Australian
National
University

Crawford School of Public Policy

CAMA

Centre for Applied Macroeconomic Analysis

Barriers to the Cross-Border Diffusion of Climate Change Policies

CAMA Working Paper 66/2024
November 2024

Trung V. Vu
Loughborough University, UK
Centre for Applied Macroeconomic Analysis, ANU

Abstract

This paper establishes a statistically and economically significant cross-country relationship between national responses to climate change and genetic distance, which is a proxy for countries' dissimilarities in cultures, ancestry, and historical legacies associated with long-term exposure to divergent historical trajectories. It finds that countries that are genetically distant to the world-leading nation-state of climate change mitigation tend to experience barriers to the cross-border diffusion of climate change policies and hence exhibit worse responses to climate change. A potential explanation is that climate change polices are more likely to spread between closely related countries with more similar preferences for the provision of the public goods of environmental and climate protection. The findings imply that strengthening climate change mitigation requires overcoming obstacles to international policy diffusion.

Keywords

genetic distance, long-term relatedness, climate change, policy diffusion

JEL Classification

O11, O13, O33, Q54

Address for correspondence:

(E) cama.admin@anu.edu.au

ISSN 2206-0332

Barriers to the cross-border diffusion of climate change policies

Trung V. Vu[1,2]
[1] Loughborough Business School, Loughborough University, UK

[2] Centre for Applied Macroeconomic Analysis, Australian National University, Australia

Abstract

This paper establishes a statistically and economically significant cross-country relationship between national responses to climate change and genetic distance, which is a proxy for countries' dissimilarities in cultures, ancestry, and historical legacies associated with long-term exposure to divergent historical trajectories. It finds that countries that are genetically distant to the world-leading nation-state of climate change mitigation tend to experience barriers to the cross-border diffusion of climate change policies and hence exhibit worse responses to climate change. A potential explanation is that climate change polices are more likely to spread between closely related countries with more similar preferences for the provision of the public goods of environmental and climate protection. The findings imply that strengthening climate change mitigation requires overcoming obstacles to international policy diffusion.

Keywords:
Genetic distance
Long-term relatedness
Climate change
Policy diffusion

JEL Classification: O11, O13, O33, Q54

Declarations of interest: None

* Correspondence: Loughborough Business School, Loughborough University,
Leicestershire LE11 3TU, UK
Email: Trung.Vu@lboro.ac.uk

1. INTRODUCTION

Climate change has emerged as one of the most pressing challenges facing the contemporary world. Several international agreements on climate change have been initiated to strengthen collective responses to changing climate conditions, such as the adoption of the United Nations Framework Convention on Climate Change (UNFCCC), the Kyoto Protocol, and the Paris Agreement in 1992, 1997, and 2015, respectively. However, many countries, under these international treaties, failed to fulfil their GHG emission reduction commitments that would be necessary to contain the rise in average surface temperature below 2°C relative to pre-industrial levels. Due to a lack of sanctioning mechanisms for addressing non-compliance, international climate change treaties primarily rely on incentives to foster compliance (Carattini, Levin, and Tavoni, 2019). However, designing "self-enforcing" international agreements on climate change appears highly difficult because of countries' temptation to free ride on others' efforts to curb GHG emissions without taking proportional domestic abatement (Nordhaus, 2015; Mason, Polasky, and Tarui, 2017). Thus, identifying the driving forces of unilateral climate change policy adoption is central to securing a better understanding of the dynamics of the global climate regime.

Several contributions to understanding the worldwide divergence in national responses to climate change emphasize the importance of cultural traits (e.g., trust or reciprocal beliefs) for fostering collective climate action.[1] Ostrom (2000) indicates that people have incentives to engage in pro-social behaviors when they believe that other players are trustworthy reciprocators. This implies that effective responses to changing climate conditions depend on the prevalence of reciprocal beliefs. On the empirical side, there is ample evidence that cultural traits fundamentally drive observed differences in climate change policies across countries.[2] However, as articulated below, climate change policies inevitably transcend national borders, suggesting the under-explored role of *international policy diffusion* in affecting national climate change mitigation. If the propensity to address climate change is influenced by policy adoption by other jurisdictions, do climate change policies spread more easily between countries with greater cultural and historical relatedness? Does international policy diffusion

---

[1] This draws on the seminal work by Ostrom (1990) establishing the central role of trust in shaping the successful management of common-pool resources, where the formation of trust is sustained over time by external enforcement and the sanctioning of noncompliance with social norms (Tabellini, 2008).

[2] See, for example, Owen and Videras (2008), Carattini, Baranzini, and Roca (2015), Volland (2017), Tam and Chan (2018), and Jo and Carattini (2021). Carattini, Levin, and Tavoni (2019) offer a comprehensive review of the literature on the economics of environmental cooperation.

affects underlying differences in climate change policies between countries? This paper attempts to address these questions in order to obtain a better understanding of the fundamental determinants of climate change policy performance. Specifically, I explore whether long-term relatedness between countries, that is, their (dis)similarities in cultures, ancestry, and historical legacies, is associated with the cross-border diffusion of climate change policies and the global divergence in national responses to changing climate conditions.

The empirical analysis exploits a deep-rooted measure of genetic distance constructed by Spolaore and Wacziarg (2009, 2018) to capture countries' dissimilarities in a variety of historical and cultural traits. Employing data for up to 161 countries, I find a statistically and economically significant relationship between genetic distance and worldwide variations in climate change policy performance. Specifically, countries that are genetically distant to the world-leading country of climate change mitigation tend to have worse climate change responses, holding other things equal. Based on a dyadic regression framework, I demonstrate that genetic distance between countries *relative* to the world frontier is positively associated with absolute differences in climate change policy performance. This implies that climate change policies tend to spread more easily between genetically proximate countries. My results withstand accounting for bilateral differences in geographical distance, geographical/agroclimatic characteristics, contemporary and early development, and different measures of historical, linguistic, and religious proximity. The core findings also remain intact when I use genetic distance for the year 1500 CE as an instrumental variable for contemporary genetic distance to mitigate concerns about post-1500 population movements.

Furthermore, I find that the role of genetic distance in shaping the worldwide divergence in climate change policies is smaller among geographically proximate countries. I also examine the relationship between genetic distance and *actual* reductions in the intensity of CO_2 emissions across countries. Results show that genetic distance is associated with emission abatement only after climate change became a globally recognized issue. This relationship is also larger among countries with higher levels of economic development. Constructing different country-level measures of pro-environmentalism, I document the cross-country relationship between genetic distance and the global divergence in public support for climate change mitigation. Accordingly, I demonstrate that genetic distance is associated with countries' dissimilarities in preferences for the provision of the public goods of environmental or climate protection, which are in turn important for shaping national climate change mitigation. Further evidence is suggestive of the long-term legacy of deep-rooted genetic distance for the cultural transmission of collective climate action across generations.

I propose several explanations for the established relationship between genetic distance and cross-country differences in climate change policy performance. The index of genetic distance between countries is based on their dissimilarities in the distribution of neutral genes, driven by random drift independent of selection pressure (Spolaore and Wacziarg, 2009). Because such random drift occurs regularly over time in sufficiently large populations, genetic distance represents a molecular clock indicating the length of time that has elapsed since two populations became separated from a common ancestor. Longer periods of ancestral separation give rise to the divergence between human societies in intergenerationally transmitted traits, such as norms, values, preferences, attitudes, beliefs, languages, and religions (Spolaore and Wacziarg, 2009, 2016b; Becker, Enke, and Falk, 2020).[3] Hence, genetically distant countries tend to differ in cultures, ancestry, and historical characteristics due to long-run exposure to divergent historical trajectories. An important caveat is that my findings by no means establish a direct influence of genes on climate change responses. Instead, genetic distance is a summary measure of long-term relatedness between countries, which arguably affects the cross-border spillovers of climate change policies and thus helps shape climate change policy performance.

I hypothesize that genetically proximate countries, with greater similarities in cultural and historical characteristics, tend to have more similar preferences for the provision of the public goods of environmental or climate protection, and comparable public support for government policies (Spolaore and Wacziarg, 2009, 2016b). For this reason, closely related countries tend to face lower barriers to the exchange of ideas, knowledge, and institutions. Hence, countries with lower genetic distance are more likely to emulate and learn about one another's policy adoption.[4] This is because policy adoption in closely related jurisdictions arguably contains

---

[3] Previous studies provide evidence of the intergenerational transmission of economic preferences, such as risk aversion, patience, social trust, and altruism (Dohmen et al., 2012). It has also been established that variations in preferences between individuals are at least partially attributable to individual differences in genes (Cesarini et al., 2009). On this basis, Becker, Enke, and Falk (2020) empirically establish that longer periods of ancestral separation between countries are associated with the global divergence in economic preferences.

[4] This proposition rhymes well with Simmons and Elkins (2004) postulating that policymakers in uncertain and poorly understood environments typically infer the appropriateness of policy adoption from the experiences of their culturally proximate counterparts. Cultural affinity is akin to a cognitive short-cut for policymakers facing a complex set of political choices (Simmons and Elkins, 2004). This line of argument is consistent with a long-standing view in sociology arguing that cultural proximity facilitates the exchange of ideas through shared beliefs and values (Rogers, 1995). It also aligns with reference group theory in social psychology where cultural proximity acts as a catalyst for policy diffusion across nations (Rose, 1993; Simmons and Elkins, 2004).

more relevant information about the potential consequences of policy adoption, thereby reducing risks and uncertainties. This argument is consistent with the observation that the development of the European Union Emissions Trading System (EU ETS) demonstrates the (political) feasibility of carbon pricing, leading to policy emulation first across countries that are culturally and historically proximate to Europe (e.g., New Zealand and Australia) and only later to more genetically distant countries (e.g., China and South Korea).[5]

Overall, this study proposes and establishes empirically that the worldwide diffusion of climate change policies decays with genetic distance between countries, which fundamentally drives large and persistent differences in national responses to climate change across the globe. As previewed earlier, I find strong empirical support for this proposition in cross-sectional and dyadic regression analyses. My findings build upon the idea that domestic climate change policies tend to spread across countries through a process of learning-based policy diffusion (Volden, Ting, and Carpenter, 2008). This is because policymakers typically rely on external information, including the costs and benefits of policy adoption by foreign jurisdictions, to assess the political feasibility and efficacy of policy adoption (Simmons and Elkins, 2004). Furthermore, policy emulation between countries can be facilitated by knowledge spillovers and peer pressure (Pitlik, 2007; Obinger, Schmitt, and Starke, 2013).[6]

Anecdotal evidence suggests that leading activities in curbing GHG emissions by European countries (e.g., the European Emission Trading System) have generated a "motivational push" for other countries to follow suit in climate change mitigation (Buchholz and Sandler, 2017; Carattini, Levin, and Tavoni, 2019). World-leading climate actors help improve international moral or political demands for climate change mitigation, thus enhancing climate policy adoption by foreign jurisdictions.[7] Existing studies establish that the UK, France,

---

[5] The ETS of New Zealand is the second-oldest scheme after the EU ETS.

[6] Beiser-McGrath and Bernauer (2022) reveal that domestic public support for environmentally friendly policies is positively linked to the implementation of emission-reducing policies in other countries due to the central role of reciprocity in forming individual support for climate change mitigation. Given that policy adoption critically depends on public opinion (Wlezien, 1995; Aklin and Mildenberger, 2020), the cross-border spillovers of pro-climate attitudes further help explain why climate change policies inevitably transcend national borders. Several studies document evidence suggesting the importance of international policy diffusion in driving unilateral climate change policy adoption (see, e.g., Sauquet, 2014; Fankhauser, Gennaioli, and Collins, 2016; Thisted and Thisted, 2020; Linsenmeier, Mohommad, and Schwerhoff, 2022).

[7] For example, the Powering Past Coal Alliance was jointly established by the UK and Canada in November 2017 to eliminate coal power generation. Following these early movers, many other countries and subnational governments, business and organizations joined this effort to initiate policies and measures to end coal burning power. As of January 2023, the Power Past Coal Alliance includes 48 nations, 48 subnational governments, and 71 organizations (see https://poweringpastcoal.org/members/).

and Germany have played a crucial leadership role in global environmental governance (Vogler and Stephan, 2007; Kelemen and Vogel, 2010). For example, the leading role of the UK is reflected in its financial and diplomatic contributions to climate change mitigation, the development of policy solutions, and ambitious commitments to GHG emission abatement (Bocse, 2020).[8] Recently, Carattini et al. (2023), by conducting a network analysis, reveal that the UK, France, and Germany have persistently proclaimed their leadership role in global environmental cooperation, as evidenced by the intensity of environmental cooperation with other countries and the importance of joining and influencing other members of the environmental cooperation network. Therefore, genetic distance between countries *relative* to the world-leading country of climate change mitigation, rather than absolute genetic distance, is relevant for understanding barriers to the international diffusion of climate change policies and national responses to changing climate conditions.

The remainder of this paper is organized as follows. Section 2 outlines the key contributions of this paper. Section 3 provides evidence of the relationship between genetic distance and climate change policy performance across countries. Section 4 discusses the role of genetic distance in driving actual reductions in the intensity of CO_2 emissions across countries. Section 5 contains evidence of the cross-country association between genetic distance and preferences for the provision of environmental public goods. Section 6 discusses alternative explanations and potential policy implications. Section 7 concludes the study.

2. RELATED LITERATURE

This paper belongs to a large and growing body of research exploring the deep roots of comparative development (see Spolaore and Wacziarg (2013) for reviews). My findings, in particular, complement and extend previous studies identifying long-term barriers to the diffusion of development across countries and subnational regions (Spolaore and Wacziarg, 2009, 2016b, 2018, 2022) by focusing on factors shaping the cross-border dissemination of climate change policies. This approach improves our understanding of the deep determinants of cross-country difference in climate change policies.[9] This article is closely related to the

---

[8] According to the climate change policy performance index of Sharma, Ang, and Fredriksson (2021), the UK remains a world leader in global warming mitigation, as evidenced by its international commitments and the availability of national legislative, fiscal, and institutional frameworks relevant for addressing climate change.

[9] Building upon Spolaore and Wacziarg (2009), previous studies establish that long-term relatedness between countries helps explain the global variation in interstate conflict (Spolaore and Wacziarg, 2016b), national happiness (Proto and Oswald, 2017), productivity (Madsen and Farhadi, 2018), financial development (Ang and

seminal work by Spolaore and Wacziarg (2009) in several aspects. First, both studies exploit genetic distance to capture long-term relatedness between countries. Second, following Spolaore and Wacziarg (2009), I use genetic distance for the year 1500 CE to isolate a plausibly exogenous source of variation in contemporary genetic distance. Finally, both studies show that genetic distance, which reflects deep-rooted barriers to the diffusion of development, helps explain worldwide comparative development.

Nevertheless, this study is considerably different to Spolaore and Wacziarg (2009) in terms of the main focus and implications. Specifically, Spolaore and Wacziarg (2009) rely on genetic distance to the United States – the global technological frontier in the twentieth century – to explain the worldwide distribution of income per capita in 1995. They also demonstrate the robustness of their findings to using the UK as an alternative frontier in the nineteenth century. This indicates that the frontier per se might change over time. The frontier of development also varies depending on the specific type of institutional or technological innovations (Spolaore and Wacziarg, 2022). Consistent with the above arguments, I use genetic distance to several world-leading countries of climate change mitigation (including the UK, France and Germany but not the United States) to identify barriers to the cross-border diffusion of climate change policies. This is in line with evidence suggesting that the United States has not played a leadership role in global climate governance as it has in economic and political development (Carattini et al., 2023). Given that the frontier is not immutable, it is important to devise different strategies to attenuate the effect of barriers to various aspects of development originating from different world frontiers. As articulated below, the findings of Spolaore and Wacziarg (2009, 2018) provide an alternative explanation for my findings based on the diffusion of technologies. However, I establish empirically that a large portion of the association between genetic distance and climate change policy performance remains stubbornly unexplained even after accounting for technological spillovers. Therefore, my findings complement Spolaore and Wacziarg's (2009) results in achieving a nuanced understanding of long-term barriers to the diffusion of multidimensional development.

Previous studies document the spread of political institutions from the United States (Spolaore and Wacziarg, 2009, 2016a, 2018). Given the importance of inclusive political institutions for the provision of environmental public goods, existing evidence implies that the diffusion of institutions is relevant for explaining the global divergence in climate change

---

Kumar, 2014), migration (Krieger, Renner, and Ruhose, 2018), international trade (Fensore, Legge, and Schmid, 2022), income inequality (Vu, 2023), and economic preferences (Becker, Enke, and Falk, 2020).

responses. However, these studies do not provide a systematic analysis of the worldwide diffusion of climate change policies. Furthermore, the extant literature has yet to focus explicitly on exploring the link between genetic distance and intergenerationally transmitted human traits related to climate change responses. It also remains unclear whether and how the international spread of broadly defined political institutions translates into noticeable climate change mitigation, reflected in substantial reductions in GHG emissions. In this regard, this paper goes beyond related studies by examining the long-term legacy of deep-rooted genetic distance for actual responses to climate change. Additionally, this paper, for the first time, provides suggestive evidence of the association between genetic distance and the global variation in preferences for the provision of the public goods of environmental and climate protection. This is important for understanding the pattern of climate change policy performance across the world.

The current study also contributes to an emerging body of research examining the determinants of climate change policy performance.[10] The existing literature jointly facilitates our understanding of the influence of socio-economic, political, and historical characteristics on climate change mitigation. However, prior studies have predominantly exploited *domestic* factors to explain international differences in climate change responses. This approach disregards the possibility that climate change policies inevitably transcend national borders. In short, the important role of international policy diffusion in driving collective responses to climate change, albeit well-documented in the policy diffusion research agenda, has been largely overlooked in the existing literature on the determinants of climate change policies. In this regard, a key distinguishing feature of this paper is to exploit deep-rooted genetic distance between countries to identify long-term barriers to the international diffusion of climate change policies. This approach sheds light on one of the deepest roots of the cross-country variation in climate change policy performance.

---

[10] Previous studies establish that corruption (Barbier, Damania, and Léonard, 2005; Oliva, 2015), democracy (Farzin and Bond, 2006; List and Sturm, 2006), political instability (Fredriksson and Svensson, 2003), trade openness (Damania, Fredriksson, and List, 2003), and female political representation (Mavisakalyan and Tarverdi, 2019) influence in environmental regulations. Other studies explore the deeper, more fundamental causes of climate change policy performance, focusing on a persistent culture of "rugged individualism" (Vu, 2024), accumulated statehood experience (Ang and Fredriksson, 2017, 2021), predicted genetic diversity (Vu, 2021), religiosity (Sharma, Ang, and Fredriksson, 2021), linguistic structures (Mavisakalyan, Tarverdi, and Weber, 2018), and legal heritage (Fredriksson and Wollscheid, 2015).

3. GENETIC DISTANCE AND CLIMATE CHANGE POLICIES

3.1. Data and the empirical strategy

3.1.1. Key variables

I exploit the Climate Change Policy Stringency Index (CCPS) of Sharma, Ang, and Fredriksson (2021) – an updated version of the Climate Laws, Institutions, and Measures Index (CLIMI) of Steves, Treisman, and Teytelboym (2011) – to capture countries' climate change mitigation. CLIMI is an internationally comparable measure of climate change policy performance, reflected in international commitments to climate change mitigation and the availability of national legislative, fiscal, and institutional frameworks relevant for addressing climate change. The construction of CLIMI relies on data on annual national communications to the UNFCCC for 95 countries between 2005 and 2010. CLIMI embodies 12 different components categorized into 4 main policy themes, including (1) international collaboration (reflected in the ratification of the Kyoto Protocol and the development of joint implementation or clean development projects); (2) domestic climate change mitigation framework (reflected in cross-sectoral climate change legislation, carbon emissions targets, and dedicated climate change institutions); (3) significant sectoral fiscal or regulatory measures or targets (reflected in energy supplies/renewables, industry, forestry, agriculture, buildings, and transport); and (4) other cross-sectoral fiscal or regulatory measures. Sharma, Ang, and Fredriksson (2021) reconstruct CLIMI but incorporate countries' ratification of the Paris Agreement as an additional sub-component of international collaboration. Furthermore, Sharma et al.'s (2021) index, bounded between 0 and 1, captures climate change mitigation efforts between 1997 and 2015 for a much wider global sample of 183 countries/territories. To enhance readability, I re-scale the outcome variable by multiplying it by 100 with higher values indicating better climate change policy performance, as depicted in Figure 1A.

Following Eskander and Fankhauser (2020), I also measure cross-country differences in climate change policy performance by using data available in the Climate Change Laws of the World database (CCLW). This globally comprehensive dataset records legislation activities (e.g., parliamentary acts, executive orders, and policies of equivalent importance) focused on reducing GHG emissions in one sector or more between 1990 and 2019 across 200 countries (CCLW, 2020). Climate change mitigation laws and policies can directly translate into emission reductions, such as the development of a cap-and-trade system or a carbon budget, or can indirectly contribute to emission abatement via developing relevant institutions or providing additional funding for research and development into low-carbon technologies

(CCLW, 2020). Furthermore, the database covers sectoral policies related to climate change mitigation (e.g., Germany's Renewable Energy Sources Act, Brazil's mandatory biodiesel requirements, and the Democratic Republic of Congo's law on the protection of the nature) (Eskander and Fankhauser, 2020).[11] Examining the emission-reducing effect of climate change mitigation laws for up to 133 countries between 1990 and 2016, Eskander and Fankhauser (2020) find that the adoption of an additional climate law is associated with a decrease in CO_2 emissions per capita by 0.78% and 1.79% in the short- and long-run, respectively. This suggests the highly predictive power of legislation activities for worldwide differences in climate change responses. I calculate the total number of climate change mitigation laws and policies passed between 1990 and 2019 to measure international differences in stock of climate laws, where higher values reflect better climate change policy performance as depicted in Figure 1B.

As mentioned previously, I measure long-term relatedness between countries by using the genetic distance index of Spolaore and Wacziarg (2009). Measuring genealogical relatedness between contemporary countries relies on an index of "expected heterozygosity" at the ethnic level. It captures the probability that two people randomly selected from a population are genetically dissimilar, yielding information on the frequency of occurrence of an allele (or a gene variant) in the population.[12] Cavalli-Sforza, Menozzi, and Piazza (1994) measure genetic distance between world societies categorized into ethnic groups by exploiting their difference in the distribution of genes. Accordingly, the F_{ST} index of genetic distance between two ethnic groups equals 0 if and only if they share identical allelic frequencies. Meanwhile, higher values of the F_{ST} genetic distance index reflect greater dissimilarities in allelic frequencies and hence greater differences in the distribution of genes. Employing Cavalli-Sforza et al.'s (1994) data on inter-ethnic genealogical relatedness, Spolaore and Wacziarg (2009) construct a weighted measure of genetic distance between contemporary countries, where the weights correspond to the proportional representations of different ethnic groups in a country's population. Figure 2 depicts cross-country differences in genetic distance to the UK.

---

[11] Due to its coverage of numerous climate laws and policies, the CCLW has been widely adopted in previous studies examining the global variation in climate change policy performance (Townshend et al., 2013; Iacobuta et al., 2018), the political economy of climate change mitigation and adaption (Fankhauser, Gennaioli, and Collins, 2015; Fankhauser, Gennaioli, and Collins, 2016), and climate governance at the national and global levels (Averchenkova, Fankhauser, and Nachmany, 2017).

[12] Specifically, the measure of expected heterozygosity for each gene is developed using information about the proportional representations of various alleles, which, for example, indicate the frequency of occurrence of an allele (gene variant) in the population. Data on allelic frequencies for numerous genes are averaged across different loci, yielding a comprehensive index of expected heterozygosity for each population.

3.1.2. Identification strategy

A potential challenge with testing the main hypothesis relates to massive post-1500 migration flows from the Old World (Europe, Africa, and Asia) to the New World (the Americas and Oceania). Specifically, Acemoglu, Johnson, and Robinson (2001) suggest that European colonizers established different types of institutions in their former colonies during the colonial (post-1500) era, which tend to persist until today.[13] Acemoglu, Johnson, and Robinson (2002) document that the historical event of European colonization caused a reversal of institutions among former colonies, which would eventually drive comparative development in postcolonial eras.[14] Furthermore, systematic and large-scale inflows of humans from genetically distant populations could significantly change genetic distance between countries. These narratives imply that the hypothesized association between genetic distance and climate change policy performance can be attributed to the persistent influence of post-1500 population movements on today's socio-economic and political development. I partially reduce this concern by augmenting all the regressions with absolute latitude, which captures the long-run effect of geographical attributes on the worldwide diffusion of human characteristics, including institutions, cultures, and human capital.[15]

Addressing the above concern requires attention to factors driving the spatial distribution of genetic distance between world societies and their persistent influence on today's economic development (Spolaore and Wacziarg, 2016b). The widely accepted theory of human origins posits that anatomically modern humans evolved from East Africa tens of thousands of years ago. The out-of-Africa migration of Homo sapiens to the rest of the world took place in a series of discrete steps, where a group of individuals departed from their parental society to establish

---

[13] European colonizers set up well-functioning (market-supporting) institutions in countries where the disease environment was conducive to their permanent settlement. In contrast, extractive (investment-hampering) institutions were established in places where the disease environment prevented Europeans from settling permanently. The persistence of these early institutions eventually shapes global income differences.

[14] According to the "reversal of fortune" hypothesis of Acemoglu, Johnson, and Robinson (2002), countries that were richer in 1500 are now poorer, while countries that were poorer in 1500 now enjoy higher income levels. The underlying idea is that Europeans established inclusive institutions in less developed former colonies but introduced extractive institutions or relied on existing autocratic institutions in wealthier societies in 1500. This created an institutional reversal among former colonies, thus shaping cross-country comparative development (Acemoglu, Johnson, and Robinson, 2002).

[15] Absolute latitude has been widely regarded as a deep determinant of worldwide differences in income per capita and institutional quality. For example, European colonizers tended to settle in countries located further away from the equator presumably due to favorable environments. Hence, they established inclusive institutions in the New World. See, for example, Spolaore and Wacziarg (2013) for comprehensive reviews of studies examining the long-run effect of geography on economic development.

a new colony further away (Ashraf and Galor, 2018). Along the migratory routes of Homo sapiens, different groups of human species became separated from one another. This gave rise to differences in allelic frequencies between human societies due to random genetic drift independent of selection pressure. Therefore, interethnic genealogical relatedness was predominantly shaped by ancestral separation along the prehistorical migratory routes of Homo sapiens (Cavalli-Sforza, Menozzi, and Piazza, 1994; Bellwood, 2014; Ashraf and Galor, 2018). Deep-rooted genetic distance between human societies would remain stable without massive and systematic movements of people across genetically dissimilar populations; this is true in precolonial times (Arbatlı et al., 2020). Given that such evolutionary process driven by genetic mutations precedes the development of modern state institutions, it plausibly affects contemporary economic development exclusively through shaping countries' dissimilarities in human characteristics.[16] While this assumption, to a large extent, remains true for much of the Old World, long-term relatedness is influenced by great human migrations into the New World during the post-1500 period (Arbatlı et al., 2020). This is in line with population geneticists highlighting that systematic and large-scale movements of humans would be required to have a substantial influence on genetic distance between countries (Cavalli-Sforza, Menozzi, and Piazza, 1994; Spolaore and Wacziarg, 2016b). To the extent that the Old World was largely unaffected by substantial inflows of humans from genetically distant populations in postcolonial eras, the aforementioned endogeneity concern applies predominantly to a sub-sample of countries that only belong to the New World.

To mitigate endogeneity concerns related to post-1500 mass migrations, I exploit genetic distance for the year 1500 as an instrumental variable (IV) for contemporary genetic distance, following Spolaore and Wacziarg (2009). This strategy exploits the fraction of contemporary genetic distance that correlates with the spatial distribution of genetic distance between prehistorically indigenous populations that have been native to their current locations well before 1500. In contrast to contemporary genetic distance contaminated by the great migrations of the post-1500 period, genetic distance between prehistorically native populations before the European colonization was not influenced by substantial inflows of humans from genetically distant societies (Cavalli-Sforza, Menozzi, and Piazza, 1994). This is because ancestral

---

[16] Genetic dissimilarities between human societies in the precolonial era, as predetermined over the prehistorical out-of-Africa exodus process, was driven by geographical and biogeographical characteristics unrelated to present-day economic development. For example, the driving forces of ancestral separation along the out-of-Africa migratory routes of Homo sapiens may include ice age shock or extinction of prey, among others (Spolaore and Wacziarg, 2016b).

separation (isolation) along the out-of-Africa migratory routes of Homo sapiens implies that genetic distance before the colonial period was not subject to the significant genetic admixture of populations whose allelic frequencies were very distinct from one another. Therefore, this IV strategy allows me to partial out the persistent influence of post-1500 movements on contemporary genetic distance and long-run institutional or economic development. This approach also relies on the highly predictive power of genetic distance in 1500 for long-term relatedness between contemporary countries, as evidenced by the strong correlation of around 0.88 between the measures of precolonial and contemporary genetic distance.

In addition, Cavalli-Sforza, Menozzi, and Piazza (1994) suggest that exploiting genealogical relatedness in 1500 as an IV also helps mitigate concerns about measurement errors in current genetic distance. The idea is that the original data of Cavalli-Sforza, Menozzi, and Piazza (1994) were collected for ancestral ethnic groups as of 1500. Furthermore, the process of matching ethnicity-level data in 1500 to their respective locations in contemporary countries is less likely to suffer from measurement issues before substantial and systematic movements of people in the colonial period (Spolaore and Wacziarg, 2009). Following Arbatlı et al. (2020), I further restrict the analysis to the Old World that was largely unaffected by large-scale and systematic migration inflows from genetically distant human societies during the colonial era. This analysis exploits dissimilarities in allelic frequencies between populations that predominantly reflect genetic distance between their respective ancestral populations before the colonial era, as predetermined over the prehistorical out-of-Africa migration process. I also mitigate concerns about post-1500 mass migration flows by augmenting the regressions with the heritage of colonial rule and legal traditions.

3.1.3. Potential confounding factors

To check for the possibility that the reduced-form relationship between genetic relatedness and climate change policies is attributed to alternative fundamental explanations, I control for several confounding factors. I first account for several geographical/agroclimatic characteristics, including absolute latitude, distance to the nearest waterway, terrain ruggedness, average land suitability for agriculture, mean elevation, and landlocked nation dummy. It has been established that absolute latitude and distance to the nearest waterway have a persistent influence on economic development through climatological, institutional, and trade-related channels (Spolaore and Wacziarg, 2013; Arbatlı et al., 2020). Thus, these geographical attributes may contribute to shaping worldwide differences in national responses to climate change. Michalopoulos (2012) also finds that mean elevation and average land suitability for agriculture give rise to the emergence of distinct ethnolinguistic groups. This may undermine collective climate action through undermining societal cohesiveness and the provision of public goods (Vu, 2021). Additionally, geographical isolation induced by terrain ruggedness may be conducive to the formation of distinct subgroups of a regional population (Michalopoulos, 2012). Thus, countries endowed with rugged terrains may experience societal non-cohesiveness, making it difficult to strengthen climate change policies. Landlocked countries could have been exposed to different barriers to international policy diffusion.

A potential concern is that my findings can be confounded by deeply rooted population diversity (Vu, 2021). Following Arbatlı et al. (2020), the baseline model specification accounts for an ancestry-adjusted measure of predicted genetic diversity, ethnic fractionalization, and ethnolinguistic polarization. This helps partial out the contribution of interpersonal and interethnic population diversity to shaping comparative cross-country development (Arbatlı et al., 2020). Ang and Fredriksson (2021) offer evidence of the long-term legacy of accumulated statehood experience for climate change policies. Hence, the baseline model is augmented with the ancestry-adjusted state history index of Borcan, Olsson, and Putterman (2018) that reflects long-term exposure to state-like polities between 3500 BCE and 1500 CE. Another concern is that countries belonging to a world region may share common cultures, geography, human characteristics, and historical legacies. These region-specific factors can be simultaneously correlated with genetic distance and the diffusion of climate change policies across jurisdictions. To account for unobserved time-invariant heterogeneity across world regions, the regression analysis is augmented with a set of binary indicators for Europe and Central Asia, Latin America and Caribbean, Middle East and North Africa, North America, South Asia, and sub-Saharan Africa; East Asia and Pacific is excluded as the base category.

3.2. Empirical estimates

3.2.1. Analysis of climate change policy performance in cross-sectional data

This section explores the relationship between genetic distance to the world-leading country of climate change mitigation and climate change policy performance. For this purpose, I specify the following cross-sectional model:

$$Y_i = \alpha + \beta GDist_i^{UK} + \gamma X_i + \delta Region_i + \varepsilon_i, \qquad [1]$$

where Y_i is a measure of climate change policy performance for country i; $GDist_i^{UK}$ is the F_{ST} measure of genetic distance to the UK; β is the main coefficient of interest capturing the association between genetic distance to the global frontier and international differences in climate change policy performance; X_i is a set of main control variables, including geographical characteristics and the deep roots of economic development; $Region_i$ is a vector of region dummies; ε_i is an unobserved error term. Table 1 contains summary statistics of key variables. Table A1 shows variables' definition and data sources (Appendix A1). In Appendix A2, Table A2 presents for the list of countries by regions, following the World Bank's classification.

Table 2 shows estimates of equation [1]. The specification from column (1) involves regressing CCPS on genetic distance to the UK, controlling for unobserved time-invariant heterogeneity across world regions. In column (2), the regression analysis is augmented with key geographical controls. The baseline model specification also accounts for the deep roots of economic development, including different measures of population diversity and accumulated statehood experience, as shown in column (3). All the main control variables and region dummies are incorporated in the full specification from column (4). Then, I re-estimate equation [1] but use the stock of climate change mitigation laws as an alternative outcome variable, as reported in columns (1) to (4) of Table 3.

Accordingly, genetic distance to the UK enters all the regressions with a negative and statistically significant coefficient. This lends support to the hypothesized negative association between genetic distance to the global frontier and climate change policy performance across countries, as illustrated in Figure 3. The estimates in column (4) of Table 2 suggest that an extra standard deviation across countries in genetic distance to the UK predicts a roughly 0.449-standard-deviation decrease in CCPS, holding other things equal. Illustratively, Belgium has a score for the F_{ST} index of genetic distance to the UK of 30.3, which is much lower than the value for Venezuela of 684. The values of CCPS of Belgium and Venezuela are 56.6 and 13.1, respectively. If Venezuela were to experience Belgium's genetic proximity to the UK, equivalent to 98% of a standard deviation of genetic distance to the UK, its score of CCPS would increase from 13.100 to 20.291; this change corresponds to approximately 42% of a standard deviation in CCPS across countries. The estimated coefficient on genetic distance to the UK retains its sign and statistical precision when I allow several observed control variables to enter the regression either individually or jointly. This indicates that the main findings are unlikely to be attributed to alternative fundamental explanations of international differences in national responses to changing climate conditions.

I now estimate the baseline model using a two-stage least squares (2SLS) estimator, consistent with the IV strategy discussed previously. According to the results reported in columns (5) and (6) of Table 2, the estimated coefficient on genetic distance to the UK is negative and statistically significant at the 1% level, conditional on unobserved time-invariant region-specific factors. The IV estimates also remain stable in size and statistical precision when all the key control variables are included in the regression. This provides additional support for the hypothesized influence of long-term relatedness between countries on climate change policy performance. The first-stage estimates suggest the highly predictive power of the IV for current genetic distance to the UK, thereby mitigating weak instrument bias. Moreover, the value of the effective F-statistic of excluded instrument of Olea and Pflueger (2013) is much larger than the rule-of-thumb threshold of 10, indicating that my findings are unlikely to be confounded by using a weak IV. I also report identification-robust Anderson-Rubin 95% confidence intervals, which are robust to weak identification and efficient in the just-identified case (Andrews, Stock, and Sun, 2019). Accordingly, none of these bound estimates contains zero, implying that my IV strategy is unlikely to be contaminated by a weak instrument problem. My findings also remain intact when using the stock of climate laws to capture the worldwide variation in climate change policy performance as shown in column (6) of Table 3. However, the results derived from the parsimonious specification from column (5) of Table 3 are imprecisely estimated at conventional levels of statistical significance.

Drawing reliable statistical inference on the cross-country relationship between genetic distance to the UK and climate change policy performance critically requires attention to the validity of the exclusion restrictions. A potential problem relates to the possibility that genetic distance to the English population in 1500 is correlated with the early formation and persistence of inclusive institutions, which could drive the global variation in contemporary climate change responses. If the IV affects national responses to climate change via its influence on early development, conventional 2SLS regressions do not consistently estimate the main structural parameter of interest (β). Admittedly, the unobserved (or observed but noisily measured) nature of early development implies that attempts to account for this channel of potential deviation from the exclusion restrictions in standard regression models are very challenging. Moreover, the exogeneity condition cannot be tested empirically due to the unobserved nature of the error terms.

To mitigate this concern, I follow Conley et al.’s (2012) adoption of the union of confidence intervals approach to re-estimate the benchmark 2SLS regressions allowing for the direct influence of the IV on the outcome variable. In order for the IV to be safely excluded from the second-stage regression, the parameter φ must be zero in the follow equation:

$$Y_i = \alpha + \beta GDist_i^{UK} + \varphi GDist_i^{UK,1500} + \gamma X_i + \delta Region_i + \varepsilon_i, \qquad [2]$$

where $GDist_i^{UK,1500}$ is genetic distance to the English population in 1500. Under the assumption of $\varphi = 0$, the structural parameter of interest (β) can be consistently estimated. The method developed by Conley, Hansen, and Rossi (2012) allows for certain degrees of violations of the exogeneity requirements ($\varphi \neq 0$) in the estimation of β. If one were to know the true direct effect of $GDist_i^{UK,1500}$ on the outcome variable, β can be consistently estimated using the above IV strategy. Specifically, the 2SLS regressions can be implemented by subtracting $\varphi GDist_i^{UK,1500}$ from both sides of equation [2]. Nevertheless, φ is unobserved and hence can take hypothesized values within a specific support interval ($\varphi \in [-2\theta, 2\theta]$), under the assumption that $\varphi \sim N(0, \theta^2)$, as proposed by Conley, Hansen, and Rossi (2012).

To conserve space, I provide Conley, Hansen, and Rossi's (2012) bound estimates of the cross-country relationship between genetic distance to the UK and climate change policy performance in Table A3 (Appendix A3). Specifically, I hypothesize that that the degree of deviation from the exclusion restrictions is 1% – 50% of the estimated coefficient on genetic distance to the UK in the baseline 2SLS regressions. As shown in column (1), the IV results remain negative and statistically significant in most cases except for extremely large violations of the exogeneity requirements (e.g., CI ($2\theta = 50\%$)). However, the results in column (2) are more sensitive to allowing for deviation from the exclusion restrictions when I use the stock of climate laws as an alternative outcome variable. Table A3 results provide partial support for the validity of the 2SLS estimates unless there are implausibly large violations of the orthogonality requirements. An important caveat is that the 2SLS estimates do not imply causal inference if genetic distance in 1500 has a very large direct influence on contemporary climate change policies, independent of its correlation with today's genetic distance.

As discussed above, Germany and France, among other European countries, have played a significant role in global climate governance (Carattini et al., 2023). Therefore, I now replicate the main analysis but consider Germany and France as alterative frontiers to explain the global variation in climate change policy performance; results are depicted in Figure 4. Accordingly, I find that a one-standard-deviation increase in genetic distance to France is associated with a decrease in CCPS by 0.537 standard deviations. The coefficient on genetic distance to Germany is also negative and precisely estimated at conventionally accepted levels of statistical significance. Results remain intact when I use the stock of climate change mitigation laws as an alternative outcome variable. In addition to France, Germany, and the UK, other European nations (including Austria, Denmark, Netherlands, Norway, Spain, and Sweden) regularly top the league table of international climate change policy performance, measured by CCPS or the stock of climate change mitigation laws. These countries, as members of the European Union, have consistently been credited for their strong commitments to reducing GHG emissions and significant contributions to strengthening global climate governance (Bocse, 2020). Through financial contributions, the establishment of policy solutions, and the adoption of ambitious emission-reducing measures, these European countries act as role models for many other countries to follow suit in climate change mitigation (Vogler and Stephan, 2007; Kelemen and Vogel, 2010; Buchholz and Sandler, 2017). As depicted in Figure 4, the main findings are robust to using these European countries as alternative frontiers.

I conduct a placebo exercise by examining the association between genetic distance to Slovenia and climate change policy performance across countries. Slovenia underwent a process of structural transformation from socialist systems of social protection to a market economy in the 1990s – the period of the early emergence of international cooperation in climate change mitigation. Slovenia has a score of CCPS of 42.4, ranked 29th out of 161 countries in the global sample. It is also characterized by a very high share of environmental taxes of total tax revenue, reflecting an enhanced ability to deliver environmental public goods in the context of a transitional economy. Nonetheless, as articulated in Section 6, Slovenia's presence in international climate agreements following its accession to the EU is mainly driven by the leadership role of EU in fostering policy emulation (Tosun and Mišić, 2022). Against this background, I select Slovenia as a placebo global frontier to check whether the main results are spurious. As depicted in Figure 4, the estimated coefficient on genetic distance is statistically insignificant when Slovenia is regarded as an alternative world-leading country of climate change mitigation. This lends credence to the hypothesis that genetic distance to the global frontier captures barriers to the cross-border spillovers of climate change policies and hence helps explain the global variation in climate change policy performance.

Appendix A3 contains further evidence of the relationship between genetic distance and climate change policy performance. To check for the robustness of my findings, I re-estimate the baseline model by restricting the analysis to countries that only belong to the Old World. As shown in Table A4, the core findings are insensitive to excluding the New World, which further mitigates concerns about post-1500 mass movements of people. The results also withstand accounting for the long-run impact of colonial legacies and early development on the nature of contemporary political institutions (Table A5).[17] Another concern is that the international diffusion of climate change policies can be attributed to geographical, linguistic, and religious distance to the global frontier. However, Table A6 results suggest the robustness of my findings to accounting for geographical distance and linguistic and religious proximity to the world frontier. In Table A7, I allow conventional correlates of climate change policies to enter the baseline regression. Accordingly, including these variables in the benchmark model fails to attenuate the coefficient on genetic distance to the UK toward zero. It is worth noting that Table A7 results do not permit causal inference because these additional controls are endogenous in regression models explaining the global divergence in climate change policy performance. Nonetheless, these estimates indicate that my findings are unlikely to be exclusively driven by conventional explanations of worldwide differences in climate change responses. The core results are also quantitatively robust to excluding each world region (Table A8) and excluding or down-weighting outliers (Table A9). Following Spolaore and Wacziarg (2009, 2018), I employ alternative measures of genetic distance to the UK; however, I still find evidence supporting the main hypothesis in most cases (Table A10). To rule out the possibility that the baseline estimates can be confounded by spatial autocorrelation in variables across countries, I estimate spatial-autoregressive models with spatial-autoregressive error terms (SARAR). However, the main results remain intact (Table A11).

3.2.2. Analysis of the diffusion of climate change policies in bilateral data

To move closer to a generalized interpretation of deep-rooted genetic distance as long-term barriers to the cross-border diffusion of climate change policies, I rely on a *dyadic* regression framework, where each country pair is a unit of observation. Consistent with the discussions in Section 1, I propose that genetic distance between countries *relative* to the global frontier is positively associated with their distance in climate change policy performance. To test this proposition, I match each of 159 countries with one another, yielding a sample of 12,720 country pairs; this is dictated by data availability. For each country pair, I calculate the absolute difference in climate change policy performance, which is regressed on bilateral genetic distance. The dyadic cross-sectional model specification, which is similar to gravity regressions

---

[17] Sharma, Ang, and Fredriksson (2021) establish that religiosity fundamentally drives international differences in climate change policies. However, my findings withstand controlling for religiosity. These results, not reported for brevity, are available on request. It is important to note that data on religiosity are only available for 69 countries. Thus, including religiosity in the baseline model significantly constrains the feasible sample size.

widely adopted to identify barriers to the cross-border flows of goods and services, can be expressed below:

$$\left|Y_i - Y_j\right| = \alpha + \beta Gdist_{i,j} + \delta Gdist_{i,j}^{UK} + \gamma X_{i,j} + \varphi f_i + \tau f_j + \varepsilon_{i,j}, \qquad [3]$$

where $\left|Y_i - Y_j\right|$ is the absolute difference in climate change policy performance between countries i and j; $Gdist_{i,j}$ is the F_{ST} measure of genetic distance; $Gdist_{i,j}^{UK} = \left|Gdist_i^{UK} - Gdist_j^{UK}\right|$ captures genetic distance between countries *relative* to the UK; $X_{i,j}$ is a vector of bilateral controls, including geographical distance and binary indicators of contiguity, common official language, colonial relationship, common sea or water, having belonged to the same country, and either country being landlocked; f_i and f_j capture unobserved time-invariant country-specific factors; $\varepsilon_{i,j}$ is an unobserved error term. Given that the standard error estimates can be confounded by interdependence between observations stemming from the presence of variables for countries i and j across various country pairs, I calculate two-way clustered standard errors at both countries in a pair.

The above dyadic regression framework permits identifying barriers to the horizontal diffusion of climate change policies. In particular, genetic distance, on average, positively relates to the difference between countries in vertical human characteristics (Spolaore and Wacziarg, 2009). Countries with greater distance to the global frontier in terms of cultural or historical traits tend to experience higher barriers to international policy diffusion. Thus, genetic distance between countries *relative* to the frontier captures their difference in barriers to the horizontal diffusion of climate change polices. This implies that country pairs with larger genetic distance *relative* to the world frontier tend to experience larger differences in climate change policy performance. Therefore, β is expected to have a positive sign and reflects the magnitude of long-term barriers to the horizontal diffusion of climate change policies across the globe. As discussed previously, bilateral genetic distance *relative* to the frontier plays a more important role in explaining barriers to climate policy spillovers, compared to bilateral genetic distance. An important noteworthy feature of the bilateral approach is that all the regressions are augmented with fixed effects for both countries i and j in order to account for unobserved time-invariant heterogeneity across countries.[18] However, the bilateral estimates

---

[18] The baseline cross-sectional estimates can be confounded by unobserved time-invariant country-specific factors. Although I attempt to incorporate a variety of possible confounding factors in the cross-country regressions, it is impossible to completely rule out concerns about unobserved heterogeneity across countries. This points to the desirability of including country fixed effects in the dyadic regression analyses.

can still be confounded by unobserved time-invariant pair-specific factors. Therefore, I augment the regression analysis with several dyadic controls.

The empirical estimates of equation [3] are reported in Table 4. Specifically, I allow $Gdist_{i,j}^{UK}$ and $Gdist_{i,j}$ to enter the OLS and 2SLS regressions individually. The coefficient on genetic distance *relative* to the UK is positive and statistically significant at the 1% level, as shown in columns (1) and (3). This is in line with my prediction that genetic distance constitutes barriers to the horizontal diffusion of climate change policies and hence predicts larger differences in CCPS across countries. The results in columns (2) and (3) are also supportive of the positive association between genetic distance and the absolute difference in CCPS. With both measures of genetic distance entering the regression jointly, the coefficient on $Gdist_{i,j}^{UK}$ retains its sign and statistical precision. By contrast, $Gdist_{i,j}$ enters the regressions with a positive but statistically insignificant coefficient, consistent with the above prediction.[19] The results also withstand the inclusion of several dyadic controls that capture the variation in relatedness across country pairs other than genetic distance. However, the dyadic estimates turn out to be statistically insignificant when I use the absolute difference in the stock of climate change mitigation laws as an alternative outcome variable, as reported in columns (5) to (8) of Table 4.[20] Overall, the bilateral estimates offer partial evidence suggesting that deep-rooted genetic distance captures barriers to the cross-border diffusion of climate change policies captured by the CCPS index of Sharma, Ang, and Fredriksson (2021).

The conventional view is that geographical proximity facilitates the cross-border dissemination of knowledge, technologies, and institutions. Furthermore, geographically proximate countries tend to have similar (fundamental) characteristics, including geography, histories, cultures, climatic conditions, and short periods of ancestral separation. Thus, geographically close countries are less likely to experience long-term barriers to the worldwide diffusion of climate change policies. The main findings withstand controlling for geographical distance, indicating that genetic distance, rather than geographical proximity, is important for explaining the cross-border movements of climate change policies. However, it is worth

---

[19] These estimates, not reported for brevity, are available upon request.

[20] This is in contrast to the cross-country evidence documenting that genetic distance bears a statistically significant correlation with the stock of climate laws across countries. While the CCLW provides internationally comparable data on climate change mitigation laws, it merely focuses on legislation at the national level. Hence, the stock of climate change mitigation laws can be imperfect proxies for international differences in climate change responses especially in countries with a considerable quantity of climate action implemented at the subnational level (CCLW, 2020). This is a potential interpretation of why the core findings cannot be generalized across country pairs when using the stock of climate laws as a measure of climate change policy performance.

examining whether the main results differ across country pairs with differential geographical proximity. To this end, I replicate the specification from Table 4, column (1) for three sub-groups of country pairs with low, medium, and high geographical distance. Specifically, country pairs whose geographical distance scores are in the first, second, or third terciles of the sample distribution are classified as low, medium, or high, respectively. As depicted in Figure 5, the coefficient on genetic distance *relative* to the UK is positive but imprecisely estimated when using a sample of country pairs with low geographical distance. By contrast, the core results retain their size and statistical significance when I use country pairs with medium or high degrees of geographical distance. These results provide partial evidence indicating that the role played by genetic distance in explaining countries' differences in the cross-border spillovers of climate change policies is decreasing with geographical distance.

Appendix A3 contains additional estimates of the relationship between genetic distance between countries *relative* to the UK and the absolute difference in climate change policy performance. Accordingly, I construct a binary indicator taking a value of 1 if both countries in each pair belong to a world region and zero otherwise, and another dummy variable for one and only one country in each pair belonging to a world region. As shown in Table A12, controlling for pairwise region dummies slightly reduces the magnitude of the coefficient on genetic distance *relative* to the UK but fails to fully absorb its statistical precision. As discussed previously, the variation in climate change policy performance across countries can be attributed to several geographical, historical, and contemporary characteristics. Hence, I create, for each country pair, the absolute differences in these factors and incorporate them in the regressions. However, the bilateral estimates remain intact in most cases (Tables A13 to A15).

4. GENETIC DISTANCE AND CO$_2$ EMISSIONS PER CAPITA

The analysis so far has focused on understanding the relationship between genetic distance and the global divergence in climate change policy performance. There is ample evidence suggesting the emission-reducing effects of climate change policies across the globe (Andersson, 2019; Eskander and Fankhauser, 2020). However, the main results do not permit an interpretation of the correlation between genetic distance and *actual* reductions in CO$_2$ emissions. Moreover, an important concern is that the baseline indicators of climate change policy performance can be imperfect proxies for true variations in collective responses to changing climate conditions across countries over years. Therefore, I now explore the relationship between genetic distance and CO_2 emissions per capita, following the approach adopted in Jo and Carattini (2021).

Analysis of the relationship between genetic distance and actual climate change mitigation critically requires attention to substantial heterogeneity in the sizeable costs associated with reductions of CO_2 emissions across countries. Specifically, the opportunity costs associated with emission abatement are typically higher for developing countries endowed with less resources. Moreover, countries at early stages of economic development arguably face higher opportunity costs of adopting low-carbon technologies due to concerns about the trade-off between economic growth and climate protection. Collective climate action is also hindered by the argument that an energy transition impedes hard-won progress in various aspects of sustainable development (e.g., health and education improvements and poverty reductions) around the developing world.[21] Therefore, developing countries are less inclined to curb GHG emissions. On this basis, I hypothesize that the cross-country relationship between genetic distance and CO_2 emissions is larger among countries with high levels of income per capita enough to cover the opportunity costs of emission abatement.

To test the above hypothesis, I first re-estimate equation [1] but use log of CO_2 emissions per capita in 2010 as the outcome variable, as shown in columns (1) and (3) of Table 5. Accordingly, genetic distance to the UK enters all the regressions with an imprecisely estimated coefficient. Then, I augment the regression analysis with log of GDP per capita and its interaction term with genetic distance to the UK. Results reported in columns (2) and (4) of Table 5 indicate a positive association between genetic distance to the UK and the intensity of CO_2 emissions depending on the level of economic development. Consistent with the above prediction, the interaction effect is larger among countries with higher levels of income per head. This reveals that the relationship between genetic distance and actual changes in climate change mitigation is heterogeneous across countries at different stages of economic development. Furthermore, I re-estimate equation [3] but replace the outcome variable by the absolute difference in log of CO_2 emissions per capita in 2010. As shown in columns (1) and (2) of Table 6, I find precise estimates of a positive but heterogeneous association between genetic distance and the absolute difference in CO_2 emissions per capita across country pairs with differential distances in the level of economic development.

---

[21] This line of reasoning is also consistent with Tol (2019) documenting that low-income countries bear a significantly higher social cost of carbon.

If genetic distance reflects worldwide differences in barriers to the horizontal diffusion of climate change responses across jurisdictions, the above results should hold only after climate change was recognized as a pressing issue facing the contemporary word. Otherwise, my findings can be attributed to conventional socio-economic and political correlates of environmental performance. There have been growing discussions on the human causes and consequences of changing climate conditions since the 1980s, leading to growing recognition of the importance of climate change mitigation. International cooperation in the climate commons began with the ratification of the UNFCCC at the Earth Summit in Rio de Janeiro (Brazil) in June 1992 (Buchholz and Sandler, 2021). Hence, if the main hypothesis is valid, the positive association between genetic distance and CO_2 emissions per capita should be smaller in size and economic significance before the Rio Earth Summit in 1992.

Following Jo and Carattini (2021), I replicate the specifications from columns (1) to (4) of Table 5 and columns (1) and (2) of Table 6 but use data for CO_2 emissions per capita in 1950. Results shown in columns (5) to (8) of Table 5 and columns (3) and (4) of Table 6 indicate that the association between genetic distance and emissions intensity for the year 1950 is statistically insignificant in all cases. This is consistent with the above prediction. Next, I replicate the specifications from column (4) of Table 5 and column (1) of Table 6 but use log of CO_2 emissions per capita measured for each year from 1960 to 2022. Results depicted in Figures 6 and 7 reveal that the positive relationship between genetic distance and CO_2 emissions per capita is larger among countries with higher levels of GDP per capita. Importantly, the interaction variable of interest becomes more precisely estimated after the adoption of the UNFCCC in 1992. This indicates that the role played by genetic distance in shaping barriers to international climate change policy spillovers is observed only after climate change became a globally recognized issue. Furthermore, these results help rule out the possibility that the main findings can be attributed to conventional explanations of the worldwide divergence in national responses to climate change.

5. GENETIC DISTANCE AND PREFERENCES FOR THE PROVISION OF ENVIRONMENTAL PUBLIC GOODS

5.1. Genetic distance and the worldwide variation in pro-environmentalism

The central hypothesis is premised on the assumption that genetic distance captures countries' dissimilarities in vertical human traits, which in turn affect the cross-border diffusion of climate change policies. Specifically, I hypothesize that countries with larger genetic distance tend to have more dissimilar preferences for the provision of the public goods of environmental or climate protection.

To test the above proposition, I construct alternative measures of pro-environmentalism at the country level using data from various waves of the World Values Survey (WVS) implemented from 1981 to 2022. I rely on surveyed respondents' attitudes toward the statement that "Protecting the environment should be given priority, even if it causes slower economic growth and some loss of jobs" (*evtprotect*); data are available in waves 3 to 7 of the WVS. A key advantage of using responses to this statement lies its wide coverage of countries and survey participants, making it convenient to construct a nationally representative measure of pro-environmentalism across 106 countries. Nonetheless, attitudes toward this statement may reflect preferences for a trade-off between economic growth and environmental protection. This presumably differs widely across countries at different levels of economic development, making it difficult to obtain an internationally comparable measure of pro-environmentalism. Thus, I mitigate this concern by using responses to the statement that global warming is a somewhat or very serious environmental problem in the world (*globwarm*) and self-reported support for increases in taxes if extra money is used to prevent environmental pollution (*evttaxes*).[22] Data on *globwarm* and *evttaxes* are available in waves 5 and 6 and waves 2 to 5 of the WVS, respectively. Responses are coded as 1 if survey participants agree with these statements, and 0 otherwise; agreement reflects a greater prevalence of pro-environmentalism. For each country in a given wave of the WVS, I calculate the fraction of survey respondents who exhibit pro-environmentalism, which are then averaged over all waves of the WVS. This yields alternative country-level measures of pro-environmentalism.

I first re-estimate equation [1] but use *evtprotect*, *globwarm*, and *evttaxes* as alternative outcome variables. As reported in panel A of Table 7, despite substantial constraints on the feasible sample size, genetic distance to the UK is negatively associated with the prevalence of pro-environmentalism in all cases. However, this relationship is imprecisely estimated at conventional levels of statistical significance when I use *evttaxes* to capture pro-environmental attitudes. The results indicate that countries with greater genetic distance to the global frontier are endowed with less public support for climate change mitigation. To generalize this finding,

---

[22] This approach is in line with previous studies highlighting the influence of public beliefs and risk perceptions of climate change on support for climate change mitigation (Leiserowitz, 2005; Lorenzoni and Pidgeon, 2006). Given the importance of (environmental) taxation for energy transitions, support for higher environmental taxes reflects individuals' willingness to contribute to the provision of environmental public goods, which affects collective responses to climate change.

I also re-estimate equation [3] by regressing the distance in pro-environmentalism between countries on their genetic distance *relative* to the UK, and present the results in Panel B of Table 7. Accordingly, I find that genetic distance *relative* to the UK positively relates to the global divergence in public support for climate change mitigation. This implies that genetic distance between countries captures their dissimilarities in preferences for government policies or, more specifically, the provision of environmental public goods, which are in turn important for collective responses to changing climate conditions.

The existing literature suggests that cultures tend to co-evolve with formal institutions (Alesina and Giuliano, 2015).[23] For this reason, countries' dissimilarities in cultural/historical legacies are more likely to establish different types of formal institutions (e.g., extractive or inclusive political institutions).[24] One could argue that genetic distance helps explain the worldwide variation in climate change policy performance via shaping the nature of formal institutions, independent of its influence on cultures (or informal institutions). To check for this possibility, I re-estimate equation [1] but use a measure of institutional quality as the outcome variable. I also implement this exercise using alternative and placebo frontier countries, in line with the preceding analysis. Figure 8 depicts the cross-country relationship between genetic distance to the frontier and institutional quality. Accordingly, the estimated coefficients on genetic distance to alternative frontier countries are negative and statistically significant at the 5% or 10% levels in most cases. Consistent with the main results, I find that genetic distance to Slovenia (a placebo frontier) enters the regression with a negative but statistically insignificant coefficient. These results provide partial evidence suggesting that genetic distance to the world frontier of climate change mitigation may be correlated with the quality of formal institutions, which is presumably a key determinant of climate change policies.

5.2. The intergenerational transmission of collective climate action

Previous studies document that cultural traits might have been transmitted across generations (see, e.g., Boyd and Richerson, 1985; Bisin and Verdier, 2000; Algan and Cahuc, 2010; Alesina, Giuliano, and Nunn, 2013). Thus, genetic distance associated with long-run exposure to divergent historical paths gives rise to the divergence in intergenerationally transmitted cultural values. This would eventually impede international policy diffusion. To provide further

---

[23] Alesina and Giuliano (2015) provide a comprehensive review of the literature on the relationship between culture and formal institutions.

[24] This argument is in line with Spolaore and Wacziarg (2016a, 2018) documenting that long-term relatedness between countries affects the cross-border diffusion of political institutions.

support for the main hypothesis, I examine the intergenerational transmission of cultural traits of cooperation in the climate commons.

A major challenge with testing for the persistence of cultural norms of collective climate action relates to the absence of a historical proxy for pro-environmental attitudes. Thus, I rely on a sample of second-generation European migrants to document partial evidence of the vertical transmission of cultural values from parents to children, following the approach adopted in Algan and Cahuc (2010).[25] I investigate the relationship between parental-country-of-origin genetic distance to the world frontier and self-reported pro-environmental behaviors among second-generation Europeans. The empirical analysis exploits variations across EU-born individuals residing in the same country but whose parents were born in a foreign nation. In other words, I rely on variations across second-generation Europeans characterized by diverse cultural backgrounds but with exposure to a homogenous institutional, economic, and educational system; this is ensured by the inclusion of country-of-residence fixed effects in the regression. This approach permits accounting for unobserved time-invariant heterogeneity across countries of residence. As such, the divergence in self-reported pro-environmental behaviors is unlikely to be attributed to economic or institutional development at the country level. This allows me to distinguish the intergenerational transmission of cultural values from economic or institutional factors.

I employ data spanning several rounds of the European Social Survey (ESS) from 2002 to 2020. To measure pro-environmental attitudes, I rely on responses to the statement that "It is important to care for nature and environment," recorded on a categorical scale between 1 and 6 with higher values corresponding to greater disagreement with this statement. For ease of interpretation, I multiply the outcome variable by minus 1 in order for higher values indicating greater support for environmental protection. I specify the following econometric model:

$$ENV_{i,c,o,t} = \beta_0 + \beta_1 Gdist_o^{UK} + \beta_2 X_{i,o} + \beta_3 f_c + \beta_4 f_t + \varepsilon_{i,c,o,t}, \qquad [4]$$

where $ENV_{i,c,o,t}$ captures pro-environmentalism of individual i participating in round t of the ESS, residing in country c, and originating from country o; $Gdist_o^{UK}$ is the measure of genetic distance to the UK at the country-of-origin level, rescaled by dividing by 1,000 to improve readability; $X_{i,o}$ denotes a vector of individual and country-of-origin controls; f_c and f_t capture

---

[25] This strategy is consistent with previous studies documenting the international transmission of gender norms, social trust, and other cultural values (Bisin and Verdier, 2000; Algan and Cahuc, 2010; Alesina, Giuliano, and Nunn, 2013).

country-of-residence and survey-wave fixed effects, respectively; and $\varepsilon_{i,c,o,t}$ is an unobserved error term. Heteroscedasticity-robust standard errors are adjusted for clustering at the country-of-origin level.

A possible problem with estimating equation [4] relates to selective migration. One might argue that migrants from countries that are genetically distant to the global frontier could have chosen to enter certain groups of countries depending on cultural/historical distance to their home countries. If differential migrant selectivity is correlated with genetic distance to the frontier, empirical estimates of equation [4] do not carry a causal interpretation of cultural transmission.[26] To partially address this concern, I augment the regression analysis with a set of country-of-origin controls for geographical attributes, the deep roots of economic development, and region dummies. This accounts for the possibility that migrant selectivity is driven by these fundamental characteristics. It is worth noting that countries in the same world region may share common histories, cultures, geography, and other slowly evolving characteristics, thereby shaping the patterns of regional migrant selectivity.

Table 8 contains estimates of equation [4]. In columns (1) to (6), I define ancestry by using the father's country of birth or the mother's country of birth. I also use the same country of birth of both parents to identify ancestry in columns (7) to (9). Accordingly, genetic distance to the UK enters all the regressions with a negative and statistically significant coefficient. This suggests that second-generation Europeans originating from countries that are genetically distant to the UK are less likely to exhibit pro-environmental attitudes. This finding underlies the argument that countries with greater genetic distance to the frontier are characterized by a less prevalence of intergenerationally transmitted norms of cooperation in climate change mitigation. To further address concerns about selective migration, I control for genetic distance *relative* to the UK between sending and receiving countries. However, the coefficient on genetic distance to the UK turns out to the imprecisely estimated in most cases.[27] Substantial reductions in the statistical precision of the main variable of interest can be attributed to a high correlation of nearly 0.7 between these measures of genetic distance. An important caveat is that the results reported in Table 8 are merely suggestive but not conclusive of a causal interpretation of the intergenerational transmission of cultural values of pro-environmentalism.

---

[26] It is noteworthy that if factors driving migrant selectivity from different countries of origin to a specific country of residence are homogenous, the results are not confounded.

[27] These results, not reported for brevity, are available upon request.

6. FURTHER DISCUSSIONS

6.1. Alternative explanations

An alternative explanation of the main findings draws on the cross-border movements of environmentally friendly goods and technologies. Specifically, one might contend that countries characterized by large distance to the fronter in terms of cultural traits of collective climate action can still benefit from the diffusion of technological innovations through economic integration, thus reducing climate change mitigation costs. If this is true, the core results can be unrelated to countries' dissimilarities in preferences for the provision of environmental public goods. Although advances in technologies have considerably reduced trade costs and hence facilitate the worldwide diffusion of low-carbon technologies (Dechezleprêtre et al., 2011; Eugster et al., 2022), cultural differences, which tend to exhibit high time persistence, remain major impediments to international trade (Disdier and Head, 2008). It is worth re-emphasizing that cultural traits are central to shaping public support for climate change mitigation and the political feasibility of climate policies. Therefore, I hypothesize that a large portion of the association between genetic distance and climate change policy performance is attributed to countries' dissimilarities in slowly evolving cultural traits despite the widespread dissemination of environmentally friendly technologies worldwide.

To test the above prediction, I now attempt to rule out the possibility that the core results are exclusively driven by the international spillovers of environmentally friendly goods and technologies via international trade. A commonly adopted approach is to incorporate potential mediating factors in standard regression models as extra covariates and observe the stability of the main coefficient of interest. This strategy, however, may yield biased and inconsistent estimates because the diffusion of technologies across countries is interrelated with and jointly determined by climate change policy performance. The relationship between CCPS and technology spillovers can be confounded by a third omitted variable (e.g., socio-economic and political characteristics). Therefore, I follow Acharya, Blackwell, and Sen (2016) to adopt sequential g-estimation and implement a simple two-step regression procedure to address concerns about intermediate variable bias.[28] This method offers an intuitive approach to estimating the partial relationship between genetic distance to the UK and climate change policy performance when holding a potential mediator (e.g., technological spillovers or pro-environmentalism) fixed at a particular level.

---

[28] See Acharya, Blackwell, and Sen (2016) for a more detailed discussion on intermediate variable bias.

To implement this exercise, in line with Acharya, Blackwell, and Sen (2016), I first distinguish pre-treatment controls from intermediate confounding characteristics. In particular, the main control variables (including geographical attributes, the deep roots of economic development, and region dummies) are allowed to enter the regressions as pre-treatment variables because they may provide alternative fundamental explanations for worldwide differences in mediating factors or the outcome variable. By contrast, the conventional proximate causes of climate change policy performance (including log of GDP per capita, manufacturing value added, trade openness, female political representation, autocratic experience, democratic experience, and years of schooling) are treated as intermediate confounding factors given that they can be influenced by genetic distance and may affect both the mediator and the dependent variable.

I first regress a measure of climate change policy performance on genetic distance to the frontier, a mediator, pre-treatment controls, and intermediate confounders. Then, I compute the *transformed* dependent variable by removing the estimated impact of the mediator. In the second-stage regression, I regress the transformed outcome variable on genetic distance to the frontier and pre-treatment variables, excluding all the intermediate confounding characteristics. This provides estimates of the average controlled direct effect (ACDE) of genetic distance to the global frontier on climate change policy performance accounting for the proposed mediator. I attempt to capture the cross-border movements of low-carbon technologies by using log of imports of environmentally friendly goods and technologies (EG) from the frontier or the rest of the world, based on the WTO's and OECD's classifications of EG. I also use total imports to measure the diffusion of broadly defined technologies. Moreover, I use log of GDP per capita to capture the role played by genetic distance in shaping the diffusion of development, as established in Spolaore and Wacziarg (2009). In line with the preceding analysis, I use the share of surveyed respondents of the WVS with pro-environmental attitudes to capture international differences in pro-environmentalism; I hypothesize that pro-environmentalism is a key mechanism underlying the baseline results.

In the interest of brevity, I depict the point estimates and 95% confidence intervals of the estimated coefficient on genetic distance to the UK in Figure 9. As illustrated in Figures 9A and 9B, the estimated coefficient on genetic distance to the UK remains negative and statistically significant in most cases. This implies that the statistically and economically significant relationship between genetic distance and climate change policy performance across countries is largely unaffected by controlling for the cross-border diffusion of EG and development across jurisdictions. As such, a large portion of the baseline estimates remains unexplained after accounting for alternative interpretations. By contrast, when I partial out the influence of pro-environmentalism, the coefficient on genetic distance to the UK turns out to be imprecisely estimated at conventional levels of statistical significance, as depicted in Figures 9C and 9D. This is consistent with my prediction that the main findings are primarily explained by cross-country differences in preferences for the provision of environmental public goods.

6.2. Policy implications

The overly deterministic nature of long-term barriers to the international diffusion of climate change policies implies that policymakers are virtually unable to change countries' dissimilarities in intergenerationally transmitted cultural and historical characteristics. Nevertheless, climate change mitigation can be fostered by enacting policies that help attenuate the long-term legacy of deep-rooted genetic distance for national responses to changing climate conditions. In this regard, a misinterpretation of my findings is that addressing climate change necessitates changes in the genetic admixture of a country's populations. Instead, policy interventions should focus on overcoming such barriers.

A potential approach is to strengthen the exchange of ideas, knowledge, and institutions between countries, for example, by promoting socio-economic, cultural, and political integration at the regional and international levels. It is argued that integration, such as the formation of free trade areas, common markets, or other intergovernmental institutional arrangements, constitutes structured communication networks between jurisdictions and thereby facilitates the spillovers of technological and institutional innovations. As proposed by Nordhaus (2015), climate change responses worldwide can be enhanced by the development of stable, cooperative climate coalitions combining regulations of trade liberalization and targets of GHG emission abatement, which helps reduce free-riding fears in climate change mitigation. Moreover, integration is central to building trust and reciprocal beliefs in the provision of the global public goods of climate protection, as evidenced by the influence of EU membership on the adoption of climate policies in post-communist countries. In this regard, the EU is considered as a credible model of climate change mitigation, thus enhancing the adoption of the EU's environmental standards among transitional economies (e.g., Bulgaria, Estonia, and Slovenia) following their accession to the EU (Tosun and Mišić, 2022). Moreover, these post-communist countries, by aligning themselves with the economic and political structures of the EU, could improve the political feasibility of adopting institutional innovations originating from the frontier. Therefore, economic integration is an effective way of mitigating barriers to the cross-border spillovers of climate change policies.

Additionally, my findings can be leveraged to evaluate countries' performance in climate change mitigation. It is expected that countries that are culturally and historically distant to the global frontier are endowed with worse climate change policies. For this reason, climate change mitigation can be strengthened by providing support for the laggards in curbing GHG emissions. For example, India, albeit endowed with a significant genetic distance to the world frontier, has played an increasingly important role in climate change mitigation at the global level, attributed to funding and other support provided by intergovernmental networks (Gupta and Parihar, 2024). Christoff and Sommer (2018) reveal that Indian climate change mitigation and adaptation projects greatly benefited from the UNFCCC's *Momentum for Change* media strategy, which relied on connections with policymakers, media outreach, and professional training to improve public support for climate change policies in India. This is an example of how intergovernmental networks can attenuate cultural barriers to adopting institutional innovations in the laggards of emission abatement, thereby increasing the political feasibility of climate change policies. In addition, investments in developing an educational system that instills cooperative behaviors in the climate commons will reduce persistent resistance to climate change mitigation in the laggards.

It is worth emphasizing that quantifying the emission-reducing impact of the aforementioned policy interventions lies outside the empirical framework of this study. Therefore, the above narratives are merely suggestive of potential approaches to overcoming the effect of deep-rooted barriers. As discussed earlier, the world frontier does vary depending on the specific innovation and is not immutable. For this reason, the established role of genetic distance as a fundamental determinant of climate change policy performance does not imply that countries' dissimilarities in vertical characteristics govern long-run outcomes. Indeed, there is room for policy interventions to break away from the long-term legacy of predetermined genetic distance. Moreover, devising effective strategies that help reduce such barriers requires identifying specific mechanisms underlying the cross-border diffusion of climate change policies and the types of cultural traits that might have fostered cooperative behaviors in the first place. Future research, by pursuing these potential avenues, will inform policymakers with better approaches to mitigating the far-reaching consequences of global climate change.

7. CONCLUSION

This article offers evidence suggesting a statistically and economically significant association between genetic distance and climate change policy responses across countries. The main results indicate that countries that are genetically distant to the world-leading country of climate change mitigation tend to have poorer climate change policy performance due to greater barriers to the international diffusion of climate change policies. Additionally, the paper documents that genetic distance to the global frontier is positively associated with the intensity of CO_2 emissions among countries with high income per capita. This reflects the heterogeneous relationship between genetic distance and actual responses to climate change among countries at different stages of economic development. Exploiting data from the World Values Survey, the paper suggests that genetic distance reflects countries dissimilarities in the prevalence of pro-environmental attitudes, which plausibly affect climate change policy adoption. Further evidence reveals that second-generation European migrants descending from countries with greater genetic distance to the global frontier are less likely to express pro-environmental views, suggesting the intergenerational transmission of cooperative behaviors in the climate commons. Overall, the results reveal that genetic distance lies at the deep roots of the international diffusion of climate change policies and thereby helps shapes worldwide differences in national responses to changing climate conditions.

Acknowledgments

The author thanks Dorian Owen for his constant support and encouragement. The author is also grateful to Christian Langpap (the handling Editor) and three anonymous referees for their insightful comments and helpful suggestions that improved the paper. The author thanks Jorge De la Roca, David Flath, Andrew Vivian, Ali Moghaddasi-Kelishomi, Anna Rita Bennato, and participants at the workshop on “Development and Economics of Emerging and Developing Countries” at Loughborough University for valuable comments. The usual caveat applies.

REFERENCES

Acemoglu, D., Johnson, S., and Robinson, J. A. (2001). The Colonial Origins of Comparative Development: An Empirical Investigation. *American Economic Review, 91*, 1369-1401.

Acemoglu, D., Johnson, S., and Robinson, J. A. (2002). Reversal of Fortune: Geography and Institutions in the Making of the Modern World Income Distribution. *Quarterly Journal of Economics, 117*, 1231-1294.

Acharya, A., Blackwell, M., and Sen, M. (2016). Explaining Causal Findings without Bias: Detecting and Assessing Direct Effects. *American Political Science Review, 110*, 512-529.

Ahlerup, P., and Olsson, O. (2012). The Roots of Ethnic Diversity. *Journal of Economic Growth, 17*, 71-102.

Aklin, M., and Mildenberger, M. (2020). Prisoners of the Wrong Dilemma: Why Distributive Conflict, Not Collective Action, Characterizes the Politics of Climate Change. *Global Environmental Politics, 20*, 4-27.

Alesina, A., and Giuliano, P. (2015). Culture and Institutions. *Journal of Economic Literature, 53*, 898-944.

Alesina, A., Giuliano, P., and Nunn, N. (2013). On the Origins of Gender Roles: Women and the Plough. *Quarterly Journal of Economics, 128*, 469-530.

Algan, Y., and Cahuc, P. (2010). Inherited Trust and Growth. *American Economic Review, 100*, 2060-2092.

Andersson, J. J. (2019). Carbon Taxes and CO2 Emissions: Sweden as a Case Study. *American Economic Journal: Economic Policy, 11*, 1-30.

Andrews, I., Stock, J. H., and Sun, L. (2019). Weak Instruments in Instrumental Variables Regression: Theory and Practice. *Annual Review of Economics, 11*, 727-753.

Ang, J. B., and Fredriksson, P. G. (2017). Statehood Experience, Legal Traditions, and Climate Change Policies. *Economic Inquiry, 55*, 1511-1537.

Ang, J. B., and Fredriksson, P. G. (2021). Does an Early Start Help or Hurt? Statehood, Institutions and Modern Climate Change Policies. *Energy Economics, 94*, 105075.

Ang, J. B., and Kumar, S. (2014). Financial Development and Barriers to the Cross-Border Diffusion of Financial Innovation. *Journal of Banking & Finance, 39*, 43-56.

Arbatlı, C. E., Ashraf, Q. H., Galor, O., and Klemp, M. (2020). Diversity and Conflict. *Econometrica, 88*, 727-797.

Ashraf, Q. H., and Galor, O. (2013). The 'out of Africa' Hypothesis, Human Genetic Diversity, and Comparative Economic Development. *American Economic Review, 103*, 1-46.

Ashraf, Q. H., and Galor, O. (2018). The Macrogenoeconomics of Comparative Development. *Journal of Economic Literature, 56*, 1119-1155.

Averchenkova, A., Fankhauser, S., and Nachmany, M. (2017). *Trends in Climate Change Legislation*. Cheltenham: Edward Elgar Publishing Limited.

Barbier, E. B., Damania, R., and Léonard, D. (2005). Corruption, Trade and Resource Conversion. *Journal of Environmental Economics and Management, 50*, 276-299.

Barro, R. J., and Lee, J. W. (2013). A New Data Set of Educational Attainment in the World, 1950–2010. *Journal of Development Economics, 104*, 184-198.

Becker, A., Enke, B., and Falk, A. (2020). Ancient Origins of the Global Variation in Economic Preferences. *AEA Papers and Proceedings, 110*, 319-323.

Beiser-McGrath, L. F., and Bernauer, T. (2022). Domestic Provision of Global Public Goods: How Other Countries' Behavior Affects Public Support for Climate Policy. *Global Environmental Politics, 22*, 117-138.

Bellwood, P. (2014). *First Migrants: Ancient Migration in Global Perspective*. Malden, MA: Wiley-Blackwell.

Bisin, A., and Verdier, T. (2000). "Beyond the Melting Pot": Cultural Transmission, Marriage, and the Evolution of Ethnic and Religious Traits. *Quarterly Journal of Economics, 115*, 955-988.

Bocse, A.-M. (2020). The UK's Decision to Leave the European Union (Brexit) and Its Impact on the EU as a Climate Change Actor. *Climate Policy, 20*, 265-274.

Borcan, O., Olsson, O., and Putterman, L. (2018). State History and Economic Development: Evidence from Six Millennia. *Journal of Economic Growth, 23*, 1-40.

Boyd, R., and Richerson, P. J. (1985). *Culture and the Evolutionary Process*. Chicago: University of Chicago Press.

Buchholz, W., and Sandler, T. (2017). Successful Leadership in Global Public Good Provision: Incorporating Behavioural Approaches. *Environmental and Resource Economics, 67*, 591-607.

Buchholz, W., and Sandler, T. (2021). Global Public Goods: A Survey. *Journal of Economic Literature, 59*, 488-545.

Carattini, S., Baranzini, A., and Roca, J. (2015). Unconventional Determinants of Greenhouse Gas Emissions: The Role of Trust. *Environmental Policy and Governance, 25*, 243-257.

Carattini, S., Fankhauser, S., Gao, J., Gennaioli, C., and Panzarasa, P. (2023). What Does Network Analysis Teach Us About International Environmental Cooperation? *Ecological Economics, 205*, 107670.

Carattini, S., Levin, S., and Tavoni, A. (2019). Cooperation in the Climate Commons. *Review of Environmental Economics and Policy, 13*, 227-247.

Cavalli-Sforza, L. L., Menozzi, P., and Piazza, A. (1994). *The History and Geography of Human Genes*. Princeton, New Jersey: Princeton University Press.

CCLW (2020). Climate Change Laws of the World Database. Retrieved from https://climate-laws.org/

Cesarini, D., Dawes, C. T., Johannesson, M., Lichtenstein, P., and Wallace, B. (2009). Genetic Variation in Preferences for Giving and Risk Taking. *Quarterly Journal of Economics, 124*, 809-842.

Christoff, P. S., and Sommer, J. M. (2018). Women's Empowerment and Climate Change Adaptation in Gujarat, India: A Case-Study Analysis of the Local Impact of Transnational Advocacy Networks. *Sustainability, 10*, 1920.

Conley, T. G., Hansen, C. B., and Rossi, P. E. (2012). Plausibly Exogenous. *Review of Economics and Statistics, 94*, 260-272.

Damania, R., Fredriksson, P. G., and List, J. A. (2003). Trade Liberalization, Corruption, and Environmental Policy Formation: Theory and Evidence. *Journal of Environmental Economics and Management, 46*, 490-512.

Dechezleprêtre, A., Glachant, M., Haščič, I., Johnstone, N., and Ménière, Y. (2011). Invention and Transfer of Climate Change–Mitigation Technologies: A Global Analysis. *Review of Environmental Economics and Policy, 5*, 109-130.

Disdier, A.-C., and Head, K. (2008). The Puzzling Persistence of the Distance Effect on Bilateral Trade. *Review of Economics and Statistics, 90*, 37-48.

Dohmen, T., Falk, A., Huffman, D., and Sunde, U. (2012). The Intergenerational Transmission of Risk and Trust Attitudes. *Review of Economic Studies, 79*, 645-677.

Drukker, D. M., Prucha, I. R., and Raciborski, R. (2013). Maximum Likelihood and Generalized Spatial Two-Stage Least-Squares Estimators for a Spatial-Autoregressive Model with Spatial-Autoregressive Disturbances. *Stata Journal, 13*, 221-241.

Eskander, S. M. S. U., and Fankhauser, S. (2020). Reduction in Greenhouse Gas Emissions from National Climate Legislation. *Nature Climate Change, 10,* 750-756.

Esteban, J., Mayoral, L., and Ray, D. (2012). Ethnicity and Conflict: An Empirical Study. *American Economic Review, 102*, 1310-1342.

Eugster, J. L., Ho, G., Jaumotte, F., and Piazza, R. (2022). International Knowledge Spillovers. *Journal of Economic Geography, 22*, 1191-1224.

Fankhauser, S., Gennaioli, C., and Collins, M. (2015). The Political Economy of Passing Climate Change Legislation: Evidence from a Survey. *Global Environmental Change, 35,* 52-61.

Fankhauser, S., Gennaioli, C., and Collins, M. (2016). Do International Factors Influence the Passage of Climate Change Legislation? *Climate Policy, 16,* 318-331.

Fariss, C. J., Anders, T., Markowitz, J. N., and Barnum, M. (2022). New Estimates of over 500 Years of Historic Gdp and Population Data. *Journal of Conflict Resolution, 66*, 553-591.

Farzin, Y. H., and Bond, C. A. (2006). Democracy and Environmental Quality. *Journal of Development Economics, 81*, 213-235.

Fearon, J. D. (2003). Ethnic and Cultural Diversity by Country. *Journal of Economic Growth, 8*, 195-222.

Fensore, I., Legge, S., and Schmid, L. (2022). Ancestry and International Trade. *Journal of Comparative Economics, 50,* 33-51.

Fredriksson, P. G., and Svensson, J. (2003). Political Instability, Corruption and Policy Formation: The Case of Environmental Policy. *Journal of Public Economics, 87,* 1383-1405.

Fredriksson, P. G., and Wollscheid, J. R. (2015). Legal Origins and Climate Change Policies in Former Colonies. *Environmental and Resource Economics, 62*, 309-327.

Friedlingstein, P., O'Sullivan, M., Jones, M. W., Andrew, R. M., Bakker, D. C. E., Hauck, J., . . . Zheng, B. (2023). Global Carbon Budget 2023. *Earth System Science Data, 15,* 5301-5369.

Gallup, J. L., Sachs, J. D., and Mellinger, A. D. (1999). Geography and Economic Development. *International Regional Science Review, 22*, 179-232.

Gupta, A. K., and Parihar, K. (2024). Global Climate Change Politics: Critical Appraisal of India’s Changing Role. *India Quarterly*, 1-16.

Iacobuta, G., Dubash, N. K., Upadhyaya, P., Deribe, M., and Höhne, N. (2018). National Climate Change Mitigation Legislation, Strategy and Targets: A Global Update. *Climate Policy*, *18,* 1114-1132.

Jo, A., and Carattini, S. (2021). Trust and CO2 Emissions: Cooperation on a Global Scale. *Journal of Economic Behavior & Organization, 190,* 922-937.

Kaufmann, D., Kraay, A., and Mastruzzi, M. (2010). The Worldwide Governance Indicators: A Summary of Methodology, Data and Analytical Issues. World Bank Policy Research Working Paper.

Kelemen, R. D., and Vogel, D. (2010). Trading Places: The Role of the United States and the European Union in International Environmental Politics. *Comparative Political Studies, 43,* 427-456.

Krieger, T., Renner, L., and Ruhose, J. (2018). Long-Term Relatedness between Countries and International Migrant selection. *Journal of International Economics, 113*, 35-54.

La Porta, R., Lopez-de-Silanes, F., Shleifer, A., and Vishny, R. W. (1999). The Quality of Government. *Journal of Law, Economics and Organization, 15,* 222-279.

Leiserowitz, A. A. (2005). American Risk Perceptions: Is Climate Change Dangerous? *Risk Analysis, 25,* 1433-1442.

Li, G. (1985). Robust Regression. In D. C. Hoaglin, F. Moseteller, & J. W. Tukey (Eds.), *Exploring Data Tables, Trends, and Shapes* (pp. 281-343). New York: Wiley.

Linsenmeier, M., Mohommad, A., and Schwerhoff, G. (2022). The International Diffusion of Policies for Climate Change Mitigation. IMF Working Paper WP/22/115.

List, J. A., and Sturm, D. M. (2006). How Elections Matter: Theory and Evidence from Environmental Policy. *Quarterly Journal of Economics*, *121*, 1249-1281.

Lorenzoni, I., and Pidgeon, N. F. (2006). Public Views on Climate Change: European and USA Perspectives. *Climatic Change*, *77*, 73-95.

Madsen, J. B., and Farhadi, M. (2018). International Technology Spillovers and Growth over the Past 142 Years: The Role of Genetic Proximity. *Economica*, *85*, 329-359.

Mason, C. F., Polasky, S., and Tarui, N. (2017). Cooperation on Climate-Change Mitigation. *European Economic Review*, *99*, 43-55.

Mavisakalyan, A., and Tarverdi, Y. (2019). Gender and Climate Change: Do Female Parliamentarians Make Difference? *European Journal of Political Economy*, *56*, 151-164.

Mavisakalyan, A., Tarverdi, Y., and Weber, C. (2018). Talking in the Present, Caring for the Future: Language and Environment. *Journal of Comparative Economics*, *46*, 1370-1387.

Mayer, T., and Zignago, S. (2011). Notes on CEPII's Distances Measures: The Geodist Database. CEPII Working Paper No 25/2011.

Michalopoulos, S. (2012). The Origins of Ethnolinguistic Diversity. *American Economic Review*, *102*, 1508-1539.

Nei, M. (1972). Genetic Distance between Populations. *American Naturalist*, *106*, 283-292.

Nordhaus, W. (2015). Climate Clubs: Overcoming Free-Riding in International Climate Policy. *American Economic Review*, *105*, 1339-1370.

Nunn, N., and Puga, D. (2012). Ruggedness: The Blessing of Bad Geography in Africa. *Review of Economics and Statistics*, *94*, 20-36.

Obinger, H., Schmitt, C., and Starke, P. (2013). Policy Diffusion and Policy Transfer in Comparative Welfare State Research. *Social Policy & Administration*, *47*, 111-129.

Olea, J. L. M., and Pflueger, C. (2013). A Robust Test for Weak Instruments. *Journal of Business & Economic Statistics*, *31*, 358-369.

Oliva, P. (2015). Environmental Regulations and Corruption: Automobile Emissions in Mexico City. *Journal of Political Economy*, *123*, 686-724.

Ostrom, E. (1990). *Governing the Commons: The Evolution of Institutions for Collective Action*. Cambridge: Cambridge University Press.

Ostrom, E. (2000). Collective Action and the Evolution of Social Norms. *Journal of Economic Perspectives*, *14*, 137-158.

Owen, A. L., and Videras, J. (2008). Trust, Cooperation, and Implementation of Sustainability Programs: The Case of Local Agenda 21. *Ecological Economics*, *68*, 259-272.

Pemberton, T. J., DeGiorgio, M., and Rosenberg, N. A. (2013). Population Structure in a Comprehensive Genomic Data Set on Human Microsatellite Variation. *G3 Genes|Genomes|Genetics*, *3*, 891-907.

Pitlik, H. (2007). A Race to Liberalization? Diffusion of Economic Policy Reform among OECD-Economies. *Public Choice*, *132*, 159-178.

Proto, E., and Oswald, A. J. (2017). National Happiness and Genetic Distance: A Cautious Exploration. *Economic Journal*, *127*, 2127-2152.

Putterman, L. (2006). Agricultural Transition Year-Country Dataset. Retrieved from https://www.brown.edu/Departments/Economics/Faculty/Louis_Putterman/

Rogers, E. M. (1995). *Diffusion of Innovations*. New York: Free Press.

Rose, R. (1993). *Lesson-Drawing in Public Policy: A Guide to Learning across Time and Space*. Washington, D.C.: CQ Press.

Sauquet, A. (2014). Exploring the Nature of Inter-Country Interactions in the Process of Ratifying International Environmental Agreements: The Case of the Kyoto Protocol. *Public Choice, 159*, 141-158.

Sauvage, J. (2014). The Stringency of Environmental Regulations and Trade in Environmental Goods. OECD Trade and Environment Working Papers No. 2014/03.

Sharma, S., Ang, J. B., and Fredriksson, P. G. (2021). Religiosity and Climate Change Policies. *Energy Economics, 101*, 105414.

Simmons, B. A., and Elkins, Z. (2004). The Globalization of Liberalization: Policy Diffusion in the International Political Economy. *American Political Science Review, 98*, 171-189.

Spolaore, E., and Wacziarg, R. (2009). The Diffusion of Development. *Quarterly Journal of Economics, 124*, 469-529.

Spolaore, E., and Wacziarg, R. (2013). How Deep Are the Roots of Economic Development? *Journal of Economic Literature, 51*, 325-369.

Spolaore, E., and Wacziarg, R. (2016a). The Diffusion of Institutions. In D. S. Wilson & A. Kirman (Eds.), *Complexity and Evolution: Toward a New Synthesis for Economics* (pp. 145-164). Cambridge, MA: The MIT Press.

Spolaore, E., and Wacziarg, R. (2016b). War and Relatedness. *Review of Economics and Statistics, 98*, 925-939.

Spolaore, E., and Wacziarg, R. (2018). Ancestry and Development: New Evidence. *Journal of Applied Econometrics, 33*, 748-762.

Spolaore, E., and Wacziarg, R. (2022). Fertility and Modernity. *Economic Journal, 132*, 796-833.

Steves, F., Treisman, D., and Teytelboym, A. (2011). Political Economy of Climate Change Policy in the Transition Region. In *The Low Carbon Transition*. EBRD and the Grantham Research Institute on Climate Change and the Environment, London School of Economics, London.

Tabellini, G. (2008). The Scope of Cooperation: Values and Incentives. *Quarterly Journal of Economics, 123*, 905-950.

Tam, K.-P., and Chan, H.-W. (2018). Generalized Trust Narrows the Gap between Environmental Concern and Pro-Environmental Behavior: Multilevel Evidence. *Global Environmental Change, 48*, 182-194.

Thisted, E. V., and Thisted, R. V. (2020). The Diffusion of Carbon Taxes and Emission Trading Schemes: The Emerging Norm of Carbon Pricing. *Environmental Politics, 29*, 804-824.

Tol, R. S. J. (2019). A Social Cost of Carbon for (Almost) Every Country. *Energy Economics, 83*, 555-566.

Tosun, J., and Mišić, M. (2022). Post-Communist Countries' Participation in Global Forums on Climate Action. *Problems of Post-Communism, 69*, 380-395.

Townshend, T., Fankhauser, S., Aybar, R., Collins, M., Landesman, T., Nachmany, M., and Pavese, C. (2013). How National Legislation Can Help to Solve Climate Change. *Nature Climate Change, 3*, 430-432.

UN (2016). UN Comtrade Database. Retrieved from https://comtradeplus.un.org/

Vogler, J., and Stephan, H. R. (2007). The European Union in Global Environmental Governance: Leadership in the Making? *International Environmental Agreements: Politics, Law and Economics, 7*, 389-413.

Volden, C., Ting, M. M., and Carpenter, D. P. (2008). A Formal Model of Learning and Policy Diffusion. *American Political Science Review, 102*, 319-332.

Volland, B. (2017). The Role of Risk and Trust Attitudes in Explaining Residential Energy demand: Evidence from the United Kingdom. *Ecological Economics, 132*, 14-30.

Vu, T. V. (2021). Do Genetically Fragmented Societies Respond Less to Global Warming? Diversity and Climate Change Policies. *Energy Economics, 104*, 105652.

Vu, T. V. (2023). Long-Term Relatedness and Income Distribution: Understanding the Deep Roots of Inequality. *Oxford Economic Papers, 75*, 704-728.

Vu, T. V. (2024). Individualism and Collective Responses to Climate Change. *Land Economics*, *100*, 398-419.

WDI (2023). World Bank's World Development Indicators. Retrieved from https://wdi.worldbank.org

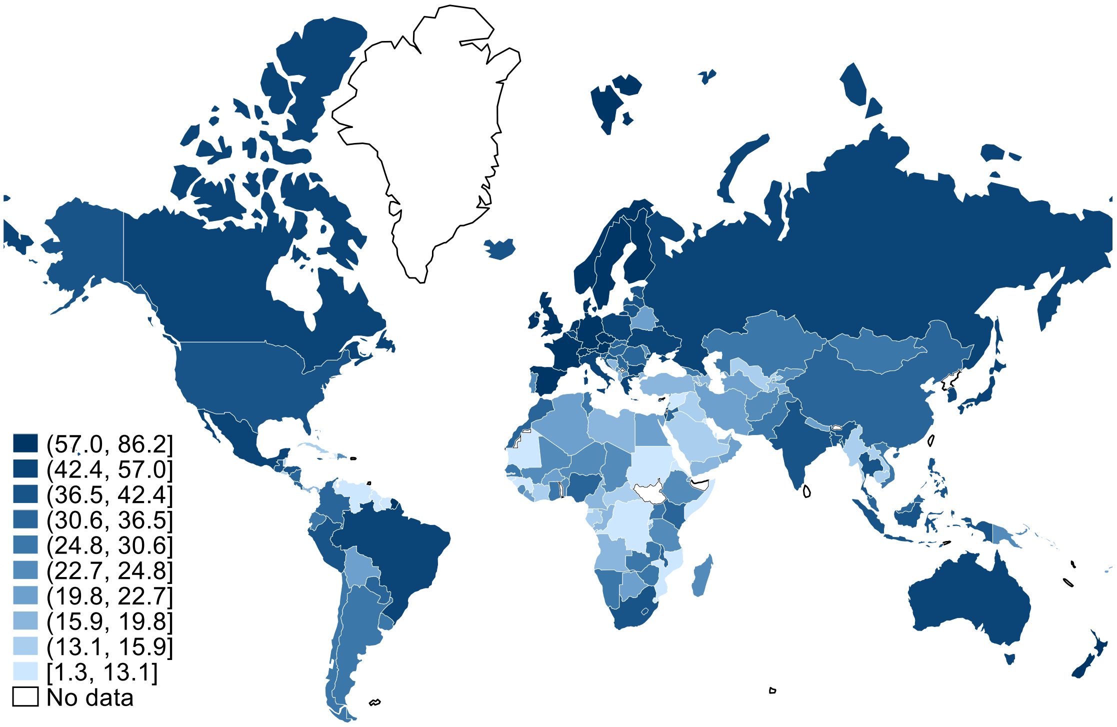
Wlezien, C. (1995). The Public as Thermostat: Dynamics of Preferences for Spending. *American Journal of Political Science, 39*, 981-1000.

WVS (2022). World Values Survey Version V3.0 (1981 - 2022). Retrieved from https://doi.org/10.14281/18241.17

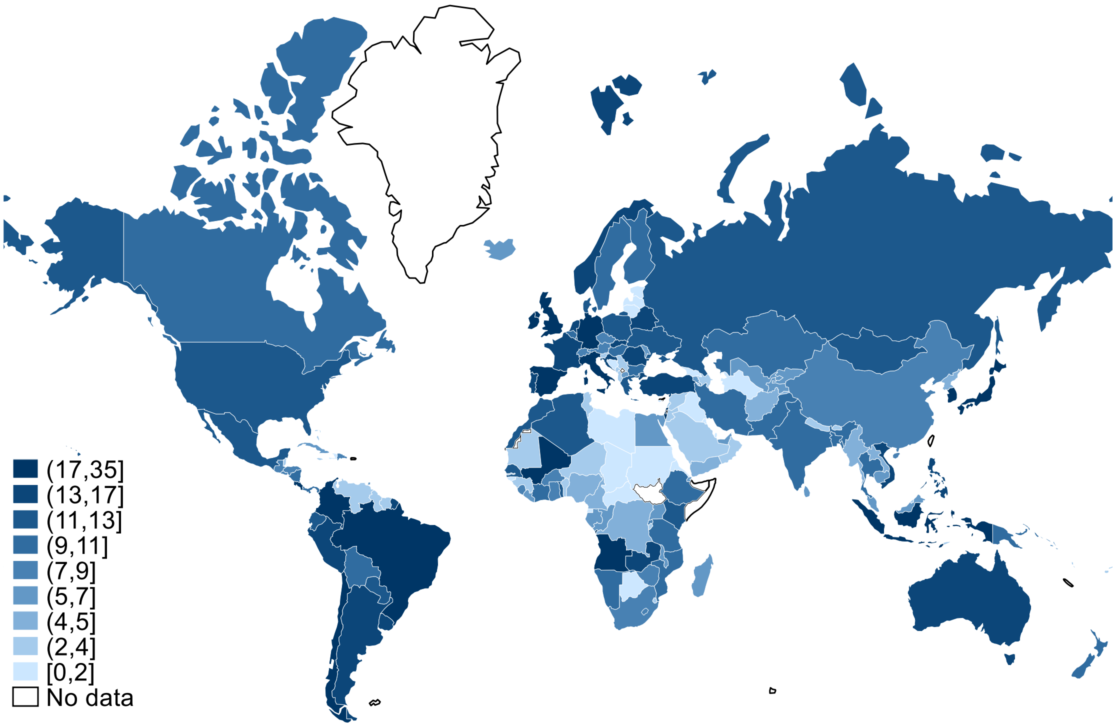
Figure 1

The cross-country variation in climate change policy performance

A. Climate change policy stringency index



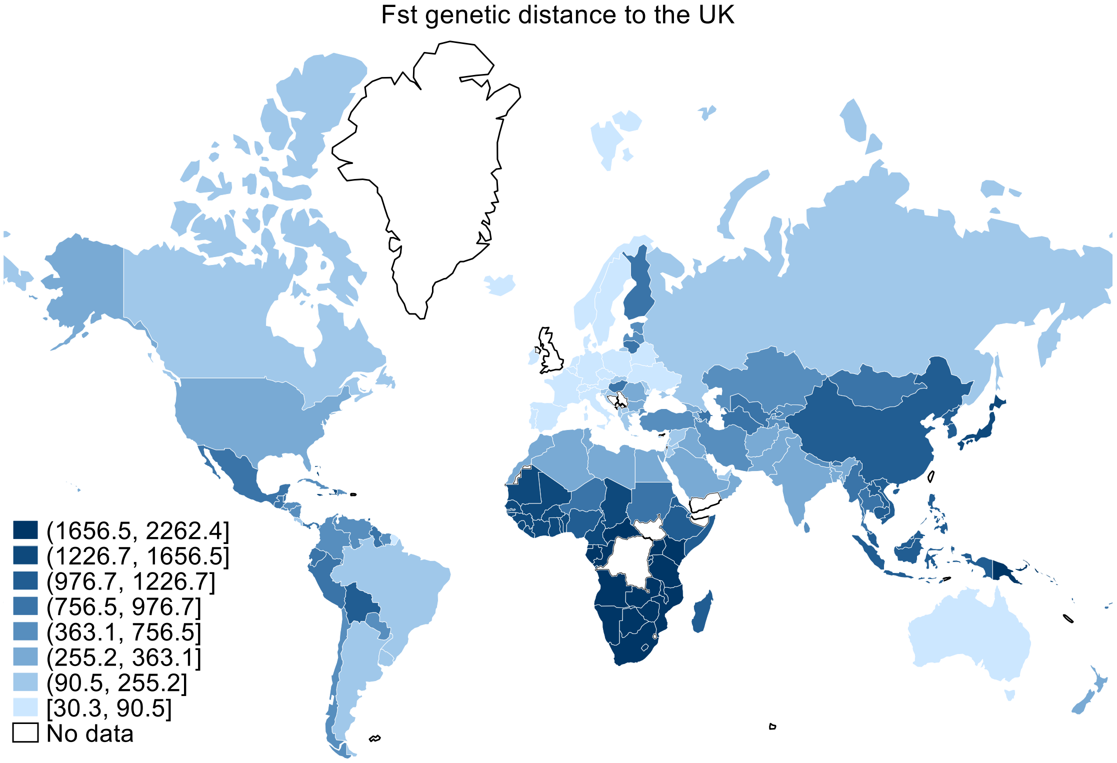
B. Stock of climate change mitigation laws



Note: This figure illustrates international differences in national responses to climate change, measured by the climate change policy stringency index and the stock of climate change mitigation laws passed between 1990 and 2019. Darker areas correspond to countries/territories with better climate change policy performance.

Figure 2

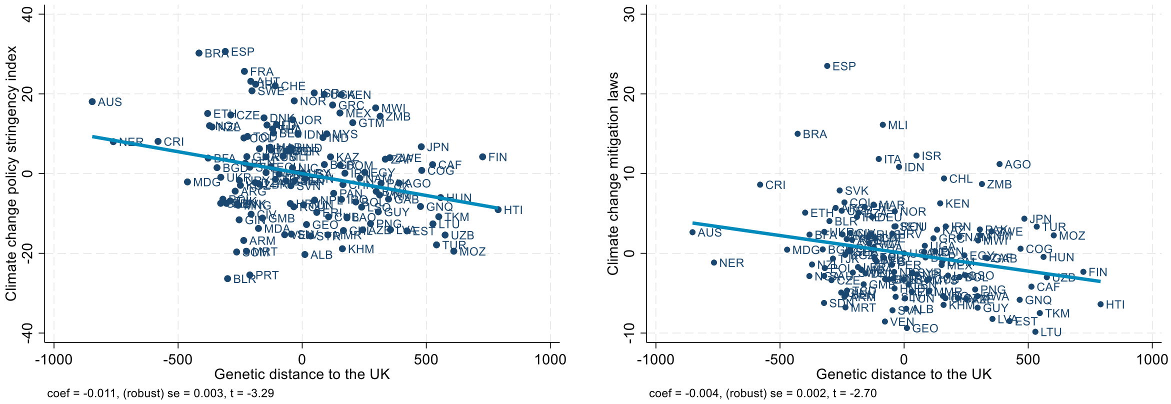
The cross-country variation in genetic distance to the UK



Note: This figure depicts the global variation in long-term relatedness between countries and the world frontier of climate change mitigation, captured by the F_{ST} measure of genetic distance to the UK. Darker areas correspond to countries/territories with greater distance to the UK in terms of cultures, ancestry, and historical legacies.

Figure 3

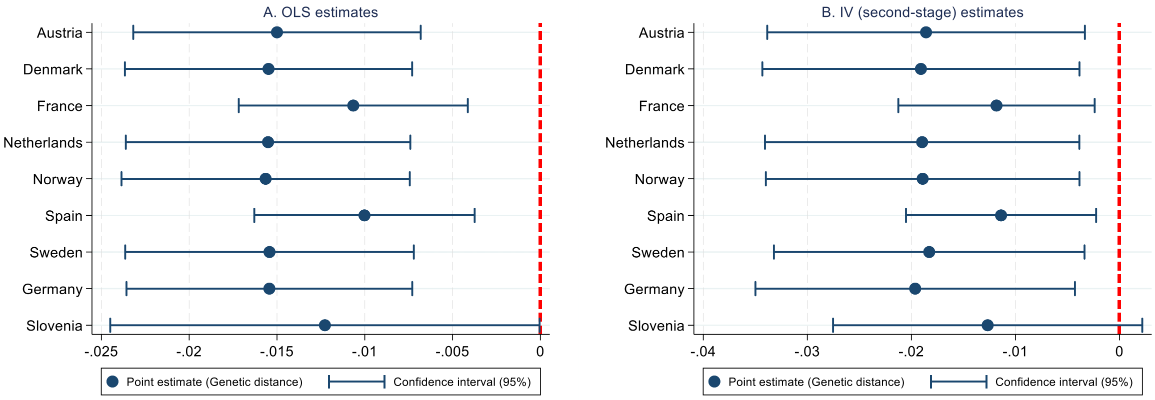
Genetic distance to the UK and climate change policy performance across countries



Note: This figure depicts the relationship between genetic distance to the UK and climate change policy performance across countries, conditional on geographical characteristics, the deep roots of economic development, and region dummies. The full estimates are reported in column (4) of Tables 2 and 3.

Figure 4

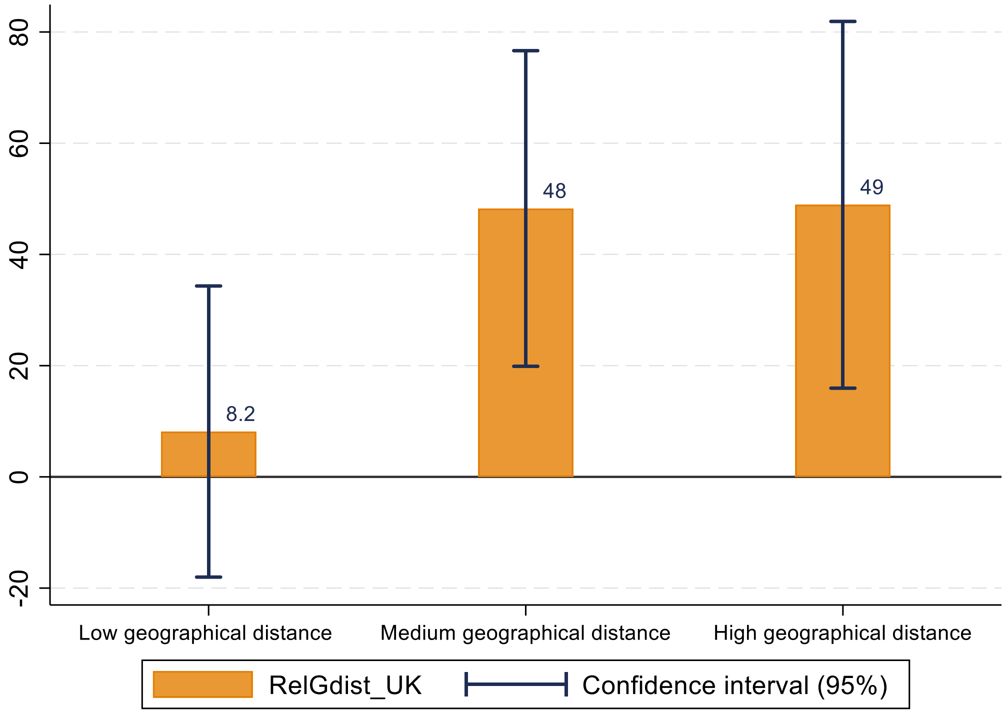
Genetic distance to alternative global frontiers and climate change policy performance



Note: This figure replicates the specifications from columns (4) and (6) of Table 2 but replaces genetic distance to the UK by genetic distance to alternative global frontiers, including Austria, Denmark, France, the Netherlands, Norway, Spain, Sweden, and Germany. Furthermore, Slovenia is selected as a placebo global frontier. To conserve space, I illustrate the point estimates and 95% confidence intervals of the coefficient on genetic distance to the frontier. All the regressions are augmented with geographical characteristics, the deep roots of economic development, and region dummies.

Figure 5

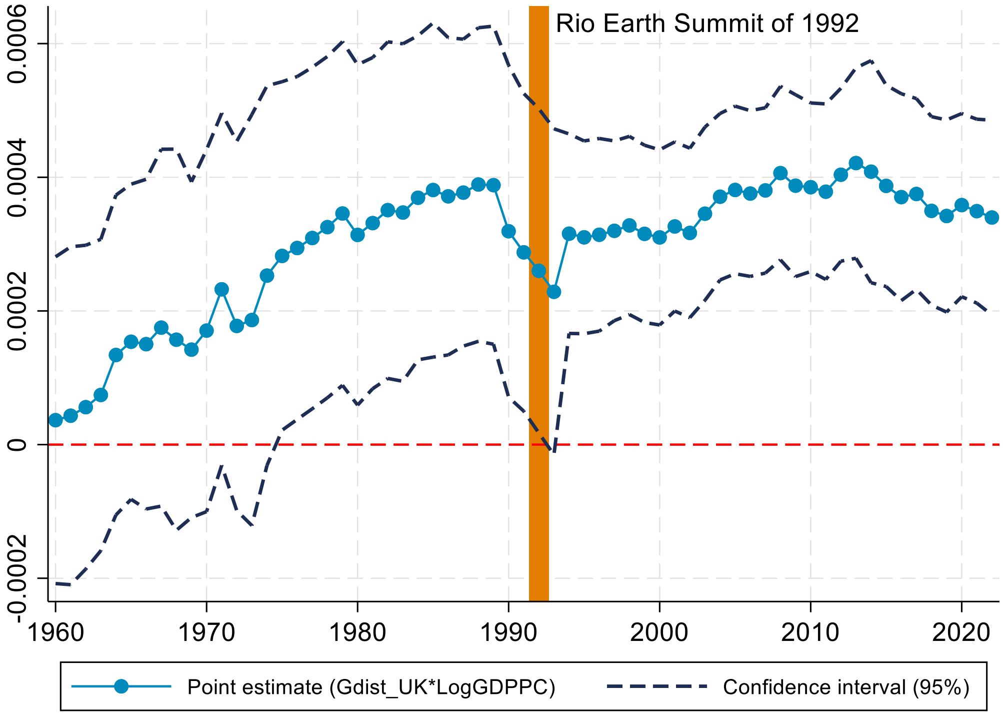
Genetic distance *relative* to the UK and absolute difference in climate change policy performance across country pairs with differential geographical distance



Note: This figure depicts the point estimates and 95% confidence intervals of the estimates of the relationship between genetic distance *relative* to the UK and bilateral differences in climate change policy performance across country pairs with differential levels of geographical distance. In particular, I re-estimate the specification from column (1) of Table 4 but use three different samples of country pairs with low, medium, or high geographical distance (whose scores are in the first, second, or third terciles of the sample distribution, respectively). All the regressions are augmented with pairwise controls and country fixed effects. Heteroscedasticity-robust standard errors are adjusted for clustering at both countries in a pair.

Figure 6

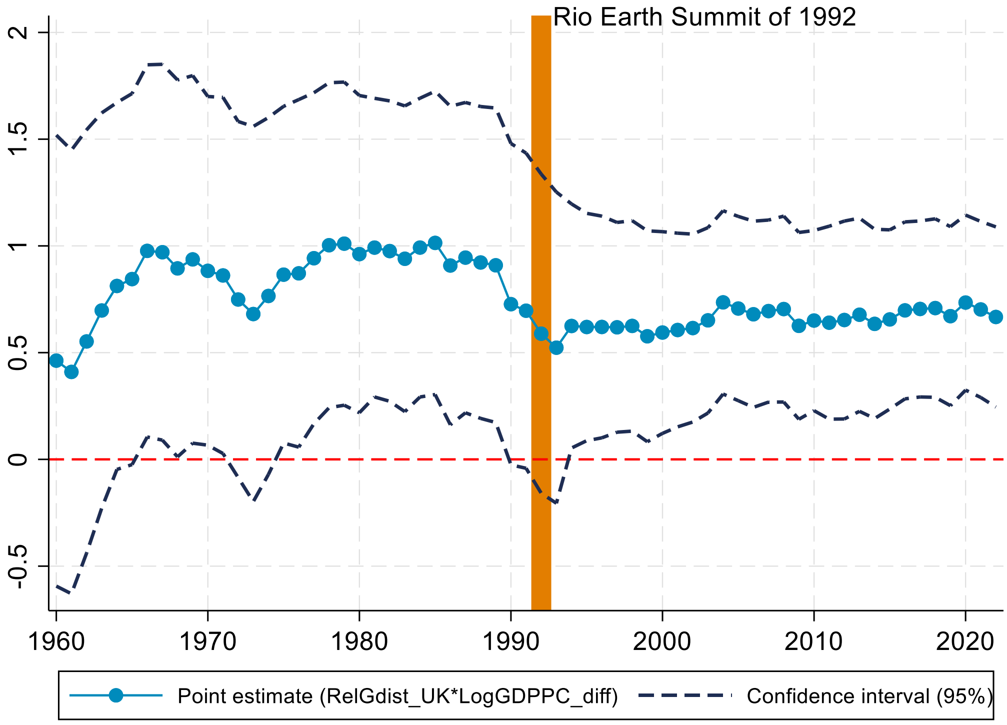
Genetic distance to the UK, economic development, and the intensity of CO_2 emissions across countries, 1960 – 2022



Note: This figure replicates the specification from column (4) of Table 5 but uses log of CO_2 emissions per capita measured for each year between 1960 and 2022. To conserve space, I depict the point estimates and 95% confidence intervals of the coefficient on the interaction term between genetic distance to the UK and income per capita. The vertical reference line shows the ratification of the UNFCCC at the 1992 Rio Earth Summit.

Figure 7

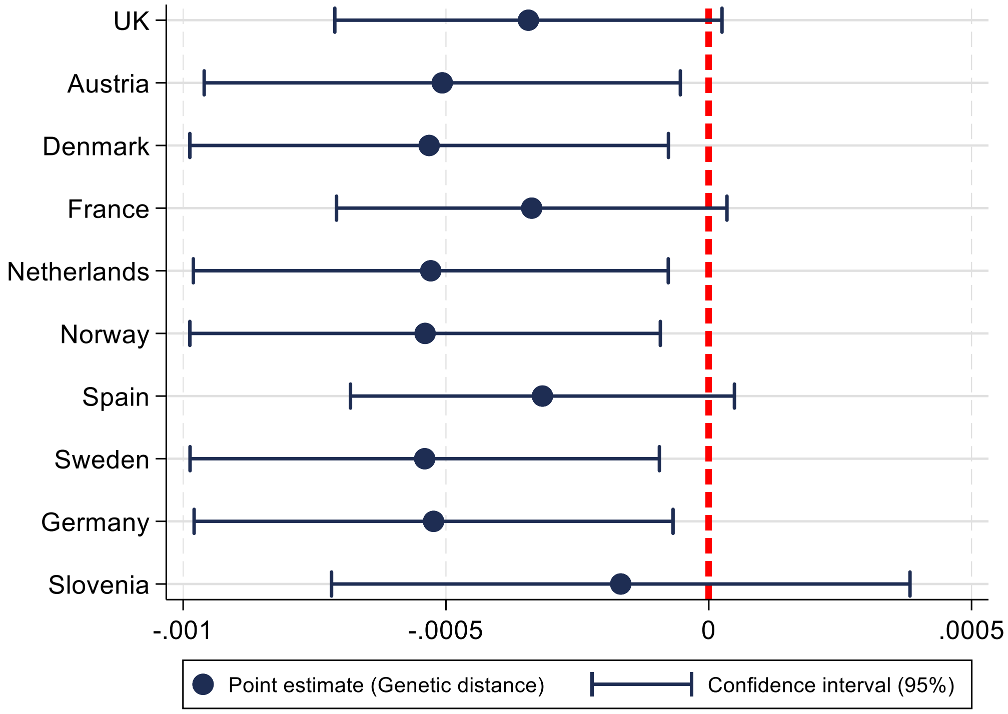
Genetic distance *relative* to the UK, absolute difference in economic development, and absolute difference in the intensity of CO_2 emissions across countries, 1960 – 2022



Note: This figure replicates the specification from column (1) of Table 6 but uses absolute difference in log of CO_2 emissions per capita measured for each year between 1960 and 2022. To conserve space, I depict the point estimates and 95% confidence intervals of the coefficient on the interaction term between genetic distance *relative* to the UK and the absolute difference in income per capita. The vertical reference line shows the ratification of the UNFCCC at the 1992 Rio Earth Summit.

Figure 8

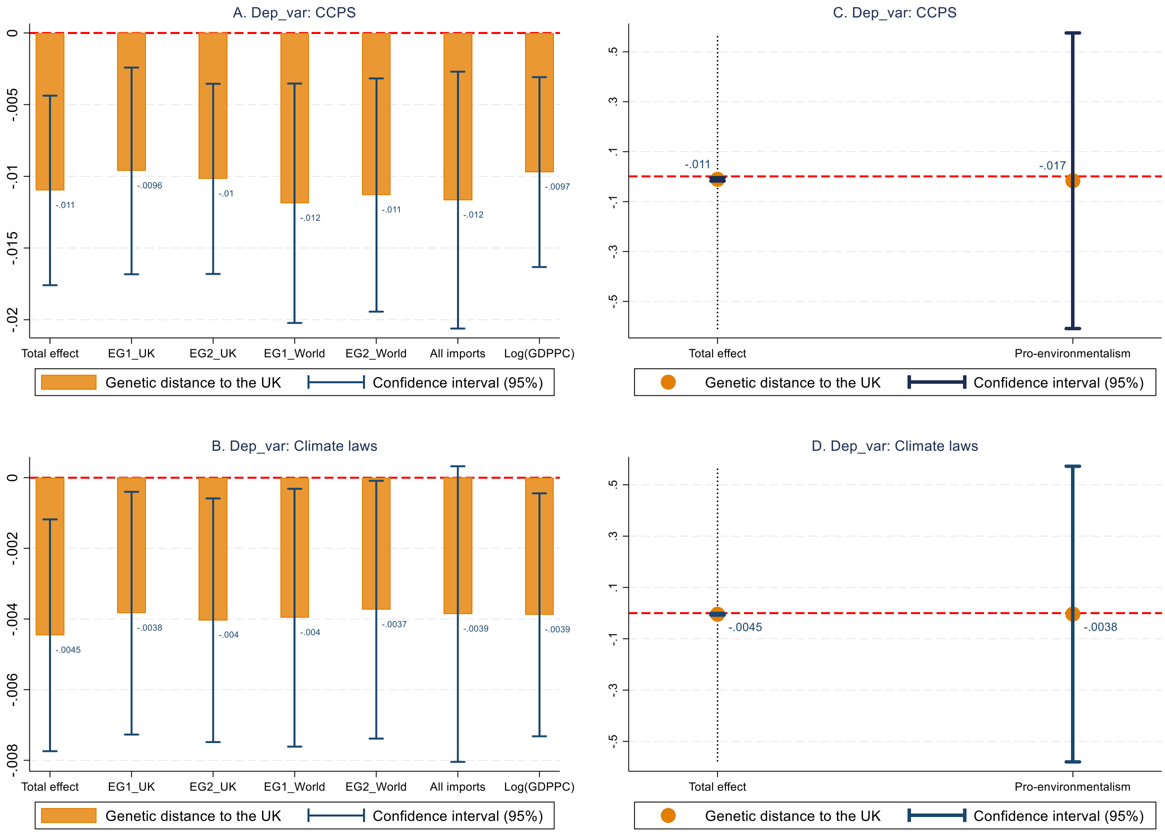
Genetic distance to alternative and placebo global frontiers and institutional quality across countries



Note: This figure depicts the point estimates and 95% confidence intervals of the cross-country relationship between institutional quality and genetic distance to alternative and placebo frontier countries. All the regressions are augmented with geographical characteristics, the deep roots of economic development, and region dummies.

Figure 9

Genetic distance to the UK and climate change policy performance across countries, ACDE estimates



Note: This figure illustrates estimates of the average controlled direct effect (ACDE) of genetic distance to the UK on climate change policy performance across countries. I follow Acharya et al.'s (2016) adoption of sequential *g*-estimation to implement a two-stage regression procedure. I depict the point estimates and 95% confidence intervals of the coefficient on genetic distance to the UK. These estimates reflect the cross-country relationship between genetic distance to the UK and climate change policy performance when holding a potential mediating factor fixed at a particular level. The mediators include log of imports of environmental goods and technologies from the UK based on the OECD's list (*EG1_UK*) and the WTO's (*EG2_UK*) list, log of imports of environmental goods and technologies from rest of the World based on the OECD's list (*EG1_World*) and the WTO's (*EG2_World*) list, log of total imports from the UK (*All imports*), log of GDP per capita (*Log(GDPPC)*), and the prevalence of self-reported *pro-environmentalism*. For ease of comparison, I depict the *Total effect* (without accounting for any mediating factors). Standard error estimates are obtained via a bootstrapping procedure using 1,000 random replications.

Table 1

Summary statistics of key variables

	N	Mean	SD	Min	Max
Panel A. Variables used in cross-sectional analyses					
Climate change policy stringency index (CCPS)	161	29.206	16.924	1.300	82.4
Stock of climate change mitigation laws (Climate laws)	160	8.675	5.907	0	35
Genetic distance to the UK	161	858.552	667.247	30.293	2262.393
Genetic distance to the English population in 1500	161	963.180	679.288	0	2288
Absolute latitude	141	26.965	17.221	1	65
Distance to the nearest waterway	141	342.269	452.985	14.176	2385.580
Terrain ruggedness	141	120.223	115.890	3.605	584.575
Average land suitability for agriculture	141	0.375	0.248	0.003	0.951
Mean elevation	141	578.585	539.586	0.522	2836.526
Landlocked nation dummy	161	0.224	0.41795	0	1
Predicted genetic diversity (ancestry-adjusted)	137	0.727	0.028	0.628	0.774
Ethnic fractionalization	141	0.469	0.253	0.012	0.930
Ethnolinguistic polarization	141	0.459	0.243	0.0003	0.958
Ancestry-adjusted state history	135	0.216	0.164	0	0.747
Log of CO$_2$ emissions per capita in 2010	160	0.651	1.615	-3.426	3.758
Log of CO$_2$ emissions per capita in 1950	143	-0.894	2.030	-6.947	3.219
Log of GDP per capita in 2010	158	8.549	1.438	5.696	11.576
Log of GDP per capita in 1950	120	7.343	0.935	5.758	10.372
Prevalence of pro-environmentalism (evtprotect)	90	53.912	12.135	3.884	85.530
Prevalence of pro-environmentalism (globwarm)	43	89.321	7.638	64.813	98.146
Prevalence of pro-environmentalism (evttaxes)	67	60.111	12.209	30.833	90.586
EG1_UK	127	10.125	2.456	5.137	15.549
EG2_UK	128	11.060	2.510	5.446	16.914
EG1_World	110	14.440	1.922	9.301	18.998
EG2_World	112	15.698	1.744	10.837	20.284
All imports	123	13.464	2.715	1.209	18.732
Panel B. Variables used in the dyadic regression analyses					
Abs. diff. in CCPS	12,880	18.467	15.225	0	81.1
Abs. diff. in Climate laws	12,720	6.435	5.327	0	35
Genetic distance *relative* to the UK	12,880	0.075	0.057	0	0.223
Genetic distance	12,880	1133.719	696.401	0	3547.446
Genetic distance *relative* to the English population in 1500	12,880	0.070	0.055	0	0.229
Geographical distance	12,720	7.571	4.349	0.094	19.650
Contiguity	12,720	0.019	0.137	0	1
Common official language	12,720	0.150	0.357	0	1
Colonial relationship	12,720	0.008	0.088	0	1
Common sea or ocean	12,880	0.113	0.316	0	1
The same country dummy	12,720	0.009	0.094	0	1
Either landlocked nation dummy	12,880	0.349	0.477	0	1
Abs. diff. in log of CO$_2$ emissions per capita in 2010	12,720	1.825	1.374	0.0001	7.184
Abs. diff. in log of CO$_2$ emissions per capita in 1950	10,153	2.314	1.700	0.0001	10.166
Abs. diff. in log of GDP per capita in 2010	12,403	1.661	1.174	0.00003	5.880
Abs. diff. in log of GDP per capita in 1950	7,140	1.051	0.803	0.0006	4.614
Abs. diff. in pro-environmentalism (evtprotect)	4,005	13.358	10.774	0.002	81.646
Abs. diff. in pro-environmentalism (globwarm)	903	8.066	7.188	0.019	33.333
Abs. diff. in pro-environmentalism (evttaxes)	2,211	13.811	10.364	0.008	59.754

Table 2

Genetic distance to the UK and climate change policy performance across countries

Dep_var: CCPS	(1)	(2)	(3)	(4)	(5)	(6)
	OLS	OLS	OLS	OLS	2SLS	2SLS
Genetic distance to the UK	-0.011***	-0.007**	-0.015***	-0.011***	-0.011***	-0.013***
	(0.003)	(0.003)	(0.003)	(0.003)	(0.004)	(0.005)
Absolute latitude		0.488***		0.393***		0.373**
		(0.146)		(0.150)		(0.145)
Distance to the nearest waterway		-0.007**		-0.007**		-0.007***
		(0.003)		(0.003)		(0.003)
Terrain ruggedness		-0.019		-0.021		-0.023
		(0.018)		(0.019)		(0.018)
Average land suitability for agriculture		-1.822		-5.889		-5.571
		(6.455)		(6.933)		(6.450)
Mean elevation		0.004		0.005		0.006
		(0.004)		(0.004)		(0.004)
Landlocked nation dummy		-3.677		-4.325		-4.265
		(3.485)		(3.486)		(3.266)
Predicted genetic diversity (ancestry-adjusted)			-177.356**	-159.217**		-160.021**
			(69.958)	(73.326)		(68.126)
Ethnic fractionalization			-13.334**	-7.432		-7.870
			(5.379)	(5.751)		(5.410)
Ethnolinguistic polarization			-5.479	-7.447		-7.333
			(5.867)	(6.064)		(5.667)
Ancestry-adjusted state history			-18.024*	-15.300*		-17.173*
			(9.577)	(9.061)		(9.584)
Standardized beta coefficient of genetic distance	-0.448	-0.285	-0.600	-0.449	-0.417	-0.519
Region dummies	Yes	Yes	Yes	Yes	Yes	Yes
Observations	161	141	130	130	161	130
R-squared	0.384	0.475	0.443	0.526		
					First-stage estimates. Dep_var: Genetic distance to the UK	
Genetic distance to the English population in 1500					0.734***	0.691***
					(0.064)	(0.070)
First-stage *F*-statistic					130.69	98.17

Anderson-Rubin CI	[-0.018, -0.003]	[-0.022, -0.004]

Note: This table reports estimates of the relationship between genetic distance to the UK and climate change policy performance across countries. Region dummies denote binary indicators for the World Bank's regions, including Europe and Central Asia, Latin America and Caribbean, Middle East and North Africa, North America, South Asia, and Sub-Saharan Africa (East Asia and Pacific is the base category). First-stage *F*-statistic denotes Olea and Pflueger's (2013) robust-weak-instrument *F*-statistics. Anderson-Rubin CI shows the weak-identification-robust 95% confidence interval, which is efficient in the just-identified case (Andrews, Stock, and Sun, 2019). An intercept, omitted for brevity, is included in all the regressions. Heteroscedasticity-robust standard errors are reported in parentheses. *** $p<0.01$, ** $p<0.05$, * $p<0.1$.

Table 3

Genetic distance to the UK and the adoption of climate change mitigation laws across countries

Dep_var: Stock of climate change mitigation laws	(1)	(2)	(3)	(4)	(5)	(6)
	OLS	OLS	OLS	OLS	2SLS	2SLS
Genetic distance to the UK	-0.004***	-0.004**	-0.004***	-0.004***	-0.003	-0.005**
	(0.001)	(0.002)	(0.001)	(0.002)	(0.002)	(0.002)
Geographical controls	No	Yes	No	Yes	No	Yes
Deep roots of economic development	No	No	Yes	Yes	No	Yes
Region dummies	Yes	Yes	Yes	Yes	Yes	Yes
Observations	160	140	129	129	160	129
R-squared	0.151	0.187	0.212	0.242		
					First-stage estimates. Dep_var: Genetic distance to the UK	
Genetic distance to the English population in 1500					0.727***	0.690***
					(0.065)	(0.070)
First-stage *F*-statistic					126.02	96.44
Anderson-Rubin CI					[-0.006, 0.0006]	[-0.009, -0.0006]

Note: This table replicates the specifications from Table 2 but uses the total number of national climate change mitigation laws passed between 1990 and 2019 as an alternative outcome variable. Geographical controls include absolute latitude, distance to the nearest waterway, terrain ruggedness, average land suitability for agriculture, mean elevation, and landlocked nation dummy. Deep roots of economic development include an ancestry-adjusted measure of predicted genetic diversity, ethnic fractionalization, ethnolinguistic polarization, and ancestry-adjusted state history. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05.

Table 4

Genetic distance and bilateral differences in climate change policy performance across country pairs

Dep_var:	Abs. diff. in climate change policy stringency index				Abs. diff. in stock of climate change mitigation laws			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
	OLS	OLS	2SLS	2SLS	OLS	OLS	2SLS	2SLS
Genetic distance *relative* to the UK	45.334***		50.584***		3.688		-0.368	
	(11.791)		(16.339)		(2.754)		(2.061)	
Genetic distance		0.003***		0.002***		0.0004		0.0001
		(0.001)		(0.001)		(0.0003)		(0.0002)
Geographical distance	-0.010	-0.040	-0.021	-0.011	-0.021	-0.030	-0.013	-0.018
	(0.057)	(0.075)	(0.041)	(0.058)	(0.018)	(0.022)	(0.016)	(0.016)
Contiguity	-2.485	-2.836*	-2.341	-3.040**	-0.766*	-0.750*	-0.877**	-0.833**
	(1.633)	(1.703)	(1.437)	(1.523)	(0.396)	(0.400)	(0.350)	(0.347)
Common official language	0.002	-0.173	0.099	-0.325	-0.659**	-0.641**	-0.735**	-0.703**
	(0.619)	(0.576)	(0.596)	(0.457)	(0.319)	(0.314)	(0.287)	(0.273)
Colonial relationship	2.099	2.487	1.970	2.655	0.236	0.230	0.337	0.299
	(2.268)	(2.358)	(2.146)	(2.261)	(1.042)	(1.022)	(1.005)	(0.992)
Common sea or water	-0.877	-0.550	-0.860	-0.660	-0.296	-0.243	-0.311	-0.290
	(0.959)	(0.953)	(0.826)	(0.840)	(0.306)	(0.295)	(0.272)	(0.267)
Same country dummy	-2.759*	-2.729*	-2.709*	-2.836*	-0.047	-0.020	-0.085	-0.064
	(1.556)	(1.603)	(1.440)	(1.478)	(0.391)	(0.391)	(0.351)	(0.349)
Either landlocked nation dummy	0.356	0.464	0.357	0.437	-0.052	-0.037	-0.053	-0.048
	(0.457)	(0.464)	(0.370)	(0.376)	(0.099)	(0.101)	(0.063)	(0.066)
Country 1 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Country 2 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Number of country 1	159	159	159	159	158	158	158	158
Number of country 2	159	159	159	159	158	158	158	158
Observations	12,720	12,720	12,720	12,720	12,561	12,561	12,561	12,561
R-squared	0.560	0.552			0.537	0.538		
			First-stage estimates. Dep_var: Genetic distance				First-stage estimates. Dep_var: Genetic distance	
Genetic distance *relative* to the English population in 1500			0.666***				0.666***	
			(0.045)				(0.045)	

Genetic distance in 1500				0.582***				0.581***
				(0.048)				(0.048)
First-stage *F*-statistic			222.85	148.15			220.48	146.10
Anderson-Rubin CI			[42.989, 58.180]	[0.002, 0.003]			[-2.521, 1.785]	[-0.0001, 0.0003]

Note: This table reports estimates of the relationship between genetic distance and bilateral differences in climate change policy performance across country pairs. Heteroscedasticity-robust standard errors reported in parentheses are two-way clustered at both countries in a pair. *** p<0.01, ** p<0.05, * p<0.1.

Table 5

Genetic distance to the UK and the intensity of CO_2 emissions across countries

Dep_var:	Log of CO_2 emissions per capita in 2010				Log of CO_2 emissions per capita in 1950			
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Genetic distance to the UK	-0.0002	-0.003***	0.0004	-0.003***	-0.0006	0.0001	0.00004	0.0030
	(0.0003)	(0.0005)	(0.0004)	(0.0006)	(0.0003)	(0.0027)	(0.0005)	(0.0029)
Log of 2010 GDP per capita		0.578***		0.576***				
		(0.066)		(0.065)				
Genetic distance to the UK × Log of 2010 GDP per capita		0.0004***		0.0004***				
		(0.0001)		(0.0001)				
Log of 1950 GDP per capita						1.363***		1.550***
						(0.248)		(0.258)
Genetic distance to the UK × Log of 1950 GDP per capita						-0.000002		-0.0004
						(0.0004)		(0.0004)
Geographical controls	No	No	Yes	Yes	No	No	Yes	Yes
Deep roots of economic development	No	No	Yes	Yes	No	No	Yes	Yes
Region dummies	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Observations	160	157	130	128	143	110	122	100
R-squared	0.543	0.899	0.701	0.910	0.560	0.728	0.686	0.775

Note: This table reports OLS estimates of the relationship between genetic distance to the UK and CO_2 emissions per capita across countries. Heteroscedasticity-robust standard errors are reported in parentheses. *** $p<0.01$.

Table 6

Genetic distance and bilateral differences in the intensity of CO_2 emissions across country pairs

Dep_var:	Abs. diff. in log of CO_2 emissions per capita in 2010		Abs. diff. in log of CO_2 emissions per capita in 1950	
	(1)	(2)	(3)	(4)
Genetic distance *relative* to the UK	0.838 (0.722)		4.122** (1.641)	
Genetic distance		0.00003 (0.0001)		0.0002 (0.0001)
Abs. diff. in log of 2010 GDP per capita	0.779*** (0.058)	0.741*** (0.070)		
Abs. diff. in log of 1950 GDP per capita			1.424*** (0.145)	1.374*** (0.161)
Genetic distance *relative* to the UK × Abs. diff. in log of 2010 GDP per capita	0.650*** (0.215)			
Genetic distance × Abs. diff. in log of 2010 GDP per capita		0.0001*** (0.00003)		
Genetic distance *relative* to the UK × Abs. diff. in log of 1950 GDP per capita			-0.060 (0.903)	
Genetic distance × Abs. diff. in log of 1950 GDP per capita				0.0001 (0.0001)
Pairwise controls	Yes	Yes	Yes	Yes
Country 1 fixed effects	Yes	Yes	Yes	Yes
Country 2 fixed effects	Yes	Yes	Yes	Yes
Number of country 1	155	155	108	108
Number of country 2	155	155	108	108
Observations	12,090	12,090	5,886	5,886
R-squared	0.789	0.790	0.688	0.685

Notes: This table reports OLS estimates of the interaction effect between genetic distance and the absolute difference in income per capita on the absolute difference in the intensity of CO_2 emissions across country pairs. Pairwise controls include geographical distance, contiguity, common official language, colonial relationship, common sea or water, same country dummy, and either landlocked nation dummy. Heteroscedasticity-robust standard errors reported in parentheses are two-way clustered at both countries in a pair. *** p<0.01, ** p<0.05.

Table 7

Genetic distance and the global variation in attitudes toward environmental pollution and global warming

Prevalence of pro-environmentalism: Share of surveyed respondents who …	Agree that protecting the environment should be prioritized even if it causes slower economic growth or job losses (*evtprotect*)		Agree that global warming is a somewhat or very serious environmental problem in the world (*globwarm*)		Support increases in taxes if used to prevent environmental pollution (*evttaxes*)	
	(1)	(2)	(3)	(4)	(5)	(6)
Panel A. Cross-country analysis. Dep_var: Prevalence of pro-environmentalism						
Genetic distance to the UK	-0.005**	-0.012**	-0.007***	-0.007*	-0.0001	-0.004
	(0.002)	(0.006)	(0.002)	(0.004)	(0.003)	(0.006)
Geographical controls	No	Yes	No	Yes	No	Yes
Deep roots of economic development	No	Yes	No	Yes	No	Yes
Region dummies	No	Yes	No	Yes	No	Yes
Observations	90	86	43	42	67	65
R-squared	0.060	0.446	0.352	0.729	0.000	0.251
Panel B. Dyadic analysis. Dep_var: Abs. diff. in prevalence of pro-environmentalism						
Genetic distance *relative* to the UK	21.381**		61.839***		12.446**	
	(10.338)		(17.716)		(5.963)	
Genetic distance		0.003**		0.005***		0.002**
		(0.001)		(0.001)		(0.0008)
Pairwise controls	Yes	Yes	Yes	Yes	Yes	Yes
Observations	3,916	3,916	861	861	2,145	2,145
R-squared	0.035	0.051	0.242	0.208	0.009	0.017

Notes: Panel A shows OLS estimates of the relationship between genetic distance to the UK and the prevalence of pro-environmentalism across countries. Panel B shows OLS estimates of the relationship between genetic distance and bilateral differences in the prevalence of pro-environmentalism across country pairs. The bilateral analysis in Panel B excludes country 1 and country 2 fixed effects to preserve as much of the variation in the prevalence of pro-environmentalism across country pairs as possible because of lower degrees of freedom afforded by using the absolute difference in self-reported pro-environmentalism. Heteroscedasticity-robust standard errors are reported in parentheses in Panel A. Heteroscedasticity-robust standard errors reported in parentheses in Panel B are two-way clustered at both countries in a pair. *** p<0.01, ** p<0.05, * p<0.1.

Table 8

Genetic distance to the UK and self-reported pro-environmentalism among second-generation European migrants

Parental country of origin:	Father's country of birth			Mother's country of birth			Parents' same country of birth		
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)
Genetic distance to the UK	-0.145***	-0.135***	-0.142***	-0.133**	-0.124**	-0.117**	-0.249***	-0.237***	-0.230*
	(0.052)	(0.049)	(0.043)	(0.058)	(0.056)	(0.052)	(0.087)	(0.084)	(0.121)
Country-of-residence fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Survey-wave fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Individual-level controls	No	Yes	Yes	No	Yes	Yes	No	Yes	Yes
Country-of-origin controls	No	No	Yes	No	No	Yes	No	No	Yes
Observations	12,977	12,931	12,806	12,129	12,090	11,999	4,484	4,472	4,400
Pseudo *R*-squared	0.010	0.014	0.015	0.011	0.014	0.016	0.013	0.017	0.021
Number of clusters	50	50	48	47	47	45	27	27	25

Notes: This table reports estimates of the intergenerational transmission of pro-environmental behaviors among second-generation European migrants. Individual-level controls include gender, employment status, educational attainment, marital status, and income levels. Country-of-origin controls include absolute latitude, distance to the nearest waterway, terrain ruggedness, average land suitability for agriculture, mean elevation, landlocked nation dummy, predicted genetic diversity, ethnic fractionalization, ethnolinguistic polarization, ancestry-adjusted state history, and region dummies. Heteroscedasticity-robust standard errors reported in parentheses are clustered at the country-of-origin level. *** p<0.01, ** p<0.05, * p<0.1.

APPENDIX

A1. Variables, data, and country coverage

Table A1

Variables' description and data sources

Variables	Description	Source
CCPS	The climate change policy stringency index that captures cross-country differences in climate change policy performance.	Sharma, Ang, and Fredriksson (2021)
Climate laws	The total number of climate change mitigation laws passed by national parliaments or governments between 1990 and 2019.	CCLW (2020)
Genetic distance to the UK	The F_{ST} index of genetic distance to the UK based on dissimilarities in allelic frequencies between countries. The country-level measure of genetic distance is a weighted average of genetic distance at the ethnicity level, where the weights correspond to the proportional representation of each ethnic group in a country's population.	Spolaore and Wacziarg (2009)
Genetic distance to the English population in 1500	The F_{ST} index of genetic distance to the English population of indigenous ethnic groups that were native to their respective current locations before the colonial period.	Spolaore and Wacziarg (2009)
Absolute latitude	The absolute latitude of a country's centroid.	Arbatlı et al. (2020)
Distance to the nearest waterway	Geographical distance to the nearest ice-free coastline or sea-navigable river, averaged across all the grid cells of a country.	Gallup, Sachs, and Mellinger (1999)
Terrain ruggedness	The ruggedness of a country's territory measured by squared root of the sum of squared differences between a chosen point on the Earth's surface and each of eight main directions of the compass (including North, Northeast, East, Southeast, South, Southwest, West, and Northwest).	Nunn and Puga (2012)
Average land suitability for agriculture	The mean suitability of a country's land areas for agriculture based on soil properties, averaged across all the grid cells of a country.	Michalopoulos (2012)
Mean elevation	Mean elevation above the sea level, averaged across all the grid cells of a country.	Arbatlı et al. (2020)
Landlocked nation dummy	A binary indicator for the landlockedness of a country.	Spolaore and Wacziarg (2013)
Predicted genetic diversity	A measure of interpersonal diversity captured by an index of predicted genetic diversity, adjusted for the ancestral composition (by territory of residence in 1500 CE) of the population of each country in 2000 CE.	Ashraf and Galor (2013)
Ethnic fractionalization	The degree of fractionalization across all the ethnic groups of a country, reflecting the probability that two individuals randomly chosen from a relevant population belong to different ethnic groups.	Fearon (2003)
Ethnolinguistic polarization	The degree of polarization across all the ethnolinguistic groups of a country.	Esteban, Mayoral, and Ray (2012)

Ancestry-adjusted state history	A normalized index of aggregate state history spanning the period 3500 BCE – 1500 CE, reflecting accumulated experience with state-like polities of the ancestors (by territory of residence in 1500 CE) of the population of each country in 2000 CE.	Borcan, Olsson, and Putterman (2018)
Colonial history dummies	A set of binary indicators for having been ruled by the UK, France, and other majoring colonizing power.	Arbatlı et al. (2020)
Legal origin dummies	A set of binary indicators for British common law and French civil law.	La Porta et al. (1999)
Years since the Neolithic Revolution	The length of time that has elapsed since a country made a historical transition to sedentary agriculture.	Putterman (2006)
Duration of human settlement	The historical length of uninterrupted human settlement.	Ahlerup and Olsson (2012)
Distance to the regional frontier in 1500	Geographical distance to regional technological frontiers for the year 1500 CE.	Ashraf and Galor (2013)
CO_2 emissions per capita	The intensity of CO_2 emissions calculated by total emissions divided by a country's population. Data were collected for each country in 1950 and on an annual basis between 1960 and 2022.	Friedlingstein et al. (2023)
GDP per capita in 2010	Income per person measured in constant 2015 US$ for the year 2010.	WDI (2023)
GDP per capita in 1950	Income per person estimated for the year 1950.	Fariss et al. (2022)
Manufacturing value added	The net output of a country's manufacturing sector (% of GDP) after adding up all outputs and subtracting intermediate inputs averaged between 2000 and 2015.	WDI (2023)
Trade openness	The value of exports and imports (% of GDP) averaged between 2000 and 2015.	WDI (2023)
Female political representation	The share of seats held by women in national parliaments averaged between 2000 and 2015.	WDI (2023)
Autocratic experience	The fraction of years under autocracy (when the Polity2 IV index is below – 5) from 1960 to 2017. The fraction of years under anocracy (when the Polity2 IV index is between – 5 and 5 is the excluded base political regime).	Arbatlı et al. (2020)
Democratic experience	The fraction of years under democracy (when the Polity2 IV index is above 5) from 1960 to 2017. The fraction of years under anocracy (when the Polity2 IV index is between – 5 and 5 is the excluded base political regime).	Arbatlı et al. (2020)
Years of schooling	Average years of schooling (total) averaged between 2000 and 2015.	Barro and Lee (2013)
Institutional quality	Average of six worldwide governance indicators, including voice and accountability, political stability and absence of violence/terrorism, government effectiveness, regulatory quality, rule of law, and control of corruption, averaged between 2000 and 2015.	Kaufmann, Kraay, and Mastruzzi (2010)
Pro-environmentalism (*evtprotect*)	The share of surveyed respondents who agree that "Protecting the environment should be given priority, even if it causes slower economic growth or some loss of jobs." Data were calculated for each country in waves 3 to 7 of the WVS and then averaged over all these waves.	WVS (2022)
Pro-environmentalism (*globwarm*)	The share of surveyed respondents who agree that global warming is a somewhat or very serious environmental problem in the world. Data	WVS (2022)

	were calculated for each country in waves 5 and 6 of the WVS and then averaged over all these waves.	
Pro-environmentalism (*evttaxes*)	The share of surveyed respondents who support increases in taxes if used to prevent environmental pollution. Data were calculated for each country in waves 2 to 5 of the WVS and then averaged over all these waves.	WVS (2022)
EG1_UK	Log of the value of imports of environmentally friendly goods and technologies from the UK in 2015 (measured in 1,000 US$). The classification of environmental goods is based on the OECD's list of 248 traded products at the six-digit level, following Sauvage (2014).	UN (2016)
EG2_UK	Log of the value of imports of environmentally friendly goods and technologies from the UK in 2015 (measured in 1,000 US$). The classification of environmental goods is based on the WTO's list of 408 traded products at the six-digit level, following Sauvage (2014).	UN (2016)
EG1_World	Log of the value of total imports of environmentally friendly goods and technologies in 2015 (measured in 1,000 US$). The classification of environmental goods is based on the OECD's list of 248 traded products at the six-digit level, following Sauvage (2014).	UN (2016)
EG2_World	Log of the value of total imports of environmentally friendly goods and technologies in 2015 (measured in 1,000 US$). The classification of environmental goods is based on the WTO's list of 248 traded products at the six-digit level, following Sauvage (2014).	UN (2016)
All imports	Log of the value of total imports from the UK in 2015 (measured in 1,000 US$).	UN (2016)
Abs. diff. in CCPS	The absolute value of the difference in CCPS between countries in each pair.	Sharma, Ang, and Fredriksson (2021)
Abs. diff. in Climate Laws	The absolute value of the difference in climate laws passed by national parliaments or governments between 1990 and 2019 between countries in each pair.	CCLW (2020)
Genetic distance *relative* to the UK	The absolute value of the difference in genetic distance to the UK between countries in each pair.	Spolaore and Wacziarg (2009)
Genetic distance	The F_{ST} index of genetic distance between countries in each pair.	Spolaore and Wacziarg (2009)
Genetic distance *relative* to the English population in 1500	The absolute value of the difference in genetic distance to the English population in 1500 between countries in each pair.	Spolaore and Wacziarg (2009)
Geographical distance	Population-weighted geographical distance between countries in each pair.	Mayer and Zignago (2011)
Contiguity	A binary indicator for two contiguous countries in each pair.	Mayer and Zignago (2011)
Common official language	A binary indicator for two countries in each pair sharing at least one common official language.	Mayer and Zignago

		(2011)
Colonial relationship	A binary indicator for two countries in each pair having been in a colonial relationship.	Mayer and Zignago (2011)
Common sea or ocean	A binary indicator for two countries in each pair sharing at least one sea or ocean.	Spolaore and Wacziarg (2018)
The same country dummy	A binary indicator for two countries in each pair having been the same country in history.	Mayer and Zignago (2011)
Either landlocked nation dummy	A binary indicator for either country in each pair being landlocked.	Spolaore and Wacziarg (2013)
Abs. diff. in log of CO_2 emissions per capita	The absolute value of the difference in log of CO_2 emissions per capita between countries in each pair. Data were calculated for each country pair in 1950 and on an annual basis between 1960 and 2022.	Friedlingstein et al. (2023)
Abs. diff. in log of GDP per capita in 2010	The absolute value of the difference in log of GDP per capita measured in constant 2015 US$ between countries in each pair. Data were calculated for each country pair in 2010.	WDI (2023)
Abs. diff. in log of GDP per capita in 1950	The absolute value of the difference in the natural logarithm of GDP per capita between countries in each pair. Data were calculated for each country pair in 1950.	Fariss et al. (2022)
Abs. diff. in evtprotect	The absolute value of the difference in pro-environmentalism (*evtprotect*) between countries in each pair.	WVS (2022)
Abs. diff. in globwarm	The absolute value of the difference in pro-environmentalism (*globwarm*) between countries in each pair.	WVS (2022)
Abs. diff. in evttaxes	The absolute value of the difference in pro-environmentalism (*evttaxes*) between countries in each pair.	WVS (2022)

Appendix A2. Country coverage (Table 2, column 1)

Table A2

List of 161 countries by the World Bank's classification of regions

Region	**Country name**
East Asia and Pacific	Australia, Brunei, China, Indonesia, Japan, Cambodia, Kiribati, Lao PDR, Myanmar, Mongolia, Malaysia, New Zealand, Philippines, Papua New Guinea, Singapore, Solomon Islands, Thailand, Tonga, and Vietnam.
Europe and Central Asia	Albania, Armenia, Austria, Azerbaijan, Belgium, Bulgaria, Belarus, Switzerland, Cyprus, Czech Republic, Germany, Denmark, Spain, Estonia, Finland, France, Georgia, Greece, Croatia, Hungary, Ireland, Iceland, Italy, Kazakhstan, Kyrgyz Republic, Lithuania, Luxembourg, Latvia, Moldova, Netherlands, Norway, Poland, Portugal, Romania, Russia, San Marino, Slovak Republic, Slovenia, Sweden, Tajikistan, Turkmenistan, Turkey, Ukraine, and Uzbekistan.
Latin America and Caribbean	Argentina, Antigua and Barbuda, The Bahamas, Belize, Bolivia, Brazil, Barbados, Chile, Colombia, Costa Rica, Cuba, Dominica, Dominican Republic, Ecuador, Grenada, Guatemala, Guyana, Honduras, Haiti, Jamaica, St. Kitts and Nevis, St. Lucia, Mexico, Nicaragua, Panama, Peru, Paraguay, El Salvador, Suriname, Uruguay, St. Vincent and the Grenadines, and Venezuela.
Middle East and North Africa	United Arab Emirates, Bahrain, Djibouti, Algeria, Egypt, Iran, Iraq, Israel, Jordan, Kuwait, Lebanon, Libya, Morocco, Malta, Oman, Qatar, Saudi Arabia, Syrian Arab Republic, and Tunisia.
North America	United States
South Asia	Afghanistan, Bangladesh, India, Nepal, and Pakistan.
Sub-Saharan Africa	Angola, Burundi, Benin, Burkina Faso, Botswana, Central African Republic, Côte d'Ivoire, Cameroon, Congo, Comoros, Eritrea, Ethiopia, Gabon, Ghana, Guinea, The Gambia, Guinea-Bissau, Equatorial Guinea, Kenya, Liberia, Lesotho, Madagascar, Mali, Mozambique, Mauritania, Mauritius, Malawi, Namibia, Niger, Nigeria, Rwanda, Sudan, Senegal, Sierra Leone, Somalia, Seychelles, Chad, Uganda, South Africa, Zambia, and Zimbabwe.

Appendix A3. Additional estimates

Table A3

Conley et al.'s (2012) bound estimates

Dep_var:	CCPS	Stock of climate change mitigation laws
	(1)	(2)
	2SLS	2SLS
Genetic distance to the UK, CI ($2\theta = 1\%$)	[-0.022, -0.003]	[-0.010, -0.0004]
Genetic distance to the UK, CI ($2\theta = 5\%$)	[-0.023, -0.002]	[-0.010, -0.0001]
Genetic distance to the UK, CI ($2\theta = 10\%$)	[-0.024, -0.001]	[-0.010, 0.0003]
Genetic distance to the UK, CI ($2\theta = 15\%$)	[-0.025, -0.0004]	[-0.011, 0.0006]
Genetic distance to the UK, CI ($2\theta = 25\%$)	[-0.027, 0.001]	[-0.011, 0.001]
Genetic distance to the UK, CI ($2\theta = 50\%$)	[-0.032, 0.006]	[-0.013, 0.003]
Geographical controls	Yes	Yes
Deep roots of economic development	Yes	Yes
Region dummies	Yes	Yes
Observations	130	129

Note: This table shows bound IV estimates of the relationship between genetic distance to the UK and climate change policy performance across countries allowing for deviation from the exclusion restrictions, following the union of confidence interval approach of Conley, Hansen, and Rossi (2012). CI ($2\theta = p\%$) reports the 95% confidence intervals of the estimated coefficient on genetic distance to the UK when the direct effect of the IV is hypothesized to be up to $p\%$ of the estimated coefficient on genetic distance to the UK reported in column (6) of Tables 2 and 3.

Table A4

Genetic distance to the UK and climate change policy performance across the Old World

Dep_var: CCPS	(1)	(2)	(3)	(4)
	OLS	OLS	2SLS	2SLS
Genetic distance to the UK	-0.008**	-0.008*	-0.011**	-0.012***
	(0.004)	(0.004)	(0.005)	(0.005)
Geographical controls	No	Yes	No	Yes
Deep roots of economic development	No	Yes	No	Yes
Region dummies	Yes	Yes	Yes	Yes
Observations	114	105	114	105
R-squared	0.398	0.537		
			First-stage estimates. Dep_var: Genetic distance to the UK	
Genetic distance to the English population in 1500			0.799*** (0.048)	0.733*** (0.060)
First-stage *F*-statistic			281.63	146.95
Anderson-Rubin CI			[-0.020, -0.003]	[-0.021, -0.003]

Note: This table replicates the main analysis using a sample of countries that only belong to the Old World. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05, * p<0.1.

.

Table A5

Robustness to accounting for historical confounding characteristics

	(1)	(2)	(3)	(4)	(5)	(6)
Panel A. OLS estimates. Dep_var: CCPS						
Genetic distance to the UK	-0.011***	-0.009**	-0.011***	-0.010***	-0.011***	-0.009**
	(0.003)	(0.003)	(0.003)	(0.003)	(0.003)	(0.004)
Panel B. IV (second-stage) estimates. Dep_var: CCPS						
Genetic distance to the UK	-0.014***	-0.013***	-0.014***	-0.012**	-0.011**	-0.013**
	(0.005)	(0.005)	(0.005)	(0.005)	(0.005)	(0.005)
Panel C. IV (first-stage) estimates. Dep_var: Genetic distance to the UK						
Genetic distance to the English population in 1500	0.698***	0.700***	0.722***	0.688***	0.705***	0.742***
	(0.069)	(0.067)	(0.078)	(0.074)	(0.072)	(0.087)
Colonial history	Yes					Yes
Legal origins		Yes				Yes
Years since the Neolithic Revolution			Yes			Yes
Duration of human settlement				Yes		Yes
Distance to the regional frontier in 1500					Yes	Yes
Geographical controls	Yes	Yes	Yes	Yes	Yes	Yes
Deep roots of economic development	Yes	Yes	Yes	Yes	Yes	Yes
Region dummies	Yes	Yes	Yes	Yes	Yes	Yes
Observations	130	130	126	126	126	126
R-squared (OLS regressions)	0.542	0.584	0.522	0.520	0.539	0.607
First-stage *F*-statistic	101.98	109.08	84.88	85.88	94.75	72.62
Anderson-Rubin CI	[-0.024, -0.005]	[-0.022, -0.004]	[-0.025, -0.005]	[-0.022, -0.003]	[-0.020, -0.002]	[-0.024, -0.003]

Note: This table replicates the main analysis but accounts for potential historical confounding characteristics. Colonial history is a set of binary variables for having been ruled by the UK, France, and other majoring colonizing power during the colonial era. Legal traditions are dummy variables for British common law and French civil law. Other controls are the length of time since a country adopted sedentary agriculture, the duration of uninterrupted human settlement, and geographical distance to regional technological frontiers in 1500 CE. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05.

.

Table A6

Robustness to accounting for geographical, linguistic and religious distance to the UK

Dep_var: CCPS	(1)	(2)	(3)	(4)	(5)	(6)
	OLS			2SLS		
Genetic distance to the UK	-0.008**	-0.008***	-0.011***	-0.011**	-0.011***	-0.012***
	(0.004)	(0.003)	(0.003)	(0.005)	(0.004)	(0.005)
Linguistic proximity to the UK	1.608**			1.388**		
	(0.658)			(0.588)		
Religious proximity to the UK		10.356***			10.121***	
		(1.918)			(1.801)	
Geographical distance to the UK			-0.0002			-0.0001
			(0.001)			(0.001)
Geographical controls	Yes	Yes	Yes	Yes	Yes	Yes
Deep roots of economic development	Yes	Yes	Yes	Yes	Yes	Yes
Region dummies	Yes	Yes	Yes	Yes	Yes	Yes
Observations	127	128	129	127	128	129
R-squared	0.532	0.615	0.517			
				First-stage estimates. Dep_var: Genetic distance to the UK		
Genetic distance to the English population in 1500				0.678***	0.680***	0.764***
				(0.064)	(0.073)	(0.075)
First-stage *F*-statistic				111.04	87.11	103.08
Anderson-Rubin CI				[-0.021, -0.002]	[-0.020, -0.003]	[-0.021, -0.003]

Note: This table replicates the main analysis but accounts for geographical distance, and linguistic and religious proximity to the UK. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05.

Table A7

Robustness to accounting for contemporary confounding characteristics

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Panel A. OLS estimates. Dep_var: CCPS							
Genetic distance to the UK	-0.011***	-0.012***	-0.010***	-0.011***	-0.008**	-0.011***	-0.008**
	(0.003)	(0.003)	(0.003)	(0.003)	(0.003)	(0.003)	(0.004)
Panel B. IV (second-stage) estimates. Dep_var: CCPS							
Genetic distance to the UK	-0.017***	-0.014***	-0.012**	-0.012***	-0.014***	-0.017***	-0.018***
	(0.004)	(0.005)	(0.005)	(0.005)	(0.005)	(0.006)	(0.005)
Panel C. IV (first-stage) estimates. Dep_var: Genetic distance to the UK							
Genetic distance to the English population in 1500	0.703***	0.703***	0.684***	0.691***	0.707***	0.618***	0.660***
	(0.069)	(0.071)	(0.072)	(0.071)	(0.066)	(0.088)	(0.094)
Log of GDP per capita	Yes						Yes
Manufacturing value added		Yes					Yes
Trade openness			Yes				Yes
Female political representation				Yes			Yes
Autocratic experience					Yes		Yes
Democratic experience					Yes		Yes
Years of schooling						Yes	Yes
Geographical controls	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Deep roots of economic development	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Region dummies	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Observations	128	128	130	130	130	113	111
R-squared (OLS regressions)	0.651	0.542	0.535	0.544	0.613	0.610	0.704
First-stage *F*-statistic	104.73	96.63	91.33	95.10	113.68	49.52	49.04
Anderson-Rubin CI	[-0.026, -0.009]	[-0.023, -0.005]	[-0.021, -0.003]	[-0.021, -0.004]	[-0.023, -0.006]	[-0.029, -0.008]	[-0.028, -0.010]

Note: This table replicates the main analysis but accounts for conventional socio-economic and political correlates of climate change policies. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05.

Table A8

Robustness to excluding regions from the global sample

Excluding	(1) EAP	(2) ECA	(3) LAC	(4) MENA	(5) NA	(6) SA	(7) SSA
Panel A. OLS estimates. Dep_var: CCPS							
Genetic distance to the UK	-0.010**	-0.008**	-0.009**	-0.011***	-0.011***	-0.011***	-0.019***
	(0.004)	(0.004)	(0.004)	(0.003)	(0.003)	(0.003)	(0.005)
Panel B. IV (second-stage) estimates. Dep_var: CCPS							
Genetic distance to the UK	-0.015***	0.003	-0.012**	-0.013***	-0.013***	-0.013**	-0.021***
	(0.005)	(0.006)	(0.005)	(0.005)	(0.005)	(0.005)	(0.007)
Panel C. IV (first-stage) estimates. Dep_var: Genetic distance to the UK							
Genetic distance to the English population in 1500	0.729***	0.668***	0.694***	0.683***	0.691***	0.693***	0.627***
	(0.069)	(0.103)	(0.069)	(0.071)	(0.069)	(0.072)	(0.105)
Geographical controls	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Deep roots of economic development	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Region dummies	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Observations	116	90	109	118	129	125	93
R-squared (OLS regressions)	0.527	0.353	0.552	0.532	0.525	0.527	0.610
First-stage *F*-statistic	111.21	42.48	99.87	91.51	98.93	93.42	35.44
Anderson-Rubin CI	[-0.025, -0.005]	[-0.006, 0.014]	[-0.022, -0.003]	[-0.023, -0.004]	[-0.022, -0.004]	[-0.022, -0.003]	[-0.036, -0.008]

Note: This table replicates the main analysis but eliminates one-at-a-time different world regions from the global sample of countries, including East Asia and Pacific (EAP), Europe and Central Asia (ECA), Latin America and the Caribbean (LAC), Middle East and North Africa (MENA), North America (NA), South Asia (SA), and sub-Saharan Africa (SSA). See Table A2 for the World Bank's classification of world regions. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05.

Table A9

Robustness of the OLS estimates to removing outliers

Dep_var: CCPS	(1)	(2)	(3)
	Cook's distance	Standardized residuals	Robust regression weights
Genetic distance to the UK	-0.011***	-0.011***	-0.011***
	(0.003)	(0.003)	(0.003)
Absolute latitude	0.407***	0.393***	0.402***
	(0.138)	(0.149)	(0.131)
Distance to nearest waterways	-0.007***	-0.007**	-0.008***
	(0.002)	(0.003)	(0.003)
Terrain ruggedness	-0.040**	-0.021	-0.023
	(0.016)	(0.019)	(0.016)
Average land suitability for agriculture	-1.617	-5.889	-6.539
	(6.398)	(6.907)	(6.222)
Mean elevation	0.007**	0.005	0.005
	(0.003)	(0.004)	(0.003)
Landlocked nation dummy	-5.400**	-4.325	-3.690
	(2.698)	(3.472)	(2.897)
Predicted genetic diversity (ancestry-adjusted)	-210.600***	-159.217**	-178.412***
	(67.076)	(73.044)	(64.261)
Ethnic fractionalization	-8.314	-7.432	-7.660
	(5.232)	(5.729)	(5.089)
Ethnolinguistic polarization	-11.294**	-7.447	-9.476*
	(5.489)	(6.040)	(5.337)
Ancestry-adjusted state history	-14.300*	-15.300*	-14.304*
	(8.454)	(9.026)	(8.113)
Region dummies	Yes	Yes	Yes
Observations	124	129	129
R-squared	0.596	0.525	0.565

Note: This table replicates the main analysis by excluding or down-weighting outlier observations. In column (1), I estimate Cook's distance and remove countries with values higher than the conventional value of four divided by the number of observations. In column (2), I exclude countries with an absolute value of the standardized residuals greater than 2.576 (the 1% two-tailed critical value of a standard normal distribution). In column (3), I follow Li (1985) to estimate robust regression weights, which are used to re-estimated the baseline model. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05, * p<0.1.

Table A10

Robustness of the OLS estimates to using alternative measures of genetic distance to the UK

Dep_var: CCPS	(1)	(2)	(3)	(4)	(5)
F_{ST} genetic distance to the UK, plurality match	-0.006**				
	(0.002)				
Nei's (1972) weighted genetic distance to the UK		-0.040**			
		(0.017)			
Nei's (1972) genetic distance to the UK, plurality match			-0.019		
			(0.013)		
F_{ST} weighted genetic distance to the UK, Pemberton et al.'s (2013) data				-649.494***	
				(166.447)	
F_{ST} genetic distance to the UK, plurality match, Pemberton et al.'s (2013) data					-217.148**
					(99.696)
Geographical controls	Yes	Yes	Yes	Yes	Yes
Deep roots of economic development	Yes	Yes	Yes	Yes	Yes
Region dummies	Yes	Yes	Yes	Yes	Yes
Observations	130	130	130	130	130
R-squared	0.507	0.509	0.497	0.546	0.506

Note: This table replicates the main analysis but uses alternative proxies for genetic distance to the UK. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05.

Table A11

Robustness to accounting for spatial dependence

Dep_var: CCPS	(1) OLS	(2) 2SLS
Genetic distance to the UK	-0.011***	-0.013***
	(0.003)	(0.005)
Spatial lag AR(1) of CCPS (λ)	0.463	0.446
	(0.284)	(0.281)
Spatial lag AR(1) of error (ρ)	0.715	0.704
	(0.468)	(0.459)
Absolute latitude	0.328**	0.309**
	(0.145)	(0.148)
Distance to nearest waterway	-0.006**	-0.006**
	(0.003)	(0.003)
Terrain ruggedness	-0.022	-0.023
	(0.016)	(0.016)
Average land suitability for agriculture	-8.077	-7.741
	(6.422)	(6.409)
Mean elevation	0.006*	0.006*
	(0.003)	(.003)
Landlocked nation dummy	-5.003*	-4.906
	(3.010)	(3.051)
Predicted genetic diversity (ancestry-adjusted)	-145.083**	-146.347**
	(67.203)	(67.453)
Ethnic fractionalization	-11.152**	-11.534**
	(5.086)	(5.206)
Ethnolinguistic polarization	-5.082	-5.036
	(5.559)	(5.571)
State history (ancestry-adjusted)	-17.809**	-19.471**
	(8.505)	(9.284)
Region dummies	Yes	Yes
Observations	130	130

Note: This table shows estimates of spatial-autoregressive models with spatial autoregressive error terms (SARAR (1,1)), derived from the generalized two-step least-squares estimator of Drukker, Prucha, and Raciborski (2013). Specifically, I use an inverse-distance spatial weighting matrix, where the weights correspond to the great-circle distances between the geodesic centroids of country pairs. Heteroscedasticity-robust standard errors are reported in parentheses. *** p<0.01, ** p<0.05, * p<0.1.

Table A12

Robustness to the inclusion of dyadic region dummies

Dep_var: Absolute difference in CCPS	(1)	(2)	(3)	(4)
	OLS	OLS	OLS	2SLS
Genetic distance *relative* to the UK	35.751***		29.649**	29.648*
	(11.523)		(12.843)	(15.266)
Genetic distance		0.002***	0.001	
		(0.001)	(0.001)	
Dyadic region dummies	Yes	Yes	Yes	Yes
Main dyadic controls	Yes	Yes	Yes	Yes
Country 1 fixed effects	Yes	Yes	Yes	Yes
Country 2 fixed effects	Yes	Yes	Yes	Yes
Observations (# of country pairs)	12,720	12,720	12,720	12,720
# of countries	159	159	159	159
R-squared	0.576	0.572	0.576	
				First-stage estimates. Dep_var: Genetic distance *relative* to the UK
Genetic distance *relative* to the English population in 1500				0.582***
				(0.044)
First-stage *F*-statistic				175.82
Anderson-Rubin CI				[21.483, 37.813]

Note: This table replicates the baseline dyadic regressions but includes dyadic region dummies in the regression. Heteroscedasticity-robust standard errors reported in parentheses are two-way clustered at both countries in a pair. *** p<0.01, ** p<0.05, * p<0.1.

Table A13

Robustness to accounting for absolute differences in the fundamental determinants of climate change policy performance

Dep_var: Absolute difference in CCPS	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
Genetic distance *relative* to the UK	21.114*	40.346***	40.824***	40.976***	40.821***	38.929***	35.597***	40.830***	46.662***	27.303**
	(10.903)	(11.932)	(12.013)	(11.975)	(11.998)	(11.809)	(11.401)	(11.988)	(12.518)	(11.410)
Abs. diff. in absolute latitude	Yes									Yes
Abs. diff. in distance to nearest waterway		Yes								Yes
Abs. diff. in terrain ruggedness			Yes							Yes
Abs. diff. in average land suitability for agriculture				Yes						Yes
Abs. diff. in mean elevation					Yes					Yes
Abs. diff. in predicted genetic diversity (ancestry-adjusted)						Yes				Yes
Abs. diff. in ethnic fractionalization							Yes			Yes
Abs. diff. in ethnolinguistic polarization								Yes		Yes
Abs. diff. in ancestry-adjusted state history									Yes	Yes
Main dyadic controls	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Country 1 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Country 2 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Observations	9,730	9,730	9,730	9,730	9,730	9,180	9,730	9,730	8,911	8,256
R-squared	0.571	0.554	0.553	0.553	0.553	0.552	0.559	0.553	0.557	0.579

Note: This table replicates the baseline dyadic regressions but controls for absolute differences in geographical attributes and the deep roots of economic development. Heteroscedasticity-robust standard errors reported in parentheses are two-way clustered at both countries in a pair. *** p<0.01, ** p<0.05, * p<0.1.

Table A14

Robustness to accounting for absolute differences in socio-economic and political correlates of climate change policies

Dep_var: Absolute difference in CCPS	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Genetic distance *relative* to the UK	33.670***	44.091***	46.209***	44.174***	29.437***	27.657**	15.718*
	(9.990)	(12.133)	(12.006)	(11.432)	(9.303)	(11.154)	(9.034)
Abs. diff. in log of GDP per capita	Yes						Yes
Abs. diff. in manufacturing value added		Yes					Yes
Abs. diff. in trade openness			Yes				Yes
Abs. diff. in female political representation				Yes			Yes
Abs. diff. in autocratic experience					Yes		Yes
Abs. diff. in democratic experience					Yes		Yes
Abs. diff. in years of schooling						Yes	Yes
Main dyadic controls	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Country 1 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Country 2 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Observations	12,403	11,935	12,561	12,561	9,045	8,001	6,441
R-squared	0.586	0.556	0.557	0.565	0.631	0.550	0.626

Note: This table replicates the baseline dyadic regressions but controls for absolute differences in conventional correlates of the worldwide divergence in climate change policies. Heteroscedasticity-robust standard errors reported in parentheses are two-way clustered at both countries in a pair. *** p<0.01, ** p<0.05, * p<0.1.

Table A15

Robustness to accounting for additional confounding characteristics

Dep_var: Absolute difference in CCPS	(1)	(2)	(3)	(4)	(5)	(6)
Genetic distance *relative* to the UK	49.011***	39.401***	41.589***	36.762***	34.436***	44.999***
	(13.405)	(13.935)	(12.541)	(11.854)	(11.271)	(13.812)
Abs. diff. in years since the Neolithic Revolution	Yes					Yes
Abs. diff. in duration of human settlement		Yes				Yes
Abs. diff. in distance to the region frontier in 1500 CE			Yes			Yes
Linguistic proximity				Yes		Yes
Religious proximity					Yes	Yes
Main dyadic controls	Yes	Yes	Yes	Yes	Yes	Yes
Country 1 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes
Country 2 fixed effects	Yes	Yes	Yes	Yes	Yes	Yes
Observations	7,750	7,750	7,750	9,316	9,453	7,626
R-squared	0.559	0.559	0.559	0.555	0.570	0.569

Note: This table replicates the baseline dyadic regressions but controls for additional confounding characteristics. Heteroscedasticity-robust standard errors reported in parentheses are two-way clustered at both countries in a pair. *** p<0.01.