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Eurasia Advantage, not Genetic Diversity: Against Ashraf and Galor's "Genetic Diversity" Hypothesis

Shiping Tang [*]

Abstract: *»Nicht genetische Vielfalt, sondern Vorteil Eurasiens. Gegen Ashraf und Galors „Genetic Diversity"-Hypothese«.* Ashraf and Galor (2012) advanced the bold thesis that genetic diversity within different human populations has been a foundational determinant of long-run economic development. We show that their results are not robust after controlling for a key missing variable – the Eurasia dummy. After controlling for the Eurasia dummy, all indicators of genetic diversity lose statistical significance in regressions with indicators of economic development as dependent variables. Ashraf and Galor's statistical results merely "reflect" – literally – Eurasia's unique advantage in supporting economic development that was mostly based on settled agriculture until about AD1500.

Keywords: Eurasia Advantage, Jared Diamond, genetic diversity, economic development.

1. Introduction: Is Economic Development within our Genetic Diversity?[1]

Ashraf and Galor (2012) advanced the bold thesis that genetic diversity within different human populations has been a more foundational determinant of economic development in the long run than geography, from the dawn of our species to today (Ashraf and Galor 2012, 1, 8-9).[2] If the theory and the evidences

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[2] For the sake of completeness and convenience, we rely on their working paper version, denoted as Ashraf and Galor (2012). The published version of their paper is cited as Ashraf and Galor (2013a). Although Ashraf and Galor (2012, 2013a) used the term "the Out of Africa Thesis" in their titles, their core explanatory variable is really "genetic diversity." I thus use "Genetic Diversity Hypothesis" in my critique of them to avoid the impression that I am against the original "Out of Africa Hypothesis" in the field of human evolution. In fact, I

presented by Ashraf and Galor (2012) hold, Ashraf and Galor (2012) surely represent a major advancement in our understanding of the deep causes of economic development in the long run, and Ashraf and Galor certainly did not understate the potential significance of their finding a bit (ibid., 8-9).

Nowadays, anything that claims to link any aspect of human genetics with human social behavior and/or macro social outcomes is bound to garner attention from the scientific community and the general public. Unsurprisingly, even before Ashraf and Galor's (2012) working paper was to be published as the lead article in *American Economic Review* (Ashraf and Galor 2013a), their provocative findings were picked by both a *Science* newspiece (Chin 2012) and a *Nature* commentary (Calloway 2012). Eventually, a mini-firestorm in the internet space resulted, partly ignited by a strongly worded critique from a group of anthropologists (Guedes et al. 2013; for other scientists' reactions, see Calloway 2012).[3]

So far, however, much of the criticism directed against Ashraf and Galor (2012), especially the critique by Guedes, et al. (2013), has been more political and ethical than scientific (Gelman 2013, 46). More prominently, without re-analyzing Ashraf and Galor's (2012) data and results, Guedes et al. (2013, 77) asserted:

> Ashraf and Galor's (2013) paper is based on a fundamental scientific misunderstanding, bad data, poor methodology, and an uncritical theoretical framework […] *this study has the potential to cause serious harm* (emphasis added).[4]

As such, Ashraf and Galor can easily dismiss their critics as largely political and unscientific and then claim "the scientific and even moral high ground" for themselves, as Gelman (2013, 46) drily noted. Indeed, in their reply to Guedes et al. (2013), Ashraf and Galor (2013b, 1) retorted exactly as such:

> these criticisms [i.e., Guedes et al. 2013] are scientifically baseless and ultimately reflective of a misunderstanding of our empirical methodology, potential unfamiliarity with the statistical techniques that we employ, and a misin-

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strongly support the original "Out of Africa Hypothesis" in the field of human evolution, just as Diamond (1997) does.

[3] See the exchanges on a website maintained by Jason Collins <www.jasoncollins.org> and another website maintained by Matter Zimmerman <www.biasedtransmission.blogspot. com> (Accessed September 16, 2013).

[4] See also a blog by another anthropologist, Rebecca Dean, "Look what the economists do with human diversity data" <www.rebeccamdean.blogspot> (Accessed September 16, 2013). The only place where Guedes et al. (2013) came close to do so has been their pointing out that a few historical data points of population density, mostly from the Americas, might have been mis-measured by Ashraf and Galor (2012), following McEvedy and Jones (1978). Yet, Guedes et al. (2013) did not test whether better measurements of these data points will significantly change Ashraf and Galor's (2012) results at all. As shown in section four below, leaving the Americas out (i.e., the sample with only the Old World) does not significantly change the statistical results.

terpretation of our findings (emphasis added; the same retort is essentially repeated on page 4 of their response).

In this contribution, we provide a systematic econometric rebuttal against Ashraf and Galor, based on Ashraf and Galor's (2012) own data. We do not question the possible link between migratory distance and predicted genetic diversity: We give Ashraf and Galor the benefit of doubt that migratory distance is a good proxy for predicted genetic diversity. Neither do we challenge the link between genetic diversity and innovation or the link between genetic diversity and cooperation/conflict, although we do wish to note that the case presented by Ashraf and Galor (2012) on these two possible causal links has been weak at best. The evidences presented by Ashraf and Galor (2012) are not from studies of human groups or even primates; rather, they are from flies, spiders, and honeybees.[5] Finally, we do not even challenge the data collected by Ashraf and Galor: We assume that all of their data are valid and accurate.[6] Instead, we attempt to unambiguously show that even with their own data, Ashraf and Galor's (2012) results cannot hold after controlling for a key variable that is missing in their inquiry. *Put it differently, Ashraf and Galor's (2012) results are an artifact of leaving out a key variable that should have been controlled.* As such, Ashraf and Galor's conclusions are on shaky ground, if not entirely unwarranted.

A key caveat is in order here. In some of the regressions reported below, the number of countries (as observations) is different from what Ashraf and Galor (2012) originally reported. This is not due to our using a different set of countries. Indeed, the original Ashraf and Galor (2012) dataset contains 208 countries, and the reason why regressions reported in Ashraf and Galor (2012) have fewer countries than the regressions reported below is because many of the independent variables they deploy have many missing values. In contrast, because we restrict our independent variables to several exogenous geographical variables and these variables have fewer missing data points, the number of countries in most of our regressions is larger than the number of countries reported by Ashraf and Galor (2012). The fact that our regressions have more countries than regressions reported by Ashraf and Galor (2012), however, does not invalidate our challenges against Ashraf and Galor (2012). This is so because when the Eurasia dummy is not controlled, we obtain almost identical results as Ashraf and Galor (2012) did: Various indicators of genetic diversity

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[5] Jason Collins has provided well-informed comments on these and other related issues in his blogspace: <www.jasoncollins.org>. See also the comments by Matt Zimmerman on Ashraf and Galor (2012) at <www.biasedtransmission.blogspot.com> (Accessed September 16, 2013).

[6] We, of course, readily admit that some of the data employed by Ashraf and Galor (2012), especially population density (PD) and rate of urbanization in pre-modern times, are subjected to serious problems of missing data and measurement error. For earlier discussions of the problems with data collected by McEvedy and Jones (1978) and Chandler (1987), see LeGates and Stout (1996, 21). See also Bandyopadhyay and Green (2012).

are statistically significant predictors of economic development and there seems to be a robust humped-shaped relation between genetic diversity and economic development. Yet, once the Eurasia dummy is controlled, various indicators of genetic diversity lose their statistical significance in almost all the regressions and the supposedly robust humped-shaped relation vanishes.

The rest of our paper is structured as follows. Section two provides a brief recount of Ashraf and Galor's (2012) key arguments, data, methods, and results. Section three presents our data and procedures for challenging Ashraf and Galor's statistical results. Section four provides our results, showing that after controlling a key variable – the Eurasia dummy that is straight from Jared Diamond's "Eurasia Advantage Thesis" (Diamond 1997) – the supposedly significant and robust effect on economic development of genetic diversity, however measured, disappears almost completely. We further show that our results are robust across different samples, using different indicators of economic development as dependent variables, and using different indicators of genetic diversity as independent variables. Building upon existing empirical testing of the Diamond Thesis (e.g. Olsson and Hibbs 2005; Putterman 2008; Petersen and Skaaning 2010), section five establishes the validity of Diamond's "Eurasia Advantage Thesis" more systematically. Section six provides a highly plausible explanation for Ashraf and Galor's (2012) misleading results and conclusions. A brief conclusion follows.

2.   Ashraf and Galor (2012): Key Arguments, Data, Methods, and Results

Ashraf and Galor (2012, 1-2) nicely summarized the central thesis and key prediction of their paper, quoted in full below, with their key empirical predictions emphasized in italics.

> The hypothesis rests upon two fundamental building blocks. First, migratory distance from the cradle of humankind in East Africa had an adverse effect on the degree of genetic diversity within ancient indigenous settlements across the globe. Following the prevailing hypothesis, commonly known as the serial founder effect, it is postulated that, in the course of human expansion over planet Earth, as subgroups of the populations of parental colonies left to establish new settlements further away, they carried with them only a subset of the overall genetic diversity of their parental colonies.

> Second, there exists an optimal level of diversity for economic development, reflecting the interplay between the opposing effects of diversity on the development process. The adverse effect pertains to the detrimental impact of diversity on the efficiency of the aggregate production process. Heterogeneity raises the likelihood of disarray and mistrust, reducing cooperation and disrupting the socioeconomic order. Higher diversity is therefore associated with lower productivity, which inhibits the capacity of the economy to operate effi-

ciently relative to its production possibility frontier. The beneficial effect of diversity, on the other hand, concerns the positive role of heterogeneity in the expansion of society's production possibility frontier. A wider spectrum of traits is more likely to contain those that are complementary to the advancement and successful implementation of superior technological paradigms.

Higher diversity therefore enhances society's capability to integrate advanced and more efficient production methods, expanding the economy's production possibility frontier and conferring the benefits of improved productivity. Higher diversity in a society's population can therefore have conflicting effects on the level of its productivity. Aggregate productivity is enhanced on the one hand by an increased capacity for technological advancement while diminished on the other by reduced cooperation and efficiency. However, if the beneficial effects of population diversity dominate at lower levels of diversity and the detrimental effects prevail at higher ones (i.e., if there are diminishing marginal returns to both diversity and homogeneity), *the theory would predict a hump-shaped effect of genetic diversity on productivity throughout the development process.*

To substantiate their thesis, Ashraf and Galor (2012) first established that migratory distance from (Addis Ababa) Ethiopia does have an inverse relationship with *observed* genetic diversity, using a small dataset from 53 ethnic groups across globe constructed by Ramachandran et al. (2005, as Figure 1 in Ashraf and Galor 2012, 2). Ashraf and Galor then went on to establish that even within this limited sample, *observed* genetic diversity has a robust and statistically significant hump-shaped relationship with population density of their respective countries at AD1500 (Ashraf and Galor 2012, 18-24, esp., Tables 1 and 2, and Figure 3).

After this reassuring start, Ashraf and Galor then went on to build a dataset on migratory distance of human populations from (Addis Ababa) Ethiopia to their present capital city and used this measure to predict "genetic diversity" of different populations in today's world (for the logic and methods for constructing "predicted genetic diversity," see Ashraf and Galor 2012, 14-5).[7] Eventually, they constructed two measures of "predicted genetic diversity": non-ancestry adjusted; ancestry-adjusted (by incorporating information on post-1500AD population flows, see Ashraf and Galor 2012, Appendix B, xiv-xvi

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[7]   Ashraf and Galor's (2012, 14-5) did not provide much rationale or information on how they extrapolate from migratory distance to predicted genetic diversity. With a bit of statistical guesswork, however, we can reveal how Ashraf and Galor (2012) extrapolated from migratory distance to "predicted genetic diversity (pdiv)." For details, see Appendix A in: Shiping Tang, 2016, Online Appendix to: Eurasia Advantage, not Genetic Diversity: Against Ashraf and Galor's "Genetic Diversity" Hypothesis, *HSR Trans* 28. doi: 10.12759/hsr.trans. 28.v01.2016. This volume of *HSR Trans* contains Appendices A-J.

and Appendix F, xl for details).[8] These two indicators of predicted genetic diversity are then employed as key explanatory variables.

Ashraf and Galor's (2012) key indicators of economic development include population density (hereafter, PD) at AD1, AD1000, AD1500 (McEvedy and Jones 1978), rate of urbanization at AD1500 (Chandler 1987; Modelski 2003; see also Bairoch 1988), and GDP per capita in 2000 (hereafter, GDPpc2000). These indicators of economic development are then deployed as key dependent variables. With numerous tables and figures, Ashraf and Galor (2012) believed that they had shown that genetic diversity has a highly significant and hump-shaped relationship with economic development.[9]

3. Missing the Eurasia Continent: Logic, Data, and Procedure

In *Guns, Germs, and Steel*, Jared Diamond (1997) provided a sweeping account for the fate of human societies in the world up to AD1500 and how the pre-1500AD world has continued to shape the post-1500AD world.

Briefly, Diamond's (1997) "Eurasia Advantage Thesis" argues that the Eurasian continent as *a whole* holds some decisive advantages over all other continents when it comes to providing the physical environment for economic development, at least until 1500AD. The Eurasia advantage has two core components. First, the Eurasia continent as a whole had been the home of most domesticated mammalian herbivores and omnivores (e.g., cow, goat, pig, and sheep) and staple crops (e.g., barley, millet, rice, and wheat). The Eurasia continent thus had "good material to work with" for developing settled agriculture (Olsson and Hibbs 2005, 913-8; see also Diamond 1997; Smith 1998; Petersen and Skaaning 2010, 205-7). Second, diffusion of domesticated animals and staple crops, together with other key agricultural technologies, has been easier on the Eurasia continent *as a whole* than other continents (e.g., Africa and the Americas) because

> the spread of food production tended to occur more rapidly along east-west axes [e.g., within Eurasia] than along north-south axes [e.g., from Eurasia to Africa], mainly because locations at the same latitudes required less evolutionary change or adaptation of domesticates than did locations at different latitudes (Diamond 2002, 705; 1997; Petersen and Skaaning 2010, 207-10).[10]

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[8] Not surprisingly, these two measures are highly correlated (Pearson r=0.750, significant at 0.001 level).

[9] Although Ashraf and Galor (2012) mostly used population density at AD1500 and GDPpc2000 as dependent variables in their main text, they have also explored the relationships between genetic diversity and other indicators of economic development as dependent variables in their Appendix A (esp. Table A1, A2, A4, and A5).

[10] We examine the second component of Diamond's Thesis in more detail in section 5 below.

Because the Eurasia continent *as a whole* holds these two key advantages, it has been a more fertile ground for generating the First Economic Revolution or the Neolithic Revolution: *the coming of settled agriculture*. Because settled agriculture provided more stable sources of protein and staple corps, it provided the key foundation for further economic development. This in turn resulted in a higher degree of urbanization and higher population density within a particular geographical area (Olsson and Hibbs 2005). A higher degree of urbanization and population density in turn supported larger sociopolitical organizations of people, eventually culminating in archaic states (Bockstette, Chanda and Putterman 2002; Putterman 2008; Borcan, Olsson, and Putterman 2014).[11] Together, these earlier advantages in food production, weaponry technology, organizational skills in war-fighting, and immunity against certain infectious diseases would later allow people from the Eurasia continent to colonize other continents, including Africa, the Americas, and Oceania (Diamond 1997; Tang 2013, ch. 2).

In short, the "Eurasia Advantage thesis" argues that the Eurasian continent as *a whole* held some decisive advantages over all other continents when it comes to providing the physical environment for economic development, at least until 1500AD. After 1500AD, the Europeans began to colonize the world and brought what they had (good or bad) to the rest of the world. Along the way, the Europeans had thus vastly complicated the picture.

Because Ashraf and Galor (2012, 1, 8-9, Appendix A4, xi-xiii) explicitly set out to challenge the Diamond Thesis, Ashraf and Galor should have included Eurasia *as a whole* as a control dummy variable.[12] Yet, they have failed to do. When this is the case, Ashraf and Galor's (2012) results might have been the product of a failure to control for a key competing variable. We set out to test this possibility.

We proceed as follows:

1) We first test the Eurasia dummy (1 if a country is classified as a European or an Asian countries in Ashraf and Galor's own data; 0 otherwise) as a possible independent explanatory factor for economic development against the four key indicators of economic development (i.e., PD at AD1, AD1000, AD1500, and GDPpc2000) as dependent variables, in three different samples: the whole world, the whole world excluding Australia, Canada, New

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[11] Here, we are not concerned with whether earlier transition to settled agriculture and hence statehood has a negative impact on subsequent political and economic development such as adoption of democracy and industrialization after 1500AD. For important works on this front, see Hariri (2012); Borcan, Olsson and Putterman (2014); Chanda, Cook and Putterman (2014). For a brief discussion, see the conclusion in Section 7.

[12] We have also tested by inserting the Europe dummy and the Asia dummy separately into the regressions, and we obtain essentially identical results. These results are reported in section 4 below and in Appendix G.

Zealand, and the United States (hereafter, ACNU), and the Old World (i.e., Africa, Asia, plus Europe).[13]

2) We then test Ashraf and Galor's key explanatory variables (genetic diversity or migratory distance, whether ancestry adjusted or not) separately and establish their plausibility as key explanatory factors for long-run economic development. We test indicators of genetic diversity that are not ancestry-adjusted against all four key indicators of economic development, again in three different samples. Consistent with Ashraf and Galor's logic, we only test ancestry adjusted measurements of predicted genetic diversity or migratory distance against PD1500 and GDPpc2000.[14] Not surprisingly, in these regressions, we obtain results that are almost identical to the results reported in Ashraf and Galor (2012).

3) We then pit the Eurasia dummy against different indicators of genetic diversity in horse-race models, again within three different samples.

4) We then add more control variables. To avoid any possibility of endogeneity, we deploy only three fixed geographical variables: landlocked (1 if a country or territory is landlocked country, 0 if not), absolute latitude of a country (taking natural log), and island (1 if a country or territory is an island, 0 if not). We exclude other bio-climate variables such as area of arable land, rain fall, and soil PH etc., because they are subjected to modification by human activities and natural causes (Pimentel et al. 1995; Montgomery 2007).[15] We also exclude other proxy indicators of economic development such as the timing of the Neolithic Revolution and ancient statehood as control variables not only because archaeological dating the exact time of these events has never been easy and conclusive, but also because these indicators are intervening variables between Eurasia (and other exogenous geographical variables) and economic development.

5) We then add distance to (regional) technological frontiers at AD1, AD1000, and AD1500 to the models in order to capture the effect of diffusion as sin-

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[13] The Eurasia dummy is easily generated by adding Ashraf and Galor's Europe dummy and Asia dummy together. Following Ashraf and Galor (2012), we also perform regressions with bootstrap procedures. Regression results with or without bootstrap procedures are almost identical. We thus report only results from regressions without bootstrap procedures here.

[14] For the sake of completeness, we also regress ancestry-adjusted indicators of genetic diversity against PD1 and PD1000. These results are reported in the appendices of *HSR Trans* 28.

[15] For instance, it is well known that the Fertile Crescent had become much less fertile in history partly due to human activities, especially agriculture supported by vast irrigation (Diamond 2011). Likewise, the pattern of rainfall has also changed significantly for northern China. Whereas the South China Sea monsoon could still reach much of northern China around 3000BC, today it can only reach the Yangtze valley (Liu 2004, ch. 2). Consequently, northern China has become much drier and less fertile. Moreover, data on rainfall, arable land etc. are all from contemporary time (i.e., post-1960), and surely we cannot use these data to explain outcomes before AD1500!

gled out by Diamond (1997). Data for these three variables are from Ashraf and Galor (2012).

6) We then test the effect upon economic development of genetic diversity vs. the three fixed geographical variables, within Eurasian countries alone. This is a litmus test whether genetic diversity has any impact upon economic development at all because the effect of Eurasia will be eliminated within this sub-sample of only Eurasian countries.

7) We then perform more robustness tests by inserting Europe and Asia into the models as two separate dummies, but always together. Again, various measures of genetic diversity have no robust relationship with economic development in these tests.

8) We then test Eurasia against genetic diversity in the limited samples of 21 countries with "observed" or "actual" genetic diversity to drive home our points. If "observed" genetic diversity has no robust significant relationship with economic development after controlling for the Eurasia dummy, then the whole enterprise of Ashraf and Galor's (2012, esp. 18-24) has no foundation to start with and hence the whole enterprise collapses.

9) Because Ashraf and Galor (2012, Table D4, xxv) reported that letting different measurements of genetic diversity take natural log does not change their overall results, we also perform such tests by using the natural log of different measurements of genetic diversity as independent variables in various samples. Again, we obtain almost identical results that strongly contradict Ashraf and Galor's claims. We report these results in the appendices of *HSR Trans* 28.

All estimations are based on a basic model below, following Ashraf and Galor (2012, 16-7):

$$\ln(y_i) = \alpha + \beta Geneticdiversity_i + \gamma Geneticdiversity_i^2 + \lambda Z_i + \varepsilon_i$$

Where y_i is a measurement of economic development for country i (e.g., PD at AD1, AD1000, AD1500, or GDPpc2000), *Geneticdiversity* is the predicted genetic diversity of country i, Z_i is a vector for control variables (e.g., the Eurasia dummy, distance to frontier at AD1, landlocked) for country i, and ε_i is an error term assumed to be normally distributed. Estimation procedures are standard OLS regressions as done by Ashraf and Galor (2012).

A caveat is in order. We drop rate of urbanization at 1500 (ur1500 in Ashraf and Galor 2012) as a dependent variable because it has far too many missing data points. We also drop other less direct indicators of economic development (e.g., the number of scientific articles published by a country divided by its population) or possible intervening variable between genetic diversity and economic development (e.g., trust) as dependent variables. After all, if genetic diversity is shown to have no robust and significant relationship with the four key indicators of economic development (i.e., PD at AD1, AD1000, AD1500, and GDPpc2000), the enterprise of Ashraf and Galor's (2012) would have

collapsed completely, and there is little need for us to further test whether genetic diversity has any impact upon trust and numbers of scientific papers published when it comes to assessing the impact on economic development of genetic diversity.

We shall hold the following two straightforward predictions:

1) If Ashraf and Galor (2012) are correct, the hump-shaped relationship between indicators of (predicted) genetic diversity and various indicators of economic development should hold in most of the models with different samples, even after controlling for the Eurasia dummy, the three other exogenous geographical variables, and distance to regional technological frontiers.

2) If, however, the Eurasia Advantage Thesis is correct, then the Eurasia dummy should have a robust and significant *positive* relationship with various indicators of economic development whereas distance to regional technological frontiers should have a robust and significant *negative* relationship with various indicators of economic development, across most of the models with different samples. *Moreover, the Eurasia dummy should replace various indicators of genetic diversity as the most potent explanatory factors for economic development in most horse-race models that pit the Eurasia dummy against various indicators of genetic diversity, in different samples.*

4.   Missing the Big Eurasia Continent: Empirical Results

4.1   Initial Test: Establishing the Plausibility of the Diamond Thesis

Our initial test firmly establishes the Eurasia dummy as a plausible key explanatory factor for economic development, lending strong support for the first key component of "the Diamond Thesis" (see also Olsson and Hibbs 2005; Putterman 2008; Petersen and Skaaning 2010). As shown in Table 1, the Eurasia dummy is highly significant in all the models when tested independently against all four key indicators of economic development as dependent variable in the three different samples at a level of $p<0.001$ (*t* statistics from 4.823 to 8.543). Indeed, the Eurasia dummy alone can explain 11.4%-32% of the variations with the four indicators of economic development.

We then test the unconditional effect on economic development of two measures of genetic diversity. As shown in Table 2A and Table 2B, when tested independently, indicators of genetic diversity, whether ancestry-adjusted or not, are significant in most of the models in all three different samples (see also Table A3-a, and A4-a). Moreover, the signs in front of the first order term and the second order term, *when they are significant*, are consistent with Ashraf and Galor's thesis: the first order term has a positive sign whereas the second order term has a negative sign. Furthermore, consistent with the results reported in Tables 5, 6, 7, D9, and D11 in Ashraf and Galor (2012), predicted genetic

diversity-ancestry adjusted is significant when GDPpc2000 is the dependent variable but insignificant when the dependent variable is indicator of economic development before AD1500. These initial results are broadly consistent with Ashraf and Galor's thesis that genetic diversity has a hump-shaped relationship with economic development (e.g., Ashraf and Galor 2012, Figures 3, 4, and 5).

One should note, however, that Ashraf and Galor's results do not always hold in these initial tests. For instance, in Model 10 and Model 11 of Table 2A, neither the first order term nor the second order term of predicted genetic diversity is significant when PD1000 and PD1500 are the dependent variables and the sample is the Old World. Moreover, in Model 6 of Table 2B, both the first order term and the second order tem of predicted genetic diversity-ancestry adjusted are significant when PD1000 is the dependent variable and the sample is the whole world excluding ACNU. Likewise, in Model 9 of Table 2B, both the first order term and the second order tem of predicted genetic diversity-ancestry adjusted are significant when PD1 is the dependent variable and the sample is the Old World. Yet according to Ashraf and Galor (2012), indicators of predicted genetic diversity-ancestry adjusted should be largely irrelevant for understanding outcomes before AD1500. These initial results, however, provide at least some support for Ashraf and Galor's (2012) claim that genetic diversity is a significant determining factor of economic development, if not one hundred percent.

4.2   Horse-Race Models: The Eurasia Advantage Demolishes "Genetic Diversity"

Once we pit the Eurasia dummy against different measures of genetic diversity, however, things fall apart almost completely for Ashraf and Galor's thesis that genetic diversity has a robust and significant hump-shaped relationship with economic development. Strikingly, once we put both predicted genetic diversity and the Eurasia dummy together into regressions, whereas the Eurasia dummy remains highly significant throughout, predicted genetic diversity – whether its first order term or its second order term – becomes thoroughly insignificant (Table 3A). Moreover, these results are robust when we add more exogenous control variables, including the three fixed geographical variables and distance to regional technological frontiers at different historical time (Table 3B). Also, inserting the two terms of predicted genetic diversity into the models does not improve the overall fit of the models with only the Eurasia dummy (compare Models 1-4 of Table 3A with Models 9-12 of Table 3A). In contrast, inserting the three fixed geographical variables and the distance to regional technological frontiers at different historical time into the models does improve the overall fit of the models significantly (compare Table 3A and Table 3B).

We obtain almost identical results when employing predicted genetic diversity-ancestry adjusted as the indicator of genetic diversity (Table 4A and Table

4B). As a matter of fact, with the presence of the Eurasia dummy, "predicted genetic diversity-ancestry adjusted" either becomes insignificant or the signs in front of the first order term and the second order term of "predicted genetic diversity-ancestry adjusted" are exactly the opposite to what Ashraf and Galor (2012) predicted (see esp. Models 7-8 in Table 4A and Models 3-4 and Models 7-8 in Table 4B).

Indeed, we obtain almost identical results when employing all possible measures of genetic diversity, from migratory distance-ancestry adjusted, to predicted genetic diversity and predicted genetic diversity-ancestry adjusted, regardless of whether we take natural log of these indicators or not (see the Appendixes).[16] Certainly, these results do not support Ashraf and Galor's claim that genetic diversity has a robust and significant hump-shaped relationship with economic development.

Results with different samples (i.e., the world excluding ACNU, the Old World) are almost identical (these results are reported in Appendix C and Appendix D). Using alternative dependent variables (e.g., PD without taking the natural log) or alternative indicators of genetic diversity (e.g., migratory distance taken natural log) does not change the results in any significant sense (these results are reported in Appendix F). Across the board, (predicted) genetic diversity, whether ancestry-adjusted or not, has no robust relationship with indicators of economic development, after controlling Eurasia as a dummy variable alone. Simply put, Ashraf and Galor's (2012) supposedly robust hump-shaped relationship between genetic diversity and (indicators of) economic development is nowhere to be found.

Because GDPpc2000 is subject to less measurement error than population density in historical time, let us dwell on the supposedly "highly significant and stable hump-shaped effect of genetic diversity on income per capita in the year 2000 CE" claimed by Ashraf and Galor (2012, 7) a bit more. In order for the hump-shaped relationship between genetic diversity and GPDpc2000 to hold, the first order term of genetic diversity (however measured, and whether ancestry adjusted or not) must have a positive sign and the second order term of genetic diversity (whether ancestry adjusted or not) a negative sign, and both terms must be statistically significant.

Unfortunately, this is not the kind of result we have obtained with Ashraf and Galor's (2012) own data. In most of the models with GDPpc2000 being the dependent variable, after controlling for the Eurasia dummy and other fixed

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[16] This should not come as a surprise. Because migratory distance and predicted genetic diversity are 100% correlated (Appendix A), the results obtained from these two independent variables are almost 100% identical (see appendix A, also compare Tables 3A, 3B with Tables B3-a, B3-b, B3-c in Appendix B). Likewise, because migratory distance-ancestry adjusted and predicted genetic diversity-ancestry adjusted too are 100% correlated (again, see Appendix A), the results obtained from these two independent variables are almost 100% identical (see appendix B, compare Table B2 and Table B4 in Appendix B).

geographical factors, both terms of genetic diversity, whether ancestry-adjusted or not, become insignificant (Tables 3A, 3B, 4A and 4B; see also results reported in the appendixes). For example, in Table 4A, although both terms of genetic diversity-ancestry adjusted are significant after controlling for the Eurasia dummy (Model 8, see also Model 4), this result is not robust once we add exogenous geographical variables and distance to technological frontiers to the models (Model 4 and Model 8 of Table 4B).

Thus, contrary to Ashraf and Galor's claim that "the highly significant and stable hump-shaped effect of genetic diversity on income per capita in the year 2000 CE is not an artifact of postcolonial migrations towards prosperous countries and the concomitant increase in ethnic diversity in these economies" (Ashraf and Galor 2012, 7; see also Ashraf and Galor 2012, 22-30, Tables 3-8, and Figures 4 and 5), there is no robust relationship between various measurements of genetic diversity and income per capita in the year 2000 CE.

Overall, our results are anything but comforting to Ashraf and Galor (2012): The various indicators of genetic diversity perform utterly dismally in most of the models with different samples. One certainly would not want to claim these results point to a robust and highly significant hump-shaped relationship between genetic diversity and economic development.

4.3   Testing Europe and Asia as Separate Dummies

Even if we test Europe and Asia as two separate dummies (rather than as the Eurasia dummy together) *but with both dummies being inserted into the models*, we obtain essentially identical results. In most of the models, both Europe and Asia have a robust and statistically significant positive relationship with various indicators of economic development, whereas indicators of genetic diversity do not (Table 5A, 5B, and 6; additional results are reported in Appendix H).[17] Indeed, some of the results point to the fact that Asia had fallen significantly behind Europe after 1500AD (i.e., there was "the Great Divergence" between Europe and Asia after 1500AD). When regressed against GDPpc2000, Asia, although remaining positive, becomes insignificant after controlling for other geographical factors (Model 4, Table 5B; Models 2 and 4, Table 6). Again, these results provide more reassuring confirmation of the Eurasia Advantage Thesis, but debilitating challenges against Ashraf and Galor's "Genetic Diversity" thesis.

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[17] The fact that distance to frontier at AD1500 becomes insignificant when regressed against GDPpc2000 is also reassuring. Likewise, the fact that the island dummy has a robust positive relationship with economic development after AD1500 in all the models is also reassuring. For a more detailed discussion, see also section 5 below.

4.4 What about the Relationship between "Observed" Genetic Diversity and Economic Development?

After thoroughly undermining Ashraf and Galor's evidences that predicted genetic diversity has a robust and significant relationship (whether hump-shaped or not) with economic development with larger samples, we now move to the limited sample of 21 countries with "observed" genetic diversity from the 53 human groups. If we can show that even "observed genetic diversity" has no robust and significant relationship with economic development, we believe that we should have driven home our counterpoints against Ashraf and Galor (2012).

And this is exactly we have obtained (Table 7). We first show that when testing independently against PD1, PD1000, PD1500, and GDPpc2000, the Eurasia dummy remains highly significant and has correct signs throughout (Models 1-4). We then show that when testing independently against PD1, PD1000, and PD1500 (but not GDPpc2000), both terms of observed genetic diversity are highly significant and have correct signs that are consistent with Ashraf and Galor's thesis. Things seem conspicuous for Ashraf and Galor. Also note that Model 7 in Table 7 reproduces the exact same results of Model 1 in Ashraf and Galor's Table 1 (Ashraf and Galor 2012, 19), so Ashraf and Galor cannot dismiss these results as errors or inconsistencies produced by different procedures on our part.

When the dependent variable is GDPpc2000, both the first order term and the second order term of observed genetic diversity become insignificant even when testing independently (Model 8, Table 5). Worse, after controlling for the Eurasia dummy, both terms of observed genetic diversity become insignificant even when the dependent variables are PD1, PD1000, and PD1500 (Models 5-8, Table 7). In contrast, the Eurasia dummy remains highly significant when the dependent variables are PD1, PD1000, PD1500, and GDPpc2000 (although only at 0.05 or 0.1 level, Models 9-12), despite the presence of both terms of genetic diversity.

With these results, there is really nothing left for Ashraf and Galor's (2012) thesis that actual or predicted genetic diversity has a robust and significant relationship with economic development with larger samples, whether hump-shaped or not.

4.5 The Litmus Test: Testing with the Eurasia Sample

There may be one last straw for Ashraf and Galor: They can claim that even though genetic diversity has not been a major determinant of economic development across the whole world, genetic diversity may still be a major determinant of economic development within Eurasia itself. If such a possibility holds, Ashraf and Galor can still claim that genetic diversity is a more foundational factor in shaping economic development than Eurasia (and other geographical factors). We thus also test genetic diversity within Eurasia alone to eliminate

the possibility that genetic diversity can significantly explain the variations in economic development within Eurasia even if it cannot significantly explain the variations in economic development beyond Eurasia.

Our results are anything but comfort for Ashraf and Galor. As shown in Table 8A, genetic diversity, whether ancestry-adjusted or not, has no statistically significant effect upon economic development even when tested independently: The models have almost no explanatory power for all four indicators of economic development. Indeed, when taking the natural log, the first order term of predicted genetic diversity, whether ancestry adjusted or not, is consistently eliminated automatically during regression due to strong collinearality, indicating that the first order term and the second order term of genetic diversity have no different impact over indicators of economic development within Eurasia (Table 8B). With these results, we see no further need to test the supposedly robust and significant relationship between other indicators of genetic diversity and indicators of economic development. For the sake of completeness, however, we perform these tests anyway (results from these tests are reported in Appendix E). Needless to say, these results lend no support for Ashraf and Galor's thesis whatsoever.

5. Diamond's Eurasia Advantage Thesis Vindicated

As noted above, Jared Diamond's Eurasia Advantage Thesis has two key components (Diamond 1997, 2002; see also Olsson and Hibbs 2005; Putterman 2008; Petersen and Skaaning 2010). First, the Eurasia continent as a whole held unique advantages for economic development over other continents, at least up until AD1500. Second, the diffusion of technologies, especially agricultural technologies, had been a key determinant of economic development before AD1500 and this component holds within and without Eurasia. In sections three and four above, we have mostly tested the first component of Diamond's Thesis against Ashraf and Galor's thesis that genetic diversity is a more foundational factor in shaping economic development and have shown that the Eurasia Advantage Thesis firmly holds its ground when pitted against various measures of genetic diversity. This section establishes the validity of the Eurasia Advantage Thesis more systematically.

We improve upon existing tests of Diamond's Thesis (e.g., Olsson and Hibbs 2005; Putterman 2008; Petersen and Skaaning 2010) on three fronts. First, we use a larger set of countries, drawing from Ashraf and Galor's (2012) dataset and Petersen and Skaaning's dataset (2010).[18]

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[18] Olsson and Hibbs' (2005) dataset covers only 84 countries with six regional clusters. Petersen and Skaaning (2010) expanded the dataset to cover 171 countries with nine regional

Second, we employ a more reliable set of geographical factors. As noted in section three above, to avoid any possibility of endogeneity, we employ only three exogenous geographical variables: the landlocked dummy, absolute latitude of a country (taken natural log), and the island dummy. We exclude other possible bio-climate variables such as area of arable land, rain fall, and soil PH etc because they have been modified in history by human activities and natural causes. Indeed, we show that there is no need to construct more elaborate indicators of geographical and biological indicators to substantiate the Eurasia Advantage Thesis (cf. Olsson and Hibbs 2005; Putterman 2008; Petersen and Skaaning 2010). We also exclude other proxy indicators of economic development such as the timing of the Neolithic Revolution and ancient statehood (e.g., Putterman 2008; Petersen and Skaaning 2010) because archaeological dating the exact time of these events has never been easy and conclusive. Third, we show that the second component of the Diamond Thesis holds in samples within or without Eurasia.

We proceed in three steps. First, we establish that both geographical components (geocom) and biological components (biocom) assembled first by Olsson and Hibbs (2005), and then expanded to cover more countries by Petersen and Skaaning (2010), are largely determined by Eurasia and the other three fixed geographical factors. Second, we show that for samples that include Eurasia, both the Eurasia dummy and diffusion components are significant determinants of economic development. Third, we show that within Eurasia, diffusion is a significant determinant of economic development. These results are presented in Tables 9-11 below, and full results are reported in Appendix F.

As shown in Tables 9 and 10, Eurasia alone accounts for 51.7-64.8% of the variations within the geographical component and the biological component across the whole world (Models 1-5, Table 9).[19] After adding the other three fixed geographical factors to Eurasia, these factors together account for 68.8-85.1% of the variations within the two components (Models 11-15, Table 9). Within Eurasia, the three fixed geographical factors account for 57-69% of the variations in the geographical component and 26.9-35.3% of variation in the biological component (Models 1 to 5, Table 10).

As shown clearly in Table 11, and Tables F1, F2, and F3 in Appendix F, with samples being the whole world, the whole world excluding ACNU, and the Old World only, the Eurasia dummy and diffusion (measured as the distance to regional technological frontiers at various historical time) are the two most important factors in shaping economic development, at least before

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clusters. Petersen and Skaaning's data are highly correlated with Olsson and Hibbs' original data, Pearson r=0.808 to 0.998, significant at 0.001 level.

[19] The Eurasia dummy is strongly correlated with geographical component and biological component by Olsson and Hibbs (2005) and Petersen and Skaaning (2010): Pearson r=0.721 to 0.806, significant at 0.001 level.

AD1500, and they remain highly significant today. Both factors are significant through almost all the models at 0.01 level (with the exception of Model 16, Table 11 and Model 16, Table E3 in Appendix E, although in both models, they just miss the cutoff level of p=0.1). Moreover, both factors have the correct signs: Eurasia is positively associated with economic development, whereas distance to regional technological frontiers is negatively associated with economic development. Together, these two factors account for up to 43% of the variations in population density at AD1, 21.4-24.4% of the variations in population density at AD1000, 26.7% of the variations in population density at AD1500, and 12.8-33.1% of the differences in GDPpc2000. These results hold firm when adding the three geographical factors (i.e., landlocked, latitude, and island): Indeed, adding the three factors often further improves the overall fit of the models significantly (Model 13-16, Table 11; see also Tables F1-F4).

More reassuringly, compared to the overall fit of the models in which Eurasia and distance to frontiers are regressed against various dependent variables independently, putting these two variables together always improve the over fit of the models significantly. Having Eurasia and diffusion together improves the overall fit of the models 12.3-35.4% over models with only Eurasia, and 61.8-161% over models with only diffusion. These results indicate that Eurasia and diffusion operate mostly independently. Adding the three other geographical factors further improves the overall fit of the models.

Finally, the fact that the island dummy has a robust positive relationship with economic development after 1500AD is also reassuring. As shown in Table 9 and Table 10, consistent with the Eurasia Advantage Thesis, the island dummy is negatively associated with both geocomponent and biocomponent at the 0.001 level. Yet, island becomes positively associated with economic development when GDPpc2000 is the dependent variable (Model 16, Table 11; see also Model 16, Table F2; Model 16, Table F3, in Appendix F), presumably because ocean-crossing became a key factor that promotes long distance trade after 1500AD. This result is consistent with what Spolaore and Wacziarg (2013) have found: whereas island dummy is positively associated with GDP per capita at 2005, it is negatively associated with years since agricultural transition at AD1500 (compare Model 1 within their Table 2, 331 with other models in which island dummy is an independent variables in their Table 1, 5, 7 on pages 328, 339, and 345 respectively). These results therefore strongly support the Eurasia Advantage Thesis.

6. What Might Have Misled Ashraf and Galor (2012)?

After establishing the validity of the Diamond Thesis, we now offer a plausible explanation for Ashraf and Galor's misleading results. We suspect that the hump-shaped relationship between genetic diversity, whether actual or predicted, mere-

ly reflects the geographical shape of the world map. If we leave out Australia, Canada, New Zealand, Papua New Guinea, and the United States for a moment, the hump part of the curves presented in Ashraf and Galors's (2012) Figure 4 (27) and Figure 5 (37) contains mostly Eurasian (i.e., European and Asian) countries. In contrast, the extreme left part of the curves contains almost exclusively African countries, whereas the extreme right part of the curves contains almost exclusively (South and North) American countries. Ashraf and Galor could have mistakenly reasoned that these hump-shaped curves point to a robust and significant hump-shaped relationship between genetic diversity (underpinned by migratory distance) and economic development without realizing that these curves merely reflect – literally – the geographical shape of the world. Indeed, if we compare the hump-shaped plots from Ashraf and Galor and the shape of the world map (Figure 1), the similarities between these two figures are simply too striking to be ignored.

There is also a more technical aspect to Ashraf and Galor's error. In most regressions with global samples, we often control the effect upon a particular outcome of a country's geographical location by controlling for "continent fixed effects." And this is precisely what Ashraf and Galor (2012, 2013a) have done. Yet, such a practice is inappropriate when trying to differentiate the effect of the Eurasia continent upon economic development from the effect of "genetic diversity (really, migratory distance)" upon economic development.

The logic is simple. Because it is the Eurasia continent as *a whole* that holds decisive advantages over other continents when it comes to providing the physical environment for economic development at least until 1500AD, the Eurasia continent must be treated as *a whole, at least until 1500AD; only after 1500 AD, did the European part and the Asian part of the Eurasia continent begin to diverge significantly in terms of economic development.* This in turn means that in the regressions done here and in Ashraf and Galor (2012, 2013a), one must control the Eurasian continent as *a whole* in regressions rather than controlling either Europe or Asia alone as it is conventionally done (i.e., by controlling for "continent fixed effects").

Indeed, if one were to control for either Europe or Asia alone as "continent fixed effects" as Ashraf and Galor (2012, 2013a) have done in some of their regression models (esp., the models in their Tables 7 and 8), one would sometimes – but not always – obtain the hump-shaped relationship between indicators of "genetic diversity"/migratory distance and indicators of economic development (i.e., indicators of "genetic diversity"/migratory distance are significant and show correct signs). But such results merely reflect the fact that only part of the Eurasia Advantage has been controlled (results shown in Appendix J). And when the whole Eurasia Advantage has been controlled, the supposedly robust hump-shaped relationship between indicators of "genetic diversity" and indicators of economic development disappears completely, as the results in the many tables presented above have unambiguously shown.

Figure 1: The Geographical Shape of the World
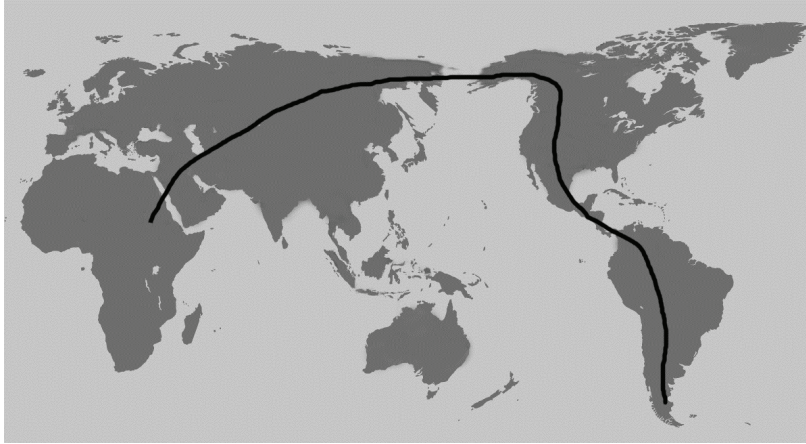
7.   Concluding Remarks

We hope we have firmly undermined Ashraf and Galor's thesis that genetic diversity of different human populations has been a more foundational factor in shaping long term economic development than the geographical factors and diffusion effect identified by Diamond (1997). Although our exercises hold important implications for a wide range of issues and point to more productive venues for future research, we shall focus on what might have misled Ashraf and Galor in their endeavor of advancing a more foundational understanding about the deep causes of long-run economic development. We believe that Ashraf and Galor might have been misled by three conceptual and logical errors.

First and foremost, Ashraf and Galor (2012, 2013a) failed to correctly grasp the two key components of Diamond's Eurasia Advantage Thesis, and thus also failed to control the Eurasia dummy when testing their genetic diversity hypotheses. The Eurasia Advantage Thesis explicitly argues that the Eurasia continent *as a whole* had held a unique advantage over other continents in providing the physical foundation for economic development in the pre-1500AD world. As shown above, once the Eurasia dummy is controlled, genetic diversity's supposedly robust and significant impact on economic development disappears almost completely. In contrast, Eurasia's powerful impact on economic development remains robust and significant throughout the models. In a nutshell, Ashraf and Galor's (2012) results merely *reflect – literally –* Eurasia's unique advantage in underpinning economic development that was mostly based on agriculture after the coming of settled agriculture until about AD1500 (see Figure 1 above).

Second, Ashraf and Galor have failed to grasp some fundamental difficulties in linking genetics with human social behavior and macro social outcomes. While linking specific gene(s) with specific biological phenotypes faces less uncertainty, linking specific gene(s) with specific human social behavior(s) is far less certain. As Benjamin et al. (2012a) show, most of the statistical association between genetic markers and human social behaviors reported so far have been false positives (see also Beauchamp et al. 2011; Benjamin et al. 2012b; Charney and English 2012, 2013). Things become decisively more complicated when we move from specific genes to genetic diversity within human populations. We simply know very little about how genetic diversity impacts human social behavior, and even less about how genetic diversity impacts macro social outcomes such as economic development.

Fundamentally, although our social behavior is constrained by the foundation shaped by our biological evolution, it is only partly so. Most of our social behavior has been the product of the interaction between biological factors and social factors, and there is no straightforward way to link our biological evolution with our social behavior, not to mention macro social outcomes such as long-run economic development. The possible linkage between genetic diversity (and genetics) and long-run economic development may be "a bridge too far."

Finally, back to genetic diversity more concretely, it is far more likely that within a wide range of genetic diversity, our biological evolution has provided us with enough intellectual and physical capacities to go around when it comes to economic development. As such, all human populations, as long as they have a large enough population supported by favorable environment, have all the biological (including genetic) potentials to develop economically: genetic difference only matters on (very) small scales (Zimmerman 2013).[20] For human populations that are large enough (e.g., at the scale of a country), their genetic makeup has not been a key determining factor of economic development. The deeper cause of the enormous variations in economic development across the globe thus does not within our genetics or genetic diversity but elsewhere. Far more plausibly, the chance for development had been foremost constrained by geography before 1500AD (Diamond 1997) and then by bad institutions and other social factors after 1500AD, although geography still matters a great deal by impacting the historical evolution of different institutions (e.g., democracy vs. autocracy) and other social factors such as cultural traits (Jones 1981; North 1990; Easterly and Levine 2003; Rodrik et al. 2004; Acemoglu and Robinson 2012; Hariri 2012; Olsson and Paik 2014; Tang 2011; Tang, Hu and Li n.d.).[21]

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[20] Zimmerman (2013) also noted that genetic diversity cannot explain (much) cognitive diversity.

[21] I am thus suggesting that that geography and institutions are not incompatible because there is a temporal dimension to the question of whether geography matters more or institutions matter more. Recall that the state is one of the most complex organizations our

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species has ever invented, and state is underpinned by a vast number of institutions. Indeed, state can be understood as a meta-institution.

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Appendix

Tab: 1: The Eurasia Advantage: Initial Tests

Independent Variables	Sample: The Whole World				Sample: the Whole World, excluding ACNU				Sample: The Old World			
	1	2	3	4	5	6	7	8	9	10	11	12
	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc200 0 (ln)	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)
Eurasia	1.652*** (8.543)	1.281*** (7.007)	1.372*** (7.380)	0.814*** (5.003)	1.537*** (8.386)	1.165*** (6.857)	1.251*** (7.151)	0.897*** (5.622)	1.512*** (6.056)	1.122*** (5.073)	1.063*** (4.823)	1.463*** (7.906)
Constant	-0.931*** (-7.062)	-0.130 (-1.055)	0.279** (2.263)	8.151*** (74.342)	-0.816*** (-6.468)	-0.014 (-0.119)	0.401*** (3.412)	8.068*** (74.231)	-0.790*** (-3.949)	0.030 (0.172)	0.589*** (3.408)	7.501*** (51.640)
Obs.	155	177	184	187	152	174	180	183	112	129	132	138
Adjusted R²	0.319	0.215	0.226	0.114	0.315	0.210	0.219	0.144	0.243	0.162	0.145	0.310
F value	72.982***	49.097***	54.462***	25.031***	70.331***	47.018***	51.134***	31.602***	36.672***	25.735***	23.262***	62.505***

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Note: we report t statistics throughout the Tables. Reporting robust regression results points to the same conclusion.

Tab: 2A: Predicted Genetic Diversity, Not Ancestry Adjusted: Initial Tests

Independent Variables	Sample: The Whole World				Sample: the Whole World, excluding ACNU				Sample: The Old World			
	1	2	3	4	5	6	7	8	9	10	11	12
	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)
Predicted genetic diversity	238.667*** (3.296)	215.589*** (3.330)	241.054*** (3.882)	155.140*** (3.002)	285.672*** (4.207)	263.637*** (4.442)	292.673*** (5.102)	142.192*** (2.731)	1065.917*** (2.951)	454.520 (-1.384)	201.84 (0.637)	890.216*** (3.289)
Predicted genetic Diversity-squared	-169.514*** (-3.177)	-153.857*** (-3.225)	-171.555*** (-3.743)	-118.265*** (-3.103)	-205.298*** (-3.177)	-190.393*** (-4.351)	-210.806*** (-4.976)	-108.298*** (-2.818)	-740.369*** (-2.979)	-320.791 (1.428)	-148.373 (-0.681)	-626.328*** (-3.358)
Constant	-83.635*** (-3.430)	-74.583*** (-3.420)	-83.225*** (-3.987)	-41.727*** (-2.400)	-98.813*** (-4.100)	-90.116*** (-4.511)	-99.912*** (-5.185)	-37.606** (-2.148)	-383.049*** (-2.920)	-159.927 (-1.465)	-66.902 (-0.582)	-307.330** (-3.131)
Obs.	155	177	184	187	152	174	180	183	112	129	132	138
Adjusted R^2	0.159	0.122	0.178	0.096	0.173	0.144	0.202	0.076	0.074	0.028	0.027	0.140
F value	15.437***	13.270***	20.750***	10.926***	16.833***	15.554***	23.723***	8.467***	5.451***	2.849*	2.791*	12.171***

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab: 2B: Predicted Genetic Diversity, Ancestry Adjusted: Initial Tests

Independent Variables	Sample: The Whole World				Sample: the Whole World, excluding ACNU				Sample: The Old World			
	1	2	3	4	5	6	7	8	9	10	11	12
	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)	PD1 (ln)	PD1000 (ln)	PD1500 (ln)	GDPpc2000 (ln)
Predicted genetic Diversity-ancestry adjusted	280.888 (1.515)	195.149 (1.152)	140.221 (0.810)	615.387*** (4.788)	386.973 (2.246)	306.342** (1.975)	265.631 (1.658)	572.293*** (4.433)	1072.382*** (2.737)	396.303 (1.157)	161.308 (0.475)	1258.647*** (4.204)
Predicted genetic Diversity-ancestry adjusted-squared	-194.765 (-1.490)	-135.075 (-1.131)	-95.888 (-0.787)	-439.272*** (-4.853)	-269.792 (-2.221)	-213.731* (-1.956)	-184.766 (-1.637)	-408.710*** (-4.494)	-744.826*** (-2.762)	-281.334* (-1.193)	-121.657 (-0.520)	-878.365*** (-4.261)
Constant	-101.206 (-1.542)	-69.887 (-1.164)	-50.252 (-0.819)	-206.441*** (-4.531)	-138.532** (-2.270)	-109.005** (-1.984)	-94.288 (-1.660)	-191.319*** (-4.181)	-385.391*** (-2.709)	-138.448 (-1.114)	-51.527 (-0.418)	-441.937*** (-4.067)
Obs.	137	154	160	162	134	151	156	158	110	126	129	131
Adjusted R^2	0.009	0.000	-0.003	0.147	0.029	0.016	0.009	0.132	0.063	0.024	0.031	0.163
F value	1.593	0.969	0.749	14.874***	2.966*	2.225	1.700	12.934***	4.656**	2.532*	3.044*	12.934***

t statistics in parenthesis; $*<0.1$; $**<0.05$; $***<0.01$.

Tab. 3A: The Eurasia Advantage vs. Predicted Genetic Diversity, horse-race (Full Sample: the Whole World)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)	9 PD1 (ln)	10 PD1000 (ln)	11 PD1500 (ln)	12 GDPpc2000 (ln)
Eurasia	1.652*** (8.543)	1.281*** (7.007)	1.372*** (7.380)	0.814*** (5.003)					1.495*** (6.105)	1.087*** (4.733)	1.009*** (4.438)	1.209*** (6.694)
Predicted genetic diversity					238.667*** (3.296)	215.589*** (3.330)	241.054*** (3.882)	155.140*** (3.002)	10.607 (0.141)	45.104 (0.636)	95.474 (1.412)	-14.497 (-0.274)
Predicted genetic Diversity-squared					-169.514*** (-3.177)	-153.857*** (-3.225)	-171.555*** (-3.743)	-118.265*** (-3.103)	-5.565 (-0.101)	-31.016 (-0.597)	-66.704 (-1.344)	3.889 (0.100)
Constant	-0.931*** (-7.062)	-0.130 (-1.055)	0.279** (2.263)	8.151*** (74.342)	-83.635*** (-3.430)	-74.583*** (-3.420)	-83.225*** (-3.987)	-41.727*** (-2.400)	-5.543 (-0.218)	-16.323 (-0.681)	-33.489 (-1.468)	16.231 (0.909)
Observations	155	177	184	187	155	177	184	187	155	177	184	187
Adjusted R²	0.319	0.215	0.226	0.114	0.159	0.122	0.178	0.096	0.321	0.219	0.255	0.270
F value	72.982***	49.097***	54.462***	25.031***	15.437***	13.270***	20.750***	10.926***	25.255***	17.404***	21.826***	23.957***

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab. 3B: Eurasia Advantage vs. Predicted Genetic Diversity, Robustness Tests (Full Sample: the Whole World)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Eurasia	1.406*** (4.954)	1.339*** (5.055)	1.326*** (5.023)	0.894*** (4.688)	1.073*** (4.038)	1.142*** (4.328)	1.174*** (4.620)	0.856** (4.459)
Predicted genetic diversity	-6.753 (-0.089)	7.800 (0.108)	48.901 (0.698)	-77.386 (-1.508)	78.223 (1.104)	63.162 (0.875)	67.549 (1.010)	-73.250* (-1.429)
Predicted genetic Diversity-squared	8.536 (0.153)	-2.728 (-0.051)	-31.491 (-0.610)	52.805 (1.397)	-53.881 (-1.034)	-43.541 (-0.820)	-45.241 (-0.918)	49.772 (1.318)
Landlocked	-0.705*** (-2.830)	-0.477** (-2.054)	-0.239 (-1.016)	-0.596*** (-3.425)	-0.486** (-2.107)	-0.302 (-1.307)	-0.076 (-0.332)	-0.553*** (-3.135)
Absolute latitude (ln)	0.138 (1.148)	-0.178 (-1.521)	-0.205* (-1.767)	0.383*** (4.686)	-0.012 (-0.106)	-0.264** (-2.273)	-0.314*** (-2.776)	0.354*** (4.224)
Island	0.071 (0.245)	0.196 (0.770)	0.412* (1.664)	0.595*** (3.286)	0.354 (1.320)	0.374 (1.476)	0.579** (2.420)	0.639*** (3.491)
Distance to Frontier AD1 (ln)					-0.442*** (-5.557)			
Distance to Frontier AD1000 (ln)						-0.293*** (-3.355)		
Distance to Frontier AD1500 (ln)							-0.278*** (-4.351)	-0.073 (-1.448)
Constant	-0.589 (-0.023)	-3.707 (-0.152)	-17.858 (-0.759)	35.117** (2.035)	-25.515 (-1.075)	-19.865 (-0.823)	-21.739 (-0.969)	34.341** (1.995)
Observations	155	177	184	187	155	177	184	187
Adjusted R²	0.348	0.242	0.275	0.407	0.457	0.285	0.341	0.410
F value	14.678***	10.369***	12.550***	22.258***	19.534***	11.032***	14.552***	19.494***

t statistics in parenthesis; * <0.1; ** <0.05; *** <0.01.

Tab. 4A: The Eurasia Advantage vs. Predicted Genetic Diversity – Ancestry Adjusted, Horse-Race (Full Sample: The Whole World)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Eurasia					1.808*** (7.626)	1.556*** (6.968)	1.656 *** (7.520)	0.721 *** (3.976)
Predicted genetic diversity-ancestry adjusted	280.888 (1.515)	195.149 (1.152)	140.221 (0.810)	615.387*** (4.788)	-230.130 (-1.361)	-282.343* (-1.733)	-340.532** (-2.104)	407.362*** (3.049)
Predicted genetic diversity –ancestry adjusted squared	-194.765 (-1.490)	-135.075 (-1.131)	-95.888 (-0.787)	-439.272*** (-4.853)	164.256 (1.379)	200.953* (1.751)	242.357** (2.126)	-292.885*** (-3.113)
Constant	-101.206 (-1.542)	-69.887 (-1.164)	-50.252 (-0.819)	-206.441*** (-4.531)	79.349 (1.326)	98.600* (1.709)	119.410** (2.082)	-133.042*** (-2.811)
Observations	137	154	160	162	137	154	160	162
Adjusted R²	0.009	0.000	-0.003	0.147	0.305	0.239	0.259	0.220
F value	1.593	0.969	0.749	14.874 ***	20.902***	17.034***	19.523***	16.110***

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.
Note: Although predicted genetic diversity-ancestry adjusted is statistically significant in Model 4 and Model 8 of Table 4A, this result is not robust once we add exogenous geographical variables and distance to technological frontiers to the models (Model 4 and Model 8 of Table 4B).

Tab. 4B: The Eurasia Advantage vs. Predicted Genetic Diversity – Ancestry Adjusted, Robustness Tests (Full Sample: The Whole World)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Eurasia	1.798*** (6.672)	1.790*** (7.183)	1.927*** (7.778)	0.472** (2.513)	1.526*** (5.986)	1.618*** (6.533)	1.767*** (7.456)	0.426** (2.248)
Predicted genetic diversity-ancestry adjusted	-298.765* (-1.721)	-282.693* (-1.679)	-317.414* (-1.875)	158.195 (1.229)	-56.370 (-0.336)	-97.545 (-0.563)	-168.683 (-1.031)	199.320 (1.520)
Predicted genetic diversity-ancestry adjusted squared	213.142* (1.741)	201.979* (1.702)	226.824* (1.901)	-115.658 (-1.274)	42.225 (0.357)	71.436 (0.585)	123.031 (1.067)	-144.347 (-1.562)
Landlocked	-0.729*** (-2.735)	-0.515** (-2.115)	-0.269 (-1.082)	-0.594*** (-3.167)	-0.474* (-1.884)	-0.305 (-1.246)	-0.069 (-0.288)	-0.537*** (-2.819)
Absolute latitude (ln)	0.098 (0.732)	-0.216* (-1.684)	-0.262** (-2.035)	0.409*** (4.163)	-0.099 (-0.757)	-0.347*** (-2.651)	-0.420*** (-3.308)	0.366*** (3.587)
Island	-0.306 (-0.896)	-0.143 (-0.479)	0.116 (0.399)	0.548** (2.540)	-0.035 (-0.110)	0.011 (0.038)	0.239 (0.870)	0.586*** (2.708)
Distance to Frontier AD1 (ln)					-0.428*** (-4.859)			
Distance to Frontier AD1000 (ln)						-0.305*** (-3.199)		
Distance to Frontier AD1500 (ln)							-0.301*** (-4.373)	-0.083 (-1.499)
Constant	103.290* (1.685)	98.980* (1.664)	111.513* (1.864)	-46.736 (-1.027)	21.297 (0.361)	36.133 (0.593)	61.011 (1.057)	-60.708** (-1.312)
Observations	137	154	160	162	137	154	160	162
Adjusted R^2	0.331	0.263	0.273	0.352	0.430	0.306	0.350	0.357
F value	12.206***	10.078***	10.970***	15.593***	15.655***	10.643***	13.250***	13.793***

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab. 5A: The Europe and Asia Advantage versus Predicted Genetic Diversity (Full Sample: The Whole World)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Europe	1.998*** (8.385)	1.594*** (6.960)	1.828*** (7.964)	1.337*** (6.694)	1.810*** (6.533)	1.382*** (5.242)	1.446*** (5.602)	1.787*** (9.021)
Asia	1.325*** (5.669)	0.998*** (4.511)	0.949*** (4.247)	0.370* (1.963)	1.153*** (4.080)	0.785*** (2.962)	0.560** (2.151)	0.655*** (3.343)
Genetic Diversity					36.661 (0.490)	64.953 (0.918)	122.355* (1.844)	24.824 (0.500)
Genetic Diversity-squared					-24.961 (-0.455)	-45.797 (-0.884)	-86.762* (-1.782)	-25.482 (-0.699)
Constant	-0.931*** (-7.713)	-0.130 (-1.067)	0.279** (2.231)	8.151*** (77.593)	-14.203 (-0.562)	-22.917 (-0.959)	-42.399* (1.894)	3.211 (0.192)
Observations	155	177	184	187	155	177	184	187
Adjusted R²	0.339	0.232	0.226	0.187	0.340	0.236	0.293	0.370
F value	40.560***	27.584***	33.886***	22.403***	20.833***	14.558***	19.976***	28.350***

t statistics in parenthesis; * <0.1; ** <0.05; *** <0.01.

Tab. 5B: The Europe and Asia Advantage versus Predicted Genetic Diversity (Full Sample: The Whole World)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Europe	1.720*** (6.025)	1.981*** (7.204)	2.243*** (8.037)	0.961*** (4.356)	1.328*** (4.114)	1.676*** (5.374)	1.795*** (5.855)	1.412*** (6.035)
Asia	1.278*** (5.414)	1.138*** (4.958)	1.241*** (5.442)	0.281 (1.616)	0.946*** (3.374)	0.843*** (3.059)	0.861*** (3.270)	0.601*** (3.065)
Genetic Diversity					92.213 (1.292)	99.390 (1.390)	100.075 (1.525)	-46.832 (-0.940)
Genetic Diversity -squared					-64.563 (-1.230)	-70.995 (-1.349)	-69.966 (-1.446)	29.677 (0.808)
Landlocked	-0.421* (-1.828)	-0.242 (-1.088)	0.029 (0.129)	-0.630*** (-3.558)	-0.464** (-2.013)	-0.247 (-1.090)	-0.043 (-0.195)	-0.518*** (-3.046)
Absolute Latitude (ln)	-0.115 (-0.981)	-0.419*** (-3.560)	-0.491*** (-4.257)	0.330*** (3.758)	-0.064 (-0.536)	-0.392*** (-3.239)	-0.432*** (-3.749)	0.254*** (3.000)
Island	0.097 (0.414)	0.199 (0.902)	0.332 (1.566)	0.796*** (4.812)	0.309 (1.148)	0.297 (1.195)	0.482** (2.059)	0.572*** (3.320)
Distance to Frontier AD1 (ln)	-0.403*** (-5.078)				-0.429*** (-5.372)			
Distance to Frontier AD1000 (ln)		-0.283*** (-3.387)				-0.307*** (-3.603)		
Distance to Frontier AD1500 (ln)			-0.214*** (-3.340)	-0.048 (-0.931)			-0.239*** (-3.789)	-0.038 (-0.776)
Constant	2.536*** (3.507)	3.111*** (4.102)	3.193*** (5.162)	7.577*** (15.361)	-30.004 (-1.257)	-31.2295 (-1.308)	-32.297 (-1.468)	25.751 (1.540)
Observations	155	177	184	187	155	177	184	187
Adjusted R^2	0.445	0.310	0.350	0.389	0.461	0.318	0.379	0.453
F value	21.573***	14.168***	34.328***	20.722***	17.436***	11.277***	14.959***	20.274***

t statistics in parenthesis; * <0.1; ** <0.05; *** <0.01.

Tab. 6: The Europe and Asia Advantage versus Genetic Diversity – Ancestry Adjusted (Full Sample: The Whole World)

Independent Variables	1	2	3	4
	PD1500 (ln)	GDPpc2000 (ln)	PD1500 (ln)	GDPpc2000 (ln)
Europe	2.143*** (8.242)	1.344*** (6.654)	2.472*** (8.298)	1.040*** (4.381)
Asia	1.217*** (4.831)	0.169 (0.858)	1.432*** (5.834)	0.139 (0.715)
Genetic Diversity- ancestry adjusted	-340.287** (-2.167)	410.387*** (3.324)	-139.785 (-0.888)	226.952* (1.810)
Genetic Diversity – ancestry adjusted-squared	240.722** (2.177)	-296.933*** (-3.416)	100.812 (0.908)	-165.461* (-1.872)
Landlocked			-0.041 (-0.179)	-0.502*** (-2.755)
Absolute Latitude (ln)			-0.551*** (-4.332)	0.251** (2.479)
Island			0.198 (0.748)	0.565*** (2.734)
Distance to Frontier AD1500 (ln)			-0.253*** (-3.759)	-0.042 (-0.780)
Constant	120.097** (2.159)	-133.098*** (-3.043)	51.722 (0.931)	-69.654 (-1.575)
Observations	160	162	160	162
Adjusted R^2	0.303	0.334	0.400	0.414
F value	18.263***	21.156***	14.232***	15.236***

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab. 7: The Eurasia Advantage vs. "Actual/Observed" Genetic Diversity, Horse-Race

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)	9 PD1 (ln)	10 PD1000 (ln)	11 PD1500 (ln)	12 GDPpc2000 (ln)
Eurasia	2.354*** 3.952	2.238*** 4.044	2.568*** 4.821	1.141** 2.156					1.684** (2.331)	1.572** (2.367)	1.966*** (3.077)	1.263* (1.918)
Actual genetic diversity					394.448*** (3.107)	390.935*** (3.327)	413.504*** (3.382)	123.146 (1.105)	204.820 (1.470)	208.844 (1.606)	185.844 (1.486)	-23.164 (-0.180)
Actual genetic diversity – squared					-289.056*** (-3.054)	-286.582*** (-3.275)	-302.647*** (-3.323)	-96.008 (-1.156)	-149.034 (-1.440)	-151.846 (-1.571)	-134.193 (-1.444)	12.251 (0.128)
Constant	-1.118** -2.798	-0.396 -1.094	0.068 0.196	7.953*** 22.956	-133.492*** (-3.161)	-131.619*** (-3.365)	-138.889*** (-3.411)	-30.261 (-0.815)	-70.643 (-1.526)	-71.365 (-1.652)	-63.556 (-1.530)	18.153 (0.424)
Obs.	20	21	21	21	20	21	21	21	20	21	21	21
Adjusted R²	0.435	0.434	0.527	0.154	0.317	0.338	0.352	0.026	0.458	0.473	0.559	0.152
F value	15.620***	16.353***	23.242***	4.649**	5.404**	6.107***	6.438***	1.265	6.353***	6.980***	9.467***	2.195*

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.
Sample: The Limited Sample of 21 Countries, with "Actual/Observed" Genetic Diversity

Tab. 8A: Genetic Diversity, Ancestry Adjusted or not, Independently Tested (Eurasia only)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Predicted Genetic Diversity	-207.674 (-0.308)	152.201 (0.247)	208.735 (0.320)	73.733 (0.143)				
Predicted Genetic Diversity-squared	160.241 (0.341)	-101.451 (-0.236)	-145.988 (-0.321)	-47.263 (-0.132)				
Predicted Genetic Diversity -ancestry adjusted					-366.259 (-0.496)	170.747 (0.256)	351.100 (0.503)	546.347 (0.943)
Predicted Genetic Diversity -ancestry adjusted -squared					270.360 (0.526)	-115.711 (-0.249)	-247.092 (-0.508)	-372.660 (-0.922)
Constant	66.47 (0.9277)	-55.848 (-0.253)	-72.890 (-0.312)	-19.639 (-0.107)	124.003 (0.468)	-61.767 (-0.259)	-122.890 (-0.491)	-191.190 (0.360)
Observations	72	80	81	85	72	79	80	81
Adjusted R^2	0.066	-0.015	-0.024	-0.013	0.058	-0.021	-0.020	0.021
F value	3.494**	0.403	0.055	0.452	3.186**	0.210	0.211	1.863

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab. 8B: Genetic Diversity, Ancestry Adjusted or not, Independently Tested (Eurasia only)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Predicted Genetic Diversity (ln)	X	X	X	X				
Predicted Genetic Diversity-squared (ln)	35.444*** (2.639)	10.587 (0.870)	-1.090 (-0.084)	9.532 (0.946)				
Predicted Genetic Diversity -ancestry adjusted (ln)					X	X	X	X
Predicted Genetic Diversity -ancestry adjusted (ln)-squared					34.752** (2.484)	7.512 (0.601)	-5.415 (-0.411)	18.522* (1.694)
Constant	-9.869** (2.458)	-2.014 (-0.553)	1.977 (0.511)	6.123** (2.037)	-9.666** (-2.310)	-1.072 (-0.287)	3.299 (0.835)	3.390 (1.036)
Observations	72	79	80	81	72	79	80	81
Adjusted R^2	0.078	-0.003	-0.013	-0.001	0.068	-0.008	-0.011	0.023
F value	6.967***	0.758	0.007	0.896	6.171**	0.361	0.169	2.868*

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Note: "X" means that the first order term of predicted genetic diversity (ln), whether ancestry adjusted or not, is consistently eliminated automatically during regression due to strong collinearity, indicating that the first order term and the second order term have no different impact over indicators of economic development.

Tab. 9: Both Geocomponents and Biocompoments are Largely Determined by Eurasia (Full Sample: The Whole World)

Independent Variables	1 Geocom1 (O&H)	2 Geocom2 (P&S)	3 Geocom3 (P&S)	4 Biocom1 (O&H)	5 Biocom2 (P&S)	6 Geocom1 (O&H)	7 Geocom2 (P&S)	8 Geocom3 (P&S)	9 Biocom1 (O&H)	10 Biocom2 (P&S)
Eurasia	1.670*** (13.962)	1.630*** (18.517)	1.438*** (13.516)	1.532*** (13.293)	1.609*** (17.666)					
Landlocked						-0.268 (-1.585)	-0.083 (-0.637)	-0.142 (-1.111)	-0.249 (-1.338)	-0.235 (-1.583)
Absolute latitude (ln)						0.713*** (10.151)	0.660*** (12.243)	0.727*** (13.802)	0.582*** (7.647)	0.611*** (9.943)
Island						-0.647*** (-3.714)	-0.677*** (-4.984)	-0.390*** (-2.937)	-0.210 (-1.113)	-0.414*** -2.681
Constant	-0.684*** (-8.735)	-0.791*** (-12.815)	-0.701*** (-9.397)	-0.701*** (-9.196)	-0.790*** (-12.338)	-1.802*** (-8.105)	-1.761*** (-10.098)	-2.009*** (-11.778)	-1.600*** (-6.615)	-1.648*** (-8.253)
Observations	112	171	171	112	170	112	171	171	112	170
Adjusted R^2	0.636	0.668	0.517	0.613	0.648	0.514	0.530	0.552	0.346	0.398
F value	94.924***	342.880***	182.673***	176.693***	312.078***	40.168***	64.812***	70.739***	20.576***	38.238***

Note: O&H is Olsson and Hibbs (2005) whereas P&S is Petersen and Skaaning (2010)
t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab. 9 (continued): Both Geocomponents and Biocomponents are Largely Determined by Eurasia (Full Sample: The Whole World)

Independent Variables	11 Geocom1 (O&H)	12 Geocom2 (P&S)	13 Geocom3 (P&S)	14 Biocom1 (O&H)	15 Biocom2 (P&S)
Eurasia	1.390*** (15.632)	1.268*** (16.968)	0.929*** (9.572)	1.314*** (10.935)	1.333*** (14.140)
Landlocked	-0.176* (-1.875)	-0.095 (-1.199)	-0.151 (-1.464)	-0.164 (-1.276)	-0.246** (-2.454)
Absolute latitude (ln)	0.367*** (8.186)	0.319*** (8.321)	0.478*** (9.600)	0.252*** (4.155)	0.255*** (5.251)
Island	-0.853*** (-8.753)	-0.690*** (-8.370)	-0.399*** (-3.735)	-0.399*** (-3.037)	-0.425*** (-4.081)
Constant	-1.387*** (-10.997)	-1.384*** (-12.797)	-1.732*** (-12.344)	-1.206*** (-7.059)	-1.257*** (-9.147)
Observations	112	171	171	112	170
Adjusted R^2	0.851	0.827	0.709	0.688	0.726
F value	159.095***	204.094***	104.746***	62.265***	113.034***

Note: O&H is Olsson and Hibbs (2005) whereas P&S is Petersen and Skaaning (2010)
t statistics in parenthesis; * <0.1; ** <0.05; *** <0.01.

Tab. 10: Determinants of Geocomponents and Biocompoments within Eurasia (Sample: Eurasia)

Independent Variables	1 Geocom1 (O&H)	2 Geocomt2 (P&S)	3 Geocom3 (P&S)	4 Biocom1 (O&H)	5 Biocom2 (P&S)
Landlocked	-0.029 (-0.160)	-0.071 (-0.568)	-0.205 (-1.436)	-0.102 (-0.418)	-0.327** (-2.296)
Absolute latitude (ln)	0.489*** (5.726)	0.473*** (6.113)	0.824*** (9.344)	0.359*** (3.113)	0.427*** (4.872)
Island	-0.964*** (-5.690)	-0.823*** (-5.518)	-0.338** (-1.987)	-0.399* (-1.897)	-0.472*** (-2.792)
Constant	-0.409 (-1.289)	-0.627** (-2.230)	-1.994*** (-6.222)	-0.435 (-0.602)	-0.493 (-1.545)
Observations	48	84	84	49	84
Adjusted R²	0.691	0.570	0.591	0.269	0.353
F value	36.041***	37.709***	40.990***	6.897***	16.108***

Note: O&H is Olsson and Hibbs (2005) whereas P&S is Petersen and Skaaning (2010) *t* statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab: 11: The Eurasia Advantage Thesis Vindicated: The Eurasia Advantage plus Diffusion (Full Sample: the Whole World)

Independent Variables	1 PD1 (ln)	2 PD1000 (ln)	3 PD1500 (ln)	4 GDPpc2000 (ln)	5 PD1 (ln)	6 PD1000 (ln)	7 PD1500 (ln)	8 GDPpc2000 (ln)
Eurasia	1.652*** (8.543)	1.281*** (7.007)	1.372*** (7.380)	0.814*** (5.003)				
Distance to Frontier AD1					-0.595*** (-7.553)			
Distance to Frontier AD1000						-0.387*** (-4.644)		
Distance to Frontier AD1500							-0.351*** (-5.059)	-0.186*** (-3.249)
Constant	-0.931*** (-7.062)	-0.130 (-1.055)	0.279** (2.263)	8.151*** (74.342)	4.255*** (7.170)	3.356*** (5.299)	3.404*** (6.702)	9.91*** (22.725)
Observations	155	177	184	187	155	177	184	187
Adjusted R²	0.319	0.215	0.226	0.114	0.267	0.105	0.118	0.049
F value	72.982***	49.097***	54.462***	25.031***	57.047***	21.570***	25.591***	10.557***

t statistics in parenthesis; *<0.1; **<0.05; ***<0.01.

Tab: 11 (continued): The Eurasia Advantage Thesis Vindicated: The Eurasia advantage plus Diffusion (Full Sample: the Whole World)

Independent Variables	9 PD1 (ln)	10 PD1000 (ln)	11 PD1500 (ln)	12 GDPpc2000 (ln)	13 PD1 (ln)	14 PD1000 (ln)	15 PD1500 (ln)	16 GDPpc2000 (ln)
Eurasia	1.275*** (6.753)	1.101*** (5.779)	1.173*** (6.155)	0.714*** (4.219)	1.422*** (6.468)	1.425*** (6.589)	1.568*** (7.229)	0.486*** (2.950)
Distance to Frontier AD1 (ln)	-0.417*** (-5.628)				-0.422*** (-5.345)			
Distance to Frontier AD1000 (ln)		-0.229*** (-2.814)				-0.279*** (-3.259)		
Distance to Frontier AD1500 (ln)			-0.214*** (-3.340)	-0.113** (-1.973)			-0.275*** (-4.188)	-0.078 (-1.498)
Landlocked					-0.433* (-1.869)	-0.262 (-1.148)	0.027 (0.117)	-0.640*** (-3.531)
Absolute Latitude (ln)					-0.062 (-0.522)	-0.305*** (-2.654)	-0.376*** (-3.279)	0.409*** (4.740)
Island					0.098 (0.419)	0.194 (0.856)	0.350 (1.597)	0.796*** (4.696)
Constant	2.343*** (3.944)	1.670** (2.566)	1.965*** (3.787)	9.044*** (19.431)	2.558*** (3.515)	2.805*** (3.636)	3.250*** (5.083)	7.624*** (15.097)
Observations	155	177	184	187	155	177	184	187
Adjusted R^2	0.432	0.244	0.267	0.128	0.439	0.274	0.304	0.359
F value	59.641***	29.478***	34.328***	14.659***	25.086***	14.272***	17.006***	21.813***

t statistics in parenthesis; * <0.1; ** <0.05; *** <0.01.