Citizenship Policy and the Spread of Communicable Diseases: Evidence from the Dominican Republic

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Abstract

We study a controversial policy in the Dominican Republic in 2013 that targeted as much as 10% of the country's population based on their foreign ancestry and limited their safe access to services such as health. Beyond the direct negative effects such policies may have on the targeted group, we argue that there may be important indirect effects from such policies through the contagion of communicable diseases. We exploit the timing and differential exposure to this policy across the country, as well as highly disaggregated epidemiological data on diseases. Our difference-in-difference strategy provides evidence of a notable increase in the caseload of Dengue, a highly contagious disease. In contrast, there are no effects for noncommunicable diseases. We provide additional evidence across different specifications and when excluding outliers such as large urban centers and border regions. We also find that the effects are not driven by dengue suitability or in dengue case reporting by authorities. We argue that these results are due to a restriction in access to health services.

Keywords: Citizenship, Communicable Diseases, Dengue, Dominican Republic

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"[...] I'm not from here, I'm not from there. I'm a nobody [...] If I'm not from here or from Haiti, where am I from?" A 15-year-old youth born in the Dominican Republic. Testimony received by the Inter-American Commission on Human Rights (Santo Domingo - December 3, 2013)

1 Introduction

Migration has long been a central concern for both policymakers and academics. For decades, research in economics has primarily focused on the impact of foreign-born workers on the host country's labor markets, often from the perspective of the receiving society (Card, 1990, 2001; Amuedo-Dorantes and Bansak, 2012; Dustmann et al., 2012; Bahar et al., 2021; Abramitzky et al., 2023; East et al., 2023). However, as new immigrants settled in their new host countries, the focus is shifting towards how governments will manage the existing population of foreign-born residents (Budiman et al., 2020). This shift highlights critical questions surrounding the regularization of migrants and their path to long-term residency or citizenship. Despite its importance, the literature has provided mixed evidence on the relationship between citizenship policies and access to public services like health and education. In particular, when examining at the potential indirect effects of these policies on non-targeted groups or native populations (Bitler and Hoynes, 2011; Bronchetti, 2014; Watson, 2014; Alsan and Yang, 2022; Jácome, 2022; Ager et al., 2023; East and Velásquez, 2024). In this paper, we ask how citizenship restrictions can affect the propagation of communicable diseases by limiting the contested citizens' access to healthcare.

We examine the impact of a citizenship policy enacted in the Dominican Republic (DR), which primarily affected Dominicans of Haitian descent (Haitian-Dominicans). In 2013, following a diplomatic crisis, the Dominican *Junta Central Electoral* (Central Electoral Board) issued the Constitutional Court Ruling 168-13 (CC-168), a decree that revoked citizenship from individuals unable to prove that both they and their parents were born to legal residents of the DR. This ruling directly challenged the citizenship status of nearly 10% of the population—over 90% of whom were of Haitian descent—plunging them into legal uncertainty and severely restricting their access to public services and goods. We explore how this citizenship policy affects the transmission of dengue, a mosquito-borne disease prevalent in many developing countries. Two key factors make our case particularly suited to addressing this question. First, while recent attention has focused on regulating migration rather than the citizenship status of existing migrant populations, large-scale rulings altering migrant regularization have been rare—except for the case of the Dominican Republic (DR). Second, the island of Hispaniola, which frequently experiences outbreaks of tropical diseases like dengue, has comprehensive administrative records on these disease outbreaks, providing a valuable data source for analysis. What is more, Dengue is highly relevant to study due to its dramatic global rise, with cases increasing tenfold between 2000 and 2019 and affecting over 129 countries. The resurgence in 2023, reaching over five million cases and spreading to new regions like Europe, is projected to keep increasing due to intensified climate change in endemic areas.

Using comprehensive administrative data on official counts of communicable and non-communicable diseases provided by the DR Ministry of Health, we address our research question by employing a difference-in-differences empirical design. We leverage the variation in policy exposure across municipalities, determined by the percentage of Haitian decedents and citizens prior to the implementation of CC-168. Our results suggest that the CC-168 significantly impacted the spread of dengue. Municipalities most affected by the citizenship ban experienced a 16% increase in dengue cases compared to the pre-policy average. We interpret these findings as evidence of both substantial direct effects on the affected citizens and indirect effects on unaffected citizens, due to restricted access to health services. The results remain robust across various specifications, functional forms, and when excluding outliers such as large urban centers and border regions, which differ in case density and policy exposure. First, we assess the influence of municipalities with high dengue cases or large Haitian-Dominican populations, demonstrating that our results remain consistent even when excluding Santo Domingo and Haiti border areas. This analysis confirms that the observed effects are not solely driven by high-exposure regions, supporting the applicability of our findings across the country.

To tackle the issue of potential misreporting in health data, we compare administrative records with the Dominican Demographic Health Survey (DHS) from 2013. This independent data source helps to validate our initial results, showing similar trends in respiratory symptoms and diarrhea related to dengue, even though the DHS does not directly measure dengue. Finally, we use a randomization inference test to substantiate the statistical robustness of our findings by resampling exposure levels to the CC-168. This test confirms that the effects we observe are not simply artifacts of sampling variability. Together, these robustness checks provide strong evidence for the reliability of our conclusions on the health impacts of the CC-168 among Haitian-Dominican populations.

This paper contributes to three main strands of the Economics literature. First, we contribute to the literature on the at-home effects of immigration and citizenship-related policies. Watson (2014), Ibáñez et al. (2021) and Rozo and Vargas (2021) focus on how immigration policies affect public services, health outcomes and local labor markets. Similarly, Amuedo-Dorantes et al. (2017), Amuedo-Dorantes and Antman (2017), and Kuka et al. (2020) study the consequences of citizenship-related policies on affected populations, primarily focusing on those directly targeted. Our contribution is unique in that we explore both the direct and indirect effects of citizenship policies. Specifically, we examine how policies targeting certain populations—such as those descended from immigrants—can negatively impact individuals whose citizenship status is uncontested. This aspect sets our work apart from existing studies like Ager et al. (2023), which examines how immigration quotas in the U.S. affected urban mortality. Our focus on citizenship enforcement in a developing country context, as opposed to entry regulations, broadens the discussion on how such policies shape local populations' well-being. The closest work to ours is the one of Ibáñez et al. (2021), that studies how

Venezuelan forced migration affects the spread of infectious diseases in Colombia, finding increased incidence of vaccine-preventable and sexually transmitted diseases, but no significant impact on vector-borne diseases. Our results suggest the opposite results but is important to highlight that the policies are different since we are focusing on a population that is already established who is suddenly targeted and lost access to health services.

Second, we contribute to the literature on the spread of communicable diseases. Prior research, such as Oster (2012), Adda (2016), and Eichenbaum et al. (2020), explores how economic activities or interventions influence the transmission of diseases. In contrast to much of this work, which looks at mitigating the impact of disease, we document how policies not directly related to health can exacerbate the disease burden. For example, Adda (2016) shows how economic activity in France contributed to the spread of seasonal influenza. Our study expands on this by focusing on citizenship policies in the Global South and demonstrating how these policies can increase the incidence of diseases like dengue.

Lastly, we engage with the literature on the effectiveness of health policies. Seminal works such as Miguel and Kremer (2004), Bleakley (2010), and Cohen et al. (2010) highlight the positive impact of health interventions on disease outcomes and broader societal benefits. For instance, Miguel and Kremer (2004) shows how deworming medication reduced absenteeism in schools and produced positive externalities for untreated individuals. Similarly, Dammert et al. (2014) investigates how mobile phone technology can encourage dengue prevention in Peru. Our contribution in this area lies in demonstrating how non-health-related policies—such as those governing citizenship—can limit the effectiveness of public health initiatives, thereby hindering disease prevention efforts. By studying the unintended consequences of citizenship policies on health, we offer new insights into how governance can both support and undermine public health.

The recent Covid-19 pandemic and many countries' responses underscore the relevance of our research and findings. In balancing fiscal constraints with controlling virus spread, nations like the Gulf countries and the United States have expanded access to health resources for temporary and irregular migrants (Amnesty International, 2020). While evaluating the impact of these measures is beyond this paper's scope, we believe such analysis would support our results and strengthen the case for acknowledging the significant positive externalities—on the host population—of extending public health services to migrants. This is a factor often overlooked in recent debates on residency and citizenship policies, such as those around the Deferred Action for Childhood Arrivals (DACA) Act.

In the following section, we delve deeper into the context of the Domincan Republic in terms of both the disease and socio-political environments. In Section 3 we provide more detail on our data sources. In Section 4 we explain our empirical approach and provide some evidence in support of our identifying assumption. Then, in Section 5 we describe the main results of our analysis, which we submit to multiple robustness tests in the succeeding section. Finally, we conclude in Section 7.

2 Context

The Dominican Republic, located on the island of Hispaniola, is the second-largest nation in the Caribbean by both area and population. Despite its economic growth and development in the 2000s, the Dominican Republic still faces ongoing challenges in providing equitable healthcare to its diverse population. The government does offer a public health system, but accessing these services is often contingent on formal citizenship, which creates barriers for migrants and their descendants. This restriction is particularly problematic given that one out of every five children is not formally registered at birth. This lack of registration severely limits their access to healthcare and other public services throughout their lives (Brito et al., 2017). For Dominican citizens who lack proper documentation, and for the Haitian-Dominican community—including both first-generation immigrants and their descendants—the struggle to obtain adequate healthcare is even more pronounced (Simmons, 2010; Rojas et al., 2011; Miller et al., 2016).

2.1 Dengue

As a Caribbean nation, the Dominican Republic is also vulnerable to frequent outbreaks of tropical diseases, adding another layer of complexity to its healthcare challenges. A common disease in these areas is the Dengue fever, a mosquito-borne illness prevalent in tropical climates, and places additional strain on the healthcare system. The combination of inadequate healthcare access and the high incidence of tropical diseases only exacerbates the already high health disparities among vulnerable populations.

Dengue virus is primarily transmitted to humans through the bites of infected female mosquitoes, especially the *Aedes aegypti* species, though other *Aedes* species can also serve as vectors. An infected individual gains immunity, but only to the specific serotype that infected them. Reinfection, therefore, is possible among those previously exposed. Moreover, those infected a second time are considered at risk for severe cases of dengue (WHO, 2009). The absence of a widely available and effective vaccine exacerbates the challenge of managing dengue. These two features result in a highly contagious and persistent illness. To put in perspective, the average estimated R0, a measure of how many new infections a single infected person is likely to cause in a fully susceptible population, is 4.74 for dengue (Liu et al., 2020) while the Delta variant of the SARS-CoV-2 virus had an estimated R0 of 5.08 (Liu and Rocklöv, 2021).

The global incidence of dengue has markedly increased over the past two decades, with reported cases rising from 500,000 in 2000 to 5.2 million by 2019, reaching an unprecedented peak across 129 countries. The spread of dengue is influenced by several factors, including longer transmission seasons, changing mosquito populations, climate change, and inadequate health systems in many endemic regions like the Caribbean and the Americas. More recently, although there was a slight decline in cases between 2020 and 2022 due to the COVID-19 pandemic, 2023 saw a resurgence in dengue cases, characterized by a significant increase in both the number and scale of outbreaks, including regions previously unaffected. By early 2023, the global number of dengue cases approached a historic high, with over five million cases and more than 5,000 deaths reported across 80 countries, primarily affecting the Americas, but also showing clusters in Europe. (World Health Organization, 2023).

The Dominican Republic is endemic for dengue, with evidence suggesting that 98% of the population in Santo Domingo, the capital, tested seropositive for the virus (Yamashiro et al., 2004). During the period from 2014 to 2016, the Dominican Republic experienced a significant dengue outbreak, which was followed by a Zika virus outbreak. In response to these concurrent crises, large-scale control measures were implemented nationwide to manage and mitigate the spread of these diseases (Kingston et al., 2022). It is important to highlight that even when climate data is useful for predicting the spread of mosquito-borne viruses like dengue, it may not fully explain the dynamics of new outbreaks. Using data from the Dominican Republic and their recent outbreak of tropical diseases, Petrone et al. (2021) suggest that in addition to climate, factors such as population size and demographics should also considered to develop effective strategies for preventing future disease outbreaks. In this paper, we argue that citizen policies could also play a role.

2.2 The Constitutional Court Ruling 168-13

The Dominican Republic and Haiti share the Caribbean island of Hispaniola and have a long history of political conflict. One of the most significant events occurred in 1937 when Dominican dictator Rafael Trujillo orchestrated the mass killing of Haitian residents in the Dominican Republic, an atrocity that entrenched deep-seated anti-Haitian sentiment in the country that persists today (Bishop and Fernandez, 2017). Decades later, marred by poverty and struck by an earthquake in 2010, many Haitians were forced to migrate to the eastern side of the island. They primarily settled near the border and in major cities, where they became cheap labor force in the agriculture and tourism sector. Many of then residing in sugarcane mills

In 2013, the situation deteriorated further during a period of heightened diplomatic tension between the two nations, triggered by a trade war. The Dominican Republic's Central

Electoral Board issued a controversial ruling known as Constitutional Court 168-13 (CC 168), which effectively removed citizenship from individuals who could not prove that both they and their parents were born to legal residents of the Dominican Republic. This decree affected approximately 10% of the country's population—over 90% of whom were descendants of Haitian migrants—leaving them in a precarious legal limbo with severely restricted access to public services and rights. This decision exacerbated the vulnerability of many Haitian-Dominican communities, deepening the ongoing socio-political challenges in the region.

The Inter-American Commission on Human Rights (IACHR) visited the Dominican Republic in 2013 and found widespread poverty, exclusion, and discrimination affecting people of Haitian descent. They also highlighted that a key issue was the lack of access to official identification and registration, resulting in severe barriers to education, healthcare, employment, and civil rights, such as marriage and entering contracts. Many individuals either lacked papers or had them withheld or destroyed, further entrenching their marginalized status. During its visit to various *bateyes*, the Commission observed migrants living in overcrowded conditions without proper sanitation, as there was a lack of clean water and latrines. These deficiencies contributed to frequent outbreaks of diseases. Additionally, medical clinics were in poor condition and often located far from the *bateyes* (Inter-American Commission on Human Rights, 2015).

Regarding access to health, the Dominican Republic State does provide free basic medical care at public hospitals regardless of nationality or immigration status. However, in practice, medical staff can deny non-citizens access to public health services on their own will. According to the testimonies collected by the IACHR, Haitians reported difficulties accessing health services. Many avoided health facilities out of fear of being denied treatment due to their Haitian origin or lack of identity documents.

3 Data

For our outcome data, we rely on *official* disease counts from the Dominican Republic's Epidemiology Direction (known by its Spanish acronym as DIGEPI). Due to the introduction of this protocol, the Dominican government made substantial efforts to gather high-frequency records. For our analysis, we use aggregated data at the municipality level on dengue cases spanning from 2012 to 2019 and on non-communicable disease diagnoses (diabetes, heart attacks, and strokes) covering the period from 2013 to 2019. The DIGEPI collects this information through patients showing up to health centers and obtaining a diagnosis from a medical professional. Because of this, our data is available at the health center-by-week level, but we aggregate up to the municipality-by-month level in our preferred estimations.[1]

In Figure A.1, we plot a time series of the monthly total of dengue cases and highlight the time when the CC-168 was passed (red vertical line). We can see that the timing of the policy was closely lead by a sharp increase in the number of dengue infections nationwide. Since our identification strategy accounts for country-level changes across time, we do not believe that this would bias our results. Nevertheless, we present evidence that supports this belief as our results persist even when we control for the local bioclimatic suitability of dengue differentially before and after the policy.

We measure exposure to the CC-168 using the 2010 Dominican Census data from IPUMS. To do so, we use a proxy for the proportion of the population of Haitian ascent. Since this proxy is taken from a self-declared immigration status and people of Haitian ascent are heavily discriminated against in the Dominican Republic, we believe that our measure is likely an underestimate. To show the robustness of our results, we construct two proxies of Haitian-Dominican presence: one based on the share of Haitian immigrants who arrived over the last 5 years (which we term long-term migrants) and the second based on the share of Haitian-born immigrants (which we term long-term migrants). Our rationale for using these measures is that, although they capture only people who were born in Haiti and emigrated

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[1] There are 155 municipalities in the Dominican Republic and our data spans 72 months.

to the DR, there should be a high correlation between this measure and the number of Haitian-Dominican people, which is what we would ideally measure directly.

Figure A.1 plots our exposure measure across municipalities. Panel (a) shows the share of short-term Haitian immigrants and Panel (b) shows the share of long-term Haitian immigrants. As expected, the largest concentrations of Haitian-Dominicans exist in the region that borders Haiti—the left end of the map—and in the tourism-centered area of Punta Cana and its surroundings—right end of the map. Despite these marked pockets of Haitian-Dominican inhabitants, the figure also shows a great degree of heterogeneity in the local exposure to the CC-168 across the rest of the country. Nevertheless, we demonstrate that our results are robust to the exclusion of these highly exposed areas in Section 6.

Additionally, we rely on epidemiological data on the predicted bioclimatic suitability of the dengue-spreading mosquito Aedes Aegyptis, as referenced above. This measure was estimated by Kraemer et al. (2015).[2] In Figure A.2, we see that there is a large amount of variation in the local suitability for the dengue-inducing mosquito. Importantly, we see that some of the areas most exposed to the CC-168 are highly suitable for the mosquitoes while others are not. For instance, the mosquito is very likely to inhabit areas towards the border region (westmost area in the map) whereas people in the Punta Cana region (towards the Southeast) are relatively unencumbered by this vector of contagion.

Finally, we obtained data on birth records, and marriage and death certificates at the municipality level. The data on birth records serves as a proxy for the local intensity of utilization of health care services. The other two sources can serve as measurements of whether the citizenry takes advantage of these administrative records that play an important part in receiving government assistance in many cases, as detailed in the section above.

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[2] We use the predicted presence of the Aedes Aegyptis mosquito and we aggregate it at the municipality level.

4 Empirical Strategy

In order to answer our research question, we rely on a *difference-in-difference* design comparing municipalities that had a differential exposure to the CC-168 both before and after its implementation. The policy was implemented at the national level so our timing variable varies only from month to month. As detailed above, we proxy the cross-sectional exposure to the CC-168 with the share of the population of Haitian ascent. Our main identifying assumption is that, absent the passing of the CC-168, the number of dengue infections in municipalities with a higher proportion of Haitian-Dominican residents would have evolved in tandem with the morbidity in municipalities with a smaller share of people of Haitian ascent.

Second, since we do not explicitly observe the share of Haitian-Dominicans in a given municipality, we must also assume that our proxy variable—the share of people who have recently immigrated from Haiti—is highly correlated with this ideal exposure measure and that any deviations from the latter are completely arbitrary. Given both of these assumptions, we can identify the effect of restricting citizenship on the spread of dengue.[3] Explicitly, we estimate the following equation:

$$y_{mt} = \delta Exposure_m \times \mathbf{1}[\text{Policy}]_t + X'_{mt}\beta + \gamma_t + \gamma_m + \epsilon_{mt} \tag{1}$$

In this regression, δ measures the impact of the CC-168 on the number of dengue cases in a given municipality (m) and month (t)—represented by y_{mt}. Where $Exposure_m$ is our proxy for the Haitian-Dominican population at the municipality level and $\mathbf{1}[\text{Pol}]_t$ is a dummy variable that takes value 1 for all months after the passing of the CC-168. In additional specifications, we include X_{mt}, which is a set of controls that vary at the municipality- and month-level. [4] The month- and municipality-level fixed effects are represented by γ_t and

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[3] Given the classical nature of the measurement error in our exposure variable, we believe that we are identifying a lower bound for the effect of this policy on the spread of dengue.

[4] In one specification, we include is the one-month-lagged number of cases in that municipality. We do this following Bertrand et al. (2004), since we believe that there could be a strong persistence within municipalities

γ_m, respectively. Lastly, all our regressions have heteroskedasticity-robust standard errors clustered at the municipality level following the difference-in-differences literature.

5 Results

In our preferred specification using the percentage of recent Haitian immigrants as our measure of exposure to the CC-168, we find that the citizenship restrictions had sizeable effects on the local spread of dengue.[5] In Table A.1 we show that a one standard deviation increase in the exposure to the policy lead to a 0.78 increase in the number dengue cases in a given month—a 16.7% increase from the pre-policy average. Put differently, a municipality in the top quartile of exposure to the policy experienced a 38.5% increase in the number of recorded dengue infections relative to the pre-ruling average in the whole country. In this table and all other specifications, standard errors are clustered at the municipality level following Bertrand et al. (2004).

We argue that this increase in the amount of dengue cases is driven not by those who were specifically targeted by the CC-168, but by those nationals whose citizenship was not contested. This follows from the features of the data collection process that we detail in Section 3. Since Haitian-Dominicans are less able to access health centers, the places where infections are recorded, it stands to reason that, in areas with higher concentration of Haitian-Dominicans (those more exposed to the policy) the number of registered dengue cases is being underestimated and mainly taking into account the infection of non-Haitian-Dominicans. Hence, not only are the results reported in Table A.1 an underestimate of the total effect of the policy, but also the effect we *are* able to capture is that on the non-targeted Dominican population. We do not mean to say that those directly affected by the citizenship removal

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in the persistence of dengue, which, if left unaddressed, could bias our estimation of standard errors. That being said, we are aware of the "Nickell bias" issue and we present results controlling for the lagged number of cases in Table A.1 to show that our point estimates are robust.

[5] In Tables A.3 and A.2 in the appendix, we show that these results are qualitatively similar if we use the number of Haitian-born residents (instead of recent immigrants) as our measure of exposure or if we aggregate our data at the yearly level.

were not also at an increased risk of getting ill, but rather that the majority of the effect that we find *in our data* likely fell on those whose citizenship was not targeted.

Since we argue that those not directly affected by the policy are those who bear the brunt of this 17% increase in the number of dengue infections, the mechanism we have in mind is one of contagion. As Haitian-Dominicans are less able to get medical attention in their communities, they become a source of increased risk of infection for their neighbors—including Dominicans whose citizenship remains uncontested. This argument can only be true because dengue is a highly contagious, viral disease. If dengue was not transmittable, we would expect to see a null effect on its prevalence following the citizenship restriction, since there would no longer be a channel through which those impacted by the policy could in turn increase the likelihood of those who attend health centers becoming ill. We show precisely this in Table A.2, where we see no increases in the number of diabetes diagnoses, heart attacks, or strokes.[6] Moreover, despite the fact that Haitian-Dominicans are overall more likely to be ailed by any of these three medical conditions, the policy seems to have had a negative effect, if any, on the number of reported cases. We reconcile the fact that we do not see a consistently null effect, but a negative one, with the fact that our data is mechanically undercounting the disease burden in areas with more Haitian-Dominicans. Therefore, the lack of contagion from the targeted population to the non-targeted citizens combined with the negative bias induced by measurement error in the number of reported cases, yields the expected weakly negative effects on the prevalence of these three non-communicable diseases.

Our results provide evidence of how removing the citizenship of a segment of the population can have sizeable effects on the health of those not targeted by the policy. We claim that these indirect effects of the policy are only possible through the spread of contagious diseases and, accordingly, show that there is no equivalent increase in the case counts for non-communicable diseases. However, in order for these results to be considered as credible

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[6] The disease counts in this table are aggregated at year level, contrary to the specification in our main results (Table A.1) that is run with monthly count data. Table A.2 in the appendix shows that our main results remain qualitatively the same when we aggregate the dengue counts at the year level. The latter table might also provide a more direct comparison to the results in Table A.2.

causal evidence of the indirect effects of citizenship restriction it is important that we validate our identification strategy. As detailed above, we are using a difference-in-differences specification. This statistical model identifies the causal effect of the policy under the assumption that, absent the CC-168, disease counts would have continued to evolve on the same trend regardless of the municipalities' proportion of Haitian-Dominicans.

Below, we show some evidence in support of this hypothesis using a difference-in-differences event study specification where we allow the effect of the policy to vary flexibly over time. Figure ?? cannot confirm our identifying assumption but it can demonstrate that, prior to the policy's implementation, there was no significant divergence in the evolution of dengue case counts across municipalities differing in the proportion of Haitian-Dominican residents in 2010. While a joint F-test for the size of all lead coefficients in this figure does reject the null hypothesis that they are all equal to zero, the figure does show that our results cannot be explained by some pre-existing divergence in the health of municipalities with varying Haitian-Dominican presence. In Figure ??, we also can see that the effect of the policy is present immediately after its implementation and persists for at least six months afterwards.

6 Robustness and Mechanisms

Besides the standard procedures for difference-in-differences estimation discussed above—using clustered standard errors and testing for statistically different trends between municipalities before the passing of the CC-168—in this section we show that our results are robust to a wide range of additional considerations. The three main problems that could arise using these data are 1) the oversized influence of outliers, 2) whether the measurement error or misreporting in the data drives our results, and 3) whether the effects we find simply represent the underlying health environment where Haitian-Dominicans live. Below, we discuss in more detail our approach to assuaging these concerns. In terms of inference, we show that our results remain statistically significant when using a randomization test—as detailed in Bertrand et al. (2004)—instead of the usual asymptotically normal approximation to the distribution of our estimand.

6.1 Sensitivity to outliers

There are two types of outliers in our setting that might affect the results we presented in the previous section: 1) municipalities with an excessive number of cases of dengue infections and 2) municipalities with a disproportionate Haitian-Dominican population. With regards to the former, densely populated areas—such as the capital of Santo Domingo—are much more likely to exhibit high infection counts as contagion can spread more easily than it can in more sparsely populated areas. Similarly, it is usually the case that these urban areas attract large shares of migrants due to their larger economies. Therefore, in Table A.3 we show that the effects of the policy that we present above remain qualitatively similar even when we do not include the capital city in our estimation. Likewise, in column 3 of the same table, re-estimate the effects of CC 198-13 on the spread of dengue without including the provinces closest to Haiti and obtain similar results. While having Santo Domingo or the border region be a driver of our results would not have directly contradicted our identification strategy, we believe that it is important to show that our results are evident across the DR.

6.2 Misreporting in case count data

In Section 3, we wrote about the process by which the Dominican government collects our administrative data on disease counts. Since it is mainly done through diagnoses determined at health centers and hospitals, it disproportionately measures the morbidity of populations that are more likely to attend and be tended to at one of these sites. Since there is evidence of Haitian-Dominicans using health services less than the rest of the Dominicans, which is exacerbated by the citizenship restrictions of the CC-168, we argue that we underestimate the number of sick individuals in areas with higher proportions of the former group of people. This is a type of misreporting that we can map to the effects of the CC-168 that we estimate and we do so above. However, it could be the case that there are other forms of misreporting that interact with our estimation in manners that we cannot observe or discern. Therefore, we turn to an independently collected source of data to validate the results that we obtain with the administrative records. This second data source is the Dominican Demographic Health Survey (DHS) of 2013.

Since this data was collected in the third quarter of that year, we can re-estimate the model in equation 1—albeit in a short window of time—using individual-level data on symptoms associated with dengue as our outcome variables. We then compare people surveyed after the policy was passed (September 2013) and those interviewed before this date across municipalities with higher exposure to the policy versus those that were less exposed, accounting for municipality and month fixed effects. We find that our results are similar even in such a short term: we find an increase in respiratory symptoms for adults and diarrhea for children, both of which are consistent with dengue.[7]

6.3 Dengue Suitability

We argue that our results stem from an increased spread of dengue from those targeted by the CC 168-13 towards the rest of the population. Haitian-Dominicans, however, live in more disease-prone environments and have lower overall healthcare access. An alternative explanation for our results is that, given the overall increase in dengue cases around the time of the policy, areas that are more suitable for this tropical disease mechanically experienced an increased infection rate and that these places are more likely to be populated by Haitian-Dominicans. We provide evidence that are inconsistent with this counterargument. First, as we show in Table 2, there seems to be no differential increase in the prevalence of non-communicable diseases in areas more affected by the citizenship restriction. This demonstrates that our results are not driven by any behavioral changes—potentially also induced by the same policy—that could drive an overall increase in the disease burden of the

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[7] The reason we do not test directly for whether people contract dengue is because the DHS does not collect this information and only asks if people have recently experience a series of symptoms.

most affected areas. More specifically, we estimate our main results in Table 1 including an interaction term between the measure of dengue suitability described in Section 3 and our policy indicator for periods following the passing of the CC 168-13. We present the results of this analysis in Table A.4. We show that, even controlling for the differential trends in dengue cases in areas more suitable for this condition, our estimate of the effect of the CC 168-13 (first row) remains economically and statistically significant. Conditional on this mechanical "inertia" effect, we find that a one standard deviation in exposure to the citizenship restriction led to a 14% increase—relative to a 16.7% increase in our main specification—in the number of dengue cases, relative to the baseline average prevalence of this illness.

6.4 Randomization inference

Following MacKinnon and Webb (2020) and Bertrand et al. (2004), we test the statistical significance of our results using a randomization test in place of the standard asymptotically normal approximation. This approach serves two main purposes: 1) it allows us to demonstrate that our results are representative of robust relationships in the data and 2) it provides an additional check on the statistical relevance of our results. In summary, the randomization inference that we conduct estimates the a modified version of equation 1 where we resample the exposure to and timing of the policy from the empirical distribution of our data. We repeat this process 300 times and use all these coefficients to generate an estimate of the finite sample distribution of the δ parameter in equation 1. The main drawback of this procedure is that it it requires that $Exposure_m \times \mathbf{1}[\text{Policy}]_t \perp\!\!\!\perp \epsilon_{mt} \mid X_{mt},\ \gamma_t,\ \gamma_m$. While this is a stronger condition than the parallel trends assumption that we need to identify δ in equation 1, we believe that it is palatable given the auxiliary nature of this exercise.

$$y_{mt} = \tilde{\delta}\ \overline{Exposure_m} \times \overline{\mathbf{1}[\text{Policy}]_t} + X'_{mt}\beta + \gamma_t + \gamma_m + \epsilon_{mt} \tag{2}$$

We present the outcome of the randomized inference test in Figure A.4. This figure plots the distribution of $\tilde{\delta_1}$ from equation 2, which is the empirical probability density function of values estimated with the resampled datasets. We then locate our estimate of δ from equation 1 within this distribution to reject the null hypothesis of a null effect. We interpret this as a validation of our asymptotic inference above and also of evidence that our results represent robust patterns in the data.

7 Conclusion

This paper documents the negative effects of tightening citizenship policy in a developing country context on the spread of communicable diseases. We argue that our results are driven by the targeted population losing access to public health services. While mechanisms other than access to healthcare may be at play, we show evidence against some of these alternatives. We concede that there may be substantial under-reporting of dengue cases in areas more affected by the citizenship removal, precisely because people are less likely to go to a clinic and get diagnosed with dengue.

For this reason, we believe that our estimates are a lower bound for the increased contagion of this tropical disease. Moreover, since it is precisely for those whose citizenship was removed that the official statistics are failing to account, we interpret our findings as evidence of indirect effects on the non-targeted population. Haitian-Dominicans were the targeted group and had their citizenship (and their public healthcare access) revoked, which mechanically biases the morbidity estimates for this sub-population downwards as they are not seen by health professionals and their conditions are not properly recorded. Therefore, the increased cases of dengue are likely to be driven by those who still seek medical attention at health clinics and hospitals, those who did not have their citizenship removed (the non-targeted population). Overall, our results point to the impossibility of containing the negative effects of policies that exclude sub-populations from access to the State in the presence of externalities, such as those induced by contagion. While our findings are restricted to the case of the Dominican Republic, this phenomenon has only become more relevant worldwide during the

Covid-19 pandemic.

These externalities pose a significant hurdle for governments that wish to exclude specific groups of people from access to government goods and services. Conversely, our findings point to the potentially sizable benefits for the "native" population stemming from increasing access to legal residency and citizenship for existing migrant groups in receiving countries. We believe these benefits have been largely overlooked in policy discussions and taking them into account could improve the support of such laws by the overall population and their legislative representatives.

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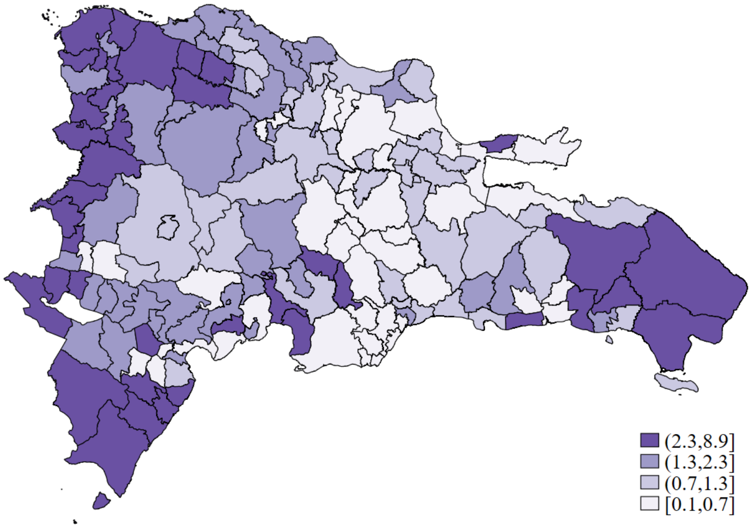
A Main Figures and Tables

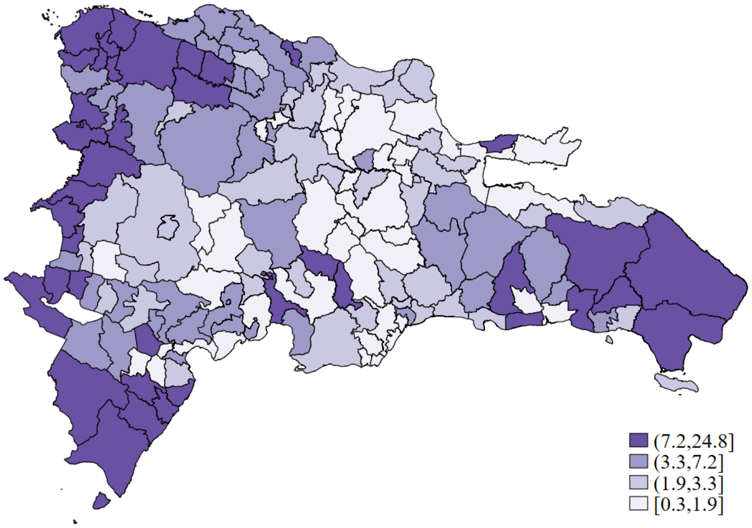
Figure A.1: Census (2010) estimates of the Haitian-Dominican population

(a) Recent Haitian immigrants



Notes: National share is 1.6%.

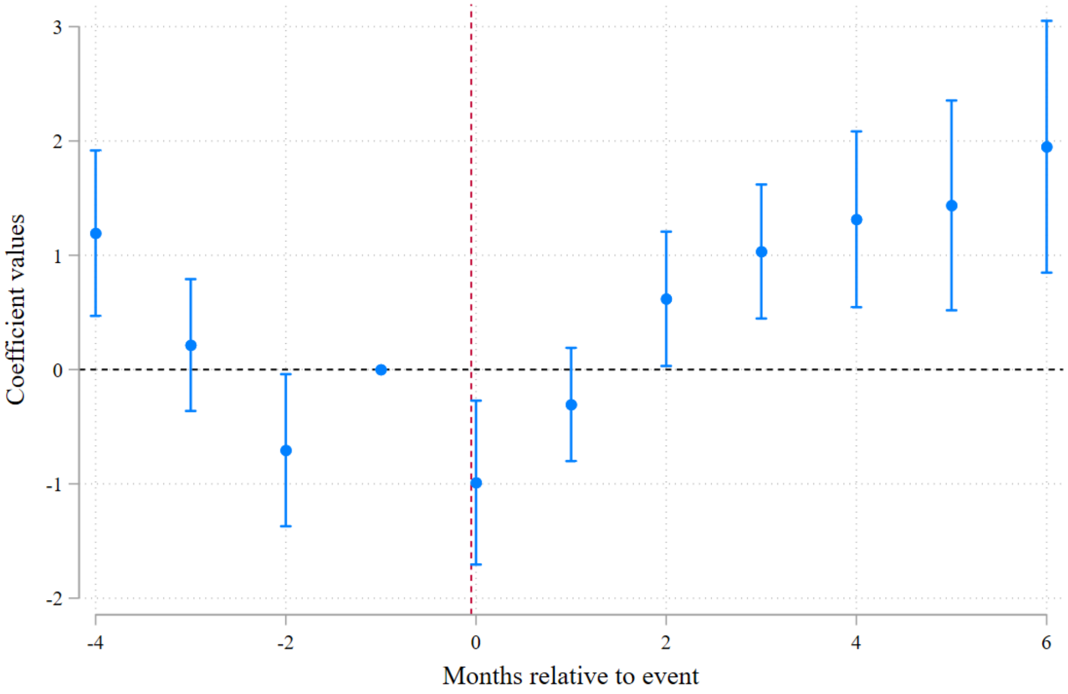
(b) Haitian-born immigrants



Notes: National share is 4.47%.

Figure A.2: Dynamic effects of the citizenship policy

(a) HD Population (%, s.d)



(b) HD Population (Top Quartile)

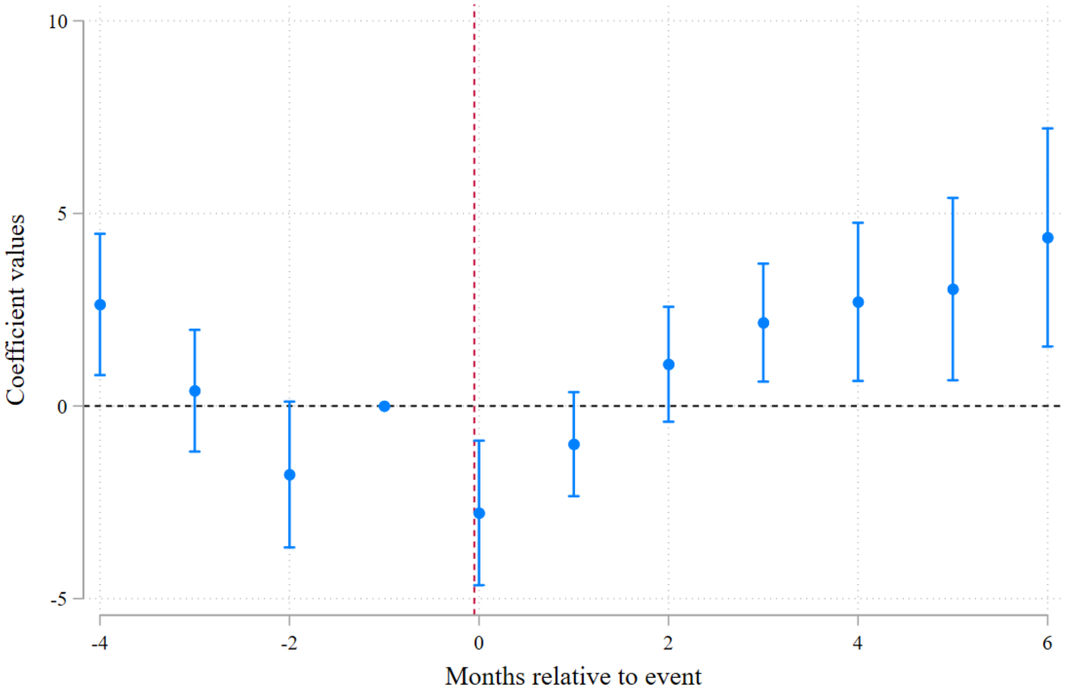
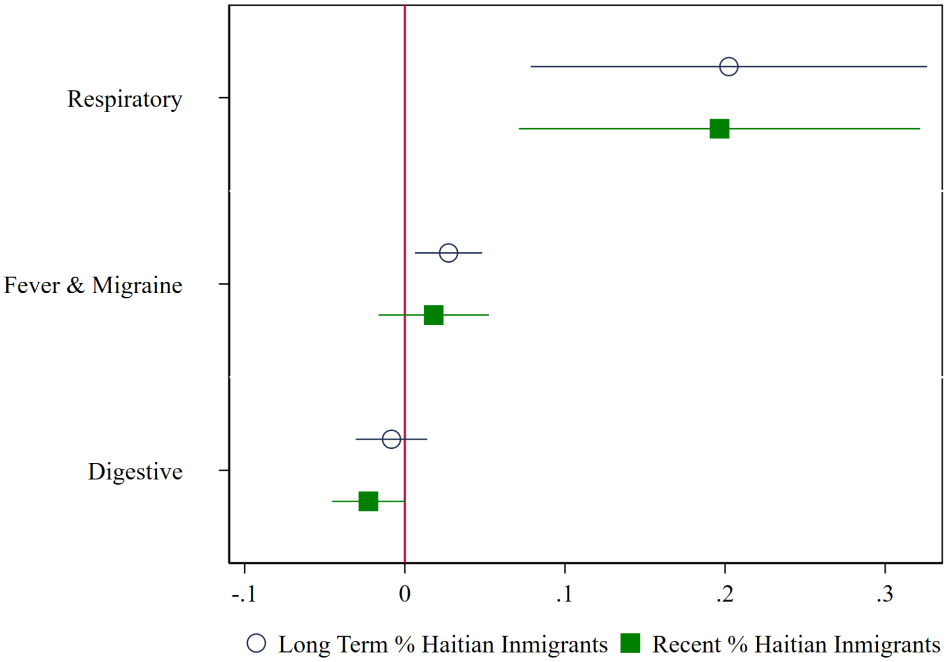


Figure A.3: Effects on Dengue symptoms using the 2013 DHS

(a) Adults



(b) Children

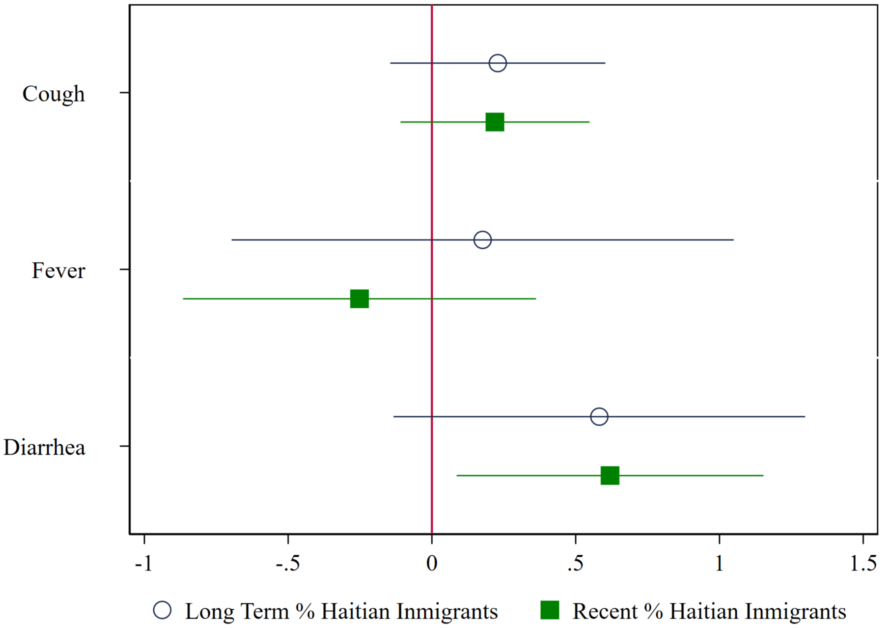
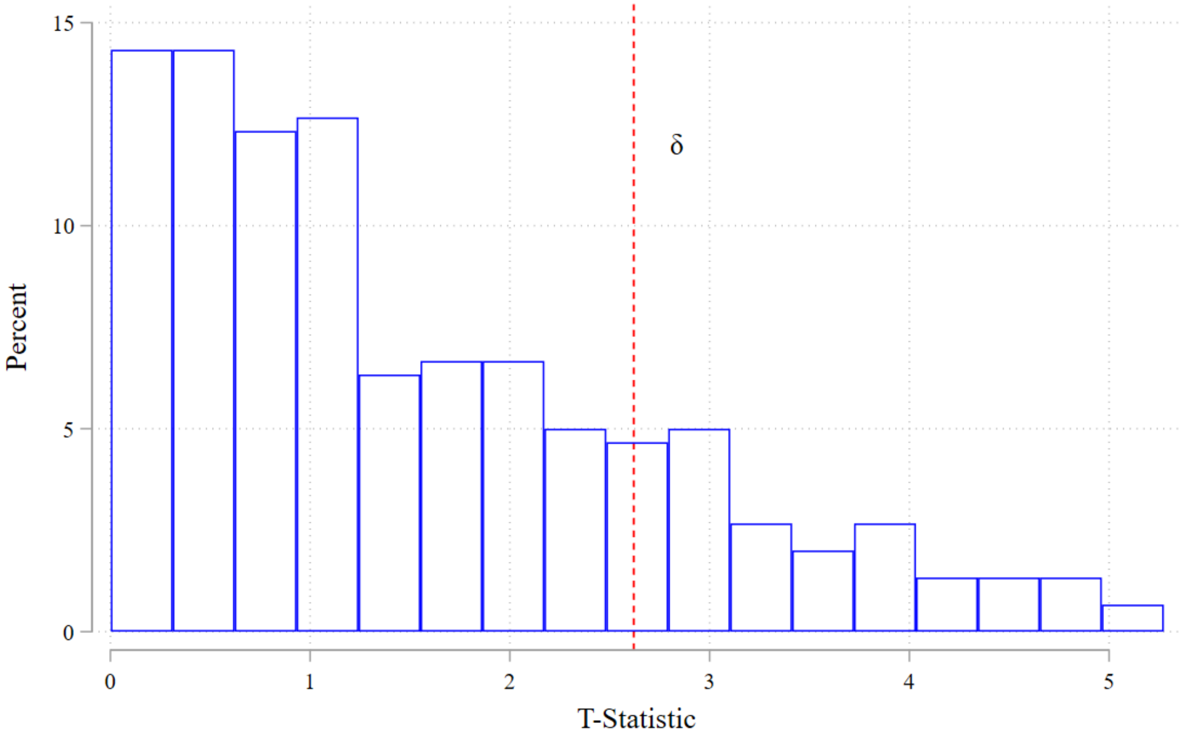


Figure A.4: T-stat distribution under resampled timing of the policy



Number of iterations: 300.

Table A.1: Effects of citizenship restriction on dengue prevalence

	(1) HD pop. (%, s.d.)	(2) HD pop. (Top Quartile)
Pol. x HD Exposure	0.781***	1.888***
	(0.283)	(0.721)
Month FE	Yes	Yes
Municipality FE	Yes	Yes
Dep. Var. Mean (2012)	4.670	4.670
N	11160	11160

Standard errors in parentheses

Errors clustered at the municipality level.

HD population proxied by share of recent Haitian migrants.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table A.2: Effects of citizenship restriction on non-communicable diseases

	HD pop. (%, s.d.)			HD pop. (Top Quartile)		
	(1) Diabetes	(2) Heartatt	(3) Stroke	(4) Diabetes	(5) Heartatt	(6) Stroke
Pol. x HD Exposure	-136.0***	-35.57***	-35.55***	-337.4**	-76.16***	-76.13***
	(51.61)	(12.51)	(12.51)	(132.4)	(23.04)	(23.04)
Year FE	Yes	Yes	Yes	Yes	Yes	Yes
Municipality FE	Yes	Yes	Yes	Yes	Yes	Yes
Dep. Var. Mean (2012)	72.78	39.18	39.18	72.78	39.18	39.18
N	833	833	833	833	833	833

Standard errors in parentheses

Errors clustered at the municipality level.

HD population proxied by share of 5-year Haitian migrants.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table A.3: Excluding Santo Domingo and the border provinces

	(1) Full sample	(2) W/o Santo Domingo	(3) W/o border
Pol. x HD Exposure	0.781***	0.607**	1.054***
	(0.283)	(0.265)	(0.350)
Month FE	Yes	Yes	Yes
Municipality FE	Yes	Yes	Yes
Dep. Var. Mean (2012)	4.670	3.685	6.470
N	11160	10656	6696
Rel. effect	0.167	0.165	0.163

Standard errors in parentheses

Errors clustered at the municipality level.

HD population proxied by share of recent Haitian migrants.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table A.4: Horse racing the HD population and disease suitability

	(1) HD pop. (%, s.d.)	(2) HD pop. (Top Quartile)
Pol. x HD Exposure	0.655***	1.557**
	(0.251)	(0.638)
Pol. x Main Vector Suit.	-1.166**	-1.155**
	(0.462)	(0.454)
Month FE	Yes	Yes
Municipality FE	Yes	Yes
Dep. Var. Mean (2012)	4.670	4.670
N	11160	11160

Standard errors in parentheses

Errors clustered at the municipality level.

HD population proxied by share of recent Haitian migrants.

The vector of contagion is the Aedes Aegypti mosquito.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

A Additional Figures and Tables

Figure A.1: Monthly dengue cases in the Dominican Republic

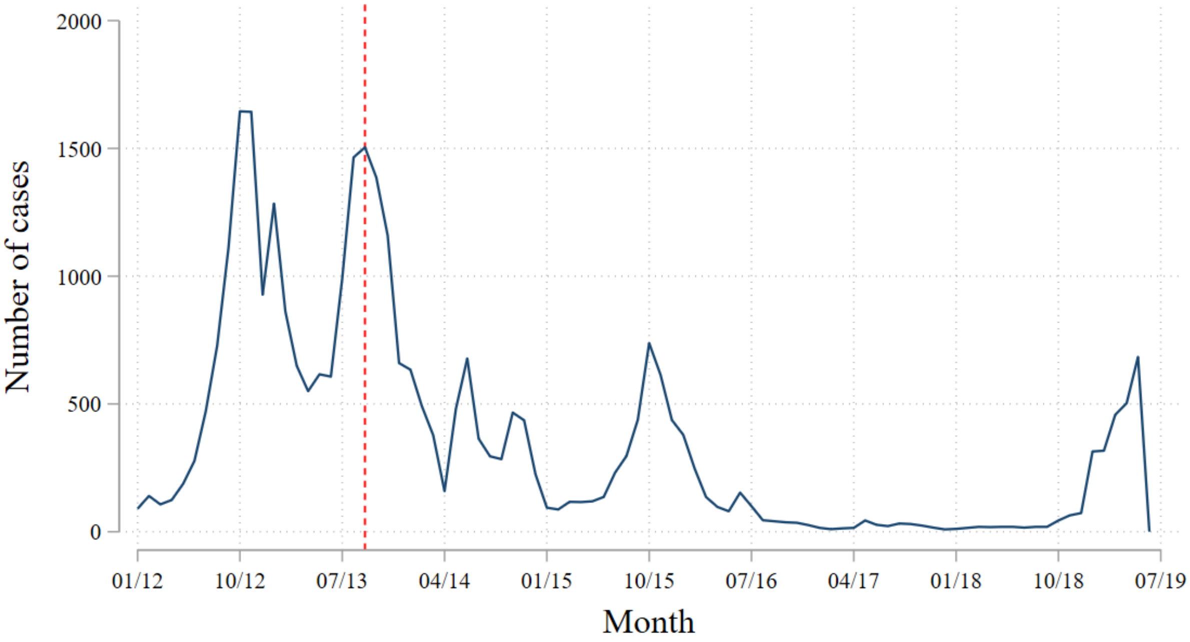


Figure A.2: Predicted presence of the Aedes Aegypti mosquito

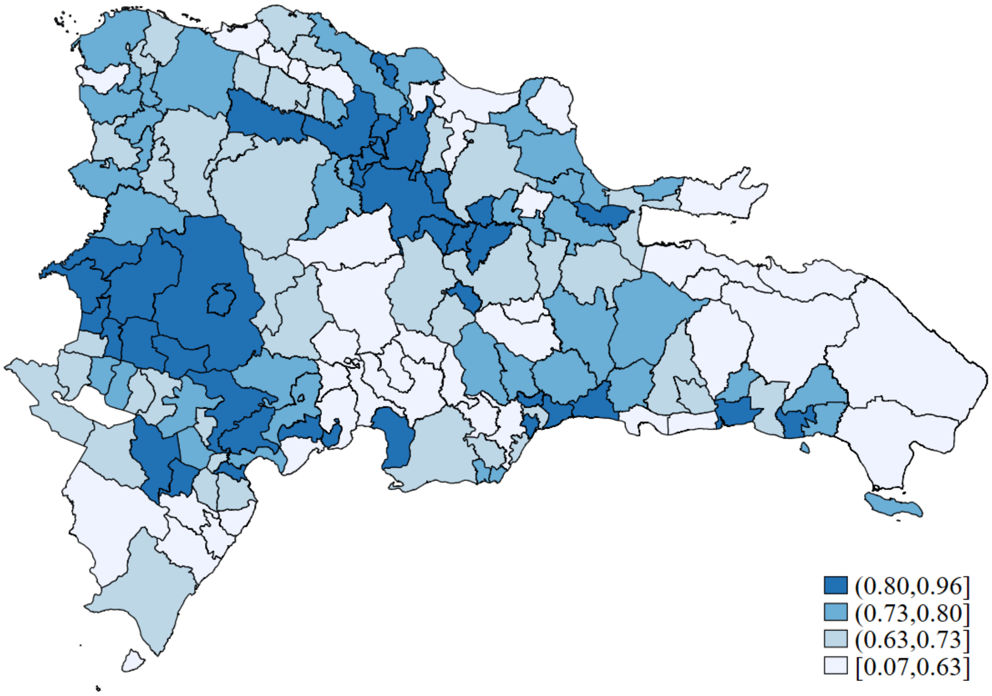


Table A.1: Effects of citizenship restriction on dengue prevalence (with lag control)

	(1) HD pop. (%, s.d.)	(2) HD pop. (Top Quartile)
Pol. x HD Exposure	0.310^{***}	0.732^{***}
	(0.0957)	(0.248)
Month FE	Yes	Yes
Municipality FE	Yes	Yes
Dep. Var. Mean (2012)	4.885	4.885
N	11005	11005

Standard errors in parentheses

Errors clustered at the municipality level.

HD population proxied by share of recent Haitian migrants.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table A.2: Effects of citizenship restriction on dengue prevalence (year x municipality level)

	(1) HD pop. (%, s.d.)	(2) HD pop. (Top Quartile)
Pol. x HD Exposure	16.25***	37.82***
	(4.891)	(12.23)
Year FE	Yes	Yes
Municipality FE	Yes	Yes
Dep. Var. Mean (2012)	61.89	61.89
N	1240	1240

Standard errors in parentheses

Errors clustered at the municipality level.

HD population proxied by share of recent Haitian migrants.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$

Table A.3: Effects of citizenship restriction on dengue prevalence (long-term Haitian immigrants)

	(1) HD pop. (%, s.d.)	(2) HD pop. (Top Quartile)
Pol. x HD Exposure	0.856^{***}	1.797^{**}
	(0.272)	(0.721)
Month FE	Yes	Yes
Municipality FE	Yes	Yes
Dep. Var. Mean (2012)	4.670	4.670
N	11160	11160

Standard errors in parentheses

Errors clustered at the municipality level.

HD population proxied by share of Haiti-born migrants.

* $p < 0.10$, ** $p < 0.05$, *** $p < 0.01$