Title

TRANSLATING PREDICTIONS OF EMERGING ZOONOTIC VIRUSES FOR POLICYMAKERS: PERSPECTIVES FROM CAMEROON

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Original Contribution

Translating Predictions of Zoonotic Viruses for Policymakers

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Abstract: Recent outbreaks of Ebola virus disease and Zika virus disease highlight the need for disseminating accurate predictions of emerging zoonotic viruses to national governments for disease surveillance and response. Although there are published maps for many emerging zoonotic viruses, it is unknown if there is agreement among different models or if they are concordant with national expert opinion. Therefore, we reviewed existing predictions for five high priority emerging zoonotic viruses with national experts in Cameroon to investigate these issues and determine how to make predictions more useful for national policymakers. Predictive maps relied primarily on environmental parameters and species distribution models. Rift Valley fever virus and Crimean-Congo hemorrhagic fever virus predictions differed from national expert opinion, potentially because of local livestock movements. Our findings reveal that involving national experts could elicit additional data to improve predictions of emerging pathogens as well as help repackage predictions for policymakers.

Keywords: Viruses, Risk, Virus diseases, Hemorrhagic fevers, Viral, Ebola virus, Bunyaviridae, Arenaviridae, Filoviridae

INTRODUCTION

Zoonotic viruses are continuing to emerge in new regions, creating an urgent need for national surveillance and preparedness. For example, the emergence of Ebola virus dis-

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ease (EVD) in West Africa and Zika virus disease in Latin America surprised both national and global communities (Feldmann 2014; Fauci and Morens 2016). Low- and middle-income countries (LMICs) afflicted by such viral diseases may lack the resources needed for integrated pathogen surveillance systems (Perry et al. 2007). However, researchers have created many predictive maps for emerging viruses that national governments could use to focus their efforts for outbreak preparedness (Clements and Pfeiffer 2009; Hay et al. 2013).

While multiple maps exist for different emerging zoonotic viruses, little is known about how these predictions compare with each other or how they are perceived by public health experts and policymakers in LMICs. Many of these maps are also made by authors who are not from LMICs, and thus critical national data may be missing. These predictive maps are also often continental or global in scale, but control measures tend to be implemented on a national level. To be most useful, predictive maps should be repackaged to address the needs of national policymakers.

Researchers also use different model types, data sets, assumptions, and parameters to generate predictions (Clements and Pfeiffer 2009; Hay et al. 2013), and these factors should be considered when translating predictions for national policymakers. A common approach to spatial disease modeling is to identify areas where the virus or viral disease has occurred and then use a model to map areas similarly suitable for the virus or host. Understanding what data and parameters were used to make a prediction is critical to interpret the prediction on a national level.

Zoonotic viruses have been known to emerge in Cameroon. All known ancestor viruses of HIV-1, called Simian immunodeficiency viruses, have been found in nonhuman primates from tropical forests in Cameroon (Peeters et al. 2014). Colloquially known as "Africa in miniature," Cameroon has many of Africa's diverse environmental regions and species that could harbor other emerging zoonotic viruses. These different environmental regions correspond with different administrative regions. Roughly, there is the Sahel in the Far North, a transition zone of savannah from the North through the Adamaoua region, and tropical rainforest in the rest of the country. Different wildlife, livestock, and vector species are present in these regions and could be hosts for emerging zoonotic viruses. Additionally, these regions are culturally diverse with different interactions between humans and animals. Therefore, Cameroon provides an ideal setting to explore predictive maps for emerging zoonotic viruses on a national level.

To understand how to make predictive maps of emerging zoonotic viruses more useful for national policymakers in Cameroon, we investigated three questions. First, how do predictions based on different modeling approaches and data sets compare with each other? Second, how well do these maps agree with national expert knowledge? Lastly, what additional information is needed for predictive maps to affect policy decisions?

Methods

Aggregating Predictions

To identify existing maps for zoonotic viruses in Cameroon, we queried Web of Science and PubMed using different Boolean search terms, for example: "virus" AND "Cameroon", "zoonosis" AND "Cameroon," and "Africa" AND "virus" AND "map." After identifying candidate zoonotic viruses that have been mapped in Cameroon, we focused on those that have significant outbreak potential and an undetermined geographic distribution. These viruses were all included on the World Health Organization's 2015 list of priority pathogens for research and development preparedness (World Health Organization 2015). We selected maps for these viruses that included Cameroon in their extent, whether or not the virus was predicted to be there. While aggregating predictions, we also recorded and categorized the data and parameters that were used to create each risk map (Tables 1, 2).

We extracted images of maps for each of the viruses from the literature. Additionally, we extracted two map images for Rift Valley fever virus (RVFV) from VectorMap (available at: http://vectormap.nhm.ku.edu/vectormap/). One of these maps was from the DoD-GEISWeb RVF monitoring project (Anyamba et al. 2009; Anyamba 2016) and the other map was from published literature (Rogers 2006). If multiple predictions were made by the same group of authors that included different input data or assumptions, we included those predictions as well.

Our goal was to produce maps at a coarse spatial scale in order to stimulate discussions with experts familiar with emerging viruses in Cameroon. We used a qualitative visual inspection procedure to align published maps to the borders of Cameroon (Supplementary Material, Text S1). This approach is potentially sensitive to the settings used to

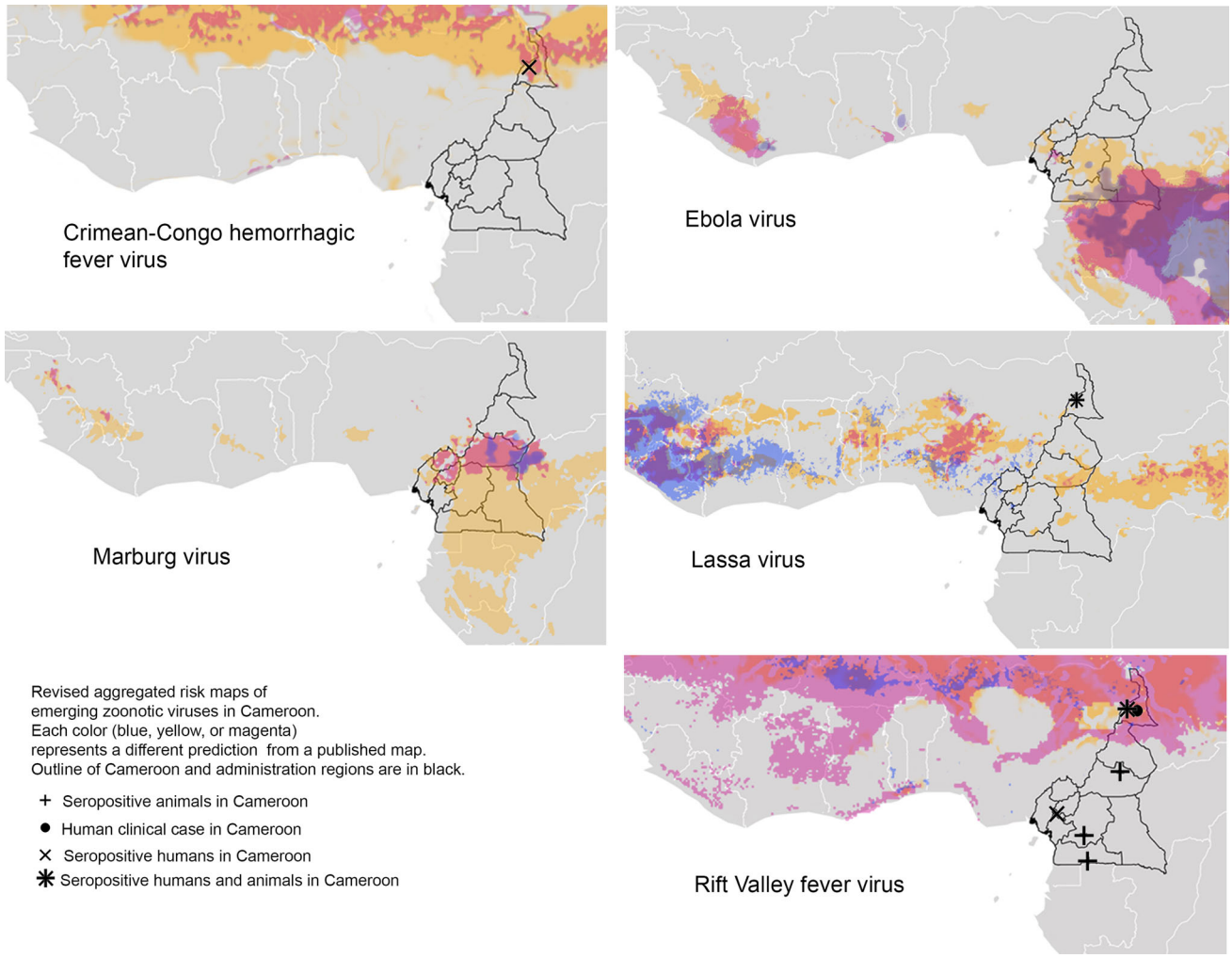

Fig. 1. Revised aggregated virus predictions with input from Cameroonian policymakers. Includes administrative regions of Cameroon and local evidence for emerging zoonotic viruses along with aggregated predictions. Crimean-Congo hemorrhagic fever virus: yellow (Randolph and Rogers 2007), magenta (Messina et al. 2015). Ebola virus: yellow (Pigott et al. 2014), magenta (Judson et al. 2016), blue (Peterson et al. 2004). Lassa virus: yellow (Fichet-Calvet and Rogers 2009) (model 2), magenta (Fichet-Calvet and Rogers 2009) (model 3), blue (Mylne et al. 2015). Marburg virus: yellow (Pigott et al. 2015) (model 2), magenta (Pigott et al. 2015) (model 1), blue (Peterson et al. 2004). Rift valley fever virus: yellow (Clements et al. 2006), magenta (Anyamba 2016), blue (Rogers 2006) (Color figure online).

display probabilistic maps such as a gamma parameter (Text S2, Figures S1-2). Alternatively, we could have used quantitative georeferencing to align the maps. However, we think that the qualitative procedure was adequate because we were interested in broad patterns of disease distributions across a large geographic region.

Assessment Strategy

In June 2016, we discussed these aggregated maps and data with 14 national experts in Cameroon, who represented 8 ministries and research institutions: the Ministry of Scientific Research and Innovation; the Ministry of Livestock, Fisheries and Animal Industries; the Ministry of Public Health; the National Veterinary Laboratory (LANAVET); the Ministry of Defense; the Chantal Biya International Reference Centre (CIRCB); Metabiota Cameroon; and Centre Pasteur du Cameroon. These experts were chosen because of their experience in research and implementing policies related to emerging pathogens. We met with experts at their respective institutions, and some experts suggested others with whom we should meet. Our conversations allowed us to compare published predictions with national expert opinion and identify how to improve predictions for national policymakers. A qualitative dis-

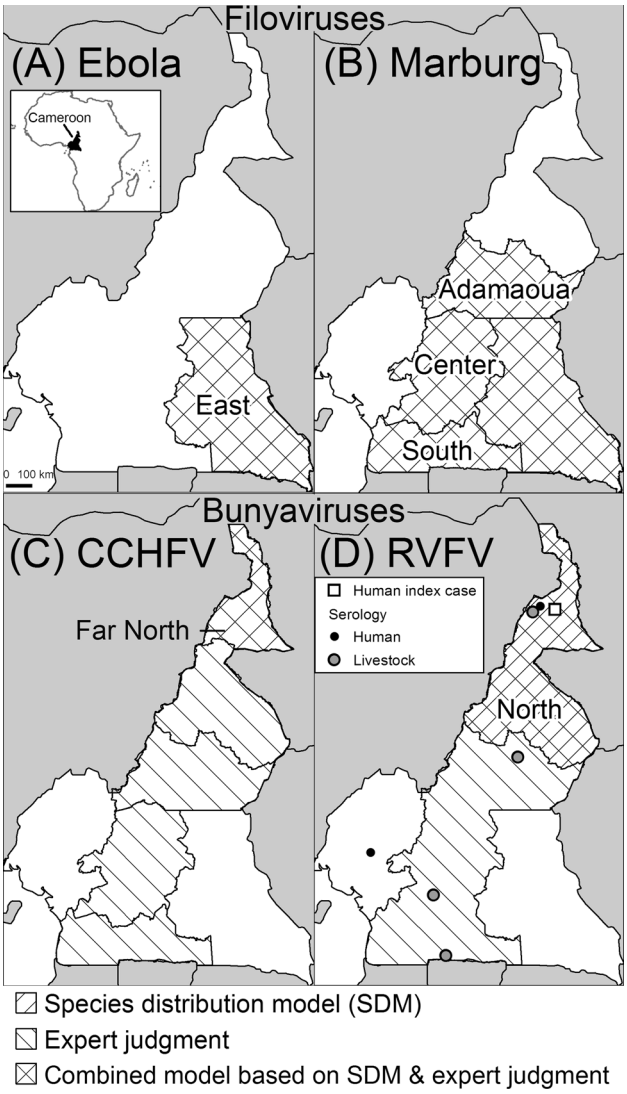

Fig. 2. Differences between expert judgment and predictions for bunyaviruses and filoviruses in Cameroon. While there was general agreement between expert judgment and species distribution models for the filoviruses (**a**, **b**), the two approaches disagreed about the distributions of bunyaviruses (**c**, **d**). Panel **d** also includes previous evidence about RVFV in Cameroon (index case and serology).

cussion instrument was used to elicit policymakers' opinions (Supplementary Text S3).

Results

Emerging Zoonotic Viruses Predicted in Cameroon

We identified five highly pathogenic, emerging zoonotic viruses that have multiple predictions within Cameroon: Crimean-Congo hemorrhagic fever virus (CCHFV), Ebola virus (EBOV), Lassa virus (LASV), Marburg virus (MARV), and RVFV. These viruses all cause viral hemorrhagic fevers. A total of 14 predictive maps were found for these viruses, with an average of 3 predictions per virus (Table 1). These maps predicted the ecological niches, distributions, and suitable habitats of these viruses based on different modeling approaches. The regions predicted in these models can be collectively interpreted as areas at risk for viral exposure. Different modeling types were used for the predictions, primarily forms of species distribution modeling. Input data and parameters were not available for all models. Environmental parameters were used for all of the predictions (14/14 predictions), while other parameters included livestock density (1/13) and putative reservoir host distributions (2/13). We describe the results from reviewing and assessing the predictions of these viruses with national experts below.

Expert Feedback

We received feedback on how to improve aggregating and sharing the predictions with national policymakers. National experts wanted to see the administrative regions of Cameroon in our aggregated maps as well as any previous evidence for the viruses in Cameroon. They also found our aggregated maps confusing when we overlaid the colors of the predictions on backgrounds with satellite images. The original maps (Figure S4) were revised based on their feedback and are shown in Fig. 1. We did not include the seropositive locations for EBOV and MARV in the revised maps because of the uncertainty of these data. National experts also emphasized that free digital copies of the maps should be made available for reports and ministry-level briefing papers. Experts also wanted to know about the quality of the models at predicting previous outbreaks in other countries as well as the data used to create the models.

Ebola Virus

There have been no reported human or animal cases of EVD in Cameroon. However, human index cases of EVD have been identified near the southern Cameroon border in the Republic of Congo and Gabon (Judson et al. 2016). EBOV is one of the five ebolaviruses in the family *Filoviridae*. The four other ebolaviruses are Sudan virus (SUDV), Tai forest virus (TAFV), Bundibugyo virus (BDBV), and Reston virus (RESTV). EBOV, SUDV, TAFV, and BDBV are known to spillover from wildlife and cause

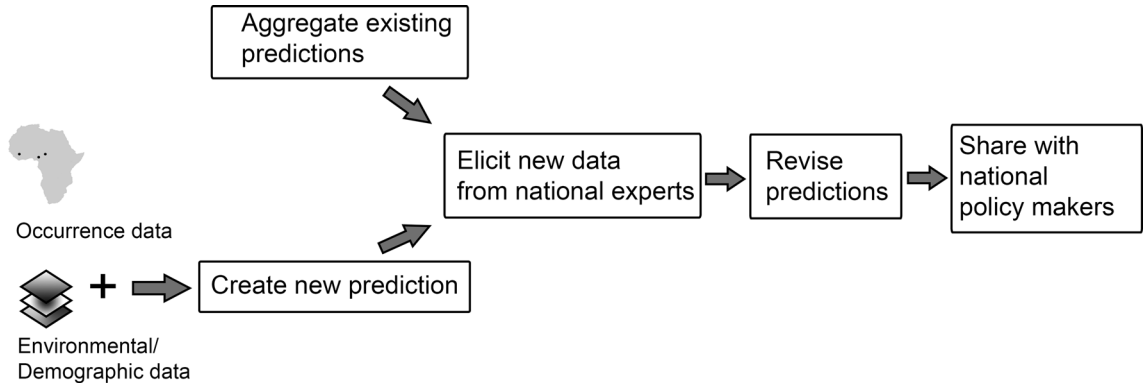

Fig. 3. A framework for translating predictions of emerging pathogens for national policymakers.

EVD in humans, while RESTV is not considered to be a human pathogen (Judson et al. 2016). Three species of fruit bats have been found to be polymerase chain reaction (PCR) positive for EBOV (Leroy et al. 2005), while other animals have been implicated as secondary hosts (Olival and Hayman 2014). These putative reservoir and secondary host species are present in Cameroon (Leroy et al. 2005). Serosurveys have found humans seropositive for filoviruses in Cameroon, predominantly those living in southern tropical rainforest (Gonzalez et al. 1989; Kuhn 2008). The seroprevalence of filoviruses in these studies in spite of scarce clinical evidence has led to speculation about non-specific assay reactivity, false positives, or the presence of nonpathogenic filoviruses (Gonzalez et al. 1989; Monath 1999).

We obtained three publications with predictions for EBOV (Peterson et al. 2004; Pigott et al. 2014; Judson et al. 2016). No occurrence data from Cameroon were used to make these predictions and all three overlapped in the tropical rainforest of the East region of Cameroon, with some predictions extending into the Central and South regions (Peterson et al. 2004; Pigott et al. 2014; Judson et al. 2016). The tropical rainforest identified in the models is similar to where most EBOV index cases have occurred (Judson et al. 2016). National experts agreed that this region might be at risk for EBOV spillover, but also acknowledged that long-distance movements by bats could put other areas at risk.

Marburg Virus

Like EBOV, MARV is another filovirus with serological evidence in humans in Cameroon (Kuhn 2008). MARV has been isolated from its reservoir host species *Rousettus aegyptiacus*, the Egyptian fruit bat, which roosts in caves and is found in Cameroon. While most human infections and wildlife detections of MARV have occurred in eastern Africa, seropositive bats have been found in the Republic of Congo and PCR positive bats have been found in Gabon (Maganga et al. 2011; Pigott et al. 2015).

We found three predictive maps for MARV from two publications (Peterson et al. 2004; Pigott et al. 2015). One publication had two predictions, one based on a model using human cases only and the other including bat serology (Pigott et al. 2015). We included both models to identify areas of consensus. Similar to the authors of the latter two models, national experts in Cameroon found the prediction that included the bat serology data to most likely represent the distribution of MARV in Cameroon. The human-only prediction was against the known ranges of host bat species in Cameroon, identifying primarily the Adamaoua region as at risk. Using only human index cases creates a prediction of area similar to where spillover events have occurred, which can be helpful for identifying places at risk for spillover, but it might not capture the full distribution of the virus in wildlife.

Lassa Virus

Human cases of LASV infection have been reported near the Cameroonian border in neighboring Nigeria, but there have been no identified human index cases in Cameroon (Mylne et al. 2015). Likewise, no actively infected wildlife have been reported in Cameroon. LASV is in the family *Arenaviridae*, and its primary reservoir host is *Mastomys natalensis*, the multimammate rat. Serosurveys found two humans and *Mastomys* spp. seropositive for LASV in the Far North region of Cameroon (Gonzalez et al. 1989). The

Table 1. Risk Map Characteristics of Predicted Emerging Zoonotic Viruses in Cameroon.

Virus	Reservoir/vector	Evidence in Cameroon	Model type	Data source[a]	# of reference cases	References
Crimean-Congo hemorrhagic fever virus	Vector: *Hyalomma* spp.	Human serology	NLMLD	NR, NR, 1	378 human	Randolph and Rogers (2007)
			BRT	A B C D, I II III IV, 1	1721 human and animal	Messina et al. (2015)
Ebola virus	**Epomops franqueti*, **Hypsignathus monstrosus*, **Myonycteris torquata*	Human serology	GARP	B, I II IV, 1	9 human	Peterson et al. (2004)
			BRT	A B, I II III IV, 1 3	23 human, 51 animal	Pigott et al. (2014)
			Maxent	B, I II IV, 1	24 human	Judson et al. (2016)
Lassa virus	*Mastomys natalensis*	Human and wildlife serology	NLMLD, step-wise	B C D, I II III IV, 1	111 human and animal	Fichet-Calvet and Rogers (2009) Model 2
			NLMLD, random	B C D, I II III IV, 1	111 human and animal	Fichet-Calvet and Rogers (2009) Model 3
			BRT	A B, I II III, 1 3		Mylne et al. (2015)
Marburg virus	*Rousettus aegyptiacus*	Human serology	GARP	B, I II IV, 1	4 human	Peterson et al. (2004)
			BRT	B, I II IV, 1	10 human	Pigott et al. (2015) Model 1
			BRT	A B, I II III IV, 1	24 human and animal	Pigott et al. (2015) Model 2
Rift valley fever virus	Vector: *Culex* spp., *Anopheles* spp., *Aedes* spp.	Human and livestock serology, suspected human case	WLC	NR, NR, 1, 4		Clements et al. (2006)
			NLMLD	NR D, NR, 1	62 unspecified	Rogers (2006)
			Multiple types	NR, NR, 1		Anyamba (2016)

BRT boosted regression tree, *GARP* Genetic Algorithm for Rule Set Production, *WLC* weighted linear combination, *OWA* ordered weighted average analysis, *NLMLD* nonlinear maximum likelihood discriminant, *NR* not reported, *EVI* enhanced vegetation index, *NDVI* normalized difference vegetation index.

[a]See Table 2 for details.

⋆ putative

Table 2. Categories of Risk Map Data.

Case data	Diagnostic assay	Parameters
A. Infections in wildlife	I. Virus isolation	1. Environmental (elevation, rainfall, temperature, etc.)
B. Spillover/index cases in humans	II. PCR	2. Human (human population density)
C. Infections in humans (secondary cases)	III. Serology[b]	3. Vector/reservoir (vector/host range)
D. Absence data[a]	IV. Descriptive	4. Other animals (livestock, secondary host range)

[a]Refers to absence reference data for model input and not pseudoabsence data.
[b]Refers to reference data that was from human and animal serosurveys.

lack of LASV infections in Central Africa despite the presence of the reservoir host species has led some to speculate that LASV is restricted to certain subspecies of *Mastomys natalensis* or that its niche is filled by arenaviruses that are nonpathogenic in humans (Gonzalez et al. 1989).

We identified three predictions for LASV from two publications (Fichet-Calvet and Rogers 2009; Mylne et al. 2015). There was sparse overlap between predictions. The authors of the first publication noted limitations of their predictions in southern Cameroon due to cloud contamination obscuring their measurements of environmental parameters (Fichet-Calvet and Rogers 2009). An additional analysis of this prediction proposed that the model underemphasized in the north and overemphasized in the south due to data quality and sampling (Peterson et al. 2014). The second publication used the occurrence data of seropositive *Mastomys* spp. in Cameroon (Mylne et al. 2015). National experts did not provide specific feedback on the LASV predictions in Cameroon.

Crimean-Congo Hemorrhagic Fever Virus

There have been no identified cases of active CCHFV infection in Cameroon, but two humans in the Far North region were seropositive for CCHFV in another study (Gonzalez et al. 1989). CCHFV is an arbovirus in the family *Bunyaviridae*. Ticks of the genus *Hyalomma* are considered to be the primary vector for the virus, transmitting CCHFV among livestock (Whitehouse 2004). It has been proposed that tick-infested migratory birds could determine the distribution of the virus, but bats have also been recently identified as possible hosts for CCHFV (Müller et al. 2016). Livestock are asymptomatic for CCHF, and humans are infected through contact with infected blood or body fluids, often during butchering (Whitehouse 2004).

We found two predictions for CCHFV risk in Cameroon (Randolph and Rogers 2007; Messina et al. 2015). The predictions overlapped similarly in the Far North region of Cameroon. No occurrence data of human or animal infections in Cameroon were used to create these predictions. One of these predictions specifically highlighted the need for increased surveillance for CCHFV in Cameroon (Messina et al. 2015). The aggregated predictions for CCHFV differed from national veterinary and livestock disease expert opinion in Cameroon. Two experts stated that there is local unpublished serological evidence for CCHFV in livestock further south in Cameroon. This difference may be due to particular patterns of livestock movement in Cameroon. In general, livestock in northern Cameroon seasonally move south for grazing during a transhumance (Xiao et al. 2015). While northern Cameroon might be more ecologically similar to where endemic CCHFV has been detected, as predicted by existing models, this transhumance could expand the area at risk for viral exposure. If viable vectors for CCHFV are present further south, this movement could expand the distribution of the virus in nature.

Rift Valley Fever Virus

In 1987, a patient with an ongoing RVFV infection was anecdotally reported in the Far North region of Cameroon (Gonzalez et al. 1989). Subsequently, serological evidence of past infection was found in humans in the Far North and Littoral regions and in livestock in the Far North, Adamaoua, Center, and South regions (Maurice 1967; Gonzalez et al. 1989; LeBreton et al. 2006). RVFV is another arbovirus in the family *Bunyaviridae*, and like CCHFV is known to infect livestock and humans. However, unlike CCHFV, it causes disease in livestock, including abortion and mortality (Linthicum et al. 2016). Most human infections occur among pastoralists and those who work with livestock

(Linthicum et al. 2016). The endemic and epizootic cycles of RVFV have been well studied, and the virus is known to circulate in sub-Saharan Africa (LaBeaud et al. 2010; Linthicum et al. 2016). *Aedes* mosquitoes are important in the endemic cycle of the virus, while *Culex* mosquitoes contribute to seasonal outbreaks, which normally occur after increased rainfall (Linthicum et al. 2016).

We found three maps for RVFV that included Cameroon in their extent (Rogers 2006; Clements et al. 2006; Anyamba 2016). The prediction from the *Rift Valley Fever Monitoring Project* has been able to predict RVFV epizootics 2–6 weeks in advance in East Africa, based on environmental parameters (Anyamba et al. 2009; Anyamba 2016). Unlike predictions for other viruses, one prediction for RVFV used livestock density as a parameter (Clements et al. 2006). There was consensus among all of the predictions in the Far North region of Cameroon, and one prediction extended into the North region. These predictions are discordant with local unpublished and published data, similar to the CCHFV predictions. Considering the published livestock data, one goat from an urban Cameroonian market and five goats from a rural southern village were seropositive for RVFV (LeBreton et al. 2006). While the goat in the urban market could have been infected in northern Cameroon before being transported to south, the rural southern goats did not have any exposure to the north, supporting that RVFV could also be circulating in southern Cameroon (LeBreton et al. 2006). Therefore, like CCHFV, RVFV could spread southwardly through livestock movement.

Discussion

None of the predictions we examined for emerging zoonotic viruses in Cameroon were made by Cameroonian first-authors or were familiar to many of the national experts with whom we met. Therefore, our discussions with national experts allowed us to assess these predictions with fresh perspectives. Multiple findings emerged from these discussions. First, we received feedback on how to improve aggregating and sharing the predictions with national policymakers. National experts recommended adding administrative regions to make the maps more useful for national policy makers who regionally allocate resources for clinical diagnostics, outbreak preparedness, and disease surveillance.

Our research also revealed that local knowledge from a variety of national experts could contribute to national predictions of emerging zoonotic viruses. We found that experts from federal ministries, reference laboratories, and uniformed services had insights on emerging pathogens. Partnerships across national agencies in Africa, such as militaries, have aided in developing surveillance programs for emerging zoonotic diseases (Witt et al. 2011; Kronmann et al. 2013). Modelers could approach these experts to refine their models. For example, we found that published predictions for filoviruses (EBOV and MARV) were consistent with expert opinion in Cameroon but that predictions for bunyaviruses (RVFV and CCHFV) were discordant, potentially due to local patterns of livestock movement (Fig. 2). Another possible reason for the discrepancies between expert judgment and species distribution models is that many of the predictions were done with data at a continental or regional scale rather than with national data. Therefore, including local knowledge or parameters may address gaps in existing predictive maps.

Because of the nuances in data and assumptions used to create predictive maps, it may be important to share existing maps with national experts to elicit new country-specific data and revise maps before they are used by national policymakers. We propose a framework for aggregating and creating predictions of emerging zoonotic viruses for national policymakers that incorporates national expert opinion (Fig. 3). Different countries could use this framework to gather predictions for emerging zoonotic pathogens and identify additional data and parameters that are nationally appropriate. For example, the predictions we studied did not rely on human parameters. One group of experts thought that adding human parameters such as landscape change, movement, hunting, and cultural practices could improve predictions of emerging zoonotic viruses, similar to the focus of USAID's Emerging Pandemic Threats program (Morse 2012). A country-tailored approach may be necessary to mobilize experts for eliciting data and feedback. We found that snowball sampling from established contacts worked well for contacting government officials compared to cold contacts by email. Platforms for distributing unpublished data such as F1000 and Scientific Data could also enable sharing of national data, but there may be a low level of awareness of these platforms in LMICs.

Our conversations with national experts identified gaps in predictions for emerging zoonotic viruses. National experts requested predictions for additional emerging zoo-

notic viruses in Cameroon, such as Dengue virus, which did not fit the criteria for our study. They also recognized the discrepancies between predictions for the same viruses. These discrepancies are due to differences in how and when the models were made. For example, the predictions for MARV reveal the differences between using only human occurrence data and adding bat serology data to the same model (Pigott et al. 2015). Meanwhile, some authors used metrics to weight the occurrence data, for example ranking virus isolation as stronger evidence than serology (Messina et al. 2015), while others used different input data. Some researchers chose to use the host ranges of putative reservoir species in their models (Pigott et al. 2014; Mylne et al. 2015), and others chose to incorporate host density (Clements et al. 2006). These choices have to be made because of lack of confirmed human index cases or wildlife infections, sparse knowledge about reservoir hosts and vectors, and little information about the drivers of zoonotic transmission. Our expert informants suggested that a summary of these characteristics, as in Table 1, should be shared so that national experts and policymakers can decide on the prediction that best fits their context and knowledge.

To our knowledge, this type of qualitative approach to aggregating and discussing risk maps has not been done before. From this experience, we found a number of limitations and areas to improve upon our method. It is difficult to gauge the quality of predictions in Cameroon because there are limited data for these viruses in Cameroon. Therefore, we do not know if the prediction maps or experts are closer to the truth. Studies in different fields of forecasting have shown that combining multiple models or expert predictions often results in a better prediction than any method alone (Araújo and New 2007). By aggregating the models, we hoped to identify areas of consensus within the models and with expert opinion. We also aimed to provide experts with a variety of predictions to stimulate discussion. An alternative approach would be to compare the quality of each model and chose the best one for the context. We chose to include predictions from 2004 to 2016, some of which had small sample sizes. Advances in statistical techniques and more recent data could make these older predictions with small sample sizes less accurate. Ensemble modeling methods could allow for a more precise approach to aggregating predictions, but this would require access to the original data for each of these models. Ensemble modeling could also help with incorporating the estimates of uncertainty that some models included as well as establish thresholds suitable to each model. To make the risk maps more easily interpretable by national experts, we converted probabilistic predictions to binary occurrence/non-occurrence in Cameroon based on a threshold. Using EVD data, we verified that the threshold that we used resulted in binary maps that were accurate based on measures of sensitivity and specificity (Figure S3). However, it is unknown whether this threshold was optimal for the other risk maps. If we had access to the inputs and model outputs, such assessments could be made independently of the original authors. Thus, risk maps are of limited utility when the underlying data are unavailable and could be more useful if authors upload the raw data to repositories. We also did not assess expert uncertainty, and some experts had less familiarity with the viruses and modeling methods than others. We might modify our approach by developing an expert prediction map first through participatory mapping and then compare it with the modeled predictions, which could reveal discrepancies more clearly and reduce biases.

After our study was conducted, additional predictions for EBOV, MARV, and LASV were published that included Cameroon in their extent (Redding et al. 2016; Peterson and Samy 2016; Schmidt et al. 2017). The predictions within Cameroon for these viruses grossly corresponded with the other predictions and expert opinion. One of the EBOV predictions incorporated seasonality, adding a temporal dimension to risk mapping (Schmidt et al. 2017). The LASV prediction used a different modeling method to make predictions for risk in future populations (Redding et al. 2016). As predictions continue to develop, it will be important to find more efficient ways of updating and comparing models.

While published predictions for emerging zoonotic viruses could be useful to national policymakers for disease prioritization, surveillance, and outbreak preparation, the current presentation of these predictions in scientific journals limits their utility for national policymakers. In order to translate these predictions for national policymakers, we need to first aggregate and repackage existing predictive maps with relevant details such as administrative regions, so that they can be compared on a national level. Next, we can share these maps with national experts to see if they agree with the predictions or if improvements can be made with additional local data and expert experience. These revised predictions can then be used by national policymakers for allocating resources to improve diagnostics, emergency preparedness, and infection control. Ultimately, increased integration of national experts into

creating predictions of emerging infectious diseases should lead to more of these studies being implemented into national policies, which could help prevent or mitigate future outbreaks of emerging zoonotic viruses.

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