Trading Epidemics*

Cosimo Beverelli[†][‡] Rohit Ticku[§]

Abstract

Can traded goods be a vector for transmitting communicable diseases? This paper identifies the causal effect of livestock imports on the spread of infectious animal diseases through an exogenous increase in demand for imported livestock. Our instrumental variable strategy exploits a surge in the import of *halal* livestock in Muslim countries during the month of Eid-al-Adha to identify the effect of livestock imports on infections in related species at the destination. Using a dataset that covers 123 countries and five livestock categories in the period between 2004 and 2019, we find that imports-to-infections elasticity is about 0.75. The relationship is driven by a contagion effect at the destination, i.e., through interaction between imported livestock, some of which might be infected, and domestic livestock. Further, countries that are likelier to import infected livestock from their partners also observe a stronger effect of livestock imports on domestic infections. These results highlight the *transmission-through-trade* from the origin to the destination.

Keywords: International trade; Livestock diseases; Religious festivals; Eid-al-Adha

JEL Classification: F14; F18; I18; Q57

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[†]Economic Research and Statistics Division, World Trade Organization. cosimo.beverelli@wto.org.

[‡]Robert Schuman Centre for Advanced Studies, European University Institute.

[§]European University Institute. rohit.ticku@eui.eu. Corresponding author.

1 Introduction

International trade in livestock has grown significantly in the last two decades. The number of livestock units traded doubled from a billion units in year 2007 to approximately two billion units in year 2017. The traded animals are also travelling ever-longer distances, which is attributed to the concentration in the slaughterhouse industry and regulatory breaches.[1] The expansion of livestock trade could potentially exacerbate the spread of communicable diseases. A 2015 study in Biomed journal noted:

> "Animal trade is an effective way of introducing, maintaining and spreading animal diseases, as observed with the spread of different strains of foot and mouth disease in Africa, the Middle East and Asia and the spread of bovine spongiform encephalopathy (BSE), for example, into Oman and Canada through the importation of infected cattle." (Hardstaff et al., 2015).

In the aftermath of Covid-19 pandemic public health officials and media have repeatedly warned about the dangers of cross-border livestock trade.[2]

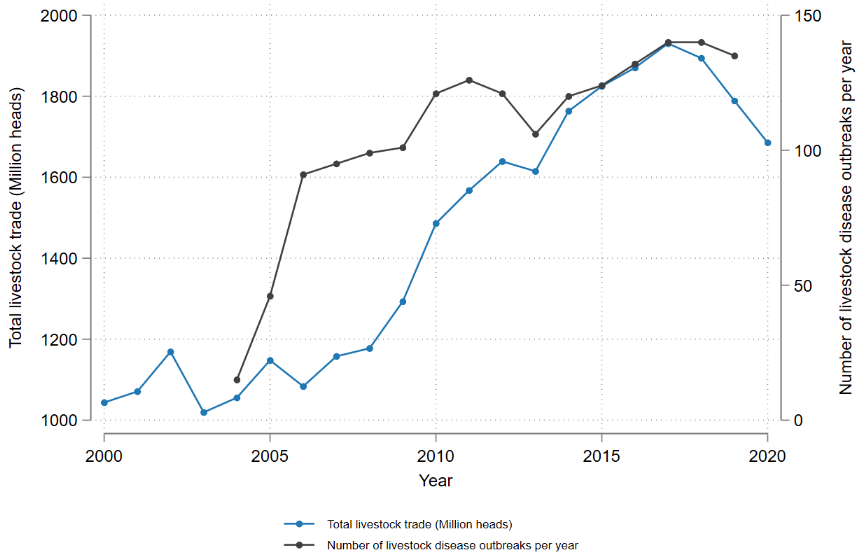
Figure 1 shows a co-movement between livestock trade and the number of disease outbreaks during the last fifteen years. While aggregate trends might suggest a link, there is no systematic evidence on the relationship between livestock trade and the spread of communicable animal diseases. Identifying the relationship is important for public policy for two reasons. First, approximately seven thousand quarantine and biosecurity (i.e. SPS) measures are currently in place among WTO member countries to regulate the spread of communicable diseases through international live animals' trade.[3] Contrary to popular perception, livestock trade may *not* contribute to animal disease outbreaks if international safeguards are efficient. Second, if these deleteri-

[1]"'Something is wrong': why the live animal trade is booming in Europe" (The Guardian, 24 January 2020).

[2]A news article in the Guardian was ominously titled "'Live animals are the largest source of infection': dangers of the export trade" (The Guardian, 21 January 2020).

[3]WTO I-TIP Goods database, Tables by Products, accessed on 29 July 2022.

Figure 1: Livestock trade and disease outbreaks



Notes: The data on the annual number of livestock heads traded is sourced from FAOSTAT while the data on livestock disease outbreaks is calculated from FAO EMPRES-i database. The EMPRES-i database records animal disease data from 2004 onwards.

ous consequences exist, we must identify the underlying mechanisms to implement appropriate policy responses.

This paper bridges the gap in the literature by identifying the causal effect of importing livestock on animal disease outbreaks in the destination country. Although we focus on diseases that impact animal species, they are directly consequential for human health, since about 60 percent of pathogens that affect humans are transmitted from animal species (Karesh et al., 2005). Further, the disease-related depletion of livestock can generate income shocks that can adversely affect individual health in developing countries (Baird et al., 2011, 2013; Burke et al., 2015). Finally, to the extent that disease shocks dampen consumer demand for livestock products or elicit state response through import restrictions, the resulting trade disruptions could severely affect farmers and exporters.[4]

Identifying the causal effect of livestock imports on disease outbreaks is challenging due to potential endogeneity. Straightforward OLS estimates are in fact likely to underestimate the true effect. This is because a disease outbreak can dampen import

[4]"'It was painful to declare it': outbreak of animal disease was blow to Sudan exports" (The Guardian, 21 January 2020).

demand for, or trigger import restrictions on, the associated live animal species in the destination country. The expected reverse causality or omitted variables are likely to bias the effect towards zero.

We address the potential endogeneity through a novel instrument that exploits an exogenous increase in the import of live animals in Muslim countries due to the festival of Eid al-Adha ('Feast of the Sacrifice'). During the festival, which lasts for four days in a given calendar year, Muslims ritually sacrifice an animal, which is shared equally with family, relatives and friends, and the poor. We expect a rise in the import of 'halal' animals for sacrifice in Muslim countries during the period of Eid al-Adha that is orthogonal to a disease outbreak. This provides the intuition for our identification strategy where we instrument the import of animals in a given livestock category, period, and importing country with a binary variable that equals one if the livestock category is halal, the period is the month of Eid al-Adha, and the importing country is Muslim.

For empirical analysis, we use FAO Empres-i data on approximately ninety-five thousand animal disease outbreaks worldwide between 2004 and 2019. Using the description of animals affected in each outbreak, we match the disease data to COMTRADE monthly trade data on five four-digit product categories of livestock in the Harmonized System (HS) classification of traded products.[5] For our matching exercise we use the strategy that we develop in Beverelli and Ticku (2021).

Results from the Instrumental Variable (IV) specification show that a 1 percent increase in the import of livestock causes 0.75 percent increase in infections in related animal species (the corresponding OLS coefficient is close to zero in magnitude). The effect is robust to controlling for domestic livestock size or policy measures to restrict the outbreak of livestock diseases. We conduct a series of exclusion restriction checks for instrument validity. By including the most restrictive set of fixed-effects possible in our IV estimation, we rule out that the instrument can impact infections through change in

[5]Approximately 87% of the disease outbreaks in FAO dataset affected livestock, 7% affected wild animals, while for the remainder we could not identify the HS-category from our matching exercise.

domestic economic activity (such as through the production or transportation of livestock) or in the quality of customs inspection during the festival period. We perform a placebo analysis to show that the festival-related import of halal meat, that is not directly related to the transmission of diseases to animals, does not affect the prevalence of animal infections. Another placebo test with an instrument that uses the timing of Eid-al-Fitr, which is an equally important festival for Muslims but does not entail ritual animal sacrifice, shows that the identified relationship is not due a spurious festival effect but specifically due to the ritual of animal sacrifice during Eid-al-Adha.

We next investigate the channels through which livestock trade can impact the prevalence of infection cases at the destination. We differentiate whether the imports-to-infections relationship is driven by a pure *import* effect or a *contagion* effect at the destination. Assuming that a given share of livestock imports are infected, an increase in livestock imports would mechanically increase the number of infected animals at the destination. Alternatively, the infected animals that enter the country might interact with domestic livestock and therefore spread infections. Our results show that the effect of livestock imports is mediated by the size of domestic livestock. The relationship between imports and infections is insignificant among countries with a small endowment of livestock. We rule out that there is a mechanical increase in infection cases due to imported livestock that might be infected. On the contrary, evidence suggests that livestock imports determine infections through a contagion effect at the destination. We then turn to the partner characteristics that can determine the likelihood of importing infected livestock. We find that countries that are likelier to import infected animals due to a contemporaneous outbreak among their partners, also observe a higher effect of livestock imports on infection cases. The evidence together highlights the transmission-through-trade from the origin to the destination.

This paper primarily contributes to the literature on international trade and health. Early empirical literature suggested that income gains from international trade would improve global health standards (Dollar, 2001; Owen and Wu, 2007). Contrary to this view, recent evidence points to the negative impact of trade on human health through various channels, including easier access to "junk food" (Giuntella et al., 2020), incentivizing risky sexual behaviour (Oster, 2012), and adverse changes in labor market conditions (Colantone et al., 2019; Adda and Fawaz, 2020; Erten and Keskin, 2021). Moreover, international commerce has enabled the spread of infectious diseases through history (Harrison, 2012; Boerner and Severgnini, 2014). The role of contemporary trade practices in spreading communicable diseases, however, remains largely unexplored. We are aware of two studies that look at the contemporary link between international trade and communicable diseases. Oster (2012) shows that trade indirectly contributed to spread of HIV in Africa by facilitating the movement of people in the logistics sector. Beverelli and Ticku (2021) show that illicit trade practices are associated with higher disease prevalence. Our paper expands this literature by identifying a direct link between international livestock trade and communicable animal diseases. Further, in contrast to Oster (2012) and Beverelli and Ticku (2021), our instrumental variable design identifies a causal relationship between trade and communicable diseases.

The paper also contributes to a growing literature at the intersection of economics and epidemiology. New research in light of the COVID-19 pandemic has highlighted environmental factors, demography, and government policies to determine COVID-19 transmission (Borjas, 2020; Carleton and Meng, 2020; Chinazzi et al., 2020; Acemoglu et al., 2020). Instead of focusing on a specific zoonotic disease, we consider a variety of pathogens that are known to afflict animal species, some of which can also cross over to human beings. We can therefore study the spread of infectious diseases over a longer time horizon as well as focus on a specific channel of transmission through international trade, which has important policy implications regarding trade regulation. Closer to our research, Antràs et al. (2020) develop a theoretical framework for the diffusion of pandemics through trade. In their model, trade-related movement of humans generate an 'epidemiological externality' across countries. Our research highlights the direct role of traded goods, that is livestock, as a vector for transmitting diseases across countries.

Finally, the paper speaks to a literature that links the observance of religious rituals to health and well-being (Almond and Mazumder, 2011; Majid, 2015; Campante and Yanagizawa-Drott, 2015; Schwab and Armah, 2019). The role of Ramadan fasting on socio-economic outcomes in Muslim countries is especially highlighted in this literature. Our paper identifies livestock imports as an additional mechanism through which a religious ritual in Muslim countries might influence health outcomes.

2 Data

We construct a dataset that covers 123 countries and the five livestock animal categories of the Harmonized System (HS) four-digit classification: 0101 (horses, asses, mules and hinnies); 0102 (bovine animals); 0103 (swine); 0104 (sheep and goats); and 0105 (poultry, fowls of the species Gallus domesticus, ducks, geese, turkeys and guinea fowls). We focus on the period from 2004 to 2019, for which data on livestock diseases is available. This section describes the main variables and their sources.

2.1 Livestock diseases

We obtain data on animal diseases from FAO's EMPRES Global Animal Disease Information System (EMPRES-i). The database contains daily information on the outbreak of thirty-two animal diseases, which is obtained from the World Organization for Animal Health (OIE) and the national health agencies. The data comprises of approximately ninety-five thousand disease outbreaks that occurred worldwide during the period from 2004 to 2019. The database records the number of animals of a species infected by a specific disease outbreak, and its consequences in terms of animal fatalities as well as the human response in the form of slaughtering infected animals. Our analysis focuses on recorded infection cases since both animal deaths and subsequent human actions are likely to be determined by country-specific institutional characteristics.

Out of the thirty-one diseases with confirmed cases in the EMPRES-i database, the OIE classifies fifteen diseases as affecting a single class of species, fourteen diseases as affecting multiple species, and two as 'other diseases' (see appendix Table A-1).[6] While it is straightforward to match diseases that affect a single species to an HS4 live animal category, it is complicated to match diseases that affect multiple species. To overcome this challenge and precisely assign diseases to an animal category k (four digit HS heading), we use a matching strategy that follows Beverelli and Ticku (2021).

All infection cases specific to HS4 category k during month/year t are summed across all locations within each country j, which yields a dependent variable, $Infections_{jkt}$, which varies by importing country, HS4-product, and month/year.

2.2 Livestock trade

We measure livestock imports as log value of imports (augmented by one) reported by importer j from all countries (M_{jkt}) for HS4 category k in month/year t. Livestock import data is sourced from UN COMTRADE and it is available monthly for the entire sample period.

2.3 Other variables

We collect data for a number of control variables that vary across the importer-HS4 category (jk) dimension over time. We include precautions at the border, the number of screening measures, and the number of surveillance measures that were issued by importer j on HS4 category k bi-annually.[7] Border precautions are applied at the

[6]One disease covered in the database, Rinderpest, is only observed in unconfirmed cases. We exclude all unconfirmed cases from the dataset to reduce measurement error. This leads to the exclusion of Rinderpest from the sample.

[7]The data on border precautions, screening, and surveillance measures are obtained from the OIE. The raw data contain information both on the type of disease and on the species affected. The matching

border posts to prevent introduction of a disease into the country and can range from quarantine, certification of health status in the exporting country, details on the zone or herd of origin of the imported animal, or testing of animals before loading the consignment. Screening measures are diagnostic tests carried out systematically either within the framework of a control programme for the disease, or for qualifying herds/flocks as free from the disease. Surveillance measures continuously investigate a given population to detect the occurrence of disease for control purposes, and may involve testing a part of the population. Besides policy measures, we also collect annual data on the stock of animals in importer *j* in HS4 product *k*. The data are obtained from FAOSTAT.

3 Empirical Strategy

3.1 Baseline model

We begin our analysis by estimating the baseline relationship between import of livestock and the prevalence of related animal diseases in the destination country. We estimate the following model using OLS:

$$log(infections)_{jkt} = \beta_1 log(imports)_{jkt} + \gamma_{jt} + \omega_{kt} + \lambda_{jky} + \epsilon_{jkt}, \quad (1)$$

where $log(infections)_{jkt}$ is the log of infection cases in importer *j* among animal species included in the livestock category *k* in month/year *t*.

The main explanatory variable, $log(imports)_{jkt}$, is the log of imports in importer *j* of animal species included in HS4 product *k* in month/year *t*. Imports are reported in values (USD) since the number of units are not reported at the monthly level in the UN Comtrade database.

We saturate the model with the most restrictive set of fixed-effects possible (γ_{jt}, ω_{kt}

with HS headings is straightforward.

and λ_{jky}). Importer-month/year fixed effects (γ_{jt}) account for importer-specific variation in economic activity or customs behavior; HS4 product-month/year fixed effects (ω_{kt}) account for seasonal fluctuations in international prices or the evolution of diseases that are specific to livestock category k; while importer-HS4 product-year (λ_{jky}) fixed effects account for all policies related to an importer-HS4 product that vary gradually. Since diseases exhibit both spatial and serial correlation we cluster standard errors at country-level and month/year-level to permit valid inference if errors are auto-correlated within country, as well as within month/year across countries. β_1 is the coefficient of interest that measures the percent increase in the number of infection cases that corresponds to a 1% increase in the import of livestock.

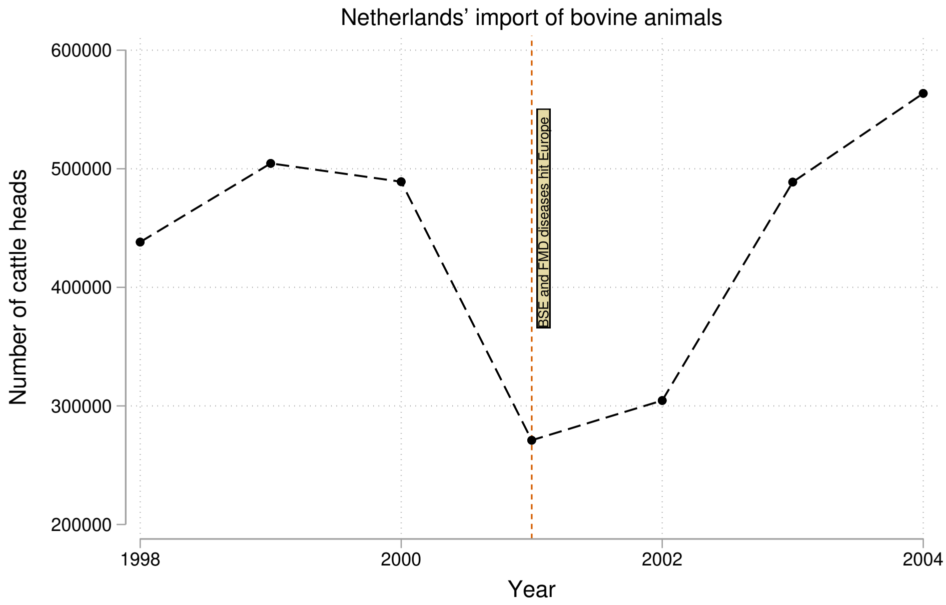
3.2 Threats to identification

Despite including a battery of fixed effects to account for potential omitted variables, the coefficient of interest (β_1) is likely to be biased towards zero for two reasons. The OLS estimate is likely to be affected by reverse causality. This is because a disease outbreak in the importing country is likely to dampen import demand for the associated animal species. Figure 2 illustrates the potential reverse causality through the example of Netherlands, where cattle imports fell sharply in 2001-02 due to the emergence of mad cow disease (BSE) and Foot and Mouth disease (FMD) (Achterbosch and Dopfer, 2006), and took another couple of years to return to the pre-outbreak levels. Besides import demand responding to a disease outbreak, the state may also regulate the entry of potentially sick animals or even impose an outright import ban, which would once again bias the OLS estimate towards zero.

3.3 Instrumental variable estimation

We use a "natural natural experiment" (Rosenzweig and Wolpin, 2000) to identify an exogenous change in the import demand for livestock. Specifically, we take advantage

Figure 2: Disease shocks and livestock imports: Case study of the Netherlands



Notes: The data on the annual number of cattle heads is sourced from FAOSTAT.

of an exogenous surge in the import of 'halal' live animals in Muslim countries during Eid-al-Adha ('Feast of the Sacrifice'). During the festival, that lasts for four days in a given calender year, Muslims are obliged to sacrifice animals, which are shared in three equal parts: for family, for relatives and friends, and for poor people. We expect a surge in the import of 'halal' live animals in Muslim countries during the four-days festival period (which shifts approximately 11 days earlier each year). The import surge due to the festival is statistically independent of a disease-induced change in consumer preferences or state action.

Based on the identifying assumption, we propose an instrumental variable design to estimate the causal effect of livestock imports on the prevalence of diseases that afflict related species in the importing country. The first stage takes the following form:

$$log(imports)_{jkt} = \delta \mathbf{Z}_{jkt} + \gamma_{jt} + \omega_{kt} + \lambda_{jky} + \mu_{jkt}, \quad (2)$$

where $\mathbf{Z}_{jkt}$ is a binary variable (Muslim × halal × Eid-al-Adha) that equals one if importer-country j is Muslim, HS4 live animal product k is halal, and t is the month/year in which Eid al-Adha takes place. The first stage in our IV specification is conceptually similar to a triple difference-in-difference estimation (Gruber, 1994), where non-Muslim countries act as a placebo group, and the specification requires a weaker set of assumptions to satisfy the exclusion restriction, due to the inclusion of more restrictive fixed effects (see discussion in Section 4.2).[8]

To categorize a country as Muslim we use the classification by Brown (2016), which identifies countries in which Islam was the preferred religion of the state's governing regime in year 2000. This measure is preferred over a simple population measure (i.e., the share of Muslims in the importing country j), since it captures the relative political power of religions within a country, which in turn would influence the social rules. Nevertheless, Figure 3 shows that this measures corresponds well to the distribution of the Muslim population.[9]

We classify livestock type as 'halal' or 'not-halal', i.e., whether a livestock animal is fit for consumption under the Islamic dietary law. Halal livestock include HS4 categories 0102 (bovine animals), 0104 (sheep and goats) and 0105 (poultry, fowls of the species Gallus domesticus, ducks, geese, turkeys and guinea fowls). The control group (not-halal) includes HS4 categories 0101 (horses, asses, mules and hinnies) and 0103 (swine).[10]

Our second stage takes the following form:

$$\mathit{log(infections)}_{jkt} = \beta_2 \widehat{\mathbf{log(imports)}}_{jkt} + \gamma_{jt} + \omega_{kt} + \lambda_{jky} + \epsilon_{jkt}. \tag{3}$$

The coefficient β_2 is a LATE of livestock imports on the prevalence of infections; a 1%

[8]In column 8 of Table 4 we present a corresponding specification on the sub-sample of Muslim countries, where we can only control for importer-product and month/year fixed effects.

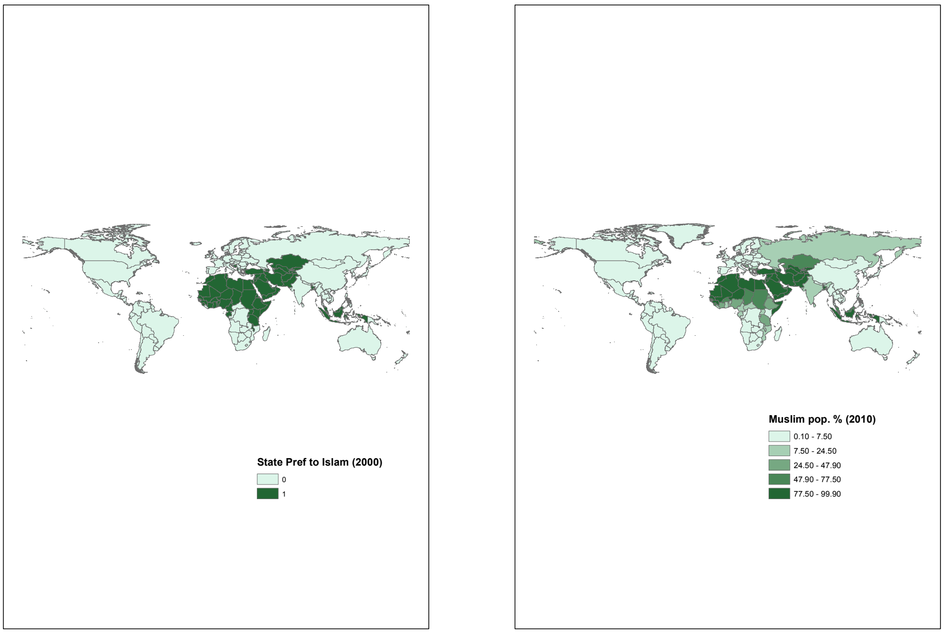
[9]Our estimation sample includes 42 countries where Islam was the preferred religion. The average Muslim population share in 2010 in these countries was approximately 62%, while the Muslim population share among the rest of the countries in the estimation sample was about 3.5%. In column 3 of Table 4 we present results from an over-identified model with a second instrument where Muslim countries are classified according to the religion of the majority in the population.

[10]While consumption of donkeys and their cross-breeds is regarded as haram (forbidden), eating horse meat is regarded as makruh (disapproved), therefore its consumption should be avoided.

Figure 3: Classification of Muslim countries

(a) Islam preference

(b) Muslim %



increase in imports of halal livestock due to Eid-al-Adha in Muslim countries causes a β_2% increase in infection cases in related species.

4 Results

4.1 Main results

Columns 1 and 2 in Table 1 shows the results from OLS for (i) all countries and (ii) for the sub-sample of Muslim countries. The coefficient of interest is small in magnitude as well as statistically not different from zero. Column (3) shows the corresponding findings from the IV estimation. The first stage results suggest that the coefficient on the festival instrument (δ) is both positively and strongly correlated with imports (the corresponding KP-F stat is above 12, which is well clear of the conventional threshold for a strong instrument). The second stage result shows that imports are positively

Table 1: Livestock imports and infection cases

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Log imports	0.014	0.015	0.744**	0.816*	0.744**	0.731**	0.745**
	(0.011)	(0.018)	(0.327)	(0.456)	(0.328)	(0.321)	(0.326)
Log stock pc				-0.298			
				(0.324)			
Border precautions					-0.001		
					(0.027)		
Screenings						0.106**	
						(0.046)	
Surveillance							-0.008
							(0.033)
Observations	36,282	6,784	34,833	34,583	34,833	34,833	34,833
R-squared	0.677	0.667					
Model	OLS	OLS	IV	IV	IV	IV	IV
First stage coeff.			0.465	0.461	0.465	0.465	0.465
First stage s.e.			0.136	0.192	0.136	0.136	0.136
KP F-test			12.03	5.788	12.03	12.01	12.08

Notes: *p<0.10, **p<0.05,***p<0.01. Dependent variable: log of infections, defined in equation (1). Robust standard errors are clustered by country and month/year. Importer-month/year, product-month/year and importer-product-year fixed effects are included in all estimation except in column (4), where we control for local animal stock per capita, which varies by importer-product-year, and therefore use importer-month/year, product-month/year, and importer-product fixed effects.

related to reported infection cases in the related species in the destination country. The point estimate implies that a 1% increase in imports is related to a 0.74% increase in infection cases among the related animal species. The coefficient from the IV estimation, which is significantly greater in magnitude than the OLS estimate, supports our prior that a naive OLS estimate is severely biased downwards due to reverse causality and omitted variables.

In column (4) we control for domestic livestock in HS-category k, to assuage concerns that the rise in infection cases is due to domestic livestock. The imports-to-infections elasticity increases to 0.8 when we control for the size of domestic livestock.[11] In columns (5) to (7) we show that elasticity is unaffected by including additional policy controls, respectively border precautions, screenings, and surveillance measures, to regulate the outbreak of diseases that afflict livestock category k in the importing

[11]Since data on domestic animal stock (per capita) only varies by importer-product-year, we cannot include importer-product-year fixed effects in the estimation of column (4). These fixed effects are replaced by less conservative importer-product fixed effects. The inclusion of importer-product fixed effects instead reduces precision in the first stage.

country j.

4.2 Checks for exclusion restriction

The instrument's validity rests on the assumption that it does not affect the outcome through any channel other than the endogenous variable. In this section we provide a battery of evidence to rule out that the festival instrument might be affecting the prevalence of infections through channels other than livestock imports. First, it is plausible the relationship is driven by enhanced economic activity (i.e., production or transportation of livestock domestically) during the festival period, which is however accounted by importer-month/year fixed effects. It is also plausible that a decline in the quality of customs inspection, due to a general upsurge in imports during the festival period, explains the higher prevalence of infections. Importer-month/year fixed effects also account for this possibility. Further, any seasonality in livestock trade or disease outbreak that coincides with the festival period would be accounted by the product-month/year fixed effects.

We perform a placebo test where we control for meat imports in category k, since there might be higher demand for halal meat, but meat imports are not directly related to transmission of diseases to animals. Column (1) of Table 2 shows that meat imports are not related to prevalence of animal infections. Thus, increase in meat consumption during the festival is a necessary but not a sufficient condition for transmission of diseases across animals. We perform a second placebo test to highlight that the festival instrument affects livestock infections through an upsurge in imports for ritual sacrifice. We construct a placebo instrument Z_1, which is a binary variable that equals one if importer j is Muslim, product k is halal and month/year t is the month of Eid-al-Fitr ("Holiday of Breaking the Fast"). Eid-al-Fitr, which marks the end of the month-long dawn-to-sunset Ramadan, is also an important festival for Muslims. However, during this festival Muslims consume sweets instead of sacrificing animals.[12] Column (2)

[12] Schwab and Armah (2019) also use Eid al-Fitr as a placebo analysis.

Table 2: Exclusion restriction checks

	(1)	(2)	(3)	(4)
Log meat imports	-4.223			
	(11.254)			
Log imports		6.218	0.850**	0.850**
		(10.458)	(0.357)	(0.357)
Log Stock pc × Time trends			0.001	-0.000
			(0.004)	(0.012)
Log Stock pc × Time trends squared				0.000
				(0.000)
Observations	43,727	34,833	33,930	33,930
Model	IV	IV	IV	IV
First stage coeff.	0.006	0.156	0.515	0.515
First stage s.e.	0.088	0.126	0.163	0.163
KP F-test	0.149	0.376	9.942	9.949

Notes: *p<0.10, **p<0.05,***p<0.01. Dependent variable: log of infections, defined in equation (1). Robust standard errors are clustered by country and month/year. Importer-month, product-month and importer-product-year fixed effects are included in all estimations. In column 2 we use a placebo instrument that relies on the timing of the Eid-al-fitr festival instead. The binary variable equals 1 if importer j=Muslim; livestock category k=halal; and month t=Eid-al-fitr.

shows that the placebo instrument does not predict the upsurge of imported animals, which reassures that the festival instrument **Z** affects infection cases through an upsurge in imports of livestock for ritual sacrifice.

In Column (3) and (4) we address concern that the initial distribution of specific livestock animals across countries might determine the surge in infections during the festival period through trends in their production or mobility. We include pre-sample controls for local livestock per capita k and interact them with linear and quadratic (monthly) time trends. The imports-to-infections elasticity is robust to controlling for trends in the evolution of domestic livestock.

4.3 Mechanisms: importer and partner characteristics

We investigate the mechanisms that determine the relationship between livestock imports and surge in infection cases at destination. We consider both importer and partner (exporter) characteristics that could mediate the relationship. We first test if the effect of livestock imports is mediated by the interaction with domestic livestock. Here,

Table 3: Mechanisms

	(1)	(2)	(3)	(4)
Log imports	-1.087	0.699**	-0.441	0.438
	(1.118)	(0.312)	(3.579)	(0.753)
Interaction term	4.774*	0.435***	4.919	1.760
	(2.767)	(0.105)	(15.473)	(4.428)
High Infection partners weighted		-5.958***		
		(1.602)		
High Screenings partners weighted			-62.391	
			(195.816)	
High Surveillence partners weighted				-22.172
				(55.541)
Observations	34,833	34,833	34,833	34,833
KP F-test	2.216	19.41	0.0583	0.265

Notes: *p<0.10, **p<0.05,***p<0.01. Dependent variable: log of infections, defined in equation (1). Robust standard errors are clustered by country and month/year. Importer-month, product-month and importer-product-year fixed effects are included in all estimations. The interaction term is the interaction between log imports and the control variable that is included in each column. In column (1) the imports are interacted with a binary domestic livestock size measure. The domestic livestock data varies by importer-product-year and the variable is absorbed by importer-product-year fixed effects.

we differentiate between a pure "import" effect and a "contagion" effect. Assuming that a given proportion of imported livestock is infected, a pure import effect would imply the increase in livestock imports mechanically raise the infection cases in the destination country. Alternatively, the results could be driven by a contagion effect, i.e., the imported animals that are infected come in contact with local livestock and this results in a surge in the infection cases. To distinguish between these two explanations we interact imports with a dummy that equals 1 if the size of the domestic livestock in importing country j in HS-category k in year t was above sample average. Column (1) of Table 3 shows that the effect of livestock imports on reported infection cases is present only in countries with substantial domestic livestock. The result thus supports the contagion explanation of our findings, i.e., the baseline effect is driven by the interaction between infected imported animals and the domestic livestock.

We then relax the assumption about a fixed likelihood of importing infected livestock, and consider that importing infected livestock is potentially dependent on partner (exporter) characteristics. We consider three types of characteristics among the partner countries that could influence the likelihood of importing infected livestock by j: i) the weighted average of infections in k across partner countries in a given month/year t (where weights are determined by the initial share of exports); ii) the weighted average of screening measures in place for livestock k across partner countries that are reported bi-annually and iii) the weighted average of surveillance measures in place for livestock k across partner countries that are reported bi-annually. We create three binary variables that classify the likelihood of importing infected livestock by partner characteristics, which equal 1 if the weighted average was above the sample mean. The first binary measure should positively determine the likelihood of importing sick livestock while the latter two binary measures should negatively determine the likelihood of doing so. We interact these binary variables with the import measure.

The coefficient of the interaction term measures if the relationship between livestock imports and infection cases at destination is mediated by the quality of the livestock imported. Results in Column (2) show that the coefficient on the interaction term is positive and statistically significant at 1% level. The point estimate implies that imported livestock is related to a greater prevalence in infection cases when it is imported from partner countries that also simultaneously experience a disease outbreak in related species.[13] These results provide further evidence for the nexus between transmission of livestock diseases through imports. In Columns (3) and (4) we estimate whether the relationship between livestock imports and infection cases at destination is mediated by the extent of livestock-health scrutiny among the partner countries. Our results suggest that scrutiny among partner countries has no effect. The findings in the last two columns should however be interpreted with caution since adding interaction terms (and their instruments) significantly weaken the associations in the first stage.

To summarize the results presented in this section, the import of livestock seems to affect the prevalence of infections in associated livestock through a contagion effect, i.e., through contact between infected livestock that is imported and the local livestock.

[13]To quantify the effect, the imports-to-infections elasticity for a country at the 75th percentile of imports, and with high weighted average of infections in partner countries, is equal to = 0.6993 + 13.0039 × 0.4354 - 5.9576= 1.14.

Moreover, the quality of imported livestock mediates the nexus between imports and infections at the destination. Countries that are exposed to a higher threat of importing sick animals from their partner countries also experience a stronger effect of livestock imports on infections in related species.

4.4 Robustness checks

In this section we provide a battery of robustness tests of the main results, displayed in Table 4. The first is the exclusion of years preceding 2010, because in the UN Comtrade data used for monthly imports only few countries report imports before this year. The results, in column (1), are very similar to the baseline result of column (3) of Table 1. Next, in column (2), we exclude Saudi Arabia from the sample, because livestock demand in the country during Eid-al-adha is highly affected by the 'Hajj pilgrimage'. This affects the type of livestock imported since Hajj pilgrims prefer to sacrifice larger ruminants, like cattle and sheep, to donate the meat to the poor (Mtimet et al., 2021). Results are robust to the exclusion of Saudi Arabia. In column (3), we present results with an over-identified model, where imports are instrumented both by the "Halal, Eid-al-Adha, preference for Islam" interaction, and by an interaction "Halal, Eid-al-Adha, high Muslim population".[14] The results of this over-identified model are also in line with the baseline results. In column (4), we exclude both Saudi Arabia and HS 0105 (live poultry), which is halal, but is not a preferred sacrificial animal for the ritual. This is because while poultry is cheap, their size limits the extent of the feast. However, poorer households can sacrifice poultry to fulfil the Eid ritual.[15] While excluding poultry we exclude Saudi Arabia, because Hajj pilgrims mainly sacrifice larger ruminants for donation. Therefore, the sub-sample that excludes poultry would also overstate the importance of livestock imports to Saudi Arabia. The coefficient on imports is similar in magnitude to the baseline effect and it is almost statistically significant at 10% level

[14]We use a dummy equal to one if at least 50% of population in j was Muslim in 2010 to construct the high Muslim population variable in this interaction.

[15]"Only chicken for Eid in rebel-besieged Yemen town", RTL Today (20 July, 2021).

Table 4: Robustness checks

	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)
Log imports (t-1)							0.285	
							(0.757)	
Log imports	0.797**	0.835**	0.680**	0.644	0.305*	0.010*	0.334***	0.238*
	(0.348)	(0.337)	(0.305)	(0.389)	(0.163)	(0.006)	(0.114)	(0.139)
Log imports (t+1)							0.119	
							(1.238)	
Observations	33,892	34,715	34,833	23,388	34,833	34,833	26,570	7,857
Model	IV	IV	IV	IV	IV	IV	IV	IV
First stage coeff.	0.441	0.443	0.355 ; 0.179	0.553	0.465	0.465	0.465	0.626
First stage s.e.	0.134	0.134	0.264; 0.264	0.164	0.136	0.136	0.136	0.153
KP F-test	11.17	11.19	10.62	12.62	12.03	12.03	0.0309	16.86

Notes: *p<0.10, **p<0.05,***p<0.01. Dependent variable: log of infections, defined in equation (1). In column (6), the dependent variable is the log of human infections. Robust standard errors are clustered by country and month/year. Importer-month, product-month and importer-product-year fixed effects are included in columns (1)-(7). Importer-product and month/year fixed effects are included in column (8), where we focus on the sub-sample of Muslim countries.

(p-value is 0.101). In column (5), we use an inverse hyperbolic sine transformation of the dependent variable (infections), and results are qualitatively similar.

In column (6) of Table 4, we show that the festival-related surge in imports of halal livestock also causes infections among humans (zoonotic cases). The result is in line with anecdotal evidence on zoonotic episodes after Eid-al-Adha (Vellucci et al., 2020). In column (7), we also add one lag and one lead of imports to the baseline specification.[16] The results show that only the contemporaneous effect matter, ruling out any anticipation or delayed effects of the festival-related surge in imports of halal livestock on infections.[17] Finally, in column (8) we provide evidence that the positive impact of imports on infections is also obtained within the sub-sample of Muslim countries.[18]

Collectively, the results presented in this section corroborate the causal relationship

[16] We accordingly construct one lead and one lag of the instrument to instrument for the lag and the lead of imports.

[17] The transmission of pathogens depends both on the survival rate of the pathogen and the proximity to other animals. According to a study on livestock in Tanzania (Ekwem et al., 2021), transmission risk is more sensitive to the survival of the pathogen in the local environment, than it is on the transmission distance. The pathogen survival versus transmission distance trade-off might explain why only the contemporaneous relationship is significant in our empirical estimation.

[18] We can estimate the IV model for the sub-sample of Muslim countries in column (8) of Table 4, with the inclusion of importer-product and month/year fixed effects. The additional inclusion of product-month/year fixed effects would absorb all the variation necessary for identification. This shows the advantage of our triple interacted instrument (Muslim × halal × Eid-al-adha), where non-Muslim countries act as a placebo group, over an instrument for livestock imports within the sub-sample of Muslim countries, that only varies by product and month/year (halal × Eid-al-adha), and where exclusion restriction is relatively weakly met through including importer-product and month/year fixed effects.

between livestock imports and the prevalence of infection cases in associated species in the destination country.

5 Conclusion

Outbreaks of infectious diseases in animal populations, and their associated costs, have grown in recent years. This has coincided with an increase in the cross-border movement of live animals. To date there is limited evidence on the role of trade-related international movement of live animals in spreading disease-carrying pathogens. This paper estimates the impact of livestock trade on the spread of communicable animal diseases.

Evidence across over 120 countries over a sixteen year period shows that commercial livestock trade is systematically related to infectious diseases in associated animal species. The relationship that we identify is due to a contagion effect i.e. the interaction of imported livestock, some of which are plausibly infected, with the local livestock animals.

In this paper we do not quantify the economic consequences of animal disease outbreaks. Future research can estimate these economic consequences, and consider the mediating role of within-country characteristics such as the local economic structure. The link between animal disease outbreaks and individual health through income shocks is another topic for future research.

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Supplement to “Trading epidemics”

Table of Contents

A Matching animal diseases to trade data

The left column of Table A-1 lists the thirty-one animal-related diseases with confirmed cases for which we have collected data from the FAO's EMPRES-i database. The right column shows the World Organization for Animal Health (OIE)'s classification of these diseases by species affected.

The OIE classifies fifteen diseases as affecting a single class of species, fourteen diseases as affecting multiple species and two as 'other diseases'. It is straightforward to match diseases that affect a single species to an HS4 live animal category. To precisely assign diseases that affect multiple species to an animal category k (four-digit HS heading), we use the description on the species affected by each outbreak that is included in the raw FAO's EMPRES-i data.

To provide an example, consider the case of the outbreak of Foot and mouth disease (FMD), which OIE classifies as affecting multiple species, in the Republic of Korea. According to FAO's EMPRES-i, in 2015 there were 159 reported outbreaks of FMD in the country. Out of these, Table A-2 presents the descriptions of animals affected from the 120 outbreaks (out of 159), with non-missing information on the number of animals infected. In this example, the dependent variable ($Infections_{jkt}$) in the observation in which j is the Republic of Korea, k is HS heading 0102, and t is 2015, is equal to the sum of recorded infections across the five outbreaks where the HS assigned is 0102, i.e. six (see row "Dom. cattle" in Table A-2).[19] The dependent variable ($Infections_{jkt}$) in the observation in which j is the Republic of Korea, k is HS heading 0103, and t is 2015, is equal to the sum of recorded infections across the 114 outbreaks where the HS assigned is 0103, i.e. 85,442 (see row "Domestic (dom.) swine" in Table A-2).[20] Notice that one event of FMD is reported to have affected both swine and cattle species (see

[19]For "Dom. cattle", which is concorded to HS heading 0102, recorded infections were equal to one in four instances, and two in one instance. Therefore, $Infections_{jkt}$ is equal to six, as reported in the last column of Table A-2.

[20]For "Domestic (dom.) swine", which is concorded to HS heading 0103, recorded infections range from one to 8,639 (mean = 749.5, median = 361.5). Their sum across the 114 observations is 85,442, as reported in the last column of Table A-2.

Table A-1: Animal diseases in FAO EMPRES-i and animal species affected in OIE classification

Disease	Animal species affected (OIE classification)
African horse sickness	Equine
African swine fever	Swine
Anthrax	Multiple
Bluetongue	Multiple
Bovine spongiform encephalopathy	Cattle
Bovine tuberculosis	Multiple
Brucellosis	Multiple
Brucellosis (Brucella abortus)	Multiple
Brucellosis (Brucella melitensis)	Multiple
Brucellosis (Brucella suis)	Multiple
Classical swine fever	Swine
Contagious bovine pleuropneumonia	Cattle
Equine infectious anaemia	Equine
Foot and mouth disease	Multiple
Glanders	Equine
Hendra Virus Disease	Multiple
Influenza - Avian	Avian
Influenza - Equine	Equine
Influenza - Swine	Swine
Japanese encephalitis	Multiple
Leptospirosis	Multiple
Lumpy skin disease	Cattle
MERS-CoV	*Other diseases*
Newcastle disease	Avian
Peste des petits ruminants	Sheep and goat
Porcine reproductive and respiratory syndrome	Swine
Rabies	Multiple
Rift Valley fever	Multiple
Schmallenberg	*Other diseases*
Sheep pox and goat pox	Sheep and goat
West Nile Fever	Multiple

row "Dom. swine, dom. cattle" in the table), and therefore we could not assign it to any HS heading.[21]

[21] FAO's EMPRES-i only provides the total number of infection cases for each outbreak. In case when

Table A-2: Example of matching: 2015 FMD outbreak in the Republic of Korea

Species description	Frequency	Percent	HS assigned	Infections
"Dom. cattle"	5	4.17	0102	6
"Domestic (dom.) swine"	114	95.00	0103	85,442
"Dom. swine, dom. cattle"	1	0.83	N.A.	382
Total	120	100		

Notes: FMD stands for Foot and Mouth Disease. N.A. stands for non-assignable. Species description as reported in the FAO's EMPRES-i database.

Table A-3 summarizes the assignment of the 94,711 disease outbreaks recorded in the FAO's EMPRES-i database to the HS4 product live animal classification. A total of 1,602 outbreaks across eight different diseases affect HS heading 0101 (horses, asses, mules and hinnies); 13,119 outbreaks across 16 diseases affect HS heading 0102 (bovine animals); 24,254 outbreaks across 13 diseases affect HS heading 0103 (swine); 11,607 outbreaks across 12 diseases affect HS heading 0104 (sheep and goats); 30,804 outbreaks across seven diseases affect HS heading 0105 (poultry, fowls of the species Gallus domesticus, ducks, geese, turkeys and guinea fowls); and 6,980 outbreaks across 17 diseases affect HS heading 0106 (live animals not elsewhere classified). Finally, 6,345 outbreaks across 24 diseases could not be assigned to any HS heading in live animals, and therefore are excluded.[22]

multiple species are infected, such as in the third row of Table A-2, we can not identify how many infection cases are attributable to different species. Hence, we leave out these outbreaks from our final sample.

[22]Cases in which it was not possible to assign observations from FAO's EMPRES-i to an HS heading typically involve descriptions that include two or more distinct live animal categories, as in row "Dom. swine, dom. cattle" in Table A-2.

Table A-3: Correspondence between animal diseases in FAO EMPRES-i and HS headings

	HS heading						
Disease	0101	0102	0103	0104	0105	0106	N.A.
African horse sickness	199	0	0	0	0	1	0
African swine fever	0	0	20,785	0	0	1	76
Anthrax	11	211	32	34	1	31	103
Bluetongue	0	4,238	1	4,108	0	15	4,283
Bovine spongiform encephalopathy	0	37	0	0	0	1	1
Bovine tuberculosis	0	9	1	0	0	0	2
Brucellosis	0	99	7	252	4	0	96
Brucellosis (Brucella abortus)	0	23	0	2	0	0	0
Brucellosis (Brucella melitensis)	0	5	0	25	0	0	10
Brucellosis (Brucella suis)	0	3	14	0	0	0	2
Classical swine fever	0	0	2,246	0	0	0	4
Contagious bovine pleuropneumonia	0	202	0	1	0	0	0
Equine infectious anaemia	142	0	0	0	0	0	45
Foot and mouth disease	0	3,118	605	382	0	23	508
Glanders	45	0	0	0	0	0	9
Hendra Virus Disease	42	0	0	0	0	0	5
Influenza - Avian	0	0	0	0	29,296	2,940	41
Influenza - Equine	682	0	0	0	0	0	4
Influenza - Swine	0	0	141	0	10	45	9
Japanese encephalitis	0	0	6	0	0	0	110
Leptospirosis	0	1	0	0	0	0	312
Lumpy skin disease	0	2,954	0	0	0	0	0
MERS-CoV	0	0	0	0	0	2,407	0
Newcastle disease	0	0	0	0	1,486	21	24
Peste des petits ruminants	0	0	0	3,100	0	6	7
Porcine reprod. and resp. syndrome	0	0	384	0	0	0	0
Rabies	38	911	11	28	1	1,402	200
Rift Valley fever	0	171	0	372	0	21	459
Schmallenberg	0	1,136	0	2,190	0	3	8
Sheep pox and goat pox	0	0	21	1,113	0	0	0
West Nile Fever	443	1	0	0	6	63	27
Total	1,602	13,119	24,254	11,607	30,804	6,980	6,345

Notes: Left column: list of diseases with confirmed cases in the FAO's EMPRES Global Animal Disease Information System (EMPRES-i). Other columns: authors' classification of animal diseases by live animal category (HS heading) affected, based on information from FAO's EMPRES-i and from USA Trade Online (`https://uscensus.prod.3ceonline.com/`). Each row assigns all the observations on each disease available in the FAO's EMPRES-i database to Harmonized System (HS) headings 0101-0106, or to the non-assignable (N.A.) category if there is not sufficient information to make a precise assignment. HS heading 0101 includes horses, asses, mules and hinnies; HS heading 0102 includes bovine animals; HS heading 0103 includes swine; HS heading 0104 includes sheep and goats; HS heading 0105 includes poultry, fowls of the species Gallus domesticus, ducks, geese, turkeys and guinea fowls; HS heading 0106 includes live animals not elsewhere classified. MERS-CoV stands for Middle East Respiratory Syndrome Coronavirus.

Among the fifteen diseases that the OIE classifies as affecting single species (Table A-1), 94% of outbreaks are on average concentrated in only one HS4 heading according to our assignment in Table A-3 (the leading HS4 heading also aligns with the OIE classification of species affected). In contrast, only 59% of outbreaks, on average, are concentrated in one HS4 heading for diseases that are listed as affecting multiple species in the OIE classification in Table A-1. For these diseases, a precise matching is essential to avoid potentially large mis-classification errors.

The twin results that the majority of disease outbreaks for 'single species' diseases are concentrated in an HS4 category that aligns with the prior OIE classification, combined with a significant dispersion of disease outbreaks across HS4 categories for OIE's 'multiple species' diseases, validate our matching exercise.