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Oasis Kodila-Tedika
Universityof Kinshasa
Department of Economics, , DRC
oasiskodila@yahoo.fr

Simplice A. Asongu
African Governance and Development Institute
Yaoundé, Cameroon.
asongus@afridev.org

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Genetic Distance and Cognitive Human Capital: A Cross-National Investigation

Oasis Kodila-Tedika & Simplice A. ASONGU

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Abstract

This paper explores the determinants of intelligence by focusing on the role played by barriers to the diffusion of competence and human capital. The results based on cross-sectional data from 167 countries consisting of 1996-2009 averages suggest that, genetic distance to global frontiers has a negative relationship with human capital. Countries that are genetically far from leading nations tend to have lower levels of human capital with the negative correlation from the USA frontier higher relative to the UK frontier. The sign is consistent with the relationship of genetic diversity and robust to the control of macroeconomic, geographical, institutional and influential variables. Policy implications are discussed.

JEL Codes: G15, O50, O16, F15, N7
Keywords: Intelligence, Human Capital, Genetic distance

1. Introduction

Why does human capital or intelligence differ across countries? The question is important because a substantial body of literature has established a significant relationship between human capital and development (e.g. Lynn & Vanhanen, 2012; Kodila-Tedika &Kanyama-Kalonda, 2012; Meisenberg & Lynn, 2012; Kodila-Tedika, 2014; Rindermann et al., 2014; Kodila-Tedika & Mustacu, 2014; Kodila-Tedika&Bolito-Losembe, 2014 ; Kodila-Tedika & Asongu, 2015).

There is a stream of studies that has addressed the question with a number of variables (Wicherts & Wilhelm, 2007; Hunt 2012). Many explanations have been advanced to elucidate the Flynn effect[1]. Some explanations to the cross-country differences from Barber (2005) include: nutrition, health, mass media diffusion, education, which have been documented to promote gains in intellectual quotient (IQ). According to Wicherts and Wilhelm (2007) and Wicherts et al. (2010), IQ differences across countries are traceable to, inter alia: the number of personal computers per 1000 people (0.66), urbanisation (0.67), fertility rates (-0.86), pupil-teacher ratio (-0.72) and secondary school enrolment ratio (0.78).

A genetical angel has also been engaged. Accordingly, studies have established a linkage between cognitive test results and the genotype of individuals (Davies et al., 2011; Hunt, 2011; Johnson et al., 2011). Notable authors that fall along this stream, include: Lynn and Vanhanen (2002, 2006), Rushton and Jensen (2005), Schwekendiek (2009), Lai (2006) and Pak (2010). Some have put forward an argument of evolutionary necessity (Kanazawa, 2004; Lynn, 2006). However, Wicherts et al. (2010) have expressed doubts about the underlying arguments and conclusions. Rushton and Jensen (2005) and Nisbett (2009) have for the most part pointed to the race and differences that exist in the ethnic composition[2]. Hunt (2012) has expressed scepticism in the face of these arguments because they are unsustainable. On the importance of genetics, the author states "*Until then, the question "Is there a genetic basis for international differences in intelligence?" has a simple answer: We do not know"* (Hunt 2012, p. 295).

The present line of inquiry attempts to address the underlying issue by responding to the question put forward by Hunt. We employ data on genetic distance compiled by Spolaore and Wacziarg (2009) who have provided a summary indicator of how populations are related to genealogy over time. According to the authors, genetic distance between populations is highly linked to per capita income differences across countries. They have disputed that genetic distance among people captures a wide range of characteristic and trait differences. In line with the narrative, the effects of this distance represents barriers to the diffusion of economic development from global technological frontiers, since variations in these characteristics stifle the flow of goods, technologies and ideas across populations, which ultimately hinder development.

[1]The Flynn effect represents a phenomenon where-by on average the Intelligence Quotient (IQ) scores have been increasing worldwide over time, with younger generations performing relatively better than their older counterparts. The average IQ score increases by about 10 points per generation.

[2] We do not believe in race superiority, whatsoever.

Ashraf and Galor (2013) along the same line have recently shown that ethnic diversity is linked to human development in a non-linear or Kuznets manner, with the countries of medium diversity having the highest levels of economic development. While the indicator of genetic diversity employed by the authors has been criticised by Guedes et al. (2013), we still employ it in order to test the robustness of our results.

Whereas genetic distance refers to genetic differences across populations, genetic diversity is defined in terms of heterogeneity across populations (Spolaore & Wacziarg, 2009). Compared to genetic diversity, the genetic distance measurement is a more interesting indicator because it has been subject to less criticism in the academic literature (Guedes et al., 2013; Asongu & Kodila-Tedika, 2015).

The argument of this study is very intuitive and is summarised in the following question. Are genetic differences the basis for differences in human capital across countries? The measurement of Spolaore and Wacziarg (2009) is interesting because, it enables us to assess if genetics explain development differences across countries. Moreover, the indicator also permits us to evaluate the role of cultural transmission. Distant genetic populations tend to differ in many characteristics that are transmitted between generations, notably: appearance, language, norms, habits, beliefs, customs and values. Authors of this index suppose that their measurement contains all sorts of intergenerational traits. On the basis that this indicator combines the highlighted dimensions, it is reasonable to think that deviations between countries can be due to differences in the perception of human capital between generations on the one hand and between geographic regions on the other hand. Hence, we could logically imagine that a generation that begun sending their children early to school should benefit from an educational advantage over that which did not. In this respect, the psychology of education plays a major role in the development of cognitive capacities (Becker et al., 2013).

The empirical approach consists of regressing the index of human capital from Meisenberg and Lynn (2011) on genetic distance. This human capital index is interesting in the perspective that it also combines education and intellectual quotient (IQ). Hence, it takes both the input and output dimensions of human capital into account, which is not the case with traditional indicators (Lutz, 2009). Our econometric results show a solid statistical linkage between genetic distance and intelligence.

The rest of the study is organised as follows. Section 2 discusses the data and empirical strategies. The results are presented and discussed in Section 3. Section 4 provides robustness checks while Section 5 concludes.

2. Data and Methodology

2.1 Data

We assess a cross-sectional sample of 167 countries which consist of 1996-2009 averages. The dependent variable is the human capital index while the independent variable of interest is the genetic distance. The former and the latter are in accordance with Meisenberg and Lynn (2011) and Spolaore and Wacziarg (2009) respectively. For robustness purposes we also employ the ethnic diversity indicator from Ashraf and Galor (2013). The control variables include: latitude, temperature, longitude, institutions, malaria and GDP per capita (in logarithm). The latitude which is measured in absolute value is calculated from La Porta et al. (1999) with some additions from the Central Intelligence Agency (CIA) World Factbook (CIA, 2010). Temperature represents average monthly temperature of nations in degrees Celsius over the period 1961-1990, computed utilising the geographical mean of data from monthly temperature reported by the Geographically based Economic data (G-Econ) project (Nordhaus, 2006) at a resolution of one degree which is based on similar data that is spatially disaggregated at a ten minute resolution (New et al., 2012). Therefore, the indicator is a spatial average of the intertemporal monthly average temperature within a nation across grid cells[3]. The Longitude indicator is consistent with Easterly and Sewadej (2001).

On the measurement of institutions, we consider an composite indicator consisting of six governance dynamics from Kaufmann et al. (2010) averaged over 1996-2009, notably: government effectiveness, regulation quality, rule of law, corruption-control, voice and accountability and political stability/no violence. The Malaria measurement is the malaria ecology index which appreciates the suitability of a nation’s climate to the breeding of mosquito as well as the prevalence of species of mosquito that essentially depend on human for survival (Kiszewski et al., 2004). GDP per capita (log) measurement is in natural logarithm of the Gross Domestic Product per capita averaged between 1996 and 2009 from Penn World Tables 7.0.

[3] We invite the interested reader to refer to the G-Econ project for more information.

The summary statistics of the variables is presented in Appendix 1. From the descriptive statistics, it can be noticed that variables are quite comparable. Moreover, from the standard deviations, we can be confident that reasonable estimated linkages would emerge owing to the substantial degree of variations. The correlation matrix is also presented in Appendix 2 to provide us with a feeling of expected signs.

2.2 Empirical specification

Consistent with Kodila-Tedika and Asongu (2015) who have investigated the effect of intelligence on financial development, we employ baseline Ordinary Least Squares (OLS) in order to investigate the linkages motivating this study. Hence, Eq. (1) below assesses the relationship between genetic distance and human capital across 167 countries.

$$HC_i = \alpha_1 + \alpha_2 GD_i + \alpha_3 X_i + \varepsilon_i \quad (1)$$

Where: HC_i (GD_i) represents the human capital index (genetic distance) for country i α_1 is a constant, X is the vector of control variables, and ε_i the error term. X entails: Latitude, Temperature, Longitude, Institutions, Malaria, and GDP per capita (log). Eq. (1) is estimated by OLS using heteroscedasticity consistent standard errors.

3. Empirical results

Table 1 below presents the OLS findings based on Eq. (1). Column 1 shows univariate regression estimates where the ratio of intelligence is regressed on the genetic distance to the United States. It is evident from the findings that these two variables demonstrate a substantial negative correlation. The GD coefficient of the first regressions is -28.366 and significant at the 1% level. This estimate shows that nations that are genetically far from the United States tend to have considerably lower levels of cognitive human capital. The corresponding coefficient of determination (R^2) of 0.423, indicates that GD explains about 42% of the total variation in human development across countries.

The significant control variables have the expected signs. The insignificance of the Latitude variable may be due to its high correlation with Temperature (see correlation matrix in Appendix 2). First, temperatures are negatively correlated with human capital, because some findings have shown that higher IQ is a compensation for cold weather (Jacob, 2010). Second, longitudes have been documented to be positively linked with the dependent variable (Kanazawa, 2008) and in the context of our study; its comparatively low magnitude may be traceable to the apparent criticism following the study of Kanazawa (Denny, 2009). Third, good institutions and per capita economic prosperity have been established to be positively associated with human capital (Meisenberg & Lynn, 2011, p. 434). Fourth, in the same vein, Meisenberg and Lynn (2011) have shown that infant mortality (life expectancy) is negatively (positively) linked to the development of human capital. Hence it is natural to infer that Malaria exerts a negative influence on the dependent variable, since like many diseases it has been shown to significantly reduce life expectancy, by increasing infant mortality, inter alia (Weil, 2010; Asongu, 2014ab).

Table 1: OLS estimates of the impact of genetic distance

	I	II	III	IV	V	VI
fst_gendist_to_US	**-28.363*****	**-18.917*****	**-17.779*****	**-14.227*****	**-12.443*****	**-10.424*****
	(1.841)	**(2.603)**	**(2.278)**	**(2.592)**	**(2.839)**	**(3.225)**
Latitude		-1.028				-9.257
		(5.487)				(5.741)
Temperature		**-0.493*****				**-0.372****
		(0.161)				**(0.165)**
Longitude		**0.038*****				**0.037*****
		(0.013)				**(0.009)**
Institutions			**0.217*****			0.044
			(0.037)			(0.035)
Malaria				**-0.585*****		**-0.188****
				(0.085)		**(0.079)**
GDP per capita (log)					**5.856*****	**4.675*****
					(0.720)	**(1.019)**
Constant	**97.303*****	**100.687*****	**82.260*****	**91.796*****	**38.681*****	**55.828*****
	(0.918)	**(4.714)**	**(2.167)**	**(1.370)**	**(7.361)**	**(10.981)**
Observations	167	96	108	108	133	81
R^2	0.423	0.472	0.465	0.444	0.690	0.754

Notes: .01 - ***; .05 - **; .1 - *; fst_gendist_to_US: Genetic distance to the United States.OLS: Ordinary Least Squares. Robust standard errors in brackets.

4. Robustness checks

In this section, we perform several robustness checks on the baseline specification in Column VI of Table1. These checks include using alternative GD indicators, considering different measures of genetic distance and controlling for influential observations.

4.1 Robustness with Respect to Influential Observations

In order to further improve the estimations, our empirical approach follows the M-estimators of Huber (1973) by using iteratively reweighted least squares (IRWLS), MM-estimator proposed by Yohai (1987) and S-estimator proposed by Salibian-Barrera and Yohai (2006) and Rousseeuw and Yohai (1984). As Midi and Talib (2008) have noted, compared to the OLS approach, the advantage of these robust estimators is that they fix simultaneously any issue arising from the existence of outliers and/or heteroskedasticity (non-constant error variances). From the findings, the signs and significance of the variables across specifications are consistent with those of the preceding tables. In Column IV, we check the sensitivity of the findings by dropping the 10 most influential countries. Next, following Nunn and Puga (2012, pp. 25-26) and Belsley et al. (1980), we adopt a systematic approach of eliminating influential observations for which DFBETA| $>2/\sqrt{N}$, where N is the number of observations; in our case, 81. Results, which are consistent with initial specifications, are presented in Column V of Table 2[4].

Table 2: Robustness checks

	I	II	III	IV	V
	M-Estimator	MM-Estimator	S-Estimator	Omit 10 Most Human genetic distance	Omit if|DFBETA| $>2/\sqrt{N}$
fst_gendist_to_US	**-9.550*** **	**-9.373** **	**-14.709*** **	**-11.489*** **	**-7.222*** **
	(3.271)	**(4.396)**	**(1.494)**	**(3.224)**	**(2.588)**
Latitude	-7.022	-5.944	**-19.369*** **	**-9.552* **	**-8.883* **
	(5.078)	(6.193)	**(4.558)**	**(5.567)**	**(4.754)**
Temperature	**-0.316** **	**-0.260** **	**-0.543*** **	**-0.371** **	**-0.377** **
	(0.134)	**(0.133)**	**(0.091)**	**(0.168)**	**(0.161)**
Longitude	**0.028*** **	**0.020*** **	**0.030*** **	**0.034*** **	**0.032*** **
	(0.007)	**(0.006)**	**(0.005)**	**(0.009)**	**(0.008)**
GDP per capita (log)	**4.652*** **	**4.612*** **	**3.500*** **	**4.401*** **	**4.583*** **
	(1.016)	**(1.095)**	**(0.691)**	**(1.033)**	**(0.927)**
Malaria	**-0.208** **	**-0.224** **	**-0.137** **	**-0.148** **	**-0.264*** **
	(0.082)	**(0.106)**	**(0.070)**	**(0.071)**	**(0.078)**
Institutions	**0.043* **	0.039	0.028	0.042	0.051
	(0.026)	(0.028)	(0.026)	(0.035)	(0.034)
Constant	**54.020*** **	**53.091*** **	**74.237*** **	**59.009*** **	**55.555*** **
	(11.367)	**(13.221)**	**(7.428)**	**(11.221)**	**(9.993)**

[4] "*The DFBETA for a predictor and for a specific observation is the difference between the regression coefficient calculated for all of the data and the regression coefficient calculated with the observation deleted, scaled by the standard error calculated with the observation deleted*" (Seif, 2014, p. 148).

Number of observations	81	81	81	77	74
R^2				0.739	0.791

Notes: .01 - ***; .05 - **; .1 - *;fst_gendist_to_US: Genetic distance to the United States. OLS: Ordinary Least Squares. Robust standard errors in brackets.

4.2. Alternate measures of genetic distance

In Table 3, we employ an alternative measure of GD and a variable of genetic diversity to assess the relationships established in Tables 1-2 and find the results to be broadly consistent. Moreover, two additional insights are worth noting. First, the negative correlation of the GD to the US is higher than the corresponding nexus of intelligence with the distance to the UK. Second, the negative correlation of genetic diversity is higher in comparison to GD to US and UK.

Table 3: Other measures of human capital diffusion

	I	II	III
fst_gendist_to_UK	-8.845***		
	(2.752)		
nei_gendist_to_US		-10.444***	
		(3.105)	
Genetic diversity			-79.897***
			(23.729)
Latitude	-9.108	-9.678	3.902
	(5.702)	(5.904)	(4.056)
Temperature	-0.378**	-0.372**	-0.279*
	(0.167)	(0.163)	(0.159)
Longitude	0.035***	0.036***	0.037***
	(0.009)	(0.009)	(0.010)
GDP per capita (log)	4.673***	4.764***	5.024***
	(1.019)	(0.991)	(0.983)
Malaria	-0.174**	-0.193**	-0.167*
	(0.081)	(0.080)	(0.092)
Institutions	0.048	0.045	0.017
	(0.035)	(0.035)	(0.040)
Constant	54.276***	54.734***	101.359***
	(1.748)	(10.600)	(22.105)
Number of observations	81	81	75
R^2	0.755	0.760	0.752

Notes: .01 - ***; .05 - **; .1 - *.fst_gendist_to_UK: genetic distance of the UK. fst_gendist_to_US: Genetic distance to the United States. Robust standard errors in brackets.

5. Concluding implications

The objective of this study has been to explore determinants of intelligence by focusing on the role played by barriers to the diffusion of competence and human capital. The results based on cross-sectional data from 167 countries consisting of

1996-2009 averages suggest that genetic distance to global frontiers has a negative relationship with human capital. Countries that are genetically far from leading nations tend to have lower levels of human capital with the negative correlation from the USA frontier higher relative to the UK frontier. The sign is consistent with the relationship of genetic diversity and robust to the control of macroeconomic, geographical, institutional and influential variables.

While the significant correlations confirm the findings of Spolaore and Wacziarg (2009) on the role of genetic distance to the USA as a barrier to economic development, they are however not consistent with a stream of studies that have concluded that the role of genetic distance disappears after controlling for additional variables, notably: (i) Angeles (2012) who has extended the empirical work of Spolaore and Wacziarg (2009) and found that the role of genetic distance dissipates after controlling for dynamics in population decent and (ii) Campell and Pyun (2015) who have examined why societies are less developed to establish that, contrary to the mainstream narrative, the nexus between GDP per capita and 'genetic distance from the US' disappears after controlling for the equator, sub-Saharan Africa and geography. The implication is that contemporary domestic human capital values may be traceable to the genetic distance to frontier or developed countries.

The negative role of genetic distance found in this study implies that the pattern may be more likely U-shaped than hump-shaped. This is essentially because if interactive regressions were involved in the specifications, corresponding estimated parameters will be interpreted as marginal impacts. Therefore, evidence of diminishing marginal effects of genetic distance on the dependent variable suggests a hump-shaped nexus. Put in other words, for a hump-shape to be established '*we expect the estimated coefficient for genetic diversity to be positive while that corresponding to the 'squared value of genetic diversity' should be negative*' (Asongu & Kodila-Tedika, 2015, p.14). It follows that the exploration of non-linear patterns in the underlying nexus could provide more regional specific insights into how the distance to the USA affects human capital development in other regions of the world. This challenging research task is not within the scope of the present inquiry and is shelved for future research.

We have also found that genetic distance to the USA is more important than the distance to the UK in the diffusion to human capital. This is logical because the USA is a relatively higher frontier nation in terms of human capital. According to the 2014 Shanghai Academic Rankings of World Universities (ARWU), in terms of contribution to knowledge, the USA has 146 universities in the Top 500 whereas the UK has 38 (ARWU, 2014).

The negative nexus with genetic diversity on human capital implies that it is more likely for the relationship to be U-shaped than hump-shaped. While the sign is consistent with Asongu and Kodila-Tedika (2015), the potential U-shaped nexus substantially runs counter to Sequeira et al. (2013) who have assessed the relationship between human capital and ancestral diversity to conclude on a strong hump-shaped relationship. Two implications boldly standout. First, like in Cook (2013) on the influence of genetic diversity on the effectiveness of vaccines and medicines and Ager and Bruckner (2013) on the impact of genetic diversity on economic development in the United States, there is a significant correlation between genetic diversity and development. Second, on the widely discussed hump-shaped nexus established by Ashraf and Galor (2013), the findings may contrast with the recent stream of literature that has confirmed the hump-shaped nexus, notably: William (2013) between genetic diversity and per capita income from a productivity perspective by means of a negative effect of social capital and positive impact on technological productivity; Ashraf et al. (2014), using nigh time light intensity and Cardella et al. (2015) on financial development. The negative relationship we find in this study has been confirmed by Asongu and Kodila-Tedika (2015) in a historical analysis of Ashraf and Galor (2013) within an African framework.

We set-out in the motivation of this study to investigate the issue raised by Hunt on whether there is a genetic basis for international disparities in intelligence. "*Until then, the question "Is there a genetic basis for international differences in intelligence?" has a simple answer: We do not know"* (Hunt 2012, p. 295). We have established that there are linkages from genetic diversity and genetic distance which can explain such differences. However, we have only partially addressed the concern because our findings should be treated as correlations, not causalities. The challenging task to advancing scientific inquiry on the underlying question in order to establish causality is left for future research.

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Appendices

Appendix 1: Summary Statistics

Variables	Obs	Mean	Std. Dev.	Min	Max
Human capital	175	84.208	10.853	61.2	106.9
fst_gendis	181	0.474	0.247	0	1
Latitude	180	0.280	0.191	0	0.778
Temperature	114	20.726	6.919	-7.633	28.193
Longitude	174	14.774	68.005	-175.2	177.97
GDP per capita (log)	140	8.871	1.188	5.902	11.173
Malaria	114	5.422	8.115	0	32.203
Institution	114	38.194	22.257	2.977	96.298

Obs: Observations. Std. Dev : Standard Deviation. Min : Minimum. Max : Maximum. Log : logarithm. fst_gendis : genetic distance.

Appendix 2 : Correlation Matrix

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Human capital(1)	1.000							
fst_gendis(2)	-0.564	1.000						
Latitude(3)	0.489	-0.473	1.000					
Temperature(4)	-0.526	0.293	-0.735	1.000				
Longitude(5)	0.227	0.135	0.122	-0.116	1.000			
GDP per capita(log)(6)	0.761	-0.530	0.426	-0.366	-0.017	1.000		
Malaria(7)	-0.563	0.387	-0.388	0.453	-0.021	-0.495	1.000	
Institution(8)	0.5853	-0.307	0.325	-0.308	0.071	0.719	-0.240	1.000

Log : logarithm. fst_gendis : genetic distance.