic frequencies for 783 microsatellite loci, after adjusting for ancestry and migration.[2]

[2] "The index of genetic diversity for contemporary national populations accounts for their ethnic compositions resulting from population flows among countries in the post-1500 era, the genetic diversity of the precolonial

Genetic diversity responds in a complicated way to climate, disease, and migration. Ashraf and Galor (2013) show that the farther a genetically similar population has migrated from the original human locus in East Africa, the lower its genetic diversity. The greatest diversity remains in the high UVR areas of Africa, but because of the serial founder effect, migrating populations have less and less diversity as they move farther away.[3]

③ From Human Adaptation to Differences in Traits and Values

Migration, genetic adaptation, and cultural adaptation lead to variations across countries in traits and values (Hibbs and Olsson 2004; Putterman and Weil 2010; Chanda, Cook & Putterman 2014; Maseland 2013; Spolaore & Wacziarg 2015). "According to the parasite-stress theory, analytical cognition is optimal when parasite stress is reduced and therefore there is less need to construct and maintain strong and permanent in-group affiliations that function to offset the negative reproductive consequences from parasites" (Fincher & Thornhill 2012: 109). Parasite burdens are strongly associated with lower measures of intelligence (Eppig *et al.* 2010). Individualism as a cultural value decreases in proportion to the group's typical pathogen burden (Chiao & Belinsky 2010; Way & Lieberman 2010; Cashdan & Steele 2013; Terrizzi *et al.* 2013). Pathogen burdens increase in-group favoritism and out-group negativity (Chiao & Blizinsky 2010) and promotes adherence to rigid behavioral sanctions (Cashdan & Steele 2013). In turn,

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ancestral population of each component ethnic group, and the genetic distances between these ancestral populations… [In addition, it] also accounts for the diversity arising from differences between subnational ethnic groups… (Ashraf & Galor 2013): 32).

[3] Some of the groups farthest away from Africa happen to have settled in high UVR areas, and their low genetic diversity means that the worldwide correlation today between heterozygotic diversity and UV exposure is not statistically significant.

compliance with these sanctions in disease-endemic regions is reinforced by socializing children to obedience rather than autonomy (Fincher *et al.* 2008). This constellation of tendencies reduces the potential for innovation and trust.

④ FROM TRAITS AND VALUES TO DEVELOPMENT OUTCOMES

These differences in traits and values affect contemporary economic and political development (among many studies, Gorodnichenko & Roland 2011; Hofstede 2011; Maseland 2013). Ashraf and Galor (2013) theorize, with empirical support, that there is an optimal amount of genetic diversity at the country level. Too little genetic diversity, they suggest, and there is not enough variety to stimulate competition and innovation. But too much diversity "raises the likelihood of disarray and mistrust, reducing cooperation and disrupting the socioeconomic order. Higher diversity is therefore associated with lower productivity, which inhibits the capacity of the economy to operate efficiently relative to its production possibility frontier" (Ashraf & Galor 2013: 3).

CHALLENGES TO ESTIMATION

Specifying and estimating these relationships runs into a host of conceptual, measurement, and statistical challenges. Unfortunately, our measures are incomplete and partial. We do not have data on the pathogen burden at historical dates relevant for evolutionary change; today's data on infectious disease burden have already benefited from the epidemiological transition that began around 1950 (Cook 2015). The effects of heat on mortality have changed greatly over the last century thanks to innovations such as air conditioning (Barreca *et al.* 2016). Our empirical work begins with the connection between UVR exposure and frequencies of the *ACP1* alleles across countries populations. We hypothesize that (1) our measure of UVR exposure has no

direct, contemporary causal connection with development outcomes such as per capita income or political rights[4] and (2) geographic patterns of UVR exposure have not changed over time. Based on studies of individuals, we hypothesize that over time UVR affects *ACP1* and other genes, whose adaptations in turn affect many traits and values (to name two, IQ and individualism), which in turn have implications for many development outcomes.

We use UVR exposure as an instrument to help assess the relationship between *ACP1* frequencies and development outcomes. We carry out a variety of tests of the satisfaction of the exclusion restriction, with positive results. In multiple analyses controlling for a variety of other variables, we find that *ACP1* frequencies are significantly related to national outcomes ranging from GDP per capita to type and quality of governance to measures of national competitiveness to health to fertility to measures of satisfaction with life. Then we will consider what the results mean—and do not mean.

MEASURES AND DATA

GENETIC DATA

Frequencies of ACP1 Alleles

We have assembled data on the frequencies of *ACP1**A, *ACP1**B, and *ACP1**C alleles in the populations of 120 countries. The data are a compilation of 153,090 global genotypes, which we believe is the largest such genetic undertaking ever. The data sources and compilation of the *ACP1* measure is detailed in Annex 2. Our research represents the first time country-level *ACP1* frequencies have been incorporated into studies of international development.

[4] But see Andersen *et al.* 2012 on the negative effects of high UVR on eyesight.

Among the 120 countries, the mean frequency of *ACP1**A is 24.0%, *ACP1**B is 73.8%, and *ACP1**C is 2.2%. Figures 2 a-c show the distributions of the frequencies. Figure 4 maps the frequencies of *ACP1**B.

Figures 2 a-c

Country Frequencies of *ACP1**A, *ACP1**B, and *ACP1**C

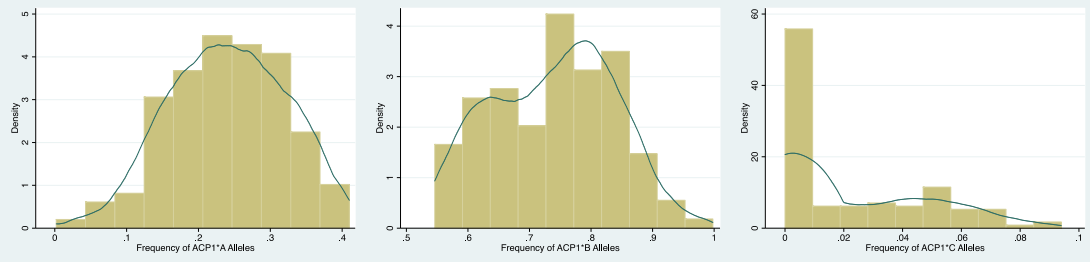
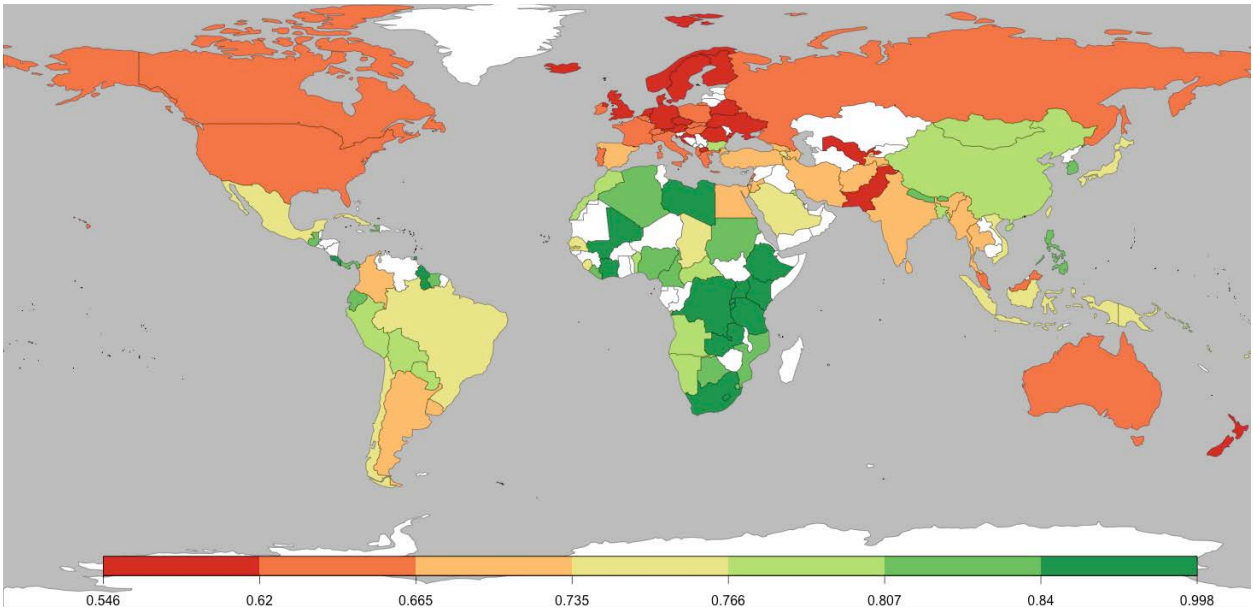


Figure 3 shows the frequencies of *ACP1**B in countries around the world.

Figure 3

Frequencies of *ACP1**B



Note: N = 120 countries. No data are available for countries in white.

Frequency of IL6 and IL10 Alleles

We have also assembled data on the frequencies of two pro- and anti-inflammatory cytokines, interleukin-6 (*IL6*-174G) and interleukin-10 (*IL10*-1082G). These, too, respond to disease burden and UV exposure and, in turn, are associated with some relevant behavioral and social outcomes (see Annexes 1 and 2 for details). Because we have data on fewer countries, we include only a few correlations in the analyses below and do not include these variables in the multivariate analyses.

Heterozygotic Diversity

As noted, we also use a measure of genetic diversity at the country level, created by Ashraf and Galor (2013).

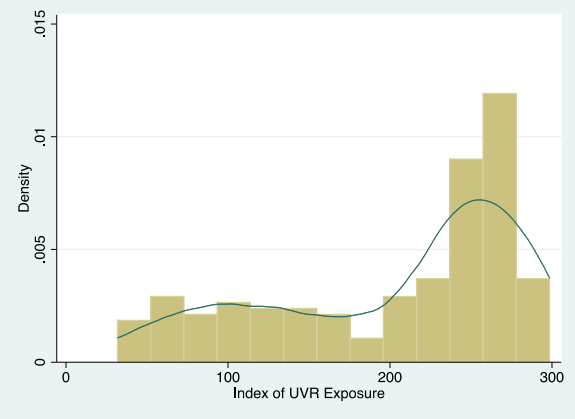
GEOGRAPHY AND CLIMATE

Among the many variables of geography and climate we examine, particularly noteworthy is the World Health Organization-derived ultraviolet (B) exposure rating.[5] These data have not been used in studies of world development (Andersen *et al.* 2012, the source of these data, remains an exception). Across 184 countries, the average of this rating is 202.0 and the standard deviation is 76.8, with a minimum of 31.8 (Iceland) and a maximum of 298.5 (Ethiopia). Figure 4 shows the distribution of country means of UVR exposure.

[5] The rating reflects biological exposure per square meter (BD/m^2), with the continuous measure scaled by dividing each averaged ultraviolet radiation dose by half of the interquartile range (Herman *et al.*, 1999). To confirm the salience of the Andersen *et al.* (2012) measure of UVR exposure, we compared it with an annual average ultraviolet index for countries based on NASA satellite recordings. For the 23 countries for which both measures are available, the correlation is 0.91.

Figure 4

Country-level Index of Ultraviolet (B) Exposure



We include geographical and climatic data assembled by Ashraf and Galor (2013) on measures of geography and climate such as temperature, rainfall, elevation, the percentage of a country's land that is arable, an index of a country's average soil quality (including such aspects as soil carbon density and pH), and mean distance in the country from the nearest waterway.

Finally, we follow Ashraf and Galor (2013) in using a measure of the time since a country experienced the Neolithic transition from hunter-gatherers to settled agriculture, adjusted for the ancestry of those now living in that country.

Development Outcomes

We examine gross national income (GNI) per capita in 2014, adjusted for purchasing power parity. We also investigate measures of democratic rights, perceptions of corruption, and an index of global competitiveness. We analyze the World Health Organization's measure disability-adjusted life years (age-standardized per 100,000 people), where higher numbers are worse. We also examine fertility and citizens' self-reported happiness.

DATA ANALYSIS

Table 2 displays correlations among the various outcomes, ultraviolet radiation, *ACP1**B, *IL6*-174G, and *IL10*-1082G.

Table 2

Correlation Matrix among Some of the Variables

	*ACP1**B	*IL6-174G*	*IL10-1082G*	UVR	lnGNIpc	Rights	Corrupt	GCI	lnDALY	lnFert	Happy
*ACP1**B	1										
IL6-174G	0.78 (68)	1									
IL10-1082G	-0.51 (58)	-0.82 (58)	1								
UVR	0.79 (119)	0.79 (76)	-0.53 (66)	1							
lnGNIpc	-0.62 (115)	-0.64 (72)	0.37 (62)	-0.59 (170)	1						
Rights	0.33 (119)	0.53 (76)	-0.35 (65)	0.59 (183)	-0.45 (170)	1					
Corrupt	-0.49 (115)	-0.53 (76)	0.37 (66)	-0.52 (166)	0.71 (150)	-0.70 (1650	1				
GCI	-0.57 (102)	-0.45 (69)	0.13 (650	-0.57 (138)	0.82 (132)	-0.44 (1370	0.82 (1380	1			
lnDALY	0.64 (116)	0.60 (73)	-0.30 (64)	0.60 (180)	-0.81 (167)	0.52 (180)	-0.67 (162)	-0.74 (135)	1		
lnFert	0.64 (119)	0.61 (76)	-0.09 (66)	0.63 (184)	-0.78 (170)	0.48 (183)	-0.56 (166)	-0.63 (138)	0.81 (180)	1	
Happy	-0.48 (102)	-0.50 (71)	0.29 (61)	-0.46 (142)	0.79 (135)	-0.53 (141)	0.69 (142)	0.72 (1250	-0.73 (139)	-0.56 (142)	1

Note: Variables are defined in the text and Annex 1. Corrupt is freedom from corruption. For Rights and lnDaly, lower numbers are better. GCI is the Global Competitiveness Index, where higher numbers are better.

As in all econometric analyses of world development, the interconnections among many possible causal variables make the estimation of independent effects difficult (Hausmann *et al.*, 2008: 7-8; see also Manski 2008 and Cohen-Cole, Durlauf & Rondina 2012). Saliman (2012) notes how many variables would have to be taken into account in a thorough study of all the hypotheses about the causes of economic development—and it is impossible with a small data set: "The data set we consider contains 88 countries and a list of 67 potential explanatory variables, giving 267 different possible subsets of regressors to include in our model. All of these

variables can reasonably be expected to influence economic growth, and we cannot be sure a priori which subset of variables we should use."[6]

Facing these difficulties, our analysis has a few advantages. We build on theoretical hypotheses based on both genetic studies of individuals and long-term economic analyses of the deep roots of development. The hypothesized theoretical mechanism lends itself directly to an instrumentation strategy. Since the *ACP1* genetic polymorphism responds to variations in UVR exposure, which is an expression of geographic location, UVR exposure is a promising instrument. As always, one must worry about the exclusion restriction: does UVR exposure exercise a direct influence on development today? In a companion paper focusing on GDP per capita in 2000, we thoroughly explore the UVR instrument, with positive results (Fedderke *et al.* forthcoming). In this paper, we confirm these findings with a broader set of outcomes and focus on the implications.

Income Per Capita

The multivariate analyses in Table 3 show that the frequency of *ACP1**B is negatively related to gross national income per capita, with or without instrumentation. Note also that just a few variables measuring certain characteristics of a country's genetic characteristics, climate, and geography—factors that might be considered beyond a country's control—statistically explain over half the variance in per capita incomes.

[6] A study of social indicators and economic development makes a related point: "The danger of more and more studies using some or all of the social and political indicators is that 'results' will emerge which are not robust. With other indicators and other specifications, as we have seen, one or another variable may show up as more important than another" (Fedderke and Klitgaard 1998).

Table 3

Explaining Log Per Capita GNI in 2014 (PPP) with Certain Genetic, Climatic, and Geographic Variables

ln GNIpc 2014	(1) OLS	(2) OLS	(3) OLS	(4) OLS	(5) IV	(6) IV
Frequency of *ACP1**B allele	-7.69*** (0.91)			-4.35*** (1.04)	-9.07*** (1.71)	-4.95*** (1.62)
Predicted genetic diversity (ancestry adjusted)		385.43*** (128.95)	112.62 (115.98)	100.44 (118.40)	13.67 (126.67)	186.50* (109.050
Predicted genetic diversity squared (ancestry adjusted)		-274.14** (91.10)	-74.94 (82.55)	-71.78 (84.44)	-13.09 (90.17)	-139.51* (78.64)
Log Neolithic transition timing (ancestry adjusted)		1.40*** (0.20)	-0.11 (0.29)	0.14 (0.31)	-0.17 (0.33)	0.49* (0.27)
Log precipitation			-0.27** (0.12)	-0.36*** (0.13)	-0.31** (0.14)	-0.27** (0.12)
Log percentage of arable land			-0.133 (0.084)	-0.141 0.096	-0.21** (0.10)	-0.20** (0.10)
Land suitable for agriculture			-0.33 (0.45)	-0.22 (0.49)	-0.22 (0.51)	-0.30 (0.39)
Log Mean distance to nearest waterway			-0.30*** (0.07)	-0.31*** (0.08)	-0.31*** (0.08)	-0.18** (0.08)
Log life expectancy in 1940						1.91*** (0.38)
Sub-Saharan Africa dummy variable			-1.81*** (0.37)	-1.08*** (0.44)	-0.45 (0.49)	0.41 (0.42)
Constant	14.74*** (0.68)	-138.02** (45.17)	-30.72 (41.00)	-19.86 (42.09)	15.70 (42.30)	-58.83 (36.98)
Number of countries	115	146	138	105	105	61
Root mean squared error	0.97	1.02	0.84	0.78	0.82	0.44
Adjusted R^2	0.38	0.35	0.55	0.61	0.57	0.76

Standard errors in parentheses. * = p ≤ 0.10. **= p ≤ 0.05. *** = p ≤ 0.01, In column (5) *ACP1**B is instrumented with ultraviolet B exposure. Durbin and Wu-Hausman tests reject exogeneity (p<0.01). Wald test rejects the hypothesis that the instrument is weak.

We performed a variety of econometric checks for endogeneity and robustness. *ACP1**B remains significant and important after including variables for genetic diversity, geography, rainfall, the timing of the Neolithic transition, and life expectancy in 1940 (before the epidemiological revolution that began about a decade later)[7]. In other analyses not reported here, we included in the IV regressions other strong covariates of UVR exposure, such as WHO's estimate of each country's burden of infectious diseases in 2004. *ACP1* remains statistically

[7] Cook (2015) develops this last variable and uses it as a proxy for the disease environment before the major improvements made possible by modern health care and prevention.

significant and practically important. Below we discuss what other factors besides this single gene the variable *ACP1**B may be picking up; the point for now is that the effect we are seeing is not removed by including many other deep roots of economic development.

GOVERNANCE

Many measures of governance exist, and their meaning and use are debated (Rothstein, 2011; Holmberg, Rothstein & Nasiritousi 2012; Fukuyama, 2013). We examine three measures:

- Freedom House assesses political rights and civil liberties on two scales from 1 (best) to 7 (worst). We combined the two into a measure we call "rights," whose mean for 183 countries is 6.68 and standard deviation is 3.92. The data are from 2014.
- Transparency International combines many sources of information to rate countries from 0 to 100 on perceptions of their "freedom from corruption" (CPI). For 166 countries in 2014, the mean is 43.59 and the standard deviation is 19.68.
- The World Economic Forum's *Global Competitiveness Report 2015-2016* includes 111 variables in 12 clusters. From these it derives an overall index of a country's competitiveness (GCI). For 138 countries, GCI ranges from a low of 2.84 to a high of 5.76; mean = 4.22, standard deviation = 0.67). Even though only about 20 of the 111 variables are related to the quality of government institutions, GCI and CPI are correlated 0.82.

We examined these outcomes in a similar fashion to the analyses of GNI per capita. Table 4 summarizes the results of the corresponding IV analyses. *ACP1**B again is a highly significant predictor. Higher frequencies of *ACP1**B are associated with worse governance, with or without instrumentation using UVR exposure.

Table 4

Explaining Governance with Certain Genetic, Climatic, and Geographic Variables

	(1) Political Rights and Civil Liberties (IV)	(2) Political Rights and Civil Liberties (IV)	(3) Freedom from Corruption (IV)	(4) Freedom from Corruption (IV)	(5) Global Competitiveness Index (IV)	(6) Global Competitiveness Index (IV)
Frequency of *ACP1**B allele	36.19*** (7.45)	13.64* (8.05)	-247.64*** (47.11)	-178.94*** (41.06)	-6.85*** (1.25)	-5.31*** (1.42)
Predicted genetic diversity (ancestry adjusted)	-97.08 (557.19)	-10.81 (547.78)	7540.30* (4109.71)	8590.95*** (2793.05)	-12.39 (91.21)	350.32*** (97.25)
Predicted genetic diversity squared (ancestry adjusted)	-93.57 (396.62)	31.58 (395.05)	-5509.81* (2913.27)	-6351.05*** (2014.30)	5.78 (64.94)	-259.46*** (70.18)
Log Neolithic transition timing (ancestry adjusted)	0.24 (1.42)	-1.05 (1.32)	-7.45 (8.15)	-9.26 (6.72)	-0.23 (0.24)	-0.22 (0.24)
Log precipitation	-0.56 (0.60)	-0.01 (0.60)	-4.18 (4.10)	-8.53*** (3.04)	0.03 (0.10)	-0.23** (0.11)
Log percentage of arable land	0.92** (0.45)	0.60 (0.51)	-6.40** (2.83)	-6.69*** (2.58)	-0.06 (0.08)	-0.04 (0.09)
Land suitable for agriculture	-3.10** (2.22)	-1.53 (1.95)	-4.59 (14.69)	5.64 (9.97)	-0.583 (0.362)	-0.10 (0.34)
Log mean distance to nearest waterway	1.03*** (0.35)	1.18*** (0.38)	-5.26** (2.20)	-7.51*** (1.93)	-0.05 (0.06)	-0.142** (0.066)
Log life expectancy in 1940		-7.64*** (1.85)		36.02*** (9.41)	-	1.07*** (0.33)
Sub-Saharan Africa dummy variable	-4.04* (2.14)	-4.43** (2.13)	22.28 (13.88)	11.41 10.86	0.03 (0.35)	0.40 (0.38)
Constant	-3.99 (199.35)	27.70 (185.98)	-1612.35 (1389.83)	-2738.00*** (948.27)	17.52 (32.66)	-110.81*** (33.10)
Number of countries	109	64	83	64	99	63
Root mean squared error	3.61	2.25	18.41	11.48	0.57	0.40
Adjusted R^2	0.13	0.57	0.26	0.72	0.28	0.64

Dependent variables are indicated in the column headings. Standard errors are in parentheses. * = p ≤ 0.10. **= p ≤ 0.05. *** = p ≤ 0.01. In all three equations, *ACP1*_B is instrumented with ultraviolet B exposure. Durbin and Wu-Hausman tests reject exogeneity (p<0.01). Wald test rejects the hypothesis that the instrument is weak (p<0.01).

Other Developmental Outcomes

We carried out similar analyses for other developmental outcomes. How do combinations of variables connected with genes, environment, and geography explain variation in outcomes including health, fertility, and self-reported happiness? Table 5 presents an overview of the results; Annex 3 contains more details.

For all these development outcomes, *ACP1**B is a powerful predictor, leading us to consider what this finding means and what it implies.

Discussion

After all our work assembling and analyzing these data, we are especially cognizant of their limitations, as well as their promise. We do not have *ACP1* frequencies for all countries, and the data we do have cannot be conceptualized as a random sample of each country's population. For many countries, the coverage of ethnic groups is incomplete. Although we believe that our compilation of 153,090 global genotypes is among the largest such genetic undertakings ever, we are keenly aware of the need for more and better data.

Importantly, this need for more research is propelled by the surprisingly strong and robust associations we discover between our imperfect and incomplete measure of the national frequencies of *ACP1* alleles and a variety of development outcomes. We also need better theorizing about what the connections between *ACP1* frequencies and health, psychology, and culture and therefore for development—and about what other causal factors are correlated with *ACP1* frequencies. Clearly, our variable *ACP1**B is a proxy for much more than a single gene.

Table 5

Overview of Findings

	ln GNI pc ppp 2014	Rights (lower is better)	Freedom from Corruption	Global Compet. Index	DALY (higher is worse)	Fertility	Happiness
Frequency of *ACP1**B allele	- ***	+ ***	- ***	- ***	+ ***	+ ***	- ***
Predicted genetic diversity (ancestry adjusted)	+ ns	- ns	+ ns	- ns	+ ns	- ns	+ ns
Predicted genetic diversity squared (ancestry adjusted)	- ns	+ ns	- *	+ ns	- ns	+ ns	- ns
Log Neolithic transition timing (ancestry adjusted)	- ns	+ ns	- ns	- ns	- *	+ ns	- *
ln precipitation	- **	- ns	+ ns	+ ns	+ *	- ns	+ ns
Log % arable land	- **	+ **	- **	- ns	+ ns	+ ns	- **
Land suitable for agriculture	- ns	- ns	- ns	- ns	- ns	- **	- **
ln Mean distance to nearest waterway	- ***	+ ***	- ***	+ ns	+ ***	+ *	- ***
Sub-Saharan Africa dummy variable	- ns	- *	+ ns	- ns	+ ns	+ ***	+ ns
Number of countries	105	109	109	99	106	109	98
Adjusted R^2	0.57	0.13	0.15	0.28	0.72	0.69	0.44

Note: All results are from the IV regressions. * = p ≤ 0.10, ** = p ≤ 0.05, *** = p ≤ 0.01. ns = not significant at p < 0.10.

To underscore this point, one thing this pattern of results does *not* mean is that the frequency of a particular gene such as *ACP1* itself has a powerful direct effect on national income or political rights or the other outcomes we have analyzed. With rare exceptions, behavioral traits are polygenic in nature (Comings 1997). Polygenic inheritance is due the additive and interactive effect of many genes interacting with the environment. As noted above, across evolutionary time *ACP1* allele frequencies have become adapted to global variations in UV radiation and infectious diseases. As noted above, after adjusting for migration effects, national-level frequencies of *IL6-174G* and *IL10-1082G*, two other adaptations to hostile climates and disease environments, are highly correlated with the frequencies of *ACP1*. Thus, the *ACP1**B variable we have been

examining is surely picking up the influences of other genetic factors that have evolved in evolutionary time in response to ultraviolet exposure and pathogen burdens. In addition, as we saw earlier in Table 1, various social and cultural adaptations to climate and disease are correlated with, possibly causally connected with, these genetic adaptations. Thus, *ACP1* frequencies are doubtless a proxy for other genetic, social, and cultural adaptations to pathogen-rich environments, which our scant current data and limitations of modeling make it difficult to untangle.

"Factors Beyond Our Control"

Let us turn now to an interpretation of this class of findings: "Much of the variance in such-and-such a development outcome across nations is explained by factors beyond a country's control, such as climate, geography, and genes." What does this mean, statistically?

A standard explanation is conveyed by Wooldridge (2009: 38, emphasis in original): "R^2 is the ratio of the explained variation compared to the total variation; thus, it is interpreted as *the fraction of the sample variation in y that is explained by x*." As Wooldridge recognizes, this interpretation depends on a number of conditions. Linear regression assumes linearity in parameter space. Curvilinearity and other issues such as outliers, clustering, and heteroskedasticity render suspect the standard interpretation of R^2 (a classic reminder is Anscombe 1973; see also Anderson-Sprecher 1994).

Suppose that linearity applies. If measures of climate, geography, and genes explain (say) half the variance in income per head, or 72 percent of the variance in fertility, does this doom a country to remain more or less where it is?

The short answer is no.

R^2 Is Large, Yet Entire Distributions Improve

Let us go back to 1970. It turns out that in that year, too, our measures of climate, geography, and genes explained over half the variance in per capita incomes. As we have seen, these same variables explain about half of the variance in per capita incomes in 2014. And yet average incomes rose from $6451 in 1970 to $15,415 in 2014.

An analogy is the heritability of human height. It is large, about 80 percent for Australians, Finns, and white Americans (Lai, 2006), meaning that across individuals in these groups at a given point in time, genetic endowments matter much more than environmental conditions. And yet, from 1850 to 1980 average heights among European males increased by 11 cm (Hatton, 2014). "The evidence suggests," notes Hatton (2014), "that the improving disease environment, as reflected in the fall in infant mortality, is the single most important factor driving the increase in height." He cites other factors including more sanitary housing and living conditions, better general education about health and nutrition, and better social services and health systems. These same changes may transform historical relationships between "deep roots" and future development outcomes.

Functional Relationships Evolve

In such a changing and adapting world, some of the variation that was fixed or limited in the past will be malleable in the future. In addition to the factors mentioned by Hatton, consider for example the impacts on development of rural education (especially of girls); good-government movements; social networks; technological change; contraceptive techniques; and international flows of goods, services, and finance, which increased by a factor of 1.5 from 1990 to 2012 and could triple in the next decade (Manyika *et al.* 2014). Changes like these are catalyzing the rapid development of low- and middle-income countries. Convergence with rich countries is well

established for social indicators like life expectancy, maternal mortality, and infant mortality. New data show that convergence in material living standards is happening much faster than previously thought.[8] For our purposes, these changes may indicate that the future explanatory power of "deep roots" variables will differ from the statistical patterns of the past.

Adapting Policies

Studying deep roots may help us rethink present policies. Consider an analogy from plant science. Suppose scientists discover that the productivity of certain bean varieties is largely heritable—meaning genetically determined—given current variations in soil, water, pests, sun, shade, and so forth. It would be premature to conclude that one bean variety that now is less productive is destined to be so under all conditions. Environmental variables are subject to change, including designed change via fertilizer, irrigation, pesticides, shade planting, cross cropping, and more. With adaptive cultivation techniques, estimates of heritability can change radically.

By analogy, we may hope to discover policies that take better account of differing climatic, geographic, and genetic conditions. And if adaptive policies are discovered and used widely,

[8] The 2014 report of the International Comparison Program (ICP) shows that the developing countries have been moving even faster than previously believed (World Bank, 2014). "For example, Indonesia and Ghana are both more than 80 percent richer than previous estimates. For Egypt and Pakistan the upward changes are more than 60 percent. These changes are dramatic. They suggest that Indonesia's economy may be as large as that of the United Kingdom, while Pakistan and Egypt are almost as large as Australia… [G]lobally, the poorest large developing countries are converging more rapidly with rich countries than we thought and this will inevitably translate into a more equal global income distribution." (Kharas and Chandy, 2014).

historical estimates of the importance geographic, climatic, and genetic factors may become obsolete.

Learning from Exceptions

Multivariate statistical studies often focus on regularities across all observations; they can also be used to identify exceptional performers. Some countries perform better than others, and they may contain lessons. Consider fertility. Our IV equation with genetic, climatic, and geographic variables explains 72 percent of the variance in log fertility. And yet, fertility levels have changed radically over the past few decades. Moreover, some countries have been exceptional performers. Ghana, for example, reduced mean fertility from 6.4 children per woman in 1998 to 4.0 in 2008. Ghana's climate, geography, and genes have not changed. What did Ghana do to achieve these outstanding results—and what lessons might be drawn?[9]

Regressions of the kinds this paper have been exploring can be helpful in identifying exceptional performers. Candidates are those countries who do much better than the equations predict. The residuals contain many sources of variance, including measurement error and variation that might be explained away with fuller specifications. The choice of econometric techniques affects the residuals. There is error that we simply call random. These facts mean that

[9] Countries can also change their governance patterns dramatically. Singapore went from a corrupt (and relatively poor) country in the 1960s to a very clean (and rapidly growing) country in the 1970s and thereafter. In just five years after 2003, the Republic of Georgia went from 113th in the world in "Ease of Doing Business" to 12th. For these and other examples, see Klitgaard (2015).

we cannot assume that countries with large positive residuals are exceptional performers—or that those with large negative residuals have done something wrong.[10]

Nonetheless, studying residuals has proved a valuable starting point. For example, Raynor and Ahmed (2013) identified 344 "exceptional companies" by looking at financial information that spans nearly half a century on more than 25,000 companies. Klitgaard and Hall (1975) identified consistently high-performing schools in four U.S. data sets. These schools turned out to have better qualified teachers and small class sizes—even though the regression coefficients on these variables across all schools were not different from zero. The method has been widely used in education since then (for example, Waits *et al.,* 2006).

Klitgaard and Fitschen (1997) used geographic information systems to array the residuals from a multivariate analysis of income averages among 190 tribal authorities in KwaZulu-Natal, South Africa. Some tribal authorities performed much better (worse) than expected based on education, rainfall, soil quality, and other predictors. Could the apparent exceptions be accounted for by geography, such as being particularly near a "white" city, a military garrison, or a highway? Some could. The authors left out those observations and focused instead on *adjacent* high-residual and low-residual tribal authorities, whose differences geography seemed unable to explain. These places would be the subject of case studies.

Table 6 provides clues about which country case studies might pay dividends. Enter here a range of skills that go beyond cross-country regressions, skills from history to sociology, anthropology to political science, biology to economics.

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[10] Especially with relatively small populations, incomplete theories, and incomplete data—our situation with these data—the statistical analysis gets complicated and tenuous. In all real-life evaluations, identifying exceptional performers is invariably a tentative exercise (Klitgaard 1978).

Table 6

Overachieving Countries in Various Development Outcomes, Given Some Genetic, Climatic, and Geographical Variables

	Ten Best Residuals	
Per Capita GNI 2014 ppp	1. Trinidad & Tobago	2. South Africa
	3. Costa Rica	4. Korea
	5. Nigeria	6. Saudi Arabia
	7. USA	8. Botswana
	9. Bulgaria	10. Switzerland
Rights	1. Mali	2. Trinidad & Tobago
	3. Costa Rica	4. Bulgaria
	5. Guyana	6. South Africa
	7. Korea	8. Mongolia
	9. Brazil	10. Panama
Disability-Adjusted Life Years	1. Costa Rica	2. Japan
	3. Korea	4. Mali
	5. Ethiopia	6. Spain
	7. Algeria	8. Rwanda
	9. Australia	10. Switzerland
Freedom from Corruption	1. Rwanda	2. Costa Rica
	3. Mali	4. Bhutan
	5. Ethiopia	6. Switzerland
	7. Japan	8. Uruguay
	9. Chile	10. Australia
Below-Expected Fertility[11]	1. South Africa	2. Trinidad & Tobago
	3. Costa Rica	4. Botswana
	5. Thailand	6. Bulgaria
	7. China	8. Japan
	9. Lesotho	10. Poland
Happiness	1. Costa Rica	2. Israel
	3. Switzerland	4. Canada
	5. Panama	6. Mexico
	7. Trinidad & Tobago	8. Mali
	9. Nigeria	10. Australia

[11] Data about *ACP1* frequencies are not available for Ghana, the success story cited in the text.

Final Remarks

Like it or not, the world will soon be awash in new genetic data about individuals, groups, and countries. The rise and spread of genome-wide association studies combined with expanded international data sharing will result in more and better genetic information being included in studies of world development. A kind of resignation may ensue: what can we do if factors beyond our control can be statistically connected to outcomes we desperately seek to improve?

Fatalism is, to say the least, premature (Putterman 2012). For the reasons we have just examined, if future research discovers that climate, geography, and population genetics explain a substantial portion of the variance in many development outcomes, this finding by itself should not engender defeatism. The frequencies of a few genes such as *ACP1*, *IL6*, and *IL10* are likely proxies for the effects of many other genes that respond to climate and disease—and may well be proxies for malleable but predictively important social and cultural variables. Conditions in the world are changing so rapidly and deeply that statistical regularities of the past do not condemn a country to remain where it now is. Research on the deep roots of development may reveal interactions between policy choices and climate, geography, and genes. And countries that do better than the rest given their deep roots can teach and inspire. In these ways, the expansion of research on the historical and evolutionary factors affecting international development can help us be more creative about what to do now and in the future.

ANNEX 1. SOME GENETIC MARKERS

In this paper we take advantage of new data we have assembled on the country-level frequencies of a particular genetic polymorphism that responds to the effects of lower folate, higher oxidative stress, increased immunosuppression, and more pathogens: *ACP1* or acid phosphatase controlled by locus 1. [12] *ACP1* is an enzyme expressed in many tissues. It has three common co-dominant alleles, *ACP1**A, *ACP1**B and *ACP1**C, with combinations defining six phenotypes characterized by different enzyme activity (from least to most active, A/A<B/A<(B/B, C/A)<C/B<C/C). These levels of activity affect cell division, differentiation, and growth.

ACP1 seems to adapt to UVR exposure in order to reduce oxidative stress. *ACP1**C carriers are least protected against oxidative stress (Apelt *et al.* 2009), and in our country-level data the frequency of the *ACP1**C allele is inversely correlated with UVR exposure (r=-0.78). The frequency of *ACP1**B is positively correlated with UVR (r=0.79).

[12] The *ACP1* gene (gene map locus chr. 2p25, OMIM**171500) encodes the Low Molecular Weight-Protein Tyrosine Phosphatase (LMW-PTP) that functions both as an acid phosphatase and a protein tyrosine phosphatase by hydrolyzing protein tyrosine phosphate to protein tyrosine and orthophosphate. It is ubiquitously expressed, and it has been demonstrated to be involved in several biochemical pathways (Bottini *et al.* 2002a). At an immunological level, by dephosphorylating a negative regulatory phosphorylation site in the ZAP-70 tyrosine kinase, LMW-PTP plays a crucial role in the activation of the signaling pathways downstream of the T cell receptor (TCR) (Bottini *et al.* 2002b). LMW-PTP is also able to modulate mitotic and metabolic signaling through the dephosphorylation of PDGF and insulin receptors, respectively (Taddei *et al.* 2000). These immune-metabolic molecular correlates of LMW-PTP are further corroborated by the several genetic-association studies conducted by analyzing the functional polymorphism of *ACP1*.

Excessive UVR produces both local and systemic immunosuppression (Beissert & Schwarz, 1999); among other genes, *ACP1* responds. It mediates the shift from pro-inflammatory to anti-inflammatory bias (Bottini *et al.* 2009). *ACP1**B is more able to adapt metabolically to heat stress and is less vulnerable to many infectious diseases (Bottini, 1999; Bottini & Gloria-Bottini, 2004). In malarial areas of the tropics, the frequency of *ACP1**C allele is close to zero (Greene *et al.* 2000).

Unfortunately, these adaptations of *ACP1* have some negative side effects in terms of various physical ailments, personality characteristics, and mental illnesses. *ACP1* is associated with inflammatory conditions, such as allergies and asthma, and with autoimmune diseases, including rheumatoid arthritis (Bottini *et al.* 2002a; Teruel *et al.* 2012; Bottini *et al.* 2007; Bottini *et al.* 2003). It is also associated with metabolic diseases, such as diabetes, obesity, and coronary artery disease (Gloria-Bottini *et al.* 2014; Banci *et al.* 2009; Bottini *et al.* 2002c). *ACP1* is correlated with mental states such as major depression, co-morbid features of Tourette syndrome, bipolar disorder, and various personality traits (Willour *et al.* 2012; Bottini *et al.* 2002d; Napolioni *et al.* 2014).

ACP1 is only one of many genes that mediate immune interactions at the interface of the individual and his environment. Other genes affect the relative secretion of pro- and anti-inflammatory cytokines that determine the Th1/Th2 balance, such as IL6 and IL10.

Interleukin-6 (IL6-174G) acts both as a pro-inflammatory cytokine to stimulate immune response during infection and an anti-inflammatory myokine in muscle fibers. IL6 has been shown to be required for resistance against many pathogens, such as bacterium *streptococcus pneumonia* (Van der Poll *et al.* 1997). The amount of IL6 produced is under control of the *IL6* gene, allowing it to be up- or down-regulated as a function of the average pathogen burden to

which populations are typically exposed. Across evolutionary time, populations exposed to high pathogen burdens adapt by positively selecting the high-producing -174 G-allele, while carriers of the low-producing -174 C-allele are gradually removed from the population by greater susceptibility to disease. Besides the comprehensive study carried out by Fumagalli *et al.* (2011) that provides evolutionary evidence of a pathogen-driven natural selection at the IL6 locus, several studies support the role of *IL6* alleles. For example, Sortica *et al.* (2014) reported higher parasitemia levels in *IL6* -174C carriers from an Amazonian population, while Doyle *et al.* (2010) showed greater illness for respiratory syncytial virus infection in *IL6* -174 C/C carriers.

IL6 is critical in the fight against infectious disease pathogens, while Interleukin-10 (IL10-1082G) is immunosuppressive. The IL6/IL10 ratio interacts with UVR. Ultraviolet radiation induces immune suppression when it is absorbed by an epidermal photoreceptor, *trans*-urocanic acid (UCA), and converted into a biologically recognizable signal, *cis*-UCA. In turn, UVR-stimulated *cis*-UCA activates a cytokine cascade (PGE2→IL4), which culminates in the activation of IL10, which induces immunosuppression by inhibiting pro-inflammatory cytokines. In this manner, UV-induced increases in IL10 suppress IL6. As a result, UV-stimulated immunosuppression impairs resistance to many infectious agents, such as bacteria, parasites, viruses, and fungi.

As with *ACP1*, these adaptations to UVR and disease have other implications for psychological and physical health. Increased IL6, decreased IL10, and increased IL6/IL10 ratio have been implicated in the pathophysiology of major depressive disorder (Rawdin *et al.* 2013). Research on individuals shows that elevated IL6 levels have a negative impact on acquiring verbal cognitive ability requiring long-term memory (Sasayama *et al.* 2012). Serum concentrations of IL6 are significantly higher in intellectual disability cases (Aureli *et al.* 2014).

Higher IL6 concentrations have also been associated with an increased rate of cognitive decline with age in both executive function and memory function (Mooijaart *et al.* 2013). Moreover, both of these cytokines are involved in learning and memory. Conversely, IL10 impairs spatial learning, and memory performance is negatively related to IL10 levels (Harvey *et al.* 2013). Taken together, these reports suggest that imbalances in the IL6/IL10 ratio may be linked to cognitive dysfunctions.

Large-scale studies of Big Five personality traits report that those individuals with lower circulating IL6 levels are higher in Conscientiousness, Openness, and Neuroticism (Turiano *et al.* 2013; Chapman *et al.* 2011).

Those suffering from coronary artery disease, an inflammatory disease, have an increased frequency of the *IL6* -174 G-allele (Elsaid *et al.* 2014). Bipolar disorder is also known to involve inflammatory dysregulation, and bipolar patients have significantly elevated levels of soluble IL6 receptor (Bai *et al.* 2014). Likewise, serum IL6 levels are significantly higher in schizophrenia patients, and the induction of epigenetic modification by IL6 has been proposed as a mechanism in the pathology of schizophrenia (Frydecka *et al.* 2014).

Thus, in regions with an elevated burden of infectious disease, high serum concentrations of IL6 and increased frequencies of the high-producing -174 G-allele are advantageous for survival. As populations migrated out of high-UVR regions into temperate zones, the immunological benefits of the high-producing G-allele began to dissipate, while the cognitive, affective, and personality attributes of the C-allele were likely to confer greater reproductive advantage. Metaphorically, in largely disease-free environments C-allele carriers were able to turn their biological attention away from disease threat, affording them the “luxury” of greater optimism, conscientiousness, and goal striving.

Our data show that *IL6*-174G and *IL10-1082G* allele frequencies are highly negatively correlated (r=-0.82). UVR exposure is positively correlated with *IL6* (r=0.79) and negatively correlated with *IL10* (r=-0.53) (Table 5 below). *ACP1**B is also correlated positively with *IL6* (r=0.78) and negatively with *IL10* (r=-0.51). Our data set currently includes only 78 countries for *IL6* and 68 countries for *IL10*, compared with 120 countries for *ACP1*. So, in our econometric work, we focus on *ACP1*. We hypothesize that measures of *ACP1* allele frequencies at the national level also capture the effects of other genes that adapt to UVR and disease.

ANNEX 2. COMPILING COUNTRY-LEVEL FREQUENCIES

ACP1

An extensive literature search was carried out on PubMed and Google free search engines using the keywords: ‘‘Acid Phosphatase locus 1’’, ‘‘ACP1’’, “LMWPTP”, “red acid phosphatase”, ‘‘polymorphism’’, “variant”, “SNP”, “Single Nucleotide Polymorphism” and “genetics” applying the following algorithm: (Acid Phosphatase locus 1 OR ACP1 OR LMWPTP OR red acid phosphatase) AND (genetics) AND (polymorphism OR variant OR Single Nucleotide Polymorphism OR SNP). The identification of eligible studies was not restricted to English language. Studies references were also analyzed to find any study not available from the electronic databases. All published studies that included allele frequency information on the samples genotyped for *ACP1* were included in the data analysis. For case-control studies, only the control group (when reported as “healthy”) was considered. *ACP1* tagSNPs (rs11553742 and rs79716074) (Faggioni *et al.* 2002) were retrieved from 1000 Genome Consortium, Phase 3 variant set (1000 Genomes Project Consortium, *et al.* 2012). The existence of a Hardy-Weinberg Equilibrium was checked for every sample population by Pearson’s chi-square, filtering all the collected data using a two-tail *p*-value less than 0.05. Mean allele frequencies were obtained by averaging the allele frequencies obtained from the population belonging to the same country and weighted according to country ethnic composition (Central Intelligence Agency 2013). For example, consider New Zealand. The literature provides *ACP1* frequencies from two studies, one for the European population living in Auckland and for the Maori. The ethnic composition of New Zealand is European 71.2%; Maori 14.1%; Asian 11.3%; “Pacific peoples” 7.6%; Middle Eastern, Latin American, African 1.1%; other 1.6%; not stated or unidentified 5.4%. Our frequency data average the *ACP1* allele frequencies of the two studies

weighted by the respective ethnic percentages. The sum of the two percentages (71.2 and 14.1) yields the "Ethnic Coverage," here 85.3%. In the data analyses for this paper, only countries were used for which the samples of ethnic groups represented 75 percent or more of the country's population.

IL6 AND *IL10*

The same strategy for data searching was used for *IL6* and *IL10* as for *ACP1*. For *IL6* and *IL10*, however, we applied to our raw average-per country *IL6* -174G>C *and IL10* -1082G>*A* frequencies a matrix transformation based on the "World Migration Matrix" of Putterman and Weil (2010), which tracks the population movements of 165 countries going as far back as the 1500s. The procedure and the use of the Putterman and Weil (2010) transformation for migration are described in detail in Napolioni and MacMurray (2016). For *ACP1*, such adjustment was not possible given the three allelic nature of its polymorphism.

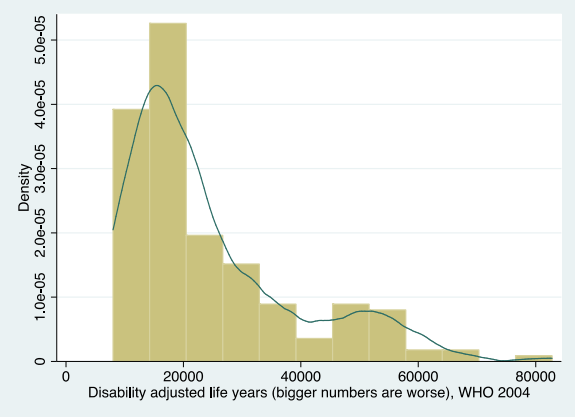
ANNEX 3. ANALYSES OF OTHER DEVELOPMENT OUTCOMES

DISABILITY-ADJUSTED LIFE YEARS

The World Health Organization estimated disability-adjusted life years (DALY) in 2004 for 180 countries.[13] Figure A-1 displays the data.

Figure A-1

Disability-Adjusted Life Years



Note: Lower values are healthier.

Table A-2 summarizes several regressions using our genetic, climatic, and geographic variables to explain country-level variation in log Disability-Adjusted Life Years.

[13] Robberstad (2005) reviews the meaning of DALY and some controversies about it. The World Health Organization explains: "One DALY can be thought of as one lost year of 'healthy' life. The sum of these DALYs across the population, or the burden of disease, can be thought of as a measurement of the gap between current health status and an ideal health situation where the entire population lives to an advanced age, free of disease and disability."

http://www.who.int/healthinfo/global_burden_disease/daly_disability_weight/en/

Table A-2

Explaining Disability-Adjusted Life Years with Certain Genetic, Climatic, and Geographic Variables (Lower DALY Is Healthier)

ln DALY	(1) OLS	(2) OLS	(3) OLS	(4) OLS	(5) IV
Frequency of *ACP1**B allele	3.68*** (0.41)			1.63*** (0.37)	3.70*** (0.64)
Predicted genetic diversity (ancestry adjusted)		-163.27*** (48.28)	-52.83 (43.16)	-21.53 (42.70)	20.47 (47.95)
Predicted genetic diversity squared (ancestry adjusted)		117.71*** (34.08)	37.06 (69.85)	16.39 (30.48)	-12.22 (34.15)
Log Neolithic transition timing (ancestry adjusted)		-0.78*** (0.07)	-0.203* (0.108)	-0.24** (0.11)	-0.217* (0.121)
ln precipitation			0.07 (0.04)	0.11** (0.05)	0.097* (0.051)
Log percentage of arable land			0.02 (0.03)	0.03 (0.03)	0.06 (0.04)
Land suitable for agriculture			-0.17 (0.17)	-0.08 (0.17)	-0.07 (0.19)
Mean distance to nearest waterway			0.13*** (0.03)	0.12*** (0.03)	0.12*** (0.03)
Sub-Saharan Africa dummy variable			0.68*** (0.14)	0.50** (0.16)	0.24 (0.18)
Constant	7.22*** (0.31)	73.04*** (16.94)	30.34** (15.27)	40.75* (22.91)	23.12 (26.04)
Number of countries	116	151	142	106	106
Root mean squared error	0.44	0.39	0.32	0.28	0.31
Adjusted R^2	0.41	0.53	0.69	0.77	0.72

Standard errors are in parentheses. Note: * = p ≤ 0.10. **= p ≤ 0.05. *** = p ≤ 0.01. In all three equations, *ACP1**B is instrumented with ultraviolet B exposure. Durbin and Wu-Hausman tests reject exogeneity (p<0.01). Wald test rejects the hypothesis that the instrument is weak (p<0.01).

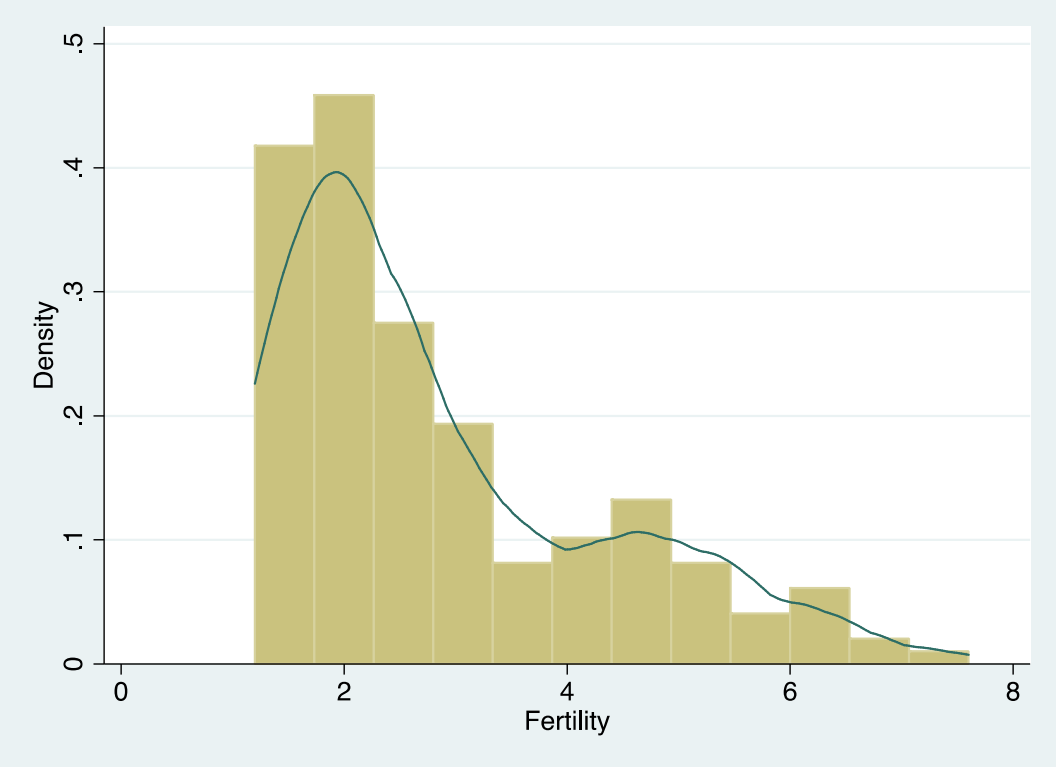
In both equations (3) and (4), higher frequencies of *ACP1**B are strongly associated with worse health outcomes measured by disability-adjusted life years (the simple correlation is 0.64). Using equation (4) in Table A-2, we see that about two-thirds of the variance in DALYs is explained by our genetic, weather, and geographic variables.

FERTILITY

Across 184 countries, the mean fertility is 2.86, with a minimum of 1.2 and a maximum of 7.6. The distribution has a long right-hand tail (see Fig. A-2, with illustrative countries indicated underneath), so we take logarithms.

Figure A-2

Distribution of Average Fertility



Live births/female	HUN 1.2	UKR 1.5	FRA 2.0	IND 2.5	SYR 3.0	GTM 3.9	CAF 4.5	SEN 5.0	NGA 6.0
	SGP 1.2	CHE 1.5	MMR 2.0	PER 2.5	ISR 3.0	IRQ 4.1	KEN 4.5	BEN 5.0	NER 7.6

Our genetic, climatic, and geographic variables explain 56 percent of the variance in mean fertility levels across countries (see Table A-2, equation 4). That same equation shows that genetic diversity has a mildly significant U-shaped relationship with fertility. *ACP1**B is highly significant. Some weather and geographic variables also have explanatory power.

Table A-2

Explaining ln Fertility with Certain Genetic, Climatic, and Geographic Variables

ln Fertility	(1) OLS	(2) OLS	(3) OLS	(4) OLS	(5) IV
Frequency of *ACP1**B allele	3.00*** (0.33)			1.11*** (0.34)	2.46*** (0.54)
Predicted genetic diversity (ancestry adjusted)		-208.15*** (43.66)	-83.13** (36.26)	-69.57* (38.78)	-43.20 (40.71)
Predicted genetic diversity squared (ancestry adjusted)		148.54*** (30.81)	56.30** (25.80)	47.79* (27.66)	29.89 (28.98)
Log Neolithic transition timing (ancestry adjusted)		-0.56*** (0.07)	0.09 (0.09)	0.08 (0.10)	0.09 (0.10)
ln precipitation			-0.01 (0.04)	-0.01 (0.04)	-0.01 (0.04)
Log percentage of arable land			-0.02 (0.03)	-0.00 (0.03)	0.02 (0.03)
Land suitable for agriculture			-0.369** (0.144)	-0.391** (0.158)	-0.38** (0.16)
Mean distance to nearest waterway			0.054** (0.021)	0.042* (0.025)	0.04 (0.03)
Sub-Saharan Africa dummy variable			0.86*** (0.12)	0.69** (0.14)	0.52*** (0.16)
Constant	-1.29*** (0.25)	78.42*** (15.32)	30.97** (12.83)	24.88* (13.79)	14.09 (14.56)
Number of countries	119	155	145	109	109
Root mean squared error	0.36	0.36	0.27	0.26	0.26
Adjusted R^2	0.40	0.46	0.69	0.71	0.69

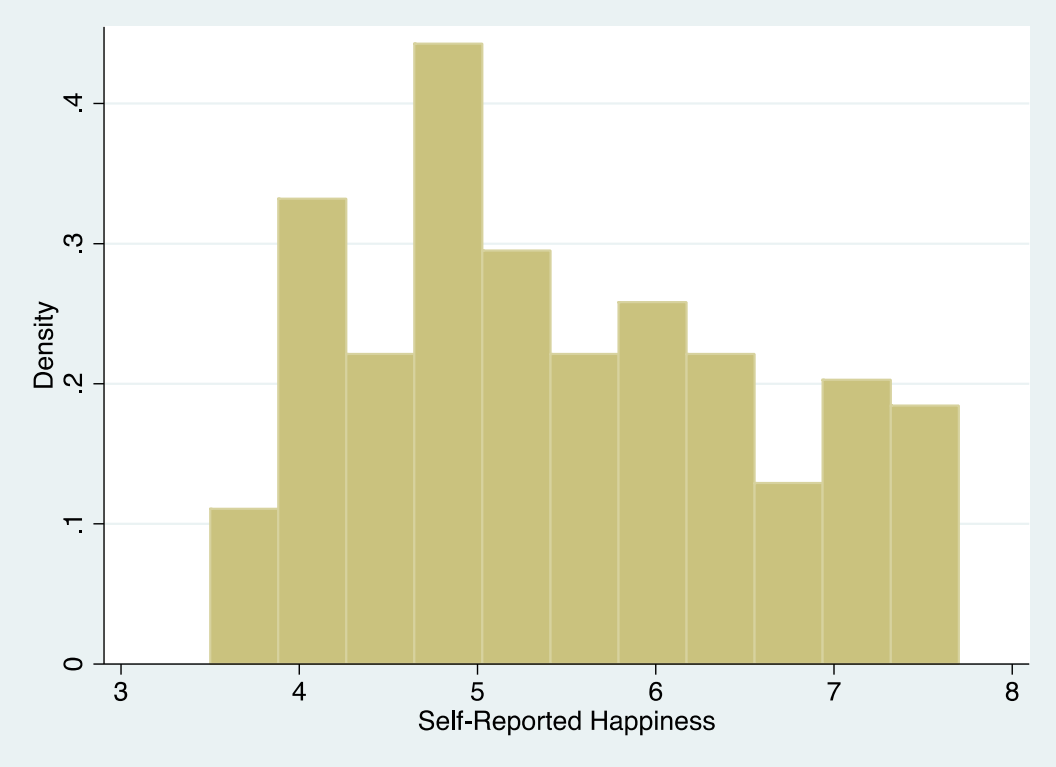
Standard errors are in parentheses. Note: * = p ≤ 0.10. **= p ≤ 0.05. *** = p ≤ 0.01. In equation (5) *ACP1**B is instrumented with ultraviolet B exposure. Durbin and Wu-Hausman tests reject exogeneity (p<0.01). Wald test rejects the hypothesis that the instrument is weak (p<0.01).

HAPPINESS

Self-reported happiness is a subject of active study and debate (for example, Deaton 2008; Proto & Rustichini, 2013; Weimann, Knabe & Schöb 2015). In the *World Happiness Report 2013* (Helliwell *et al.* 2013), across 142 countries the mean happiness level is 5.47, with a minimum of 3.5 (Benin) and a maximum of 7.7 (Norway, Switzerland, and Denmark). Figure A-2 displays the variation in country means (the standard deviation is 1.11).

Figure A-3

Histogram of Country Mean Self-Reported Happiness



BEN SYR HTI LAO NGA KAZ ESP BRA PAN SWE

BDI GAB SDN CHN RUS ECU TTO GBR CRI DNK

As before, we use our genetic, climatic, and geographic measures to explain the observed variation in country means. Table A-3 provides some results.

Table A-3

Explaining Country Mean Self-Reported Happiness with Certain Genetic, Climatic, and Geographic Variables

Happiness	(1) OLS	(2) OLS	(3) OLS	(4) OLS	(5) IV
Frequency of *ACP1**B allele	-5.63*** (1.03)			-4.85*** (1.20)	-9.58*** (1.91)
Predicted genetic diversity (ancestry adjusted)		387.39*** (133.47)	182.92 (135.37)	73.18 (141.10)	3.59 (146.59)
Predicted genetic diversity squared (ancestry adjusted)		-282.49*** (94.36)	-131.52 (96.51)	-56.87 (100.87)	-11.75 (104.60)
Log Neolithic transition timing (ancestry adjusted)		0.567*** (0.190)	-0.38 (0.31)	-0.55 (0.34)	-0.62* (0.35)
ln precipitation			0.04 (0.14)	-0.07 (0.16)	0.02 (0.17)
Log percentage of arable land			-0.14 (0.10)	-0.18 (0.12)	-0.25** (0.12)
Land suitable for agriculture			-0.71 (0.50)	-1.12** (0.54)	-1.08** (0.55)
Mean distance to nearest waterway			-0.21*** (0.08)	-0.22** (0.19)	-0.25*** (0.09)
Sub-Saharan Africa dummy variable			-1.47*** (0.43)	-1.08** (0.53)	-0.37 (0.59)
Constant	9.70*** (0.76)	-131.53*** (46.76)	-95.61 (69.32)	-8.68 (49.89)	22.21 (52.19
Number of countries	102	138	129	98	98
Root mean squared error	1.03	0.97	0.90	0.85	0.87
Adjusted R^2	0.22	0.23	0.36	0.48	0.44

Standard errors are in parentheses. Note: * = p ≤ 0.10. **= p ≤ 0.05. *** = p ≤ 0.01.

Surprisingly, *ACP1**B is the strongest predictor of mean self-reported happiness. As noted in the text, clearly *ACP1**B is standing for more than this one gene: we believe it represents a suite of correlated variables that have reacted over time to climate and disease. Almost half the variance in mean country happiness is explained by these few variables representing geography, climate, and genes.

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