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RESEARCH PAPER

A Genetic Component to National Differences in Happiness

Michael Minkov[1] · **Michael Harris Bond**[2]

Abstract National differences in subjective well-being (SWB) have been attributed to socioeconomic, climatic, and genetic factors. We focus on one particular facet of SWB—happiness or positive affect—measured by the nationally representative World Values Survey (WVS). We find that national percentages of very happy people across the three latest WVS waves (2000–2004, 2005–2009, 2010–2014) are consistently and highly correlated with national prevalence of the rs324420 A allele in the FAAH gene, involved in the hydrolysis of anandamide, a substance that reportedly enhances sensory pleasure and helps reduce pain. Climatic differences are also significantly associated with national differences in happiness, whereas economic wealth, recent economic growth, rule of law, pathogen prevalence, and the distribution of short versus long alleles in the serotonin transporter gene SLC6A4 are not significant predictors of national happiness.

Keywords Genes · Happiness · Positive affect · Climate · National wealth

1 Introduction

A number of recently published studies have shown associations between measures of national culture and national prevalence of specific genetic polymorphisms (e.g., Chiao and Blizinsky 2010; Fischer 2013; Kong 2014; Minkov et al. 2015; Minkov and Bond 2015; Mrazek et al. 2013; Way and Lieberman 2010, etc.). Although all these studies are

✉ Michael Minkov
michaelminkov@yahoo.com

Michael Harris Bond
ssmhb@polyu.edu.hk

[1] Varna University of Management, ul. Tsarigradsko Shose 149 B, 1784 Sofia, Bulgaria

[2] Department of Management and Marketing, Faculty of Business, Hong Kong Polytechnic University, Kowloon, Hong Kong, SAR, China

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characterized by various limitations, some of which are very serious (Eisenberg and Hayes 2011; Minkov et al. 2015), the search of genetic components of national culture is becoming a promising research field, as the data base of available markers grows.

National culture is closely related to aggregate national personality traits (Hofstede and McCrae 2004). A decade ago, Allik and McCrae (2004) expressed the opinion that genetic differences between nations may account for national differences in aggregated personality traits. This hypothesis has never been tested in depth. However, some preliminary findings suggest that Allik and McCrae may be right. Minkov et al. (2015) have reported an association between a national genetic index and aggregate national neuroticism. Since neuroticism is associated with subjective well-being (SWB), this suggests that national differences in SWB may have a genetic component.

In this article we focus on a particular facet of SWB—happiness or positive affect—and test the hypothesis that national measures of that facet have a genetic component that remains statistically significant after controlling for other plausible predictors.

It is well-known that national measures of happiness are not perfectly stable. A stable factor, such as a nation's genetic profile, cannot explain on its own any fluctuations in any measure. At best, it can explain only the stable element in the observed national differences in happiness. The object of our study is precisely to explain that stable element.

1.1 Previously Reported Predictors of National Differences in Subjective Well-Being

There is a vast array of studies explaining national differences in SWB. Although a variety of different predictors has been proposed, the available evidence suggests some convergence in the results. Analyses of large-scale studies of SWB, such as the nationally representative World Values Survey (WVS; www.wordlvaluessurvey.com), are quite unequivocal. Minkov's (2009) analysis of WVS data from representative populations in 97 countries led to the conclusion that the strongest predictor of national differences in SWB are average differences in life control or freedom of choice endorsed by that nation's population, i.e., the feeling that one controls one's life and can live it as one wishes. Interesting as this finding may be, it is circular as it does not explain what accounts for national differences in perceived freedom of choice.

Inglehart et al. (2008) report the same finding: the main predictor of happiness differences across nations is the feeling of freedom of choice. These authors go a step further in their analysis. They find that, at the national level, this sense of freedom is a function of national economic development, democratization, and increasing social tolerance. This suggests that the distal predictors of national differences in happiness are two strongly correlated variables: national wealth and the rule of law. However, this argument cannot explain why the highest percentages of very happy people in the WVS are consistently found in northern Latin America and West Africa (Nigeria and Ghana). These regions rank low in national wealth and economic growth. They may have free elections, but they are characterized by little effective rule of law, since they have the highest murder and robbery rates in the world as well as high levels of corruption (Minkov 2011).

Other studies report a similar association between national wealth and happiness. Based on such findings, Jorm and Ryan (2014) concluded that economic growth in poor countries will improve global subjective well-being even though higher-income countries need to focus on other determinants of well-being. Di Tella et al. (2003) found that movements in reported well-being are associated with movements in gross national domestic product. The statistical correlations that these studies report across a large number of nations may be

significant, but the mystery of the high happiness levels in northern Latin America and West Africa remains.

An alternative explanation is provided by van de Vliert (2009). This author recognizes the association between national wealth and SWB, but analyzes climatic factors as well, such as harshness of summers and harshness of winters. From the perspective of this theory, people from poor societies in geographic areas that do not have excessive climatic variation are likely to be happier than people in poor societies with excessive climates. Van de Vliert's theory thus may be able to explain the happiness paradox of Latin America and West Africa. However, his explanation of the relatively high happiness of Scandinavians is less convincing. In his view, people in rich countries need a cold climate to be happy, because it provides much-needed stimulation for productive activity. In an affluent society, people cannot be happy without dealing with some challenge. This hypothesis is yet to be proven.

If climatic factors are associated with subjective well-being, it is plausible that pathogen prevalence (Murray and Schaller 2010) will also be correlated with it, as pathogen prevalence is related to climate. Inglehart et al. (2013) launched the idea that parasite (pathogen) prevalence may account for cultural and economic factors that ultimately affect happiness.

Recently, Proto and Oswald (2014) offered a genetic explanation. In their view, "national happiness" (the term used in the title of their publication) has a genetic component. Happier nations have a lower prevalence of a specific genetic polymorphism: short alleles in the 5-HTTLPR variable number tandem repeat (VNTR) of the serotonin transporter gene. Individual-level studies have associated that polymorphism with negative affect and depressiveness.

At this point, we must dwell on the confusing terminology used in various studies of SWB. This construct is defined as "a person's evaluative reaction to his or her life—either in terms of life satisfaction (cognitive evaluations) or affect (ongoing emotional reactions)" (Diener and Diener 1995, p. 653). These two facets of SWB have also been defined as "cognitive" (or "evaluations of one's life according to subjectively determined standards") and "hedonic balance" (or "the balance between pleasant affect and unpleasant affect") (Schimmack et al. 2002, p. 582). Unfortunately, many published studies do not distinguish clearly between these two facets of SWB.

The WVS regularly fields two items that address SWB. One of these (item v10 in the more recent WVS waves) asks the respondents, "Taking all things together, would you say you are"…. The possible answers are: "very happy", "rather happy", "not very happy", and "not at all happy". Another question (item v23 in the latest WVS wave) asks, "All things considered, how satisfied are you with your life as a whole these days? Using this card on which 1 means you are 'completely dissatisfied' and 10 means you are 'completely satisfied' where would you put your satisfaction with your life as a whole?"

Although the happiness item and the life satisfaction item are highly correlated at the national level (Minkov 2009), they do not measure the same thing in all countries. Similarly, at the individual level, their within-nation correlation also varies across nations from high to only moderate. The happiness item seems to tap the hedonic element of SWB, whereas the life satisfaction item elicits a cognitive appraisal. Evidence for this distinction comes from sub-Saharan Africa. In a number of countries in that region, respondents evidently dissociate happiness and life satisfaction, because these countries score high on the former and low on the latter. Interviews that the first author of this article regularly conducts with Nigerian students confirm this perceived dichotomy. Nigerians say that happiness means being in a good mood, probably an innate personality trait. Life

satisfaction, however, comes from an appraisal of one's achievements. Thus, it is possible to be in a good mood in a country like Nigeria, but it is hard to be satisfied with one's life, as one cannot achieve much in such a national culture.

If Proto and Oswald (2014) are right, and national differences in SWB do have a genetic element, it should manifest itself in the hedonic component of SWB. We can expect associations between a national genetic index and national differences in aggregate Big-Five personality traits, or specific facets of such traits, such as positive affect, in accordance with the argument of Allik and McCrae (2004). Genes may somehow be involved in the cognitive element of SWB as well, yet we lack individual-level studies that suggest a plausible mechanism. As for the hedonic element, we explain below why a genetic contribution to its strength at both the individual and national levels is plausible.

1.2 Potential Genetic Contributors to Happiness

Serotonin is a chemical in the human brain that maintains mood balance. It has been found to play a role in susceptibility to depression and suicide (Young 2007). The SLC6A4 gene encodes the serotonin transporter protein (SERT or 5-HTT). The short (S) allelic variant of the serotonin transporter-linked polymorphic region (5-HTTLPR) is associated with reduced SERT availability and function compared with the long (L) form, as well as with anxiety and neuroticism (Homberg and Lesch 2011). This pattern of relationships suggests that Proto and Oswald's (2014) hypothesis concerning the association between the 5-HTTLPR polymorphism and national differences in happiness is plausible. However, those authors did not test that hypothesis appropriately, because they did not have sufficient data concerning the worldwide prevalence of the S and L alleles. Working with a small and globally unrepresentative sample of nations can result in erroneous conclusions about the association between national differences in genes and personality or culture (Eisenberg and Hayes 2011; Minkov et al. 2015).

Anandamide is a naturally occurring endogenous brain cannabinoid that has been shown to enhance sensory pleasure (Mahler et al. 2007). It also plays an important role in pain suppression (Walker et al. 1999). Anandamide is degraded by the enzyme fatty acid amide hydrolase (FAAH; McKinney and Cravatt 2005), which suggests that inhibition of FAAH may be an approach to anti-anxiety therapy (Kathuria et al. 2002). Mice that lack FAAH display reduced pain sensation (Cravatt et al. 2001). Pharmacological blockade of FAAH produces anxiolytic (anxiety-reducing) effects (Gaetani et al. 2003).

The FAAH gene encodes a protein that is responsible for the hydrolysis of anandamide (National Center for Biotechnology Information 2015). It has a single nucleotide polymorphism (SNP) known as rs324420. The A allele of this SNP is associated with increased anandamide signaling (Conzelmann et al. 2012), as well as reduced FAAH expression and decreased anxiety (Dincheva et al. 2015). Similar conclusions were reached by Hariri et al. (2009): the A allele was associated with reduced threat-related reactivity and increased reward-related reactivity. Also, Conzelmann et al. (2012) found an association between the A allele and reduced brain reactivity toward unpleasant faces as well as enhanced reactivity towards reward.

Collectively, these findings suggest that A-allele carriers may be less prone to anxiety and, consequently, report higher baseline happiness. Nations with a higher prevalence of the A allele may thus have higher percentages of happy people. This hypothesis has never been tested so far.

2 Method

We used the nationally representative WVS (www.worldvaluesurvey.com) to calculate average national percentages of respondents who reported that they were "very happy". In the 2010–2014 WVS wave, these percentages range from 67.5 in Mexico to 5.3 in Egypt, dwarfing the national differences in the percentages of respondents who have chosen any of the other three response options. We know from empirical studies that positive affect and negative affect are not two sides of the same coin; they appear to be independent dimensions (Kuppens et al. 2006; Schimmack et al. 2002). In this study, we are interested in national differences in happiness rather than unhappiness; that is, positive affect rather than negative affect. Therefore, we analyze only the percentages of people who state unambiguously that they are happy. Minkov (2013) shows that selection of ambiguous positions on a four-point Likert scale, such as "somewhat…" or "rather…", usually results in poor predictive properties at the national level. This is so because selection of the "somewhat" or "rather" position on the WVS four-point Likert scale apparently denotes uncertainty and ambiguity on the part of the respondent.

To minimize the effect of ephemeral situational factors (such as a sudden rise of unemployment) and random measurement error, we averaged the data from the three latest WVS waves: 2000–2004, 2005–2009, and 2010–2014. Table 1 shows correlations between the national percentages of very happy people in these three waves. The high correlations suggest high stability in the observed national differences in happiness and justify the averaging of the data into a single 2000–2014 national happiness index, reflecting percentages of people in nationally representative studies who regularly experience positive affect.

To validate our happiness index, we used a measure by Kuppens et al. (2006): a national positive affect index (component 1 in Table 1 in that publication).

Since the number of WVS countries that are represented in all three waves from 2000 to 2014 is relatively small, we decided to include also those nations that are represented in at least two waves during that period. We used the three-wave index as a dependent variable and data from two waves at a time to predict scores on the three-wave index by means of linear regressions. R square values exceeded .95, attesting to the high reliability of the estimates.

To enlarge our index even more, we also calculated predicted scores for countries that were studied only once by the WVS in 2000–2014. Although these regression models also showed highly acceptable reliability ($R^2 > .90$), we took a conservative approach and analyzed the resulting happiness index separately.

Table 1 Correlations between national percentages of World Values Survey respondents who report that they are "very happy", WVS waves 2000–2004, 2005–2009, 2010–2014

	Percentage very happy 2005–2009	Percentage very happy 2000–2004
Percentage very happy 2010–2014	.83* ($n = 36$)	.78* ($n = 24$)
Percentage very happy 2005–2009		.80* ($n = 22$)

* Correlation significant at the .001 level

Table 2 Sources of rs324420 A allele estimates

Country	Source
Algeria	Estimate based on converging data for Algerian Mozabites (Berbers) in Kidd (2014) and Palestinian Arabs in Kidd (2014)
Andorra	Estimate based on converging data for Spain in De Luis et al. (2013) and French in Kidd (2014)
Argentina	Estimate based on data for Spain, assuming a small Amerindian admixture
Australia	Estimate based on data for European Americans in Kidd (2014)
Austria	Estimate based on Germany
Belarus	Estimate based on Russia
Botswana	Estimate based on data for southern African Bantu populations in Kidd (2014)
Brazil	Estimate based on Spain, as well as data for West African Blacks in Kidd (2014), taking into account Brazil's racial composition
Bulgaria	Estimate based on nearly converging data for Greece and Hungary
Burkina Faso	Estimate based on data for West Africans in Kidd (2014)
Canada	Estimate based on data for European Americans in Kidd (2014)
Cambodia	Data for Khmers in Kidd (2014)
Chile	Estimate based on Argentina
China	Data for Han in Kidd (2014)
Colombia	Estimate based on Spain, as well as data for Amerindians and West African Blacks in Kidd (2014), taking into account Colombia's racial composition
Cyprus	Estimate based on Greece
Denmark	Jensen et al. (2007)
Ecuador	Estimate based on Spain, as well as data for Amerindians in Kidd (2014), taking into account Ecuador's racial composition
Egypt	Estimate based on converging data for Algeria and Palestine
El Salvador	Estimate based on Spain, as well as data for Amerindians in Kidd (2014), taking into account El Salvador's racial composition
Estonia	Kidd (2014)
France	Kidd (2014)
Germany	Doehring et al. (2007)
Ghana	Estimate based on data for West Africans in Kidd (2014)
Greece	Marinos et al. (2014)
Hong Kong	Data for Han in Kidd (2014)
Hungary	Kidd (2014)
India	Data for Indian and Pakistani ethnic groups in Kidd (2014). Despite the significant divergence between the data for Dravidians in the south of India and the northern populations, a median value is plausible for India as a whole
Indonesia	Calculated from data for Malays (healthy controls) in Sim et al. (2013)
Ireland	Kidd (2014)
Iraq	Estimate based on data for Palestinians in Kidd (2014)
Italy	Estimate based on data from Kidd (2014)
Japan	Estimate based on data from Kidd (2014)
Jordan	Estimate based on data for Palestinians in Kidd (2014)
Korea	Kidd (2014)
Laos	Kidd (2014)

Table 2 continued

Country	Source
Malaysia	Calculated from data for Chinese and Malays (healthy controls) in Sim et al. (2013), as well as Dravidian populations in Sim et al. (2013), taking into consideration Malaysia's ethnic composition
Mexico	Estimate based on Spain and data for Amerindians in Kidd (2014), taking into consideration Mexico's racial composition
Mongolia	Kidd (2014)
Morocco	Estimate based on Algeria
New Zealand	Estimate based on data for European Americans in Kidd (2014)
Nigeria	Estimate based on data for Hausa and Yoruba in Kidd (2014)
Norway	Estimate based on Denmark
Pakistan	Estimate based on data for Pakistani populations in Kidd (2014)
Palestine	Kidd (2014)
Peru	Estimate based on data for Quechua (Kidd 2014) and Spain, taking into account Peru's racial composition
Romania	Estimate based on nearly converging data for Greece and Hungary
Russia	Kidd (2014)
Rwanda	Estimate based on data for southern African Bantu populations in Kidd (2014)
Singapore	Calculated from data for Chinese and Malays (healthy controls) in Sim et al. (2013), as well as Dravidian populations in Sim et al. (2013), and Han in Kidd (2014), taking into account Singapore's ethnic composition
South Africa	Estimate based on data for southern African Bantu populations in Kidd (2014), assuming a small, predominantly European admixture
Spain	De Luis et al. (2013)
Sri Lanka	Estimate based on data for South Indian populations in Kidd (2014)
Sweden	Estimate based on Denmark
Switzerland	Estimate based on Germany
Syria	Estimate based on Palestine
Taiwan	Data for Han in Kidd (2014)
Thailand	Estimate based on data for Khmers in Kidd (2014)
Tunisia	Estimate based on Algeria
Uganda	Estimate based on data for southern African Bantu populations in Kidd (2014)
Ukraine	Estimate based on data for Russians in Kidd (2014)
United Kingdom	Estimate based on data for converging data for Irish and European Americans in Kidd (2014)
Venezuela	Estimate based on Spain, as well as data for Amerindians and West African Blacks in Kidd (2014), taking into account Venezuela's racial composition
Vietnam	Estimate based on Laos
Yemen	Estimate based on converging data for Palestinians and Yemenite Jews in Kidd (2014)
Zambia	Estimate based on data for southern African Bantu populations in Kidd (2014)
Zimbabwe	Estimate based on data for southern African Bantu populations in Kidd (2014)

Although our study focuses on national differences in positive affect, not life appraisal, we did consider the life satisfaction item (v23 in the 2010–2014 WVS). However, as we demonstrate in the Sect. 3, it proved to be out of place in an analysis of the relationship between genes and SWB at the national level.

Table 3 Estimates of national prevalence of the rs324420 A allele and average percentage of respondents "very happy", world value survey waves 2000–2004, 2005–2009, 2010–2014

	Prevalence of rs324420 A allele (%)	Average percentage "very happy" 2000–2004, 2005–2009, 2010–2014, with predictions from 2 waves	Average percentage "very happy" 2000–2004, 2005–2009, 2010–2014, with predictions from 2 + 1 waves
Albania	NA	NA	10.6
Algeria	12.0	17.5	17.5
Andorra	20.0	NA	27.9
Argentina	23.0 (estimate)	32.8	32.8
Armenia	NA	NA	30.5
Australia	23.0 (estimate)	34.6	34.6
Austria	20.0 (estimate)	NA	NA
Azerbaijan	NA	NA	37.0
Belarus	26.0 (estimate)	NA	12.8
Botswana	20.0	NA	NA
Brazil	25.3 (calculated)	33.8	33.8
Bulgaria	16.0 (estimate)	NA	11.1
Burkina Faso	42.5	NA	24.0
Canada	23.0 (estimate)	NA	45.0
Cambodia	09.0	NA	NA
Chile	23.0 (estimate)	31.0	31.0
China	13.0	16.1	16.1
Colombia	35.0 (calculated)	50.7	50.7
Cyprus	18.2 (estimate)	32.3	32.3
Denmark	26.3	NA	NA
Ecuador	35.0 (calculated)	NA	53.2
Egypt	11.0 (estimate)	11.1	11.1
El Salvador	32.0 (estimate)	NA	NA
Estonia	32.0	NA	12.7
France	21.0	NA	35.4
Germany	20.0	22.2	22.2
Ghana	42.5	48.6	48.6
Greece	18.2	NA	NA
Hong Kong	13.0	15.8	15.8
Hungary	14.0	NA	NA
India	20.0 (calculated)	30.8	30.8
Indonesia	17.0 (estimate)	23.2	23.2
Iran	NA	NA	20.0
Iraq	11.0 (estimate)	10.0	10.0
Ireland	23.0	NA	NA
Israel	NA	NA	28.8
Italy	12 (estimate)	NA	18.5
Japan	20.0 (estimate)	29.8	29.8
Jordan	11.0 (estimate)	20.9	20.9
Kazakhstan	NA	NA	30.5

Table 3 continued

	Prevalence of rs324420 A allele (%)	Average percentage "very happy" 2000–2004, 2005–2009, 2010–2014, with predictions from 2 waves	Average percentage "very happy" 2000–2004, 2005–2009, 2010–2014, with predictions from 2 + 1 waves
Korea	16.7	13.2	13.2
Kuwait	NA	NA	39.2
Kyrgyzstan	NA	NA	29.2
Lebanon	NA	NA	19.1
Laos	28.0	NA	NA
Libya	NA	NA	36.6
Malaysia	16.0 (calculated)	45.2	45.2
Mali	NA	NA	38.2
Mexico	46.0 (estimate)	60.8	60.8
Moldova	NA	7.6	7.6
Mongolia	10.0	NA	NA
Morocco	11.0	22.6	22.6
Netherlands	NA	35.7	35.7
New Zealand	23.0 (estimate)	35.0	35.0
Nigeria	42.5	59.8	59.8
Norway	26.3 (estimate)	NA	NA
Pakistan	24.0 (calculated)	34.2	34.2
Palestine	11.0	NA	12.5
Peru	37.0 (calculated)	34.1	34.1
Philippines	NA	44.4	44.4
Poland	NA	22.0	22.0
Puerto Rico	NA	NA	55.4
Republic of Macedonia	NA	NA	20.0
Romania	16.0 (estimate)	11.3	11.3
Russia	26.0	13.4	13.4
Rwanda	18.0	26.4	26.4
Saudi Arabia	NA	NA	45.3
Serbia	NA	10.7	10.7
Singapore	13.0 (calculated)	34.5	34.5
Slovenia	NA	NA	19.0
South Africa	20.0 (calculated)	41.8	41.8
Spain	20.0	16.4	16.4
Sri Lanka	12.0	NA	NA
Sweden	26.3 (estimate)	39.9	39.9
Switzerland	20.0 (estimate)	NA	40.0
Syria	11.0 (estimate)	NA	NA
Taiwan	13.0	24.4	24.4
Tanzania	NA	NA	57.3
Thailand	9.0 (estimate)	38.8	38.8
Trinidad	NA	NA	50.4

Table 3 continued

	Prevalence of rs324420 A allele (%)	Average percentage "very happy" 2000–2004, 2005–2009, 2010–2014, with predictions from 2 waves	Average percentage "very happy" 2000–2004, 2005–2009, 2010–2014, with predictions from 2 + 1 waves
Tunisia	11.0 (estimate)	NA	18.0
Uganda	18.0	NA	27.2
Ukraine	26.0 (estimate)	14.4	14.4
United Kingdom	23.0 (estimate)	NA	48.7
Venezuela	35.0 (calculated)	NA	57.9
Vietnam	28.0 (estimate)	37.4	37.4
Yemen	11.0 (estimate)	NA	19.1
Zambia	18.0	NA	19.7
Zimbabwe	18.0	31.0	31.0

Latest data concerning the national prevalence of 5-HTTLPR polymorphisms in the serotonin gene, plus additional estimates, are available from Table 1 in Minkov et al. (2015). We adopted their expanded index, based on their estimate that the prevalence of the S allele is about 44 % in the Arab countries and about 70 % in Indonesia and the Philippines.

Our main source for rs324420 allele frequencies was Kidd (2014). This is an allele frequency database maintained by Yale University population geneticist Kenneth Kidd, and supported by the US National Science Foundation. The rs324420 table is available at http://alfred.med.yale.edu/alfred/SiteTable1A_working.asp?siteuid=SI379351C. We expanded Kidd's data with data from peer-reviewed journals. Table 1 provides details.

As Kidd's (2014) data are for ethnic groups, not nations, we had to make estimates for multi-racial nations, such as those of the Americas. Estimates of the ethnic or racial composition of these countries are provided by the Central Intelligence Agency (2012). We made estimates of the prevalence of the A allele in each main ethnicity in the Americas based on data for Amerindians, West Africans, and US Afro-Americans from Kidd (2014). Our estimates of the prevalence of the A allele in Whites in Latin Americas was the prevalence of that allele in Spaniards (De Luis et al. 2013). Although Latin America has descendants of other European groups as well, the Spanish estimate is plausible, as it seems to be a European average.

Thus, our estimates of the prevalence of the A allele in the main ethnic and racial groups in the American nations are as follows: Amerindians—47 %, Whites—20 %, Blacks outside the US—42.5 % (the same as in Nigerians). We made the assumption that those categorized as "mestizos" on average have a 50 % Amerindian heritage versus 50 % European, whereas "mulattos" have a 50 % West African heritage versus 50 % European. Details are provided in Table 2.

We expanded our genetic database further, assuming that some neighboring nations, such as Germany, Austria, and Switzerland, or the Scandinavian nations, are so similar genetically as to be nearly indistinguishable. Minkov et al. (2015) provide evidence that this assumption is plausible.

Table 3 shows national prevalence of the rs324420 A allele as well as two average national happiness indices for 2000–2014, one with predicted scores from two WVS waves

Table 4 Zero-order correlations between national happiness 2000–2014 and its potential predictors

	National prevalence of the S allele in 5-HTTLPR	National prevalence of the A allele in FAAH	GDP per person in 2005	GDP per person growth 2012/1998	KK rule of law index 2005	Harshness of summers plus harshness of winters	Pathogen prevalence
National happiness index 2000–2014 (with predicted scores from two waves at a time)	−.18 ($n = 39$)	.73* ($n = 38$)	.08 ($n = 45$)	−.18 ($n = 43$)	.04 ($n = 45$)	−.51* ($n = 47$)	.20 ($n = 45$)
National happiness index 2000–2014 (with predicted scores from two plus one waves at a time)	−.12 ($n = 61$)	.63* ($n = 56$)	.18 ($n = 82$)	.04 ($n = 75$)	.09 ($n = 83$)	−.33* ($n = 85$)	.08 ($n = 83$)

* Correlation significant at the .001 level

at a time, and one with predicted scores from two plus one WVS waves. Of note, national prevalence of the A allele is not significantly correlated with any of the other independent variables in our study. Therefore, its predictive properties are independent of those of the other predictors.

Data on the harshness of summers and harshness of winters are provided by van de Vliert (2009).

Our historical pathogen prevalence data are from Murray and Schaller (2010).

Our national wealth data (GDP per person) are from the World Bank (2014). We used GDP per person in 2005, which is approximately the middle of the period for which we made estimates of average national wealth. To obtain a measure of speed of economic growth, starting shortly before the period of our initial happiness data and ending shortly before the period of the latest happiness data, we calculated GDP-per-person change from 1998 to 2012 by dividing GDP per person in 2012 by GDP per person in 1998.

The KK rule of law index for 2005 is from the International Bank for Reconstruction and Development/The World Bank (2007).

3 Results

To validate our national happiness index for 2000–2014, we obtained zero-order correlations between its two versions and component 1 (national scores on positive affect) in Kuppens et al. (2006). The two versions of our happiness index (with predicted scores from two WVS waves at a time, and with predicted scores from two plus one waves at a time) correlate with component 1 at .55 ($n = 29$, $p = .002$) and .65 ($n = 39$, $p < .001$). Obviously, our index and component one measure something quite similar, although they are derived from very different cross-cultural studies. The second correlation is not far lower than the correlation between percentage "very happy" in 2010–2014 and percentage "very happy" in 2000–2005 in the WVS.

Despite confirming this validation, we tested the hypothesis that the happiness measures in some of the WVS waves are not significantly associated with the variable of main

Table 5 Final results of the regression analyses with national happiness 2000–2014 (with predictions from two waves) as the dependent variable

R	R^2	SE	*F* change	Sig. *F* change	*N* (countries)
Model summary					
.788	.622	8.56	28.76	<.0001	38

Independent variables	Std beta	*T*	Sig.	Correlations		VIF
				Zero-order	Partial	
Model						
National prevalence of the A allele in FAAH	.630	5.99	<.0001	.69	.71	1.02
Harshness of summers plus harshness of winters	−.390	−3.70	.001	−.48	−.53	1.02

interest in this study, national prevalence of the rs324420 A allele. It is possible that even if our average 2000–2014 happiness index is highly correlated with prevalence of the A allele, this is so because of a high significant correlation in only one or two of the three WVS waves, masking the fact that the happiness measures in one or two other waves yield insignificant or very low correlations with the genetic index. This would be a blow to the theory of genetic determinism of national happiness, since national genetic patterns evolve very slowly. They should produce similar effects across three happiness surveys within a decade or decade and a half.

We found that percentage of very happy people, as measured by each of the three latest WVS waves (2000–2004, 2005–2009, 2010–2014) is highly and significantly correlated with rs324420 A allele prevalence at .63 ($n = 43$), .54 ($n = 41$), and .84 ($n = 26$). All these correlations are significant at the .001 level.

We applied this test to the WVS life satisfaction item (mean national values) as well. We found striking inconsistencies across the three waves. While the 2010–2014 measure correlates with rs324420 A allele prevalence at .47 ($p = .002$, $n = 42$), the 2005–2009 measure yields a weak and insignificant correlation of .30 ($p = .057$, $n = 40$). More disturbingly, the 2010–2014 life satisfaction measure yields a weak and insignificant correlation with GDP per person in 2012: $r = .26$ ($p = .073$, $n = 49$), even though the 2004–2009 life satisfaction measure correlates with GDP per person in 2005 at .53 ($p < .001$, $n = 46$). Barring serious measurement errors, this volatility suggests powerful situational influences on national averages in life satisfaction.

Table 4 provides zero-order correlations between the two versions of the national happiness index 2000–2014 (with predicted scores from two WVS waves at a time, and with predicted scores from two plus one waves at a time) and the independent variables.

Table 4 suggests that the only plausible predictors of the national happiness index 2000–2014 are the prevalence of the A allele in FAA and climate. Our linear regression models confirmed that the other independent variables are not significant predictors of national happiness, yielding results far from statistical significance. Therefore, in Tables 5 and 6 we provide models with the only two significant predictors of our two happiness indices.

Table 6 Final results of the regression analyses with national happiness 2000–2014 (with predictions from two + one waves) as the dependent variable

R	R^2	SE	F change	Sig. F change	N (countries)
Model summary					
.677	.46	10.12	22.39	<.0001	56

Independent variables	Std beta	T	Sig.	Correlations		VIF
				Zero-order	Partial	
Model						
National prevalence of the A allele in FAAH	.569	5.61	<.0001	.60	.61	1.01
Harshness of summers plus harshness of winters	−.318	−3.13	.003	−.37	−.32	1.01

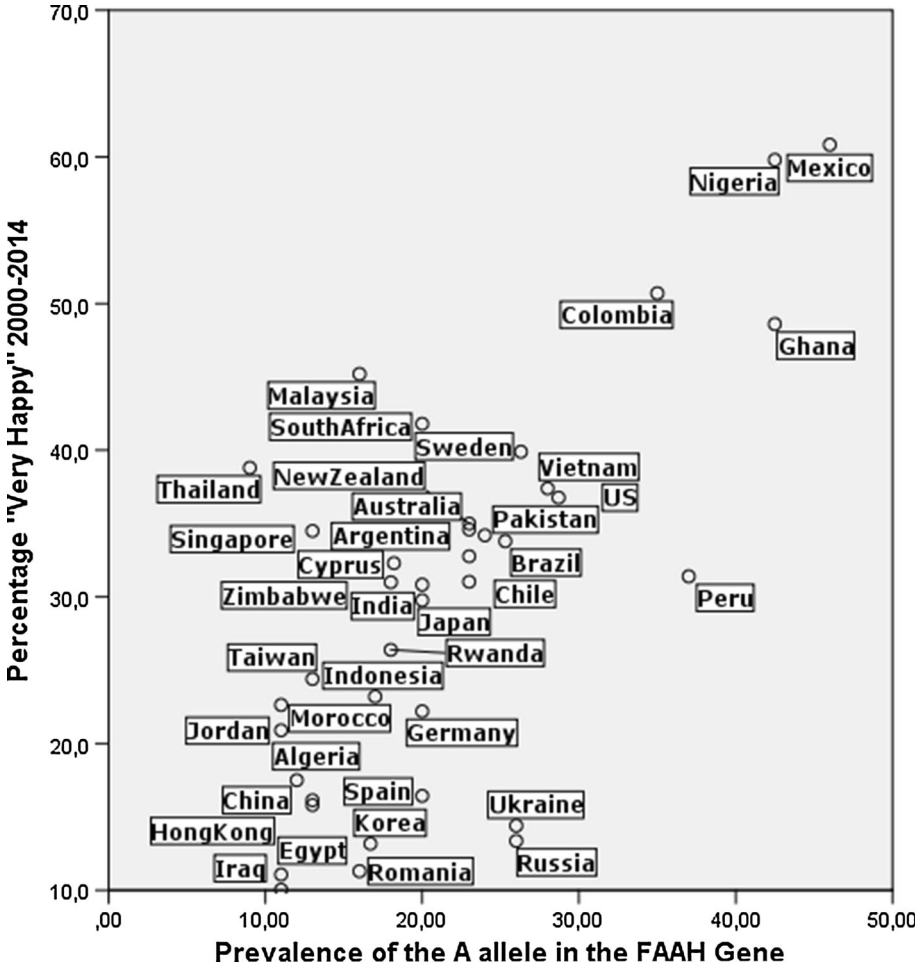

Fig. 1 Visual illustration of the relationship between prevalence of the A allele in the FAAH gene and national happiness

Since national prevalence of the A allele in the FAAH gene is the best predictor of national differences in happiness, we illustrate this relationship in Fig. 1.

We also ran a series of regression analyses with Kuppens et al.'s (2006) component 1 as the dependent variable. Regardless of the number or combination of independent variables in the regression models, the outcome was the same as in the case of the happiness indices from the WVS, except that this time the climatic variable did not reach statistical significance. Across 30–33 countries, only national prevalence of the A allele in FAAH was a significant predictor, explaining about 33 % of variance in the dependent variable.

We were advised to test the predictive properties of the same independent variables with respect to single happiness measures (percentage "very happy") from the three latest waves of the WVS, rather than the composite happiness indices that we obtained by averaging data from the three latest waves. When the dependent variable was happiness in 2010–2014, the regression model included 36 nations. Prevalence of the A allele in FAAH

Table 7 Percentage "very happy" by main ethnicity in Malaysia and Singapore

Malaysia 2010–2014	Malay	59.7
	Indian	57.0
	Chinese	47.6
Singapore 2010–2014	Malay	49.9
	Indian	47.5
	Chinese	35.6
Malaysia 2005–2009	Malay	43.3
	Indian	33.9
	Chinese	32.8
Singapore 2000–2004	Indian	44.0
	Malay	42.1
	Chinese	25.2

was the best significant predictor ($b = .551$, $t = 5.18$, r partial $= .684$, $p < .0001$), followed by climatic harshness ($b = -.556$, $t = -4.514$, r partial $= -.636$, $p < .0001$). The other independent variables were not significant predictors. We obtained very similar results for happiness in the 2005–2009 wave (35 countries), except that this time we also had a third-ranking significant predictor, rule of law. When the dependent variable was happiness in 2000–2004 (25 countries) only A allele in FAAH was a significant predictor.

We also tried replacing van de Vliert's (2009) composite "harshness of summers plus harshness of winters" variables with his "harshness of winters" and "harshness of summers", entered as separate independent variables together with A allele prevalence. "Harshness of summers" was not a significant predictor of happiness. "Harshness of winters" reached statistical significance ($p = .025$) but its predictive property was somewhat lower ($b = -.314$) than that of "harshness of winters plus harshness of summers". When other independent variables were entered in the model, these results did not change appreciably.

We tested the hypothesis that our results are affected by our incorrect estimates of the A allele in FAAH in some countries, whose A allele data in our study are actually based on neighboring countries or other countries with a similar ethnic composition. After dropping all such estimates, the number of countries in our model for the 2000–2014 composite happiness index (with predictions from 2 + 1 waves) fell to 26. The results were essentially the same as before: The best predictor was always A allele prevalence, followed by the climatic variable. We also built separate models for happiness in 2010–2014, 2005–2009, and 2000–2004. The number of countries fell to 24, 17, and 14, respectively. Despite the small number of countries and the somewhat different composition of the three country samples in those three models, our previous results remained unchanged: A allele prevalence was always the best predictor, followed by "harshness of winters plus harshness of summers". There were no other significant predictors.

We also compared the percentages of "very happy" respondents in two ethnically diverse countries—Malaysia and Singapore—whose different ethnicities have co-existed for a long time. This situation controls for a potential recent-arrival effect that can enhance or suppress the average happiness of a group of immigrants. The results are presented in Table 7.

The results demonstrate clear differences between countries and ethnicities. The observed ethnic differences and rankings are stable, with a single exception: Indians score slightly higher (instead of slightly lower) than Malays in Singapore 2000–2004.

Unfortunately, we do not have genetic data for the Indians who live in Malaysia and Singapore and can only speculate that the observed stability in these rankings of ethnic groups has a genetic component.[1]

Although our study focuses on happiness as a form of positive affect, and not on life satisfaction, we were advised to test the predictive properties of our independent variables with respect to average life satisfaction as measured by the World Values Survey. When all independent variables were entered simultaneously, in a model with 35 countries, the 2010–2014 measure of life satisfaction was predicted only by prevalence of the A allele in FAAH ($b = .441$, $t = 2.63$, partial $r = .445$, $p = .014$). However, the 2005–2009 measure of life satisfaction was predicted only by "harshness of winters plus harshness of summers" ($b = -.540$, $t = -2.371$, partial $r = -.415$, $p = .025$). Thus, the predictors of life satisfaction depend on the period of study and country sample.

4 Discussion

This is the first study showing that national differences in happiness, defined as the hedonic component of SWB or positive affect, have a genetic component. Somewhat surprisingly, these differences are not associated with the polymorphisms of the serotonin gene, but only with those in the FAAH gene. Nations with the highest prevalence of the A allele in rs324420 of the FAAH gene have the highest percentages of very happy people, and this association is quite strong. Vice versa, nations with the lowest prevalence of that allele have the lowest percentages of very happy people. The former group of nations consists mostly of northern Latin American countries, with relatively high percentages of Amerindians or people of mixed Euro-American descent, as well as West African countries. The data in Kidd (2014) are unequivocal: Amerindians have the highest prevalence of the rs324420 A allele in the FAAH gene. The main tribes of Nigeria—Hausa and Yoruba—are next in the ranking.

The lowest prevalence of the A allele is found in some Arab and East Asian nations, most of which have low happiness scores. Differences in happiness between Northern and Central or South Europeans also seem attributable to the genetic differences between them, since Northern Europeans have a much higher prevalence of the A allele.

However, Northeast Europeans (Russians and Estonians) are not among the nations that have a very low prevalence of the A allele. Their very low happiness scores are obviously not due to a deficiency of anandamide alone. They may be a lasting effect of the economic and political difficulties that the East European nations continue to experience in their transition to capitalism and democracy, in accordance with the findings of Veenhoven (2001) and Inglehart et al. (2008). Alternatively, it is possible that other, hitherto unknown, genes explain the low happiness scores of East Europeans.

[1] We were advised that genetically heterogeneous countries, such as Malaysia and Singapore, can be expected to have greater internal dispersion of happiness scores than genetically homogeneous countries, such as Japan. However, heterogeneity versus homogeneity should not be measured simply as presence or absence of diverse ethnic groups, but also in terms of the structure of the population. It is possible that a country like Singapore, where over 80 % are ethnic Chinese, the remaining less than 20 % Indians and Malays create a relatively low dispersion. Vice versa, in a country with large socioeconomic inequality, such as the US, South Africa, and Brazil, there may be a relatively large dispersion even among the same ethnic group. We cannot expect that the FAAH genes will explain all the variance in positive affect at the individual level. Factors such as socioeconomic status may play an equally important role.

We must also acknowledge that a few nations in the WVS evidence large fluctuations in their percentages of very happy people that obviously have nothing to with their genetic heritage. Some of these fluctuations are fully explicable by the changing socioeconomic conditions in those countries. The percentage of very happy people in Rwanda has risen dramatically recently, apparently because the effect of the 1994 genocide is beginning to wear off. Inversely, the percentage of very happy people in Egypt has fallen recently, most likely as a result of the political turmoil and economic difficulties that Egyptians have experienced in recent years. Although our analysis cannot capture these changes, it seems plausible to accept that they can affect not only a nation's cognitive appraisal of its well-being, but also the positive affect that most citizens experience.

Our analysis suggests that differences in economic growth do not explain differences in happiness. This finding must not be misinterpreted. It does not necessarily prove that happiness and economic growth have nothing in common. First, strictly speaking, we have not studied the effect of economic growth on happiness but the effect of differences in economic growth on differences in happiness. These are two different types of study. Second, the effect of national economic growth in the past decade may not have been evenly distributed, especially across the members of rich nations. Instead, the benefits of that growth may have accrued mostly to those who were already rich. This phenomenon may have suppressed the potential effect of growing national wealth on national happiness.

It was not the aim of this study to examine the predictors of national differences in life satisfaction in detail. Yet, our brief analysis of that variable suggests somewhat greater volatility than in the case of happiness. The results depend on the period of study and the country sample. We can tentatively conclude that, since happiness and life satisfaction are not completely independent, the genetic factor is probably involved in both, although its effect on the latter is not as strong as on the former. It appears that situational factors at the national level can more strongly suppress the effect of genetic factor on differences in life satisfaction.

The results of our study may sound somewhat disturbing for nations that are not endowed with beneficial genes and climatic factors. However, we must reiterate that we have studied only national differences, not absolute measures. In other words, we have not shown that a nation's genetic and climatic heritage doom a particular country to a specific happiness score. Despite that heritage, a nation's happiness score can rise or fall as a function of various situational factors. What our study shows is that despite these situational factors, differences in happiness between nations remain relatively stable.

We have also found that national differences in genetic heritage do not provide a good explanation of national differences in life satisfaction. The genetic effect of genes and climate on the way that most people in a particular nation evaluate their lives may be considerably smaller than the genetic effect on hedonic balance.

There are limitations to our study. First, we worked with a number of estimated scores. However, our findings hold even if we drop estimates based on neighboring countries or countries with a similar ethnic composition. Also, although it is possible that some of our estimates are far from perfect, it is highly unlikely that all of them are skewed in the same wrong direction. Our findings would be seriously challenged if future genetic studies discovered that, for instance, in terms of the prevalence of the A allele of the FAAH gene, the Hong Kong Chinese are genetically closer to Amerindians than to the Han of the People's Republic, or that the Amerindians of Columbia are more similar to Arabs than to Mexican and Brazilian Amerindians. Yet, this is highly unlikely. In fact, Minkov et al. (2015) worked with a variety of different estimates concerning the prevalence of the S allele in 5-HTTLPR and showed that the final results are little affected.

We must also acknowledge that it seems somewhat surprising that the prevalence of a single genetic allele can have such an enormous effect on national differences in happiness. But we must point out that Dincheva et al. (2015) reported unusually high effects of the rs324420 polymorphism at the individual level, whereas aggregation to a higher level of analysis, such as nations, in principle results in higher effects than those observed at the individual level. Although many genes that have so far been tested for relationships with personality and cognition tend to yield minuscule effects at the individual level, the FAAH gene may be an exception.

Further, the geographic distribution of the rs324420 polymorphism is fairly clear. It replicates some well-known genetic contrasts, especially those between Asian and Amerindian populations. It is quite possible that the FAAH gene is not the only one involved in the national happiness equation. Other, at present unknown, genes may produce similar effects and their polymorphisms may have a similar geographic distribution. In that sense, the FAAH gene may be a marker for a large package of genes that affect national differences in happiness.

The geographic distribution of the rs324420 polymorphism warrants a study in its own right. What environmental factors have resulted in population differences in the occurrence of the A allele in FAAH? The main problem in attempting an answer to that question is that we do not know the time when the rs324420 polymorphism appeared. When geneticists reach consensus on that point, researchers should examine the climatic and other environmental conditions across the globe at that time and attempt to correlate those data with prevalence of the A allele at the ethnic, rather than national level.

Yet, we cannot fail to notice the high occurrence of the A allele in equatorial and tropical environments in the Americas and Africa and the lower occurrence of that allele around the Mediterranean Sea than in Northern Europe. It seems that some equatorial and tropical environments select for a higher occurrence of the A allele as a counterbalance to environmental stressors. A similar process may have occurred across Northern Europe. Although current estimates of pathogen prevalence and climatic differences do not correlate significantly with A allele occurrence at the national level, a different picture could emerge if environmental factors in the past, at the time of the appearance of the rs324420 polymorphism, were compared with ethnic data from the same period.

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