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Geography, Climate, and Genes in Development Studies

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Abstract

Over the coming decade, much more genetic data will enter into the study of economic development. This paper provides an example and emphasizes the uses and misuses of such information. It has assembled for the first time national frequencies of the *ACP1* genetic polymorphism and the Interleukin-6 (IL6-174G) and Interleukin-10 (IL10-1082G) cytokines. These three respond over the centuries to ultraviolet radiation and infectious diseases. The study also looks at a national measure of heterozygotic diversity. In particular, it finds 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. These associations do not seem explainable by reverse causation nor by the influence of some of the usual variables in studies of long-run development. Nonetheless, these results do not mean that a few genes have a direct causal effect on world development. The *ACP1*B variable is surely picking up the influences of many genetic and cultural adaptations over evolutionary time in response to ultraviolet exposure and pathogen burdens. This study's findings thus support other research indicating the importance of disease environments in shaping both genetic and sociocultural adaptations that have influence on development outcomes today. The paper concludes with a discussion of what such strong associations mean and do not mean, in hopes of guiding future studies of genes and other deep roots of economic development.

JEL classification: O1, O4, I15, I18

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1. 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. Theories of international development do not provide accepted models for how various outcomes vary with geographic, climatic, and genetic variables (Spolaore and Wacziarg 2013). The outcomes themselves are contentious in definition and measurement. Across the many variables that plausibly matter, longitudinal data range from weak to absent. Even if excellent data were available, estimating dynamic relationships across times and places would confront challenges ranging from heterogeneity to nonstationarity (Söderbom et al. 2015). As a result of these problems, estimating a full causal model is likely to be impossible. At best it is possible to mark out some empirical patterns and apparent exceptions to them. Fortunately, new data on a particular genetic adaptation to climate and disease are available, which makes it possible 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 some cross-country variation in various measures of world development. One of the authors (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. Surprisingly, it is found that *ACP1* frequencies are significantly related to GDP per capita to type and many other development outcomes.

Are the correlations a sign of causation or simply an artifact? This paper uses exposure to ultraviolet radiation as an instrument in assessing the relationship between *ACP1* frequencies and development outcomes. The study carries out a variety of tests of the satisfaction of the exclusion restriction, with encouraging results. The effects of the ACP1 variable are not readily explainable by reverse causation or by the influence of some of the usual variables in studies of long-run development. But as will be explained, *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, historical 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, the study expects 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.

2. Data Analysis

This study's empirical analysis builds 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 in evolutionary time to variations in UVR exposure, which is a function of geographic location, UVR exposure is a promising instrument. UVR data have not been used in studies of world development (Andersen, Dalgaard, and Selaya 2016 is an exception). The study also uses a measure of genetic diversity at the country level, created by Ashraf and Galor (2013). For many fewer countries, we assembled data about two pro- and anti-inflammatory cytokines, interleukin-6 (*IL6*) and interleukin-10 (*IL10*), whose evolution also responds to UVR and the disease environment; but this paper leaves the analysis at the

Table 1. Explaining Log Per Capita GNI in 2014 (PPP) with Certain Genetic, Climatic, and Geographic Variables

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

Source: Authors' calculations based on data from the World Bank (GNI per capita); Andersen, Dalgaard, and Solaya (2016) (ultraviolet B exposure); Fedderke, Klitgaard, and Napolioni (2017) (*ACP1**B); and Ashraf and Galor (2013) (the other variables).

Note: Standard errors in parentheses. 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. ***$p \leq 0.01$, **$p \leq 0.05$, *$p \leq 0.10$.

level of correlations. For details about the assembling of the ACP1 and IL6 data, see Fedderke, Klitgaard, and Napolioni (2017).

The study includes 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, the paper follows 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.

The multivariate analyses in table 1 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.

The study 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). In other analyses the study 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*

Table 2. 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

Source: Authors' calculations based on data from the World Bank (GNI per capita); Freedom House (2013) (rights is a sum of political rights and civil liberties); Transparency International (2013) (freedom from corruption); World Economic Forum (2014) (global competitiveness index); World Health Organization (2008) (DALY); Andersen, Dalgaard, and Solaya (2016) (ultraviolet B exposure); Fedderke, Klitgaard, and Napolioni (2017) (*ACP1**B); and Ashraf and Galor (2013) (the other variables).

Note: ns = not significant at $p < 0.10$. In all equations, *ACP1**B is instrumented with ultraviolet B exposure. Durbin and Wu-Hausman tests reject exogeneity ($p < 0.01$). Wald tests reject the hypothesis that the instrument is weak ($p < 0.01$). ***$p \leq 0.01$, **$p \leq 0.05$, *$p \leq 0.10$.

remains statistically significant and practically important. Below the study discusses what other factors besides this single gene the variable *ACP1**B may be picking up; the point for now is that the effect that is being seen is not removed by including many other deep roots of economic development.

Similar analyses were carried out for other developmental outcomes: measures of democratic rights, perceptions of corruption, and an index of global competitiveness; the World Health Organization's measure disability-adjusted life years, where higher numbers are worse; fertility; and citizens' self-reported happiness. As table 2 summarizes, for each of these development outcomes, *ACP1**B is a powerful predictor.

3. Discussion

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. As noted above, over evolutionary time *ACP1* allele frequencies have become adapted to global variations in UV radiation and infectious diseases. National-level frequencies of *ACP1**B are highly correlated with the frequencies of two other adaptations to hostile climates and disease environments *IL6-174G* ($r = 0.78$) and *IL10-1082G* ($r = -0.51$), after adjusting these two variables for migration effects. Moreover, in response to the disease environment many aspects of human culture have evolved, including individualism and political attitudes (Thornhill and Fincher 2014; Murray and Schaller 2016). Thus, *ACP1* frequencies are doubtless a proxy for other genetic, social, and cultural adaptations to pathogen-rich environments, which the scant current data and limitations of modeling make it difficult to untangle.

This paper notes that heterozygotic diversity—recently reviewed in Ashraf and Galor (2018)—is no longer statistically significant when *ACP1* is included in the regressions. This paper wonders if their emphasis on the variance of selectively neutral genetic traits (and in Ashraf and Galor 2013 a measure of genetic distances among countries based on selectively neutral genetic traits) masks the importance of mean differences of adaptive genetic traits.

Interpretations and Misinterpretations

The paper now turns to a separate question. If only a few measures of climate, geography, and genes can explain over half the variance in income per capita, does this doom a country to remain more or less where it is?

Consider 1970. In that year, too, the measures of climate, geography, and genes explained over half the variance in per capita incomes. And yet mean incomes rose from $6451 in 1970 to $15,415 in 2014.

An analogy is human height. It is about 80 percent heritable among Australians, Finns, and white Americans (Lai 2006). 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.

Furthermore, in this 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). For the purposes of this study, these changes may indicate that the future explanatory power of "deep roots" variables will differ from the statistical patterns of the past.

Studying deep roots may also make it possible to 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, it may be possible to discover policies that take better account of differing climatic, geographic, and genetic conditions. And if adaptive policies are discovered and used widely, historical estimates of the importance geographic, climatic, and genetic factors may become obsolete.

Finally, studies of deep roots may go beyond the 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. The study's 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?

The 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). 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 may make it possible to be more creative about what to do now and in the future.

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