

GENETIC DISTANCE AND DIFFERENCES IN HAPPINESS ACROSS NATIONS: SOME PRELIMINARY EVIDENCE

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ABSTRACT

Survey studies worldwide have revealed large differences in happiness, both within and across nations. Many of the within-nation differences have a genetic basis, as twin studies have shown. Is there also a genetic component in the large differences across nations? In this paper, we report an initial exploration of this question in 104 nations. We estimate the relative importance of the genetic component in a bilateral analysis, calculating the correlation between the distance in genetic profile and average happiness, measured as satisfaction with life-as-a-whole. In this analysis, genetic distance explains 8.4% of the variance in cross-national differences in happiness. However, after controlling for cultural, institutional, economic, and geographical differences between countries, the explained variance is significantly reduced. We conclude that the direct effect of genetic distance is probably small.

ÖZET: Genetik mesafe ve uluslararası mutluluk farklılığı: Ön kanntlar

Dünya genelinde yapılan çalışmalar mutluluk açısından hem ülkeler içinde hem de ülkeler arasında büyük farklılıkların olduğunu ortaya koymuştur. İkizler üzerinde yapılan çalışmaların gösterdiği üzere bir ülke içindeki farklılıkların çoğunun genetik bir temeli vardır. Peki, ülkeler arasındaki büyük farklılıklarda da genetik bir unsur söz konusu mudur? Bu çalışmada, bu soru 104 ülke üzerinden ele alınmaktadır. Genetik unsurun göreceli önemi iki yönlü bir analizle tahmin edilmiş, genetik profildeki mesafe ile bir bütün olarak yaşam doyumu olarak ölçülen ortalama mutluluk arasındaki korelasyon hesaplanmıştır. Bu analize göre genetik mesafe mutluluk açısından ülkeler arasında bulunan farklılığın %8,4'ünü açıklamaktadır. Ancak, ülkeler arasındaki kültürel, kurumsal, ekonomik ve coğrafi farklılıklar kontrol edildiğinde açıklanan varyans anlamlı şekilde azalmaktadır. Genetik mesafenin doğrudan etkisinin muhtemelen çok küçük olduğu sonucunavarılmıştır.

Anahtar Kelimeler: Mutluluk, genetik, ülkeler

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1. INTRODUCTION

Over the past decades, evidence has accumulated on the heredity of happiness. Research on twins has shown that 30%-50% of the variation in happiness across individuals can be attributed to genetic variation (e.g. Tellegen et al., 1988, Lykken and Tellegen, 1996; Nes et al., 2006; Stubbe et al., 2005; Schnittker, 2008; Bartels and Boomsma, 2009).¹ In the search for the genetic roots of happiness, individual heterogeneity in happiness has been linked to the monoamine oxidase A gene (Chen et al., 2013), the oxytocin receptor gene (Saphire-Bernstein et al., 2011), and the serotonin transporter gene (De Neve, 2011; De Neve et al., 2012). Research in behavioural genetics has shown that genetic influences on happiness are shared with certain personality traits. Most notably, a common genetic architecture may underlie the strong association between happiness and personality traits such as extraversion, neuroticism, and conscientiousness (Weiss et al., 2008).

Although individual-level studies on the heredity of happiness are gaining momentum in the social sciences and life sciences, limited attention has been paid to the role of genetics in explaining cross-national differences in levels of happiness. Although there are cross-national differences in gene frequencies (Cavalli-Sforza et al., 1994; Spolaore and Wacziarg, 2009), studies on cross-national differences in happiness have predominantly focused on economic, social, and cultural factors. Direct links have not been established between differences in gene frequencies and happiness (Diener and Suh, 1999; Inglehardt and Klingemann, 2000; Tov and Diener, 2007).

The absence of a genetic factor in cross-national studies on happiness is not surprising; within the narrow range of variation inside any given country, genetic factors might account for most of the variance, whereas in the broader range of cross-national variation, cultural and economic factors may also play a role. However, as noted by Diener and Suh (1999: 448), “*if individual differences within cultures are largely inheritable, it is conceivable that differences between groups might at least in part be due to genetic differences between populations*”. In this light, several studies have identified cross-national differences in personality traits (see, e.g., data collections by Martin and Lynn (1995) and Schmitt et al. (2007)) and have linked these differences to cross-national differences in happiness (e.g., Lynn and Steel, 2006). Nevertheless, most scholars have attributed these cross-national differences in personality to cultural factors rather than to genetic factors (Allik and McCrae, 2004). At the same time, it is important to consider that such cultural differences in happiness might be due to genetic differences between populations that are unaccounted for in empirical examinations.

This research is one of the first studies to examine the influence of genetics on cross-national differences in happiness levels. To the authors' knowledge, only the paper by Proto and Oswald (2014) studies the relationship between genetic distance and cross-national differences in happiness. Using genetic distance data obtained from Spolaore and Wacziarg (2009) and happiness indicators for more than 100 countries from Gallup and the World Values Survey, Proto and Oswald (2014) find a positive correlation between the proximity of a country to the genetic makeup of Denmark (the happiest country in their sample) and the average level of happiness in that country. In subsequent analyses, Proto and Oswald (2014) focus on the influence of specific genetic effects by showing that small cross-national differences in the proportion of the population that has the short version of the 5-HTTLPR polymorphic allele (a version of a gene that is present at a specific location) can result in considerable cross-national differences in happiness.⁶

¹ A full review of this literature is available in the Bibliography of Happiness, Section Pe ‘Heritability of Happiness’ (Veenhoven 2014a). See Bartels (2015) for a recent meta-analysis of this literature.

This paper builds on⁷ the previous literature by exploring data on genetic distances and differences in happiness in 104 nations, comparing 5,356 country pairs. In other words, this study employs a bilateral approach that involves an estimation of a measure of the absolute differences in happiness across all available country pairs. Subsequently, we regress this measure on the genetic distance between countries, controlling for other differences between countries. By taking country pairs instead of countries as the unit of analysis, we utilise not only information on the proximity of a country to the genetic makeup of Denmark but also the database on genetic distance by Spoloare and Wacziarg (2009) to its fullest extent. In addition, we include a large set of cultural, institutional, economic, and geographical distances between countries that may confound the relationship between genetic distance and absolute differences in happiness between countries.

The remainder of this article is organised as follows. The next section provides a discussion of our data and methodology. The empirical results are presented in section 3. We conclude with a discussion of our findings in section 4.

2. DATA AND METHODOLOGY

2.1 Happiness

Happiness can be defined as the degree to which a person evaluates the overall quality of his or her present life-as-a-whole positively (Veenhoven, 1984). According to Veenhoven (1984, 2009), the evaluation of life draws on two sources of information, the ‘components’ of happiness: (1) how well we feel in general, or the *hedonic level of affect*, and (2) how well our life-as-it-is compares to standards of how-life-should-be, or the level of *contentment*.

Happiness is commonly measured using self-reports, in which questions on happiness can be framed in many ways: directly or indirectly and using single or multiple items. Based on the different components of happiness, questions may concern (1) overall happiness, using either ‘happiness’ or ‘life satisfaction’ as the keyword, (2) experienced emotions, and (3) perceived differences between what one wants from life and what one gets.

In this research, we focus on overall happiness by utilising data from the data file ‘States of Nations’, which is part of the World Database of Happiness (Veenhoven, 2014b). Our dependent variable, which measures the absolute difference score in average life satisfaction across nations for the 2000-2009 period, is based on responses to the survey question, “*Taken together, how satisfied or dissatisfied are you with your life-as-a-whole these days on a scale from 0 (not satisfied) to 10 (very satisfied)?*” (used in the Gallup World Poll). For countries for which data were only available on a 10-point scale (1-10) (obtained from the World Values Survey question), average life satisfaction scores were re-estimated using the transformation procedure described by Veenhoven (1993).² Of the 104 countries in our common sample, average satisfaction varies between 2.8 (Tanzania) and 8.5 (Costa Rica) (see [Table 1](#)). Whereas countries in Sub-Saharan Africa are generally the least happy, countries in Western Europe and Latin America show the highest average life satisfaction scores.

2.2 Genetic Distance

In the genetics literature, several measures have been introduced to capture the genetic distance between populations. In principle, these genetic distance measures are based on differences in

⁶ It should be noted that all life satisfaction scores were obtained from surveys with representative population samples. Average scores may be inflated in some countries due to undersampling of rural and illiterate populations. This distortion is partly corrected by weighting afterwards but may still affect the average life satisfaction scores. This means that the real differences in happiness are likely to be somewhat larger than what can be obtained from the data.

allele frequencies. An allele is a version of a gene that is present at a specific location, known as the locus for that gene. New alleles that are the result of mutation can perish or spread within a given population. In a situation in which a population is split into two smaller populations, mutations after the division will only exist in one of the two populations. Allelic drift or random fluctuations in the occurrence of other alleles (due to the essentially random process of reproduction) also generate genetic differences between isolated populations.³ Genetic distance can be interpreted as a general metric for very long-term divergence in characteristics transmitted across populations. In other words, genetic distance measures the time that has elapsed since two populations had the same common ancestor. Hence, populations that share more recent common ancestors (a small genetic distance) have had less time to diverge concerning traits and characteristics that are transmitted across generations (i.e., vertically transmitted traits and characteristics). Accordingly, genetic distance can be interpreted as the measure of historical relatedness between populations.

In this research, we use the F_{ST} (Fixation Index; also known as the co-ancestor coefficient) distance between pairs of countries from Spolaore and Wacziarg (2009) as an indicator of genetic distance. This database builds on the work of Cavalli-Sforza et al. (1994), which presents data on differences in allele frequencies between populations across a range of neutral genes based on protein and blood group analyses. The Cavalli-Sforza et al. (1994) data contain information on 120 alleles for 42 ethnic groups. The largest genetic distance is observed between Mbuti Pygmies and Papua New Guineans, and the smallest genetic distance is observed between the Danish and the English. Using information from Alesina et al. (2003) on the ethnic composition of countries, a weighted measure of genetic distance between countries can be estimated. Note that a higher F_{ST} score is associated with larger differences between countries because a longer separation time means a greater genetic distance computed from a set of neutral genes. **Figure 1** shows the phylogenetic tree of the largest countries in our databases. This branching diagram shows the inferred relationships among the various populations in the different countries based upon similarities and differences in their genetic characteristics. Not surprisingly, differences are smallest between countries that are situated on the same continent.

2.3 Control Variables

As indicated by Brulé and Veenhoven (2015), most differences in happiness between countries can be attributed to societal characteristics, such as economic development and the quality of institutions. Because countries that are genetically close may also be close in terms of culture, institutions, economy, and climate (see also Spolaore and Wacziarg, 2009), we include control variables that may confound the relationship between genetic distance and cross-national differences in happiness. In other words, we test whether the effect of genetic distance on absolute difference in happiness levels across countries is robust to controlling for other factors that drive differences in happiness between countries, thereby avoiding omitted variable bias. These control variables are related to (1) cultural distance between countries, (2) institutional distance between countries, (3) economic distance between countries, and (4) geographical distance between countries. These variables are discussed in more detail below. Descriptive statistics and a correlation table of the variables included in our regression are provided in **Tables 2 and 3**.

Cultural Distance

As proxies for cultural distance between countries, we use linguistic distance and religious distance. The linguistic distance between two countries is measured as the inverse of the common language index provided by Melitz and Toubal (2012). This linguistic similarity index

⁷ Please note that most of these genetic changes are neutral in the sense that they do not involve any environmental advantage to the individual who possesses these genes (Kimura, 1968). These neutral genes are used to estimate genetic distance between populations because they tend to be uncorrelated with environmental characteristics.

is based on (1) countries sharing the same official language, (2) countries sharing the same native language, and (3) the linguistic proximity between different native languages. Religious distance is measured as the inverse of the shared common religion presented in the work of Alesina et al. (2003) on religious fractionalisation and has previously been used in the work of Disdier and Mayer (2007). The religion similarity index is defined for each religion using its family and sub-family and takes the value of 1 if two religions are similar, 0.5 if two religions are part of the same sub-family, 0.25 if they are part of the same family, and 0 if they are part of different families. The index of religious proximity between countries is estimated as the sum of the products of the share of each religion weighted by the religion similarity index for all religions practiced by at least 3% of the population in each country.

Institutional Distance

With respect to social-institutional distance, we include 4 indicators reflecting differences in welfare and demography between countries: (1) the absolute difference in healthcare expenditures (as % of GDP), (2) the absolute difference in the level of education, (3) the absolute difference in income inequality between countries, and (4) the difference in institutional quality between countries. Country data on healthcare expenditures are obtained from the World Development Indicators. Income inequality (2000-2008 period) is measured as a Gini coefficient of family income distributions and is obtained from the CIA World Factbook. Education is measured as the gross enrolment ratio incorporating all three levels of education (primary, secondary, and tertiary) for the 2000-2004 period and is obtained from the UN Human Development Index. Our measure of differences in institutional quality is based on Kaufmann's six dimensions of governance quality (Kaufmann et al., 2004). These dimensions include voice and accountability, political stability, effectiveness of government, quality of regulation, rule of law, and control of corruption. These indicators are constructed on the basis of factor analysis and reflect different aspects of the quality of governance. A more detailed description of these dimensions can be found in Kaufmann et al. (2004). Following Burger et al. (2009), we measure the institutional distance between pairs of countries using the index developed by Kogut and Singh (1988):

$$IQD_{ij} = \frac{1}{6} \sum_{k=1}^6 \frac{(I_{ki} - I_{kj})^2}{V_k},$$

where I_{ki} indicates the i^{th} country score on the k^{th} dimension and V_k is the variance of this dimension across all countries.

Economic Distance

With respect to the economic distance between countries, we include 3 indicators reflecting differences in wealth between countries: (1) the absolute difference in the natural log of the GDP, (2) the absolute difference in average annual GDP growth (in percentage points), and (3) the absolute difference in the inflation rate (in percentage points; based on Consumer Price Indices). All variables are averages for the 2000s and are obtained from the World Bank Development Indicators database.

Geographical Distance

Because populations that are genetically distant tend to be geographically dispersed, we control for the geographical distance between countries in our regressions. To take into account the geographical distance between countries, we include two variables: physical distance and contiguity. Physical distance is measured as the population-weighted average of the straight line distance ('as the crow flies') between the 20 largest cities in the origin and destination countries and is obtained from CEPPII (Mayer and Zignagno, 2006). The Boolean contiguity variable takes

the value of 1 if two countries are adjacent. Contiguity requires either a land border or a small body of water separating the two countries.

2.4 Empirical Strategy

To examine whether genetic distance has an influence on the difference in happiness across countries, we adopt a bilateral approach that encompasses an estimation of a measure of the *absolute differences in happiness across all available country pairs* and regress it on genetic distance, controlling for other types of distances between countries. More specifically, we use the following simple reduced-form model specification:

$$|H_i - H_j| = \alpha_0 + \alpha_1 GD_{ij} + \alpha'_3 X_{ij} + \varepsilon_{it}, \quad (1)$$

where H_i is a measure of the average life satisfaction level in a country i , H_j is a measure of the average life satisfaction level in a country j , GD_{ij} is our measure of genetic distance, and X_{ij} is a set of control variables capturing cultural, social-institutional, economic, and/or geographical distances between countries. Please note that other factors affect cross-national differences in happiness. However, in this study, we are primarily interested in the effect of genetic distance on the absolute difference in average life satisfaction scores between nations, and we control for variables that may confound this relationship. Equation (1) is estimated using Ordinary Least Squares. Standard errors are corrected for the clustering of observations of each country in the country pair using the two-way cluster-robust variance estimator provided by Cameron et al. (2011). In all regressions, we use a common sample of 5,356 country pairs ((104 countries*103)/2) for which information on all the different distance measures is available to allow for comparison across the different estimations.

3. EMPIRICAL RESULTS

All models are estimated using the statistical program Stata. We find a modest bivariate correlation of 0.29 between genetic distance and the absolute difference in life satisfaction (see also [Table 3](#)). [Figure 2](#) shows the relationship between genetic distance and the difference in the average level of life satisfaction (scale 0-10) between countries. We find a moderate slope coefficient of 0.469 for genetic distance with a standard error of 0.083. [Table 4](#) reports the estimates of the regressions using as a dependent variable the absolute difference in average life satisfaction between countries. Six specifications are estimated; our baseline regression model only includes genetic distance. Subsequently, we add cultural distance variables (column 2), institutional distance variables (column 3), economic distance variables (column 4), and geographical distance variables (column 5). A comparison of the results of specifications 2-5 with specification 1 enables us to gauge to what extent the different dimensions of bilateral distances between countries moderate the effect of genetic distance on cross-national differences in life satisfaction. Finally, we present our full specification (column 7).

Turning to the main results, genetic distance is positively correlated with absolute difference in average life satisfaction levels, and this effect is statistically significant and meaningful at the 1% significance level. A one-standard-deviation increase in genetic distance is associated with an increase in absolute difference in average life satisfaction of 0.29 points, where genetic distance explains 8.4% of the variance in the absolute difference in average life satisfaction levels between countries. Controlling for cultural distance (column 2) and geographical distance (column 5) barely attenuates this relationship. However, institutional distance (column 3) and economic distance (column 4) considerably moderate the relationship between genetic distance and absolute difference in life satisfaction. When all control variables are added in our full specification (column 7), the estimated effect genetic distance coefficient reduces to 0.110 and is only significant at the 10% level. Likewise, the effect size is very small:

a one-standard-deviation increase in genetic distance is now associated with an increase in absolute difference in average life satisfaction of less than 0.07 points. Adding genetic distance as an explanatory variable to our model with control variables (moving from column 6 to 7 in [Table 4](#)) would increase the R^2 by only 0.2%.

4. ALTERNATIVE MEASURES OF GENETIC DISTANCE

Genetic distance can be measured either by examining dominant groups (i.e., the population with the largest shares in each country's population) or by taking into account the genetically diverse populations of some countries by using a weighted distance measure. As noted by Spolaore and Wacziarg, the weighted FST is very highly correlated with the FST measure based on dominant groups (in our common sample, the correlation is 0.93). Despite the fact that it does not really matter for estimation purposes which of the measures we use, we use the weighted FST measure in our initial regressions because it is considered a more precise measure of genetic distance (Spolaore and Wacziarg, 2009). The FST measure based on dominant groups is used in our robustness check.

In addition to the FST genetic distance measures, we use Nei's standard genetic distance (Nei, 1972). Whereas the FST genetic distance measures assume that genetic differences between populations arise due to genetic drift, Nei's genetic distance measures take into account that genetic differences between populations can arise due to genetic drift or mutation. Nei's genetic distance measure has a weighted variant and a variant based on dominant groups, and the correlation with the FST measures is generally high (0.88-0.93).

As a robustness check, [Table 5](#) presents our baseline and full model specifications, shown in columns 1 and 6 of [Table 5](#), re-estimated using different measures of genetic distance between countries (i.e., standard FST distance, weighted Nei genetic distance, and standard Nei genetic distance) (see discussion above). All estimations point in the same direction: there is initially a positive effect of genetic distance on the absolute difference in average life satisfaction between nations, which largely disappears when including control variables, most notably those reflecting differences in the institutional and economic environment between countries.

5. DISCUSSION

In this exploratory analysis of differences in average happiness across 104 nations, we observed that a one-standard-deviation difference in genetic distance is associated with a 0.29 difference (more than one-fourth of a standard deviation) in average happiness, but this effect is reduced to less than 0.07 points (one-sixteenth of a standard deviation) when differences in other country characteristics are controlled for, particularly differences in economic prosperity. Whereas in our model without control variables genetic distance explains 8.4% of the variance in cross-national differences in happiness, the explained variance is significantly reduced after controlling for cultural, institutional, economic, and geographical differences between countries. Although our results are in line with the findings of Proto and Oswald (2014), the effect sizes these authors found were generally larger.

Does this mean that the effect of genetic differences is negligible? On the one hand, we know that genetic differences are an important determinant of differences in happiness between individuals within countries. At the same time, 93%-95% of the total human variability is found within a population, whereas only 3%-5% is found between populations (Rosenberg et al., 2002). In this light, it is not surprising that genetic differences are not a very important determinant of variations in happiness between countries.

At the same time, it can be argued that the observed effect is conservative. Our measure of genetic distance does not capture all genetic differences between countries; it only captures differences in some alleles. Hence, part of the variation in genetic distance is not accounted for

in the data used here, and our measure of genetic distance is essentially a measure of differences in long-term characteristics between two countries. This detail is important because there are most likely specific genes that drive differences in happiness between people. Although happiness is not linked to a single gene, Caprara et al. (2009) suggest that there is something like a general and genetically influenced 'positive orientation' in which fairly overlapping sets of genes influence self-esteem, life satisfaction, and optimism.

In addition, our estimation strategy obscures the view of the effect of genetic distance in two ways. First, it can be argued that genetic and other long-term invariant (or slowly changing) differences between countries (such as culture and geography) are difficult to separate empirically. This is the case with religious, linguistic and geographical distances, which are typically part of the same evolutionary history. Although these variables account for differences in culture and climate, which can confound the relationship between genetic differences and differences in subjective well-being, these factors may also erase true variance in genetics.

Second, genetic differences may influence happiness indirectly through their effect on the economy and society. In other words, the difference in happiness between nations could be attributed to the differential presence of various genes that foster the economic and societal functioning of individuals. If we consider that happiness, particularly its affective component, functions as an orientation device for choosing organisms (Veenhoven, 2009), this implies that there is little genetic variation in this basic affective signal structure among humans. Rather, the variation seems to be in other inherited traits, such as sociability and activity level, which foster the development of a liveable society in contemporary conditions. In this regard, several economists have linked genetic differences and differences in economic development (Spolaore and Wacziarg, 2009), innovation (Spolaore and Wacziarg, 2012), and political stability (DeSmet et al., 2011). Likewise, Cioa and Blizenski (2010) link genetic difference with cross-national differences in collectivism-individualism. Controlling for societal differences between countries could therefore result in an underestimation of the effect of genetic factors on happiness. However, further research on the effect of genetic factors on happiness is needed to verify this suggestion.

6. CONCLUDING REMARKS

This exploratory study shows that genetics may only explain a small part of the differences in life satisfaction across nations; our estimates range between 8.4% and 0.2%. At the same time, it must be acknowledged that it is difficult to empirically separate genetic factors from cultural and geographical time-invariant factors, and cross-national genetic differences could still influence cross-national differences in happiness through their effects on economic and societal functioning.

In this regard, the understanding of differences in happiness in nations can be enriched by considering specific genetic factors. A first step for future research is to generate better data about genetic distance between nations. Specifically, one could focus on specific genes that are associated with certain personality traits and psychological conditions that influence people's happiness levels. For example, it would be interesting to examine cross-national differences with regard to the monoamine oxidase A gene (Chen et al., 2013), the oxytocin receptor gene (Saphire-Bernstein et al., 2011), or the serotonin transporter gene (De Neve, 2011; De Neve et al., 2012). From the behavioural genetics literature, it has been established that these genetic differences are associated with differences in happiness through their effect on personality.

A good example in this regard is the analysis by Proto and Oswald (2014), which links cross-national differences in happiness to cross-national differences in the proportion of the population that has the version of an allele (5-HTTLPR) that is related to higher probabilities of clinical depression. It is well established that genes play a role in causing depression (heritability is approximately 30%-40%; Sullivan et al., 2000). Clinical depression is strongly associated with

unhappiness (Koivumaa-Honkanen et al., 2004; Rapaport et al., 2005), and most of the relationship between depression and unhappiness can be explained by genes (Nes et al., 2013). Given that gene research is growing rapidly, more cross-national data on specific gene frequencies will become available in the near future, which will help us to pinpoint *how* and *to what extent* cross-national differences in happiness have a genetic origin.

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Table 1: Average Life Satisfaction across Nations in our Sample for the 2000-2009 Period

Rank	Country	Score	Rank	Country	Score	Rank	Country	Score	Rank	Country	Score
1	Costa Rica	8,50	27	Trinidad and Tobago	7,02	53	South Korea	6,02	79	Armenia	5,03
2	Denmark	8,24	28	Spain	7,00	54	Estonia	5,98	80	Pakistan	5,03
3	Switzerland	8,01	29	Singapore	6,88	55	Slovakia	5,91	81	Ukraine	4,98
4	Finland	7,89	30	Paraguay	6,87	56	Philippines	5,89	82	Zambia	4,97
5	Norway	7,86	31	Slovenia	6,87	57	Tunisia	5,89	83	Mauritania	4,95
6	Mexico	7,85	32	Uruguay	6,75	58	Iran	5,88	84	Cambodia	4,89
7	Sweden	7,82	33	Italy	6,71	59	South Africa	5,82	85	Moldova	4,86
8	Panama	7,79	34	Jamaica	6,70	60	Portugal	5,71	86	Uganda	4,81
9	Australia	7,73	35	El Salvador	6,68	61	Egypt	5,66	87	Mali	4,71
10	Colombia	7,72	36	Chile	6,64	62	Nigeria	5,65	88	Macedonia	4,66
11	Ireland	7,61	37	France	6,61	63	Turkey	5,56	89	Albania	4,62
12	Canada	7,60	38	Thailand	6,58	64	Russian Federation	5,55	90	Bulgaria	4,41
13	Dominican Republic	7,59	39	Malaysia	6,55	65	Kyrgyzstan	5,54	91	Burkina Faso	4,36
14	Austria	7,58	40	Bolivia	6,50	66	Lithuania	5,53	92	Georgia	4,26
15	Netherlands	7,56	41	Czech Republic	6,50	67	India	5,51	93	Rwanda	4,23
16	Venezuela	7,52	42	Japan	6,50	68	Hungary	5,46	94	Cameroon	3,94
17	Brazil	7,48	43	Greece	6,44	69	Algeria	5,39	95	Haiti	3,90
18	New Zealand	7,46	44	Ecuador	6,42	70	Morocco	5,38	96	Mozambique	3,84
19	United States	7,44	45	Poland	6,38	71	Latvia	5,36	97	Niger	3,75
20	Argentina	7,34	46	China	6,31	72	Nepal	5,32	98	Madagascar	3,73
21	Belgium	7,33	47	Laos	6,24	73	Azerbaijan	5,28	99	Kenya	3,67
22	Guatemala	7,20	48	Peru	6,22	74	Bangladesh	5,28	100	Sierra Leone	3,55
23	United Kingdom	7,14	49	Malawi	6,20	75	Ghana	5,22	101	Zimbabwe	3,05
24	Germany	7,12	50	Kazakhstan	6,13	76	Belarus	5,18	102	Benin	3,02
25	Nicaragua	7,09	51	Vietnam	6,11	77	Tajikistan	5,10	103	Burundi	2,94
26	Honduras	7,02	52	Croatia	6,02	78	Sri Lanka	5,06	104	Tanzania	2,82

Source: Veenhoven (2014)

Table 2: Descriptive Statistics (N=5,356)

Variable	Mean	Standard Deviation	Minimum	Maximum
Genetic Distance	1.06	0.68	0	3.36
Difference in Satisfaction with life	1.52	1.11	0	5.68
Religious Distance	0.83	0.25	0	0.99
Linguistic Distance	0.87	0.16	0	0.99
Difference Health Expenses (% GDP)	2.44	1.82	0	9.20
Difference Education Levels	20.63	15.78	0	82.14
Difference Income Inequality	10.71	7.84	0	38.20
Difference Institutional Quality	1.02	0.77	0	3.39
Difference Log GDP per Capita (x1000)	1.92	1.36	0.00	6.48
Difference GDP Growth	2.60	2.28	0.00	19.35
Difference Inflation Rate	11.92	45.58	0.00	341.09
Geographical Distance (x1000)	7.57	4.41	0.16	19.65
Not Sharing Border	0.97	0.17	0	1

Table 3: Correlation Matrix of Main Variables Included in Models

Variable	1	2	3	4	5	6	7	8	9	10	11	12	13
1. Difference in Average Life Satisfaction	1.00												
2. Genetic Distance (x1000)	0.29	1.00											
3. Religious Distance	0.13	0.05	1.00										
4. Linguistic Distance	0.23	0.32	-0.49	1.00									
5. Difference Health Expenses (% GDP)	0.17	-0.00	0.07	0.07	1.00								
6. Difference Education Levels	0.45	0.32	0.10	0.24	0.26	1.00							
7. Difference Income Inequality	0.06	0.11	-0.04	0.11	0.09	0.04	1.00						
8. Difference Institutional Quality	0.27	-0.02	0.08	0.06	0.51	0.37	0.15	1.00					
9. Difference Log GDP per Capita (x1000)	0.47	0.25	0.10	0.11	0.50	0.63	0.10	0.70	1.00				
10. Difference GDP Growth	0.16	0.13	0.17	0.14	0.23	0.06	0.01	0.24	0.21	1.00			
11. Difference Inflation Rate	0.18	0.14	0.05	0.03	-0.04	0.02	0.03	0.12	0.05	0.38	1.00		
12. Geographical Distance (x1000)	0.14	0.31	0.11	0.19	0.01	0.02	0.31	0.01	0.05	0.02	0.01	1.00	
13. Not Sharing Border	0.11	0.16	0.13	0.21	0.10	0.12	0.11	0.10	0.15	0.05	0.00	0.25	1.00

Table 4: OLS on Absolute Difference in Average Life Satisfaction between Countries

	(1) Baseline	(2) + Cultural Distance	(3) +Institutional Distance	(4) +Economic Distance	(5) +Geographical Distance	(6) Only Control Variables	(7) Full Model
Genetic Distance (x1000)	0.469*** (0.083)	0.401** (0.085)	0.303** (0.073)	0.268** (0.067)	0.431** (0.088)		0.110# (0.064)
Religious Distance		0.245# (0.134)				0.095 (0.123)	0.135 (0.120)
Linguistic Distance		0.836** (0.162)				0.432** (0.143)	0.329* (0.143)
Difference Education Levels			0.023** (0.003)			0.016** (0.003)	0.015** (0.003)
Difference Income Inequality			0.000 (0.004)			-0.002 (0.004)	-0.002 (0.004)
Difference Institutional Quality			0.221** (0.070)			-0.104 (0.070)	-0.073 (0.066)
Difference Health Expenses (%GDP)			0.003 (0.022)			-0.025 (0.018)	-0.021 (0.019)
Difference Log GDP per Capita (x1000)				0.348** (0.026)		0.298** (0.050)	0.282** (0.049)
Difference GDP Growth				-0.001 (0.012)		0.011 (0.012)	0.009 (0.012)
Difference Inflation Rate				0.003** (0.000)		0.004** (0.000)	0.004** (0.000)
Geographical Distance (x1000)					0.012 (0.009)	0.028** (0.008)	0.024** (0.008)
Not Sharing Border					0.369** (0.088)	-0.020 (0.067)	-0.038 (0.069)
Constant	1.032*** (0.064)	1.254** (0.077)	0.492 ** (0.073)	0.536 (0.073)	0.624** (0.066)	0.613** (0.069)	0.563** (0.078)
Observations	5,356	5,356	5,356	5,356	5,356	5,356	5,356
R-squared	0.084	0.107	0.245	0.274	0.090	0.314	0.316
Standardised Beta Genetic Distance	0.289	0.247	0.187	0.165	0.266	N/A	0.067

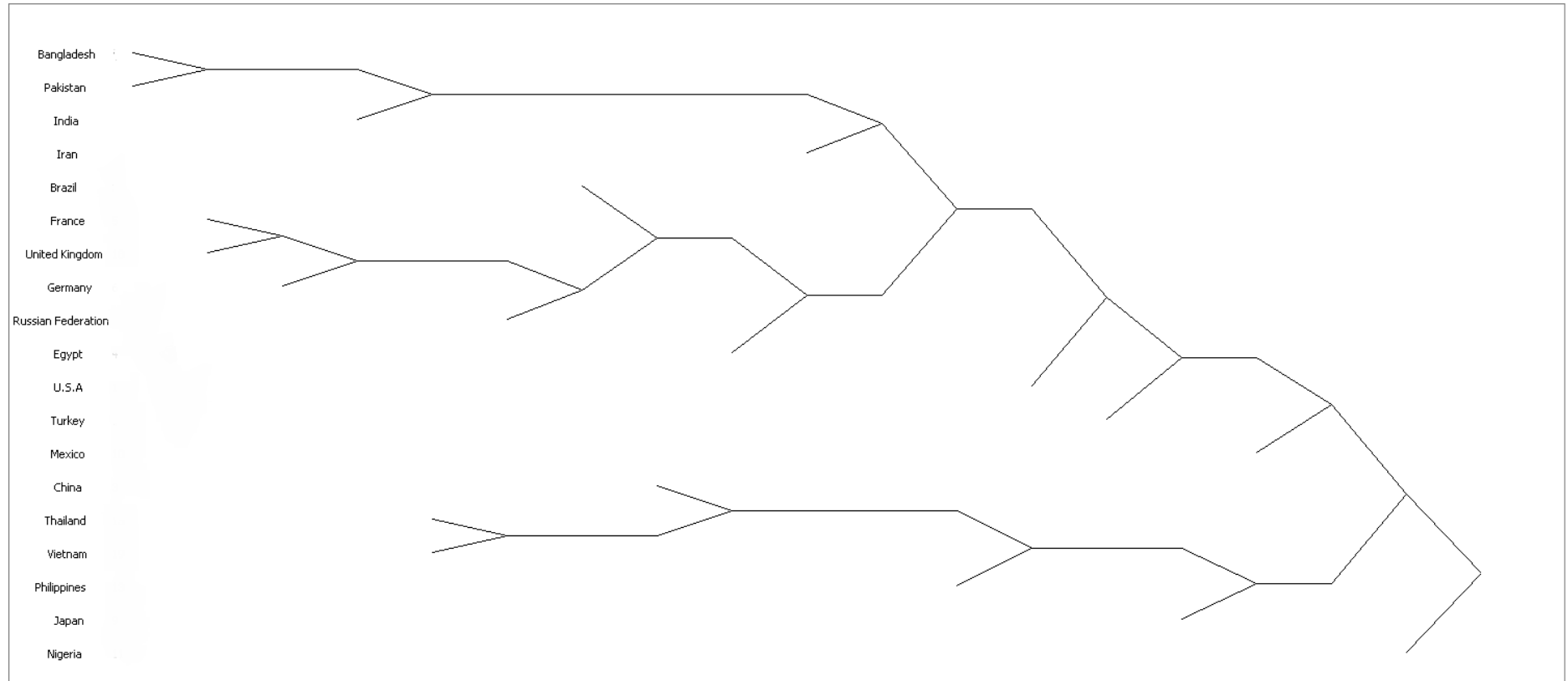
Two-way cluster-robust standard errors in parentheses; ** p<0.01, * p<0.05, #p<0.10

Table 5: OLS on Absolute Difference in Average Life Satisfaction between Countries – Alternative Genetic Distance Measures

	(7) Baseline FST Dominant	(8) Full Model FST Dominant	(9) Baseline Nei Weighted	(10) Full Model Nei Weighted	(11) Baseline Nei Dominant	(12) Full Model Nei Dominant
Genetic Distance (x1000)	0.334** (0.068)	0.067 (0.048)	2.844** (0.519)	0.788# (0.409)	2.138** (0.409)	0.666* (0.291)
Religious Distance		0.122 (0.120)		0.152 (0.121)		0.153 (0.119)
Linguistic Distance		0.350* (0.143)		0.319* (0.145)		0.299* (0.145)
Difference Education Levels		0.016** (0.003)		0.015** (0.003)		0.015** (0.003)
Difference Income Inequality		-0.002 (0.004)		-0.003 (0.004)		-0.002 (0.004)
Difference Institutional Quality		-0.086 (0.067)		-0.062 (0.066)		-0.068 (0.066)
Difference Health Expenses (%GDP)		-0.023 (0.019)		-0.024 (0.019)		-0.025 (0.018)
Difference Log GDP per Capita (x1000)		0.289** (0.049)		0.276** (0.050)		0.279** (0.050)
Difference GDP Growth		0.010 (0.012)		0.009 (0.012)		0.010 (0.012)
Difference Inflation Rate		0.004** (0.000)		0.003** (0.000)		0.003** (0.000)
Geographical Distance (x1000)		0.025** (0.008)		0.023** (0.008)		0.023** (0.008)
Not Sharing Border		-0.033 (0.089)		-0.039 (0.070)		-0.041 (0.069)
Constant	1.163** (0.055)	0.579** (0.075)	1.038** (0.067)	0.567** (0.078)	1.144** (0.055)	0.569** (0.073)
Observations	5,356	5,356	5,356	5,356	5,356	5,356
R-squared	0.059	0.315	0.095	0.319	0.077	0.319
Standardised Beta Genetic Distance	0.243	0.049	0.369	0.102	0.231	0.072

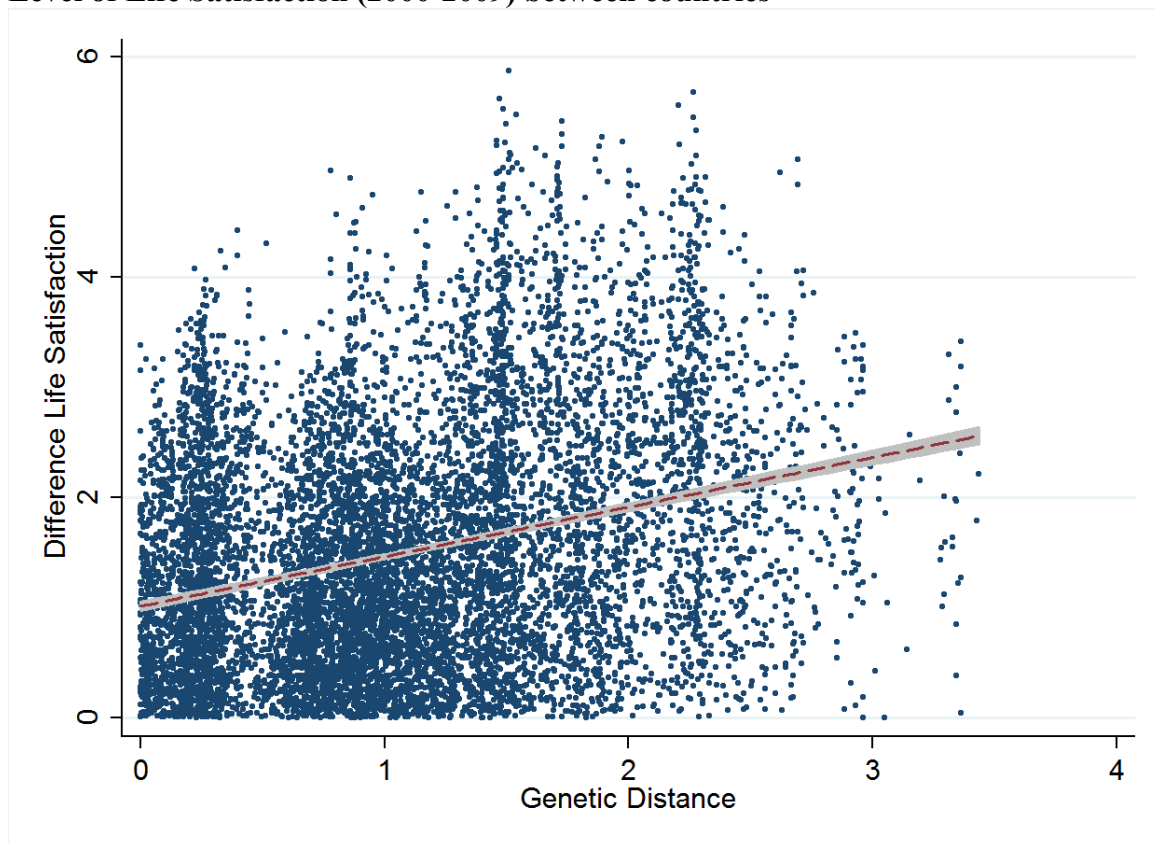
Two-way cluster-robust standard errors in parentheses; ** p<0.01, * p<0.05, #p<0.10

Figure 1: Genetic Distance between Largest Countries in our Database



Source: own computations based on Spolaore and Wacziarg (2009)

Figure 2: Relationship between Genetic Distance and Absolute Difference in Average Level of Life Satisfaction (2000-2009) between countries



Source: own computations based on Spolaore and Wacziarg (2009) and Veenhoven (2014)