Title

Predictors of human-infective RNA virus discovery in the United States, China and Africa,
an ecological study

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Abstract

Background The variation in the pathogen type as well as the spatial heterogeneity of predictors make the generality of any associations with pathogen discovery debatable. Our previous work confirmed that the association of a group of predictors differed across different types of RNA viruses, yet there have been no previous comparisons of the specific predictors for RNA virus discovery in different regions. The aim of the current study was to close the gap by investigating whether predictors of discovery rates within three regions—the United States, China and Africa—differ from one another and from those at the global level.

Methods Based on a comprehensive list of human-infective RNA viruses, we collated published data on first discovery of each species in each region. We used a Poisson boosted regression tree (BRT) model to examine the relationship between virus discovery and 33 predictors representing climate, socio-economics, land use, and biodiversity across each region separately. The discovery probability in three regions in 2010–2019 was mapped using the fitted models and historical predictors.

Results The numbers of human-infective virus species discovered in the United States, China and Africa up to 2019 were 95, 80 and 107 respectively, with China lagging behind the other two regions. In each region, discoveries were clustered in hotspots. BRT modelling suggested that in all three regions RNA virus discovery was best predicted by land use and socio-economic variables, followed by climatic variables and biodiversity, though the relative importance of these predictors varied by region. Map of virus discovery probability in 2010–2019 indicated several new hotspots outside historical high-risk areas. Most new virus species since 2010 in each region (6/6 in the United States, 19/19 in China, 12/19 in Africa) were discovered in high risk areas as predicted by our model.

Conclusions The drivers of spatiotemporal variation in virus discovery rates vary in different regions of the world. Within regions virus discovery is driven mainly by land-use and socioeconomic variables; climate and biodiversity variables are consistently less important predictors than at a global scale. Potential new discovery hotspots in 2010–2019 are identified. Results from the study could guide active surveillance for new human-infective viruses in local high risk areas.

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Introduction

RNA viruses are the primary cause for emerging infectious diseases with epidemic potential, given that they have high rate of evolution and high capacity to adapt to new hosts (Woolhouse et al., 2016). In recent decades, infectious diseases caused by severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS-CoV), Bundibugyo Ebola virus and SARS-CoV-2 present major threats to the health and welfare of humans (Albarino et al., 2013; Ksiazek et al., 2003; Mackay et al., 2015; World Health Organisation, 2020). Detection of formerly unknown human-infective RNA viruses in the earliest stage after the emergence are essential for controlling the infections they cause. Measures to implement early detection include not only advanced diagnostic techniques (Lipkin et al., 2013), but more importantly the idea where to look for them (so-called hotspots) (Morse et al., 2012).

Socio-economic, environmental, and ecological factors related to both virus natural history and research effort have been found to affect the discovery of emerging RNA viruses (Jones et al., 2008; Morse et al., 2012; Rosenberg, 2015; Zhang et al., 2020). However, these factors are highly spatially heterogeneous, making the generality of any associations with discovery debatable. For example, the United States, China, and Africa have experienced different rates of socio-economic, environmental, and ecological changes in the last one hundred years. The United States has always had better resources to discover new viruses. For example, the Rockefeller Foundation—a U.S. foundation—supported the discovery of 23 arboviruses in Latin America, Africa, and India in 1951–1969 (Rosenberg, 2015). China has seen urban land coverage more than double and GDP per capita increase by seven times since the 1980s (Ritchie, 2018; Roser, 2013). Nine out of 223 human-infective RNA viruses have been originally discovered in China, and all were discovered after 1982 (Zhang et al., 2020). In

contrast, effective surveillance is challenging in less developed regions such as large parts of Africa given resource constraints (Petti et al., 2006).

There have been no previous comparisons of the specific predictors for RNA virus discovery in different regions. In this study, we applied a similar methodology from our previous study of global patterns of discovery of human-infective RNA viruses (Zhang et al., 2020) to investigate whether predictors of discovery rates within three regions—the United States, China and Africa—differ from one another and from those at the global level, using three new virus discovery data sets. We also mapped discovery probability in three regions in 2010–2019 using the fitted models and historical predictors. According to findings from our previous study (Zhang et al., 2020), the main predictors for virus discovery at the global scale were GDP-related. This suggests that the patterns of virus discovery we have identified may have been largely driven by research effort rather than the underlying biology. In this study, by focusing on more restricted and homogenous regions where the research effort is less variable, we expected to identify predictors more associated with virus biology.

Materials and Methods

Data sets of human-infective RNA viruses in three regions

We performed an ecological study, and the subject of interest is each human-infective RNA virus species. With reference to a full list of human-infective RNA virus species (Zhang et al., 2020), we geocoded the first report of each in humans in the United States, China, and Africa separately. The latest version as of 31 December 2019 included 223 species (**Table 1S**), with *Human torovirus* abolished and a new species—*Heartland banyangvirus*—added by ICTV in 2018 (International Committee on Taxonomy of Viruses, 2018). We defined discovery location as where the initial human was exposed to/infected with the virus, as suggested in the first report of human infections from peer-reviewed literature.

91 We followed the same search terms, databases searched, and inclusion or exclusion criteria as
 92 our global data set for data collection (Woolhouse et al., 2018). Reference databases included
 93 PubMed, Web of Science, Google Scholar, and Scopus. Two Chinese database [i.e. China
 94 National Knowledge Infrastructure (CNKI) and Wanfang Data] were also searched when
 95 collecting data for China. Reference lists of relevant studies and reviews were also checked
 96 manually to find potential earlier discovery papers. The following key words were used for
 97 the retrieval: virus full name or abbreviations or virus synonyms; and human* or person* or
 98 case* or patient* or worker* or infection* or disease* or outbreak* or epidemic*; and region
 99 name (Chin* or Taiwan or Hong Kong or Macau; United States or US or USA or America*;
 100 Africa* or all African country names). Virus synonyms and abbreviations include early
 101 names used in the discovery paper and all subtypes provided by the ICTV 10th report (*Full*
 102 *ICTV Online (10th) Report: https://talk.ictvonline.org/ictv-reports/ictv_online_report/*).
 103 Evidence which met the following criteria from peer-reviewed literatures were included: (a)
 104 Diagnostic methods for RNA virus infection in humans were clearly described, through either
 105 viral isolation or serological methods; (b) Specific virus species name or subtypes falling
 106 under that species were clearly provided; (c) Both natural infection and iatrogenic or
 107 occupational infections were accepted. Evidence which met the following criteria were
 108 excluded: (a) Uncertain species due to cross-reactivity with related viruses; (b) Diagnostic
 109 methods for virus infection were not specified; (c) Description of clinical symptoms or
 110 pathogenicity were not considered as human infection of one certain virus species; (d) Report
 111 of '[virus name]-like' or 'potential [virus name] infections'; (d) Intentional infections
 112 including experimental inoculation or vitro infections; (e) Non-peer-reviewed literature,
 113 including media reports, thesis, or unpublished data. Literature selection was performed by
 114 two individuals independently and discrepancies were resolved by discussion with a third
 115 individual.

All locations were geolocated as precisely as possible using methods from our previous paper (Zhang et al., 2020). For each region, a polygon was created for those locations at administrative level 3 (county for the United States; city for China; for Africa, it varies between different countries) and above. Details of data types for virus discovery database in three regions was summarised in **Table 2S**. The majority of discovery locations in the United States and Africa involved point data, while in China the majority involved polygon data at province level. A bootstrap resampling procedure was developed for polygon data covering more than one grid cell (details below). Discovery date of human infection was defined as the publication year in the scientific literature.

Spatial covariates

As for our global analysis (Zhang et al., 2020), a suite of global gridded climatic, socio-economic, land use, and biodiversity variables (n=33) postulated to affect the spatial distribution of RNA virus discovery were compiled, each at a resolution of 0.5°/30" (except university count having a resolution at country level for Africa and state/province for the United States and China). Data for the United States, China and Africa were extracted by restricting the coordinates within each region. The definition, original resolution, and source of each variable were the same as our previous paper (Zhang et al., 2020). All predictors were aggregated from their original spatial resolution to 1°×1° resolution; data for climatic variables, population, GDP, and land use data without full temporal coverage were extrapolated back to 1901; both following methods from our previous paper (Zhang et al., 2020).

Boosted regression trees modelling

We used Poisson boosted regression trees (BRT) model to examine the relationship between discovery of RNA virus and 33 predictors for each 1° resolution of grid cell across each

region separately, following codes from our previous study (Zhang et al., 2020) and one previous paper (Allen et al., 2017). As a tree-based learning method, BRT model can automatically capture complex relationships and interactions between variables, and also can well account for spatial autocorrelation within the data (Crase et al., 2012). We compared Moran's I values of the raw virus data and the model residuals to estimate the ability of the BRT model to account for spatial autocorrelation (Cliff et al., 1981). In order to minimise the effect of spatial uncertainty of virus discovery data, we performed 1000 times bootstrap resampling for those discovery locations reported as polygons. We assumed each grid cell in the polygon has the equal chance to be selected, and for each virus record we selected one grid cell randomly from the polygon for each subsample. A ratio of 1:2 for presence to absence constituted each subsample, i.e., for each grid cell with virus discovery, two grid cells with no discovery were randomly selected from 'virus discovery free' areas at all time points within the region. Take the United States as an example, each subsample included 95 grid cells with virus discovery and 190 with no virus discovery. We then matched the virus data with all predictors (using the nearest decade for time-varying predictors). We assumed that the virus count in any given grid cell in each decade followed a Poisson distribution, and we calculated the virus discovery count in each grid cell by decade as the response variable.

All BRT models were fitted in R v. 3.6.3, using packages dismo and gbm. BRT models require the user to balance three parameters including tree complexity, learning rate, and bag fraction. Tree complexity reflects the order of interaction in a tree; learning rate shrinks the contribution of each tree to the growing model; bag fraction specifies the proportion of data drawn from the full training data at each step. We set these parameters as recommended from Elith et al (Elith et al., 2008), and make sure each resampling model contained at least 1000 trees. BRT models identified the final optimal number of trees in each model using a 10-fold cross validation stagewise function (Elith et al., 2008). The three parameter values of the

optimal model as well as the mean optimal number of trees across 1000 replicate models for all three regions were summarised in **Table 3S**.

By fitting 1000 replicate BRT models, the relative contribution plots and partial dependence plots with 95% quantiles were plotted. We defined variables with a relative contribution greater than the mean (3.03%) as influential predictors in all three regions (Shearer et al., 2018). The partial dependence plots depict the influence of each variable on the response while controlling for the average effects of all the other variables in the model. The map of virus discovery probability across each region in 2010–2019 was derived from the means of the predictions of 1000 replicate models, using values of the 33 predictors in 2015. In order to show discovery hotspots, we converted the prediction map of virus count to a map of probability.

Two statistics were calculated to evaluate the model's predictive performance: a) the deviance of the bootstrap model (Elith et al., 2008), b) intraclass correlation coefficient (ICC) calculated from 50 rounds of ten-fold cross-validation, by following methods from our previous paper (Zhang et al., 2020). For the ten-fold cross-validation, we selected 50 data sets randomly from the 1000 bootstrapped subsamples. We took the first data set and divided into ten subsets. For each round of ten-fold cross-validation, the unique combinations of 9 subsets constituted the training sets and were used to fit models, and the remaining one was used as a test set to evaluate the predictive performance of the model. We repeat the same process as above for the remaining 49 data sets. One intraclass correlation coefficient (ICC) was calculated from each round of validation and the median with 95% quantiles across all 50 rounds was calculated. The ICC varies between 0 and 1, with an ICC of less than 0.40 representing a poor model, 0.40–0.59 representing a fair model, 0.60–0.74 representing a good model, and 0.75–1 representing an excellent model (Cicchetti, 1994).

Exploratory subgroup analyses (distinguishing viruses firstly discovered in regions and those that had been discovered elsewhere in the world) were performed. We used the same BRT modelling approach as we described above, and relative contribution of each predictor was calculated for each subgroup. We were unable to perform subgroup analysis for China because only 9 human-infective RNA viruses have been firstly discovered in it, and BRT model cannot be fitted to a sample as small as 9.

The R software, version 3.6.3 (R Foundation for Statistical Computing, Vienna, Austria) was used for all statistical analyses. All maps were visualised by using ArcGIS Desktop 10.5.1 (Environmental Systems Research Institute).

Results

The numbers of human-infective virus species discovered in the United States, China and Africa up to October 2019 were 95, 80 and 107 respectively (**Table 1S**). Most first discoveries have been in eastern United States (especially in areas around Maryland, Washington, D.C., and New York), eastern China (developed cities including Beijing, Hong Kong, Shanghai, and Guangzhou), and southern and central Africa (Pretoria and Johannesburg, South Africa; Borno State and Ibadan, Nigeria) (**Figure 1**). A total of 60 virus species were previously reported in all three regions, and 27, 12, 37 species were only found in the United States, China, and Africa respectively (**Figure 2**). In all three regions, smaller proportions of viruses were vector-borne [United States: 23.2% (22/95); China: 21.3% (17/80); Africa: 27.1% (29/107)] and strictly zoonotic [United States: 30.5% (29/95); China: 16.3% (13/80); Africa: 33.6% (36/107)], compared to large proportions for both virus types at the global scale [vector-borne: 41.7% (93/223) and strictly zoonotic: 58.7% (131/223)] (**Figure 2**). The 60 shared species were also disproportionally vector-borne [11.7% (7/60)] and strictly zoonotic [7% (4/60), **Figure 2**].

Figure 1 Spatial distribution of human-infective RNA virus discovery in three regions, 1901–2019. A, United States. B, China. C, Africa. Red dots represent discovery points or centroids of polygons, with the size representing the cumulative virus species count.

Figure 2 Shared human-infective RNA virus species count in three regions. Under/By the species count the ratios of vector-borne (V) to non-vector-borne (N) viruses and strictly zoonotic (Z) to human transmissible (T) viruses were shown.

221 The discovery curves for the United States and Africa have seen a broadly similar pattern,
 222 with China lagging behind these two regions (**Figure 3**). In comparison with the world, the
 223 median time lag of the virus discovery was 0 [interquartile range (IQR): 2.5], 12 (IQR: 29.5)
 224 and 2 (IQR: 10.5) years in the United States, China and Africa, respectively (**Figure 1S**). In
 225 China, the time lag was noticeably shorter for viruses discovered after 1975 [before 1975: a
 226 median lag of 30.5 (IQR: 30.5) years; after 1975: 2.5 (IQR: 7) years, p value of Wilcoxon
 227 rank sum test < 0.001].

228

229 **Figure 3 Discovery curve of human-infective RNA virus species in three regions and the world**

230 In the United States, six variables including three predictors related to land use [urbanized
 231 land: relative contribution of 35.8%, urbanization of cropland (i.e. the percentage of land area
 232 change from cropland to urban land): 8.0%, growth of urbanized land: 4.1%], two socio-
 233 economic variables (GDP growth: 10.0%; GDP: 5.7%), and one climatic variable (diurnal
 234 temperature change: 4.9%) were identified as important predictors for discriminating between
 235 locations with and without virus discovery (**Figure 4A**). The partial dependence plots shown

in **Figure 2S** suggested non-linear relationships between the probability of virus discovery and most predictors. All important predictors presented a positive trend over narrow ranges at lower values.

In China, twelve variables including four socio-economic variables (GDP: 12.7%, university count: 7.5%, GDP growth: 4.6%, population growth: 4.4%), five predictors involving land use [pasture: 8.3%, urbanized land: 8.1%, vegetation: 5.8%, cropland: 5.3%, urbanization of secondary land (the percentage of land area change from secondary land to urban land; secondary land is natural vegetation that is recovering from previous human disturbance): 3.3%], and three climatic variables (maximum precipitation: 4.5%, precipitation change: 3.8%, diurnal temperature range: 3.3%) were identified as important predictors for discriminating between locations with and without virus discovery (**Figure 4B**). GDP, urbanized land, university count, vegetation, GDP growth, maximum precipitation, population growth, and urbanization of secondary land presented a positive trend over narrow ranges at lower levels; pasture, cropland, precipitation change, and diurnal temperature range had non-monotonic/ negative impacts, with highest risks at lower values (**Figure 3S**).

In Africa, ten variables including two socio-economic variables (GDP growth: 21.2%, GDP: 13.0%), seven predictors related to land use (urbanized land: 9.4%, growth of cropland area: 5.6%, urbanization of cropland: 5.5%, growth of urbanized land: 5.1%, urbanization of pasture: 3.8%, vegetation, 3.7%, cropland: 3.2%), and one biodiversity variable (mammal species richness: 3.1%) were identified as important predictors for discriminating between locations with and without virus discovery (**Figure 4C**). All important predictors presented a positive trend over narrow ranges at lower positive values, except mammal species over a large range (**Figure 4S**).

259

260 **Figure 4 Relative contribution of predictors to human-infective RNA virus discovery in three regions. A,**
 261 **United States. B, China. C, Africa. The boxplots show the median (black bar) and interquartile range (box) of**
 262 **the relative contribution across 1000 replicate models, with whiskers indicating minimum and maximum and**
 263 **black dots indicating outliers.**

Our BRT models reduced Moran's I value below 0.15 in all three regions (**Figure 5S**), suggesting that BRT models with 33 predictors have adequately accounted for spatial autocorrelations in the raw virus data in all three regions. The model validation statistics for each region are shown in **Table 4S**. Combining these measures, our BRT model predictions range from fair to good (Cicchetti, 1994).

In all three regions, human-infective RNA virus discovery was best predicted by land use and socio-economic variables, followed by climatic variables and biodiversity (**Figure 5**), whereas virus discovery was more associated with climatic variables and biodiversity at the global level. The comparison between three regions showed that: climatic variables contributed most to the discovery of human-infective RNA viruses in China; land use contributed most to the discovery in the United States; socio-economic variables and biodiversity contributed most to the discovery in Africa and least to discovery in the United States.

Figure 5 Cumulative relative contribution of predictors to human-infective RNA virus discovery by group in each model of different regions. The relative contributions of all explanatory factors sum to 100% in each model, and each colour represents the cumulative relative contribution of all explanatory factors within each group.

We mapped human-infective RNA virus discovery probability in 2010–2019 for the three regions, based on the fitted BRT models and values of all 33 predictors in 2015 (**Figure 6S–Figure 8S**). Outside contemporary risk areas where human-infective RNA viruses were previously discovered in the United States (**Figure 1A**), we predicted high probabilities of virus discovery across southern Michigan, central-Northern Carolina, central Oklahoma, southern Nevada, and north-eastern Utah (**Figure 6A**). Outside contemporary risk areas where human-infective RNA viruses were previously discovered in China (**Figure 1B**), we predicted high probabilities of virus discovery across other eastern China area as well as two western areas including south-central Shaanxi and north-eastern Sichuan (**Figure 6B**). Outside contemporary risk areas where human-infective RNA viruses were previously discovered in Africa (**Figure 1C**), we predicted high probabilities of virus discovery across northern Morocco, northern Algeria, northern Libya, south-eastern Sudan, central Ethiopia and western Democratic Republic of the Congo (**Figure 6C**). Most new virus species since 2010 in each region (6/6 in the United States, 19/19 in China, 12/19 in Africa) were discovered in high-risk areas (85% percentiles of predicted probability across each region) as predicted by our model. Of all the 37 (United States: 6; China: 19; Africa: 12) viruses discovered in high-risk areas in 2010–2019, 13 (United States: 2; China: 7; Africa: 4) viruses were discovered at the potential new hotspots where there have not been any virus discoveries before 2010.

Figure 6 Predicted probability of human-infective RNA virus discovery in three regions in 2010–2019. A, United States. B, China. C, Africa. The triangles represented the actual discovery sites from 2010 to 2019, and the background colour represented the predicted discovery probability.

Based on our subgroup analysis (distinguishing viruses firstly discovered in regions and those that had been discovered elsewhere in the world), discoveries of human-infective RNA viruses firstly discovered from either United States or Africa were better predicted by climatic and biodiversity variables, while discoveries of viruses that had been discovered from elsewhere in the world were better predicted by socio-economic variables (**Figure 9S**).

Discussion

To our knowledge, this analysis represents the first investigation of human-infective RNA virus discovery in three large regions of the world which have experienced distinct socio-economic, ecological and environmental changes over the last 100 years. In total, 95 human-infective RNA virus species had been found in the United States; 80 in China; 107 in Africa.

The discovery maps of human-infective RNA virus in the three regions indicated areas with historically high discovery counts: eastern and western United States, eastern China, and central and southern Africa. BRT modelling suggested that the relative contribution of 33 predictors to human-infective RNA virus discovery varied across three regions, though climatic and biodiversity variables were consistently less important in all three regions than at a global scale. We mapped the probability of human-infective RNA virus discovery in 2010–2019 which would continue to be high in historical hotspots but, in addition, we identified several new hotspots in central-eastern and southwestern United States, eastern and western China, and northern Africa. These results offer a tool for public health practitioners and policy-makers to better understand local patterns of virus discovery and to invest efficiently in surveillance systems at the local level.

In all three regions, GDP and/or GDP growth were identified as important predictors for virus discovery, especially in Africa where GDP and GDP growth were identified as the leading predictors. This is consistent with our previous analysis that GDP and GDP growth play a major role in discovering viruses (Zhang et al., 2020). In general, sufficient economic, human and material resources, the availability of advanced infrastructure and technology, and greater research capabilities in the relative higher-income areas enable the virus discovery (Rosenberg et al., 2013). That this effect applied both within one continent and within single countries such as the United States and China suggested that most virus discoveries were likely passive, i.e. the viruses were detected when they arrived in a location with the resources to detect them. This is plausible because in all regions in our study, human-transmissible viruses accounted for the larger proportion, and our previous analysis suggested richer areas were more likely to first capture transmissible viruses (e.g. Influenza virus, Rhinovirus, Rabies lyssavirus, Measles morbillivirus, Mumps orthorubulavirus, Rubella virus, and Norwalk virus) capable of spreading to multiple areas (Zhang et al., 2020). Temporally,

in China the rate of discovery increased after economic growth accelerated in the 1980s (**Figure 3**). We note in publications describing first virus discoveries that most historical virus discoveries in Africa received support from the United States and Europe, and this may explain why Africa saw an increased number of virus discoveries after 1950—30 years earlier than China (**Figure 3**). Notably, in China the relative contribution of GDP growth to virus discovery was not as substantial as that in Africa. In contrast, university count was found to be associated with virus discovery, suggesting virus discovery likely being a significant area of research in Chinese universities. Our model also suggested the overall socio-economic factors contributed less in the United States than other two regions. The possible explanation is that the socio-economic level across the whole United States is relatively high and homogenous.

Predictors other than GDP and university count are likely to be linked to virus natural history. In all three regions, the area of urban land and further urbanization made great contribution to virus discovery. This reinforced previous studies that urbanization was linked to the detection of new human pathogens through the denser urban population, increased human-wildlife contact rate, spill-over of human infection from enzootic cycle, and the contamination of the urban environment with microbial agents (Hassell et al., 2017; Olival et al., 2017; Weaver, 2013). In the United States, land use contributed most to virus discovery in comparison to other regions—urbanized land, urbanization of cropland, and growth of urbanized land alone had a relative contribution of 47.9%. However, the leading role of urbanization to virus discovery in the United States remains unclear. There might be many factors contributing to this, e.g. the underlying relationships between urbanization and economic growth as well as population growth, but we can't untangle these from this study.

Consistent with our previous work, population growth was identified as a less prominent predictors (Zhang et al., 2020). In China, population growth—though with greater influence than other regions—contributed less than urbanized land and three other land types on virus discoveries. This reinforces our previous interpretation that urbanization brings larger changes on human living environment than human population size/growth, and therefore may have influenced virus discovery more greatly.

Climate had less influence on human-infective RNA virus discovery in all three regions in comparison to other predictors, in contrast to virus discovery at a global scale (Zhang et al., 2020). The underlying reason may be that the proportion of vector-borne viruses—whose distribution and abundance is strongly associated with the impact of climate on vector populations (Li et al., 2014)—in all three regions (United States: 23.2%; China: 21.3%; Africa: 27.1%) were less than that in the world (41.7%) (**Figure 3**). Vector-borne viruses tend to have more restricted global ranges, so are less likely to appear in a study of any one region (Zhang et al., 2020).

In addition, a relative smaller proportion of strictly zoonotic viruses in three regions (United States: 30.5%; China: 16.3%; Africa: 33.6%) than that in the world (58.7%) (**Figure 2**) made biodiversity contribute less to virus discovery in the three regions than in the world (Zhang et al., 2020). With exposure to denser mammals played a slightly larger role in virus discovery in Africa than in China and the United States (**Figure 6S–Figure 8S**).

Our discovery probability maps for 2010–2019 in three regions captured most historical hotspots, though several small new areas in central-eastern and southwestern United States, eastern and western China, as well as northern Africa would also make greater contribution to virus discovery (**Figure 6**). Our model has a good predictive ability, given 84% (37/44) new virus species in 2010–2019 were discovered in high-risk areas we have defined—85%

percentiles of discovery probability within each region. Further, 35% (13/37) of those viruses discovered in high-risk areas since 2010 were discovered at the potential new hotspots where there had not been any virus discoveries in the past.

Our subgroup analyses suggested in both the United States and Africa, discoveries of viruses firstly discovered in regions were more likely to be associated with climatic and biodiversity variables while discoveries of viruses had been discovered elsewhere in the world were more likely to be associated with socio-economic variables. This is plausible, again because after a novel virus was discovered elsewhere in the world, it is usually areas with a higher socio-economic level firstly capture the virus in the local region.

This study had limitations. First, one common problem for data collected from literature review is the time lag between virus discovery and publication, in which case the virus data are likely to be matched to covariates in later decades. Second, we acknowledge that it is possible we have not identified the earliest report for some well-known viruses such as yellow fever virus, measles virus, especially in the post-vaccination era. Third, we were unable to identify robust and comprehensive data for all three regions on virus discovery effort, although we interpret GDP and university count as being an indirect measure of resources available for this activity.

The study adds to our previous study (Zhang et al., 2020) in several ways. First, we firstly construct data sets of human-infective RNA virus discovery reflecting the viral richness in three broad regions of the world. Second, we reduced the heterogeneity of the predictors by focusing on regions, including those predictors reflecting the research effort. Research effort is less variable within restricted regions and therefore has less effect on virus detection. This implies our predicted hotspots stand closer to the virus geographic distribution in nature. Third, the predicted hotspots derived from regional analysis have a higher precision than at a

global scale, e.g. specific areas in the United States and China were identified as hotspots from regional analysis, rather than the whole eastern area from the global analysis. This helps target areas for future surveillance.

In conclusion, a heterogeneous pattern of virus discovery-driver relationships was identified across three regions and the globe. Within regions virus discovery is driven more by land-use and socio-economic variables; climate and biodiversity variables are consistently less important predictors than at a global scale. We mapped with good accuracy that in 2010–2019 three regions where human-infective RNA viruses had previously been discovered would continue to be the discovery hotspots, but in addition, several new areas in each region would make great contribution to virus discovery. Results from the study could guide active surveillance for new human-infective viruses in high risk areas.

Author contributions

Feifei Zhang, Conceptualization, Data preparation, Formal analysis, Methodology, Validation, Visualization, Interpretation, Writing - original draft, Writing - review and editing; Margo Chase-Topping, Methodology, Interpretation, Writing - review and editing; Chuan-Guo Guo, Data preparation, Methodology, Validation, Interpretation, Writing - review and editing; Mark E.J. Woolhouse, Conceptualization, Methodology, Interpretation, Writing - original draft, Writing - review and editing, Funding Acquisition.

Competing interests

The authors disclose no conflicts of interest.

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Data availability

The authors confirm that all data or the data sources are provided in the paper and its Supplementary Materials. The final datasets and codes used for the analyses are available via figshare at <https://doi.org/10.6084/m9.figshare.15101979>.

References

- Albarino, C. G., Shoemaker, T., Khristova, M. L., Wamala, J. F., Muyembe, J. J., Balinandi, S., . . . Stroher, U. (2013). Genomic analysis of filoviruses associated with four viral hemorrhagic fever outbreaks in Uganda and the Democratic Republic of the Congo in 2012. *Virology*, 442(2), 97-100.
- Allen, T., Murray, K. A., Zambrana-Torrel, C., Morse, S. S., Rondinini, C., Di Marco, M., . . . Daszak, P. (2017). Global hotspots and correlates of emerging zoonotic diseases. *Nat Commun*, 8(1), 1124.
- Cicchetti, D. V. (1994). Guidelines, criteria, and rules of thumb for evaluating normed and standardized assessment instruments in psychology. *Psychological Assessment*, 6(4), 284-290.
- Cliff, A. D., & Ord, J. K. (1981). *Spatial processes: Models and applications*. London: Pion Limited.
- Crane, B., Liedloff, A. C., & Wintle, B. A. (2012). A new method for dealing with residual spatial autocorrelation in species distribution models. *Ecography*, 35(10), 879-888.

Elith, J., Leathwick, J. R., & Hastie, T. (2008). A working guide to boosted regression trees. *J Anim Ecol*, 77(4), 802-813.

Full ICTV Online (10th) Report: https://talk.ictvonline.org/ictv-reports/ictv_online_report/. Retrieved from

Hassell, J. M., Begon, M., Ward, M. J., & Fevre, E. M. (2017). Urbanization and Disease Emergence: Dynamics at the Wildlife-Livestock-Human Interface. *Trends Ecol Evol*, 32(1), 55-67.

International Committee on Taxonomy of Viruses. (2018). Virus Taxonomy: The ICTV Report on Virus Classification and Taxon Nomenclature. Retrieved from https://talk.ictvonline.org/ictv-reports/ictv_online_report/

Jones, K. E., Patel, N. G., Levy, M. A., Storeygard, A., Balk, D., Gittleman, J. L., & Daszak, P. (2008). Global trends in emerging infectious diseases. *Nature*, 451(7181), 990-993.

Ksiazek, T. G., Erdman, D., Goldsmith, C. S., Zaki, S. R., Peret, T., Emery, S., . . . Anderson, L. J. (2003). A novel coronavirus associated with severe acute respiratory syndrome. *N Engl J Med*, 348(20), 1953-1966.

Li, L. M., Grassly, N. C., & Fraser, C. (2014). Genomic analysis of emerging pathogens: methods, application and future trends. *Genome Biol*, 15(11), 541.

Lipkin, W. I., & Firth, C. (2013). Viral surveillance and discovery. *Curr Opin Virol*, 3(2), 199-204.

Mackay, I. M., & Arden, K. E. (2015). MERS coronavirus: diagnostics, epidemiology and transmission. *Virol J*, 12, 222.

Morse, S. S., Mazet, J. A., Woolhouse, M., Parrish, C. R., Carroll, D., Karesh, W. B., . . . Daszak, P. (2012). Prediction and prevention of the next pandemic zoonosis. *Lancet*, 380(9857), 1956-1965.

Olival, K. J., Hosseini, P. R., Zambrana-Torrel, C., Ross, N., Bogich, T. L., & Daszak, P. (2017). Host and viral traits predict zoonotic spillover from mammals. *Nature*, 546(7660), 646-650.

Petti, C. A., Polage, C. R., Quinn, T. C., Ronald, A. R., & Sande, M. A. (2006). Laboratory Medicine in Africa: A Barrier to Effective Health Care. *Clinical Infectious Diseases*, 42(3), 377-382.

Ritchie, H. (2018). "Urbanization". Published online at OurWorldInData.org. Retrieved from: <https://ourworldindata.org/urbanization>.

- Rosenberg, R. (2015). Detecting the emergence of novel, zoonotic viruses pathogenic to humans. *Cell Mol Life Sci*, 72(6), 1115-1125.
- Rosenberg, R., Johansson, M. A., Powers, A. M., & Miller, B. R. (2013). Search strategy has influenced the discovery rate of human viruses. *Proceedings of the National Academy of Sciences*, 201307243.
- Roser, M. (2013). "Economic Growth". Published online at OurWorldInData.org. Retrieved from: <https://ourworldindata.org/economic-growth>
- Shearer, F. M., Longbottom, J., Browne, A. J., Pigott, D. M., Brady, O. J., Kraemer, M. U. G., . . . Golding, N. (2018). Existing and potential infection risk zones of yellow fever worldwide: a modelling analysis. *Lancet Global Health*, 6(3), E270-E278.
- Weaver, S. C. (2013). Urbanization and geographic expansion of zoonotic arboviral diseases: mechanisms and potential strategies for prevention. *Trends Microbiol*, 21(8), 360-363.
- Woolhouse, M., & Brierley, L. (2018). Epidemiological characteristics of human-infective RNA viruses. *Sci Data*, 5, 180017.
- Woolhouse, M., Brierley, L., McCaffery, C., & Lycett, S. (2016). Assessing the Epidemic Potential of RNA and DNA Viruses. *Emerg Infect Dis*, 22(12), 2037-2044.
- World Health Organisation. (2020). Coronavirus disease (COVID-2019) situation reports. Retrieved from <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation430>
- Zhang, F., Chase-Topping, M., Guo, C. G., van Bunnik, B. A. D., Brierley, L., & Woolhouse, M. E. J. (2020). Global discovery of human-infective RNA viruses: A modelling analysis. *PLoS Pathog*, 16(11), e1009079.

1 Supplementary materials

2 *Supplementary tables*

3 Table 1S Summary of the human-infective RNA virus data sets in the United States, Africa and China

Species	Original discovery year	United States					China					Africa				
		Reported?	Discovery year	location	Lat	Lon	Reported?	Discovery year	location	Lat	Lon	Reported?	Discovery year	location	Lat	Lon
Argentinian mammarenavirus	1958	No					No					No				
Brazilian mammarenavirus	1994	Yes ¹	1995	New Haven, Connecticut	41.31	-72.93	No					No				
Cali mammarenavirus	1971	Yes ²	1974	Houston, Texas	29.76	-95.37	No					No				
Chapare mammarenavirus	2008	No					No					No				
Guanarito mammarenavirus	1991	No					No					No				
Lassa mammarenavirus	1970	Yes ³	1970	New Haven, Connecticut	41.31	-72.93	No					Yes ³	1970	Lassa, Borno State, Nigeria	10.69	13.27
Lujo mammarenavirus	2009	No					No					Yes ⁴	2009	Lusaka, Zambia	-15.39	28.32
Lymphocytic choriomeningitis mammarenavirus	1934	Yes ⁵	1934	St. Louis county, Missouri	38.61	-90.41	No					No				
Machupo mammarenavirus	1964	No					No					No				
Mobala mammarenavirus	1985	No					No					Yes ⁶	1985	Bouboui and Gomoka village, Boali town, Central African Republic	4.89	18.14
Whitewater Arroyo mammarenavirus	2000	Yes ⁷	2000	Alameda County, California	37.60	-121.72	No					No				
Mamastrovirus 1	1975	Yes ⁸	1981	Martin County, California	40.22	-123.10	Yes ⁹	1981	Guangzhou, Guangdong	23.13	113.26	Yes ¹⁰	1981	Lebowa, South Africa	-23.5	29.5
Mamastrovirus 6	2008	Yes ¹¹	2009	St. Louis, Missouri	38.63	-90.20	Yes ¹²	2010	Hong Kong	22.40	114.11	Yes ¹³	2009	Maiduguri, Borno State, Nigeria	11.83	13.15
Mamastrovirus 8	2009	Yes ¹⁴	2009	St. Louis, Missouri	38.63	-90.20	Yes ¹⁵	2013	Nanjing, Jiangsu and Lanzhou, Gansu	31.95	118.78	Yes ¹³	2009	Maiduguri, Borno State, Nigeria	11.83	13.15
Mamastrovirus 9	2009	Yes ¹⁶	2009	Accomack and Northampton Counties, Virginia	37.71	-75.81	Yes ¹⁷	2019	Jinan, Shandong	36.68	117.11	Yes ¹³	2009	Maiduguri, Borno State, Nigeria	11.83	13.15
Mammalian 1 orthobornavirus	1985	Yes ¹⁸	1985	Philadelphia, Pennsylvania	39.95	-75.17	Yes ¹⁹	1999	Taiwan	23.70	120.96	Yes ²⁰	1992	Rural area of East Africa	-1.28	34.53
Mammalian 2 orthobornavirus	2015	No					No					No				

Norwalk virus	1972	Yes ²¹	1972	Norwalk, Ohio	41.24	-82.62	Yes ²²	1995	Henan	33.88	113.48	Yes ²³	1993	Pretoria, Gauteng province, South Africa	-25.75	28.23
Sapporo virus	1980	Yes ²⁴	1988	Houston, Texas	29.76	-95.37	Yes ²⁴	1988	Shanghai	31.23	121.47	Yes ²⁵	1997	Pretoria, Gauteng province, South Africa	-25.75	28.23
Vesicular exanthema of swine virus	1998	Yes ²⁶	1998	Corvallis, Oregon	44.56	-123.26	No					No				
Alphacoronavirus 1	2007	No					No					No				
Human coronavirus 229E	1966	Yes ²⁷	1966	Chicago, Illinois	41.88	-87.63	Yes ²⁸	1975	Kunming, Yunnan	25.07	102.68	Yes ²⁹	1998	Kumasi, Ghana	6.70	-1.62
Human coronavirus NL63	2004	Yes ³⁰	2005	New Haven, Connecticut	41.31	-72.93	Yes ³¹	2005	Hong Kong	22.40	114.11	Yes ³²	2008	Cape Town, Western Cape Province, South Africa	-33.90	18.57
Betacoronavirus 1	1967	Yes ³³	1967	Bethesda, Maryland	38.98	-77.09	Yes ³¹	2005	Hong Kong	22.40	114.11	Yes ³⁴	2011	Pretoria, Gauteng province, South Africa	-25.75	28.23
Human coronavirus HKU1	2005	Yes ³⁵	2006	New Haven, Connecticut	41.31	-72.92	Yes ³⁶	2005	Hong Kong	22.40	114.11	Yes ³⁴	2011	Pretoria, Gauteng province, South Africa	-25.75	28.23
Middle East respiratory syndrome-related coronavirus	2012	Yes ^{*37}	2014	Lake county, Indiana	41.45	-87.37	Yes ^{*38}	2015	Huizhou, Guangdong	23.09	114.40	Yes ^{*39}	2014	Monastir, Tunisia	35.79	10.82
Severe acute respiratory syndrome-related coronavirus	2003	Yes ^{*40}	2003	Atlanta, Georgia	33.75	-84.39	Yes ⁴¹	2003	Hong Kong	22.40	114.11	Yes ⁴²	2004	Pretoria, Gauteng province, South Africa	-25.75	28.23
Human torovirus (been abolished)	1984	No					No					No				
Bundibugyo ebolavirus	2008	No					No					Yes ³²	2008	Bundibugyo and Kikyo town, Bundibugyo District, Western Uganda	0.71	30.06
Reston ebolavirus	1991	Yes ⁴³	1991	Reston, Fairfax County, Virginia	38.96	-77.35	No					No				
Sudan ebolavirus	1977	No					No					Yes ⁴⁴	1977	Maridi, South Sudan	4.91	29.45
Tai Forest ebolavirus	1995	No					No					Yes ⁴⁵	1995	Abidjan, Cote-d'Ivoire	5.36	-4.01
Zaire ebolavirus	1977	No					No					Yes ⁴⁶	1977	Yambuku village, Democratic Republic of the Congo	2.83	22.22
Marburg marburgvirus	1968	Yes ^{*47}	2009	Denver county, Colorado	39.55	-105.78	No					Yes ⁴⁸	1975	Johannesburg, South Africa	-26.20	27.90
Aroa virus	1971	No					No					No				
Bagaza virus	2009	No					No					No				
Banji virus	1959	No					No					Yes ⁴⁹	1959	Maponde's Kraal(Usutu river), South Africa	-26.52	31.67
Cacipacore virus	2011	No					No					No				
Dengue virus	1907	Yes ⁵⁰	1914	Savannah, Georgia	32.02	-81.12	Yes ⁵¹	1967	Southwest Taiwan	23.06	120.59	Yes ⁵²	1927	Durban, KwaZulu-Natal Province, South Africa	-29.86	31.02

Edge Hill virus	1985	No					No					No				
Gadgets Gully virus	1991	No					No					No				
Ilheus virus	1947	No					No					No				
Japanese encephalitis virus	1933	Yes ^{*33}	1953	Waltham, Massachusetts	42.38	-71.24	Yes ³⁴	1941	Beijing	40.01	116.41	Yes ³⁵	2017	Cunene, Angola	-16.28	15.28
Kokobera virus	1964	No					No					No				
Kyasanur forest disease virus	1957	No					Yes ³⁶	2009	Hengduanshan Mountain, Yunnan	27.50	99.00	Yes ³⁷	2014	Djibouti, Republic of Djibouti	11.57	43.15
Langat virus	1956	No					No					No				
Louping ill virus	1934	Yes ³⁸	1934	New York	40.71	-74.01	No					No				
Murray Valley encephalitis virus	1952	No					No					No				
Ntaya virus	1952	No					No					Yes ³⁹	1952	Bwamba county, Uganda	0.75	30.02
Omsk hemorrhagic fever virus	1948	No					No					No				
Powassan virus	1959	Yes ⁶⁰	1973	Middlesex County, New Jersey	40.54	-74.37	No					No				
Rio Bravo virus	1962	Yes ⁶¹	1962	Dallas city, Texas	32.78	-96.80	No					No				
Saint Louis encephalitis virus	1933	Yes ⁶²	1933	St. Louis City, Missouri	38.63	-90.20	No					No				
Tembusu virus	1975	No					Yes ⁶³	2013	Shandong	36.40	118.77	No				
Tick-borne encephalitis virus	1938	Yes ^{*64}	1979	Cleveland, Ohio	41.51	-81.69	Yes ⁶⁵	1956	Bali village, Wuchang, Heilongjiang	44.91	127.16	No				
Uganda S virus	1952	No					No					Yes ⁶⁶	1952	Bwamba county, Uganda	0.75	30.02
Usutu virus	2009	No					No					No				
Wesselsbron virus	1957	No					No					Yes ⁶⁷	1957	Lake Simbu region, Maputaland, KwaZulu-Natal, South Africa	-27.36	32.32
West Nile virus	1940	Yes ⁶⁸	2001	New York	40.71	-74.01	Yes ⁶⁹	2013	Jiashi County, Xinjiang	39.58	77.18	Yes ⁷⁰	1940	Omogo, West Nile district, Uganda	0.42	33.21
Yellow fever virus	1901	Yes ⁷¹	1904	Laredo, Texas	27.51	-99.51	Yes ^{*72}	2016	Beijing	40.01	116.41	Yes ⁷³	1928	Larteh, Ghana	5.94	-0.07
Zika virus	1952	Yes ^{*74}	2011	Northern Colorado	39.55	-105.78	Yes ^{*75}	2016	Gan County, Ganzhou city, Jiangxi	25.86	115.02	Yes ⁷⁶	1952	Zika, Uganda	0.12	32.53
Hepacivirus C	1989	Yes ⁷⁷	1989	Emeryville, California	37.83	-122.29	Yes ⁷⁸	1990	Qidong county, Jiangsu	31.88	121.72	Yes ⁷⁹	1990	Johannesburg, South Africa	-26.20	27.90
Pegivirus C	1995	Yes ⁸⁰	1995	Chapel Hill, North Carolina; Rochester, Minnesota; Dallas,	35.91	-79.06	Yes ⁸¹	1996	Beijing	40.01	116.41	Yes ⁸⁰	1995	Cairo, Egypt	30.04	31.24

				Texas												
Pegivirus H	2015	Yes ⁸²	2015	New York city, New York	40.71	-74.01	Yes ⁸³	2018	Guangzhou, Guangdong	23.13	113.26	Yes ⁸⁴	2019	Ebolowa, Cameroon	2.92	11.15
Pestivirus A	1988	Yes ⁸⁵	1989	Whiteriver, Arizona	33.83	-109.97	No					Yes ⁸⁶	1988	Zambia	-13.13	27.85
Andes orthohantavirus	1996	No					No					No				
Bayou orthohantavirus	1995	Yes ⁸⁷	1995	Louisiana	30.98	-91.96	No					No				
Black creek canal orthohantavirus	1995	Yes ⁸⁸	1995	Miami-Dade County, Florida	25.76	-80.34	No					No				
Choclo orthohantavirus	2000	No					No					No				
Dobrava-Belgrade orthohantavirus	1992	No					No					No				
Hantaan orthohantavirus	1978	No					Yes ⁸⁹	1980	Zhejiang	29.14	119.79	No				
Laguna Negra orthohantavirus	1997	No					No					No				
Puumala orthohantavirus	1980	No					No					No				
Sangassou orthohantavirus	2010	No					No					Yes ⁹⁰	2010	Sangassou village, Macenta district, Forest Guinea	8.24	-9.32
Seoul orthohantavirus	1982	Yes ⁹¹	1987	Mississippi	32.57	-89.88	Yes ⁹²	1982	Jiangsu	33.14	119.79	Yes ⁹³	1986	Jos, Nigeria	9.90	8.86
Sin Nombre orthohantavirus	1993	Yes ⁹⁴	1993	New Mexico	34.52	-105.87	No					No				
Thailand orthohantavirus	2006	No					No					No				
Thottopalayam thottimvirus	2007	No					No					No				
Tula orthohantavirus	1996	No					No					No				
Orthohepevirus A	1983	Yes ^{*95}	1987	Los Angeles County, California	34.05	-118.24	Yes ⁹⁶	1989	Kashi county, Kashi city, Xinjiang	39.46	75.99	Yes ⁹⁷	1985	Medea town, Algeria	36.26	2.75
Orthohepevirus C	2018	No					Yes ⁹⁸	2018	Hong Kong	22.40	114.11	No				
Crimean-Congo haemorrhagic fever orthonairovirus	1967	No					Yes ⁹⁹	1985	Bachu, southern Xinjiang	39.79	78.55	Yes ¹⁰⁰	1967	Kisangani, Tshopo province, Democratic Republic of the Congo	0.53	25.19
Dugbe orthonairovirus	1969	No					No					Yes ¹⁰¹	1969	Ibadan, Nigeria	7.35	3.88
Nairobi sheep disease orthonairovirus	1969	No					No					Yes ¹⁰²	1991	Mombasa; Malindi; and Kilifi, Coast Province, Kenya	-3.34	39.57
Thiafora orthonairovirus	1989	No					No					No				
Influenza A virus	1933	Yes ¹⁰³	1935	Philadelphi, Pennsylvania	39.95	-75.17	Yes ¹⁰⁴	1950	Beijing	40.01	116.41	Yes ¹⁰⁵	1951	Johannesburg, South Africa and Cape Town, South Africa	-26.20	27.90
Influenza B virus	1940	Yes ¹⁰⁶	1940	Irvington village, Greenburgh town,	41.03	-73.87	Yes ¹⁰⁷	1957	Beijing	40.01	116.41	Yes ¹⁰⁸	1970	Arusha, Arusha Region, Tanzania	-3.37	36.69

				Westchester County, New York												
Influenza C virus	1950	Yes ¹⁰⁹	1950	Ann Arbor city, Michigan	42.28	-83.74	Yes ¹¹⁰	1957	Beijing	40.01	116.41	Yes ¹¹¹	1968	Johannesburg, South Africa	-26.20	27.90
Dhori thogotovirus	1985	No					No					No				
Thogoto thogotovirus	1969	No					No					Yes ¹⁰¹	1969	Ibadan, Nigeria	7.35	3.88
Avian orthoavulavirus 1	1943	Yes ¹¹²	1943	Washington, D. C.	38.91	-77.04	No					No				
Hendra henipavirus	1995	No					No					No				
Nipah henipavirus	1999	No					No					No				
Canine morbillivirus	1955	Yes ¹¹³	1955	Buffalo, New York	42.89	-78.88	No					No				
Measles morbillivirus	1911	Yes ¹¹⁴	1911	Washington, D. C.	38.91	-77.04	Yes ¹¹⁵	1958	Beijing	40.01	116.41	Yes ¹¹⁶	1963	Dakar, Senegal	14.72	-17.47
Human respirovirus 1	1958	Yes ¹¹⁷	1958	Washington, D. C.	38.91	-77.04	Yes ¹¹⁸	1964	Zhejiang	29.14	119.79	Yes ¹¹⁹	1963	Cape Town, Western Cape Province, South Africa	-33.90	18.57
Human respirovirus 3	1958	Yes ¹¹⁷	1958	Washington, D. C.	38.91	-77.04	Yes ¹²⁰	1987	Guangzhou, Guangdong	23.13	113.26	Yes ¹¹⁹	1963	Cape Town, Western Cape Province, South Africa	-33.90	18.57
Achimota pararubulavirus 2	2013	No					No					Yes ¹²¹	2013	Volta, Ghana	6.05	0.37
Human orthorubulavirus 2	1956	Yes ¹²²	1956	Cincinnati, Ohio	39.10	-84.51	Yes ¹²³	1975	Nanjing, Jiangsu	31.95	118.78	Yes ¹²⁴	1967	Accra, Ghana	5.60	-0.19
Human orthorubulavirus 4	1960	Yes ¹²⁵	1960	Bethesda, Maryland	38.98	-77.09	Yes ¹²⁶	2005	Hong Kong	22.40	114.11	Yes ¹²⁷	2010	Ndiop village, Sine Saloum region, Senegal	15.18	-16.74
Mammalian orthorubulavirus 5	1959	Yes ¹²⁸	1959	Stanford, California	37.42	-122.17	No					No				
Menangle pararubulavirus	1998	No					No					No				
Mumps orthorubulavirus	1934	Yes ¹²⁹	1934	Nashville, Tennessee	36.16	-86.78	Yes ¹³⁰	1958	Beijing	40.01	116.41	Yes ¹³¹	1955	Johannesburg, South Africa	-26.20	27.90
Simian orthorubulavirus	1968	No					No					No				
Sosuga pararubulavirus	2014	No					No					Yes ¹³²	2014	-	3.76	32.82
Tioman pararubulavirus	2007	No					No					No				
Bunyamwera orthobunyavirus	1946	Yes ¹³³	1964	Southern Florida	26.92	-81.21	No					Yes ¹³⁴	1946	Bwamba County, Uganda	0.75	30.02
Bwamba orthobunyavirus	1941	No					No					Yes ¹³⁵	1941	Bwamba county, Western Province of Uganda	0.75	30.02
California encephalitis orthobunyavirus	1952	Yes ¹³⁶	1952	Kern county, California	35.49	-118.86	Yes ¹³⁷	1984	Longhua, Shanghai	31.22	121.43	Yes ¹³⁸	1961	Uganda	1.37	32.29
Caraparu orthobunyavirus	1961	No					No					No				

Catu orthobunyavirus	1961	No					No					No				
Guama orthobunyavirus	1961	No					No					No				
Guaroa orthobunyavirus	1959	No					No					No				
Kairi orthobunyavirus	1967	No					No					No				
Madrid orthobunyavirus	1964	No					No					No				
Marituba orthobunyavirus	1961	No					No					No				
Nyando orthobunyavirus	1965	No					No					Yes ¹³⁹	1965	Kisumu, Kenya	-0.09	34.77
Oriboca orthobunyavirus	1961	No					No					No				
Oropouche orthobunyavirus	1961	No					No					No				
Patois orthobunyavirus	1972	No					No					No				
Shuni orthobunyavirus	1975	No					No					Yes ¹⁴⁰	1975	Ibadan, Nigeria	7.38	3.95
Tacaiuma orthobunyavirus	1967	No					No					No				
Wyeomyia orthobunyavirus	1965	No					No					No				
Candiru phlebovirus	1983	No					No					No				
Punta Toro phlebovirus	1970	No					No					No				
Rift Valley fever phlebovirus	1931	No					Yes* ¹⁴¹	2016	Beijing	40.01	116.41	Yes ¹⁴²	1931	Rift Valley of Kenya Colony	-0.28	36.07
Sandfly fever Naples phlebovirus	1944	No					No					Yes ¹⁴³	1951	Cairo, Egypt	30.04	31.24
Heartland banyangvirus	2012	Yes ¹⁴⁴	2012	Andrew and Nodaway Counties, Missouri	39.82	-94.59	No					No				
Huaiyangshan banyangvirus	2011	No					Yes ¹⁴⁵	2011	Huaiyangshan	31.37	115.39	No				
Uukuniemi phlebovirus	1970	No					No					No				
Human picobirnavirus	1988	Yes ¹⁴⁶	1993	Atlanta, Georgia	33.75	-84.39	Yes ¹⁴⁷	2000	Lulong County, Hebei	39.94	116.94	No				
Equine rhinitis A virus	1962	No					No					No				
Foot-and-mouth disease virus	1965	No					Yes ¹⁴⁸	1999	Guangzhou	23.13	113.26	Yes ¹⁴⁹	2002	Alexandria Governorate, Egypt	30.74	29.74
Cardiovirus A	1947	Yes ¹⁵⁰	1961	New Orleans, Louisiana	29.95	-90.07	Yes ¹⁵¹	2015	Changchun, Jilin	43.87	125.34	Yes ¹⁵²	1948	Entebbe, Uganda	0.05	32.46
Cardiovirus B	1963	Yes ¹⁵³	2007	San Diego, California	32.72	-117.16	Yes ¹⁵⁴	2009	Lanzhou, Gansu	36.06	103.79	Yes ¹⁵⁵	2009	Cameroon	5.03	12.40
Cosavirus A	2008	No					Yes ¹⁵⁶	2010	Shanghai	31.23	121.47	Yes ¹⁵⁷	2012	Maiduguri, Borno State, Nigeria	11.83	13.15
Cosavirus B	2008	No					Yes ¹⁵⁸	2016	Zhenjiang, Jiangsu	32.19	119.43	No				

Cosavirus D	2008	No					No					Yes ¹⁵⁷	2012	Maiduguri, Borno State, Nigeria	11.83	13.15
Cosavirus E	2008	No					No					Yes ¹⁵⁷	2012	Maiduguri, Borno State, Nigeria	11.83	13.15
Cosavirus F	2012	No					No					No				
Enterovirus A	1949	Yes ¹⁵⁹	1949	New York	43.30	-74.22	Yes ¹⁶⁰	1985	Tianjin	39.34	117.36	Yes ¹³¹	1955	Johannesburg, South Africa	-26.20	27.90
Enterovirus B	1949	Yes ¹⁵⁹	1949	Wilmington	39.74	-75.54	Yes ¹⁶¹	1960	Fuzhou, Fujian	26.07	119.30	Yes ¹⁶²	1953	Middelburg, Transvaal, South Africa	-25.77	29.46
Enterovirus C	1909	Yes ¹⁶³	1909	New York city, New York	40.71	-74.01	Yes	1941	Beijing	39.90	116.41	Yes ¹⁶⁴	1933	Monrovia, Liberia	6.29	-10.76
Enterovirus D	1967	Yes ¹⁶⁵	1967	Berkeley, California	37.87	-122.27	Yes ¹⁶⁶	1979	Shanghai	31.23	121.47	Yes ¹⁶⁷	1973	Morocco	31.79	-7.09
Enterovirus E	1961	Yes ¹⁶⁸	1961	Denver, Colorado	39.74	-104.99	No					No				
Enterovirus H	1965	No					No					No				
Rhinovirus A	1953	Yes ¹⁶⁹	1956	Baltimore, Maryland	39.29	-76.61	Yes ¹⁷⁰	1975	Guangzhou, Guangdong	23.13	113.26	Yes ¹⁷¹	1963	Cape Town, Western Cape Province, South Africa	-33.90	18.57
Rhinovirus B	1960	Yes ¹⁷²	1961	Chicago, Illinois	41.88	-87.63	Yes ¹⁷³	2008	Beijing	40.01	116.41	Yes ¹⁷⁴	2008	Pretoria, Gauteng province, South Africa	-25.75	28.23
Rhinovirus C	2006	Yes ¹⁷⁵	2006	New York city, New York	40.71	-74.01	Yes ¹⁷⁶	2007	Hong Kong	22.40	114.11	Yes ¹⁷⁴	2008	Pretoria, Gauteng province, South Africa	-25.75	28.23
Erbovirus A	2005	No					No					No				
Hepatovirus A	1973	Yes ¹⁷⁷	1973	Bethesda, Maryland	38.98	-77.09	Yes ¹⁷⁸	1978	Shanghai	31.23	121.47	Yes ¹⁷⁹	1977	Dakar, Senegal	14.72	-17.47
Aichivirus A	1991	Yes ¹⁸⁰	2013	Cincinnati, Ohio	39.10	-84.51	Yes ¹⁸¹	2009	Shanghai	31.23	121.47	Yes ¹⁸²	2008	Monastir, Tunisia	35.77	10.82
Parechovirus A	1958	Yes ¹⁸³	1958	Cincinnati, Ohio	39.10	-84.51	Yes ¹⁸⁴	2009	Shanghai	31.23	121.47	Yes ¹⁵⁷	2012	Ouagadougou, Burkina Faso	12.24	-1.56
Parechovirus B	2003	No					No					No				
Salivirus A	2009	Yes ¹⁸⁵	2009	Northern California	38.84	-120.90	Yes ¹⁸⁶	2010	Shanghai	31.23	121.47	Yes ¹⁸⁷	2009	Maiduguri, Borno State, Nigeria	11.83	13.15
Avian metapneumovirus	2011	Yes ¹⁸⁸	2011	Memphis, Tennessee	35.15	-90.05	No					No				
Human metapneumovirus	2001	Yes ¹⁸⁹	2003	Rochester, New York	43.16	-77.61	Yes ¹⁹⁰	2003	Hong Kong	22.40	114.11	Yes ¹⁹¹	2003	Johannesburg, South Africa	-26.20	27.90
Human orthopneumovirus	1957	Yes ¹⁹²	1957	Baltimore, Maryland	39.29	-76.61	Yes ¹⁹³	1975	Kunming, Yunnan	25.07	102.68	Yes ¹⁹⁴	1965	Cape Town, Western Cape Province, South Africa	-33.90	18.57
Colorado tick fever virus	1946	Yes ¹⁹⁵	1946	Denver, Colorado	39.74	-104.99	Yes ¹⁹⁶	1996	Nanjing, Jiangsu	31.95	118.78	No				
Eyach virus	1980	No					No					No				
Corriparta virus	1967	No					No					No				
Great Island virus	1963	No					No					No				

Lebombo virus	1975	No					No					Yes ¹⁴⁰	1975	Ibadan, Nigeria	7.38	3.95
Orungo virus	1976	No					No					Yes ¹⁹⁷	1976	Ibadan, Nigeria	7.38	3.95
Mammalian orthoreovirus	1954	Yes ¹⁹⁸	1954	Cincinnati, Ohio	39.10	-84.51	Yes ¹⁹⁹	1995	Xuzhou, Jiangsu	34.26	117.19	Yes ²⁰⁰	1963	Johannesburg, South Africa	-26.20	27.90
Nelson Bay orthoreovirus	2007	No					Yes* ²⁰¹	2009	Hong Kong	22.40	114.11	No				
Rotavirus A	1973	Yes ²⁰²	1976	Washington, D. C.	38.90	-77.04	Yes ²⁰³	1979	Beijing	40.01	116.41	Yes ¹⁹⁷	1976	Johannesburg, South Africa	-26.20	27.90
Rotavirus B	1984	Yes ²⁰⁴	1985	Baltimore, Maryland	39.29	-76.61	Yes ²⁰⁵	1984	Jinzhou, Liaoning	41.10	121.13	Yes ²⁰⁶	1987	Kenya	-0.02	37.91
Rotavirus C	1986	Yes ²⁰⁷	1995	Providence, Rhode Island	41.82	-71.41	Yes ²⁰⁸	1999	Beijing	40.01	116.41	Yes ²⁰⁹	1999	Pretoria, Gauteng province, South Africa	-25.75	28.23
Rotavirus H	1987	No					Yes ²¹⁰	1987	Huaihua, Hunan Province	27.55	109.96	No				
Banna virus	1990	No					Yes ²¹¹	1990	Xishuangbanna, Yunnan Province	21.90	100.80	No				
Primate T-lymphotropic virus 1	1980	Yes ²¹²	1980	Bethesda, Maryland	38.98	-77.09	Yes ²⁰⁵	1984	Shenyang, Liaoning	41.80	123.38	Yes ²¹³	1984	Ibadan, Nigeria	7.38	3.95
Primate T-lymphotropic virus 2	1982	Yes ²¹⁴	1982	Seattle, Washington	47.61	-122.33	Yes ²¹⁵	2013	Henan and Hubei	32.21	112.96	Yes ²¹⁶	1991	Franceville, Gabon	-1.63	13.60
Primate T-lymphotropic virus 3	2005	No					No					Yes ²¹⁷	2005	Océan department, South Province, Cameroon	2.50	10.50
Human immunodeficiency virus 1	1983	Yes ²¹⁸	1984	Washington, D. C.	38.90	-77.04	Yes ²¹⁹	1986	Hong Kong	22.40	114.11	Yes ²²⁰	1984	Kisangani, Tshopo province, Democratic Republic of the Congo	0.53	25.19
Human immunodeficiency virus 2	1986	Yes* ²²¹	1988	New Jersey	40.06	-74.41	Yes* ²²²	2000	Fuzhou, Fujian	26.07	119.30	Yes ²²³	1986	Dakar, Senegal	14.72	-17.47
Simian immunodeficiency virus	1992	Yes ²²⁴	1992	Atlanta, Georgia	33.75	-84.39	No					Yes ²¹⁷	2005	Cameroon	7.37	12.35
Central chimpanzee simian foamy virus	2012	No					No					Yes ²²⁵	2012	Near Dja Nature Reserves, Southern Cameroon	4.50	13.50
Eastern chimpanzee simian foamy virus	1971	No					No					Yes ²²⁶	1971	Kenya	-0.02	37.91
Grivet simian foamy virus	1997	No					No					No				
Guenon simian foamy virus	2012	No					No					Yes ²²⁵	2012	Near Iolodrof, Southern Cameroon	3.23	10.73
Taiwanese macaque simian foamy virus	2002	No					Yes ²²⁷	2012	Yunnan	25.18	101.86	No				
Australian bat lyssavirus	1998	No					No					No				
Duvenhage lyssavirus	1971	No					No					Yes ²²⁸	1971	Pretoria, Gauteng province, South Africa	-25.75	28.23
European bat lyssavirus	1989	No					No					No				
European bat 2	1986	No					No					No				

lyssavirus																
Irkut lyssavirus	2013	No					Yes ²²⁹	2013	Tonghua county, Jilin	41.68	125.76	No				
Mokola lyssavirus	1972	No					No					Yes ²³⁰	1972	Ibadan, Nigeria	7.38	3.95
Rabies lyssavirus	1903	Yes ²³¹	1910	Southern California	34.57	-116.76	Yes ²³²	1981	Beijing	40.01	116.41	Yes ²³³	1933	Carolina, Mpumalanga, South Africa	-26.07	30.12
Bas-Congo tibrovirus	2012	No					No					Yes ²³⁴	2012	Mangala village, Boma Bunu Health Zone, Democratic Republic of Congo (DRC)	-4.04	21.76
Ekpoma Yestibrovirus	2015	No					No					Yes ²³⁵	2015	Irrua, Edo State, Nigeria	6.74	6.22
Ekpoma 2 tibrovirus	2015	No					No					Yes ²³⁵	2015	Irrua, Edo State, Nigeria	6.74	6.22
Alagoas vesiculovirus	1967	No					No					No				
Chandipura vesiculovirus	1967	No					No					No				
Cocal vesiculovirus	1964	No					No					No				
Indiana vesiculovirus	1958	Yes ²³⁶	1958	Beltsville, Prince George's County, Maryland	39.05	-76.90	No					No				
Isfahan vesiculovirus	1977	No					No					No				
Maraba vesiculovirus	1984	No					No					No				
New Jersey vesiculovirus	1950	Yes ²³⁷	1950	Madison, Wisconsin	43.07	-89.40	No					No				
Piry vesiculovirus	1974	No					No					No				
Barmah Forest virus	1986	No					No					No				
Chikungunya virus	1956	Yes ^{*238}	2006	Minnesota	46.44	-93.36	Yes ⁵¹	1967	Southwest Taiwan	23.06	120.59	Yes ²³⁹	1956	Newala district, Tanzania	-10.64	39.24
Eastern equine encephalitis virus	1938	Yes ²⁴⁰	1938	Southwestern Massachusetts	42.19	-73.09	No					No				
Everglades virus	1970	Yes ²⁴¹	1970	Homestead, Florida	25.47	-80.48	No					No				
Getah virus	1966	No					Yes ²⁴²	1992	Baoting County, Hainan	18.98	109.83	No				
Highlands J virus	2000	Yes ²⁴³	2000	Florida	27.66	-81.52	No					No				
Madariaga virus	1972	No					No					No				
Mayaro virus	1957	Yes ^{*244}	1999	Ohio	40.42	-82.91	No					No				
Mosso das Pedras virus	2013	No					No					No				

Mucambo virus	1965	No					No					No				
Ndumu virus	1961	No					No					Yes ²⁴⁵	1961	Ndumu, Maputaland, KwaZulu-Natal, South Africa	-26.93	32.26
Onyong-nyong virus	1961	No					No					Yes ²⁴⁶	1961	Entebbe, Uganda	0.05	32.46
Pixuna virus	1991	No					No					No				
Rio Negro virus	1993	No					No					No				
Ross River virus	1972	No					Yes ²⁴⁷	1999	Hainan	19.16	109.94	No				
Semliki Forest virus	1979	No					No					Yes ²⁴⁸	1990	Bangui, Central Africa	4.36	18.58
Sindbis virus	1955	No					No					Yes ²⁴⁹	1955	Cairo, Egypt	30.04	31.24
Tonate virus	1976	No					No					No				
Una virus	1963	No					No					No				
Venezuelan equine encephalitis virus	1943	Yes ²⁵⁰	1943	New York	40.71	-74.01	No					No				
Western equine encephalitis virus	1938	Yes ²⁴⁰	1938	Fresno, California	36.75	-119.77	No					No				
Whataroa virus	1964	No					No					No				
Rubella virus	1942	Yes ²⁵¹	1942	Washington, D. C.	38.91	-77.04	Yes ²⁵²	1979	Hangzhou, Zhejiang	29.87	119.33	Yes ²⁵³	1963	Cape Town, Western Cape Province, South Africa	-33.90	18.57
Hepatitis delta virus	1977	Yes ²⁵⁴	1979	New Jersey	40.06	-74.41	Yes ²⁵⁵	1980	Taipei, Taiwan	24.96	121.51	Yes ²⁵⁶	1984	Harare, Zimbabwe	-17.83	31.03

4 Notes: Yes denotes the virus was ever discovered from the region; * denotes the virus was ever discovered from the region, but imported from other regions; No denotes the
5 virus species has never been discovered from the region; The lat and long denote the coordinate of discovery points or centroids of polygons

6 Table 2S Resolution and covered grid cells for virus discovery data

		Polygon data			Point data	Total
		Country level	State/Province level	City/County level		
United States	Virus counts	NA	14 (14.7%)	11 (11.6%)	70 (73.7%)	95
	Gridded cell counts	NA	189	12	72*	273
China	Virus counts	NA	22 (27.5%)	47 (58.7%)	11 (13.8%)	80
	Gridded cell counts	NA	161	70	12*	243
	Virus counts	7 (6.5)	5 (4.7%)	15 (14.0%)	80 (74.8%)	107
Africa	Gridded cell counts	307	22	17	80	426

7 *Grid cell counts here include viruses first detected in multiple points from the literature, NA, not applicable

8 Table 3S Model parameters

Model	Tree complexity	Learning rate	Bag fraction	No. of trees
United States	2	0.0020	0.5	1430
China	2	0.0035	0.5	1473
Africa	2	0.0030	0.5	1446

9 Table 4S Model validation statistics for analyses in three regions

Model	% of deviance explained (95% quantiles)	ICC (95% quantiles)
United States	50.5% (44.3%–56.8%)	0.66 (0.60–0.70)
China	42.0% (32.4%–50.8%)	0.52 (0.41–0.60)
Africa	42.4% (34.2%–50.0%)	0.51 (0.44–0.62)

10 ICC, intraclass correlation coefficient

11 *Supplementary Figures*

12
13 **Figure 1S Time lag of human-infective RNA virus discovery between the three regions and the world.** A, United States. B, China. C, Africa. The blue dots represent the
14 original discovery year of each virus in the world; the red dots represent the discovery year of each virus in three regions; and the segments between them represent the time
15 lag.

Figure 2S Partial dependence plots showing the influence on human-infective RNA virus discovery for all predictors in the United States. Partial dependence plots show the effect of an individual explanatory factor over its range on the response after factoring out other explanatory factors. Fitted lines represent the median (black) and 95% quantiles (coloured) based on 1000 replicated models. Y axes are centred around the mean without scaling. X axes show the range of sampled values of explanatory factors.

Figure 3S Partial dependence plots showing the influence on human-infective RNA virus discovery for all risk factors in China. Partial dependence plots show the effect of an individual explanatory factor over its range on the response after factoring out other explanatory factors. Fitted lines represent the median (black) and 95% quantiles (coloured) based on 1000 replicated models. Y axes are centred around the mean without scaling. X axes show the range of sampled values of explanatory factors.

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Figure 4S Partial dependence plots showing the influence of human-infective RNA virus discovery for all risk factors in Africa. Partial dependence plots show the effect of an individual explanatory factor over its range on the response after factoring out other explanatory factors. Fitted lines represent the median (black) and 95% quantiles (coloured) based on 1000 replicated models. Y axes are centred around the mean without scaling. X axes show the range of sampled values of explanatory factors.

Figure 5S Moran's I across different spherical distances. A, United States; B, China; C, Africa. The solid line and dots represented the median Moran's I value, and the grey area represented its 95% quantiles generated from 1000 samples (Blue: Raw virus data) or replicate BRT models (Red: Model residuals). We used the fixed spherical distance as the neighbourhood weights—as there is no general consensus for selecting cut-off values, we chose spherical distances ranging from one time to fifteen times of distance of 1° grid cell at the equator, i.e. 110km to 1650km, considering the area of three regions. Our BRT models reduced Moran's I value from a range of 0.19–0.50 for the raw virus data to 0.009–0.04 for the model residuals in the United States A), 0.11–0.45 to -0.01–0.09 in China B), 0.05–0.31 to -0.004–0.15 in Africa C), suggesting that BRT models with 33 predictors have adequately accounted for spatial autocorrelations in the raw virus data in all three regions.

Figure 6S Distribution maps for 32 predictors in 2015 in the United States. The values of these explanatory variables and latitude in each grid cell were used to predict the virus discovery in the corresponding grid cell in the United States in 2010–2019. Explanatory variables were log transformed where necessary to get better visualization, not meaning they entered the model by logged values.

50
51 **Figure 6S Continued**

Figure 7S Distribution maps for 32 predictors in 2015 in China. The values of these explanatory variables and latitude in each grid cell were used to predict the virus discovery in the corresponding grid cell in China in 2010–2019. Explanatory variables were log transformed where necessary to get better visualization, not meaning they entered the model by logged values.

57
58 **Figure 7S Continued**

Figure 8S Distribution maps for 32 predictors in 2015 in Africa. The values of these explanatory variables and latitude in each grid cell were used to predict the virus discovery in the corresponding grid cell in Africa in 2010–2019. Explanatory variables were log transformed where necessary to get better visualization, not meaning they entered the model by logged values.

63
64 **Figure 8S Continued**

Figure 9S Cumulative relative contribution of predictors to human-infective RNA virus discovery by group in each model of subgroups. Subgroup 1 represents viruses firstly discovered from the region (United States or Africa); Subgroup 2 represents viruses firstly discovered elsewhere in the world. The relative contributions of all explanatory factors sum to 100% in each model, and each colour represents the cumulative relative contribution of all explanatory factors within each group.

References

1. Barry M, Russi M, Armstrong L, et al. Brief report: treatment of a laboratory-acquired Sabia virus infection. *The New England journal of medicine* 1995; **333**(5): 294-6.
2. Buchmeier M, Adam E, Rawls WE. Serological evidence of infection by Pichinde virus among laboratory workers. *Infection and immunity* 1974; **9**(5): 821-3.
3. Buckley SM, Casals J. Lassa fever, a new virus disease of man from West Africa. 3. Isolation and characterization of the virus. *Am J Trop Med Hyg* 1970; **19**(4): 680-91.
4. Briese T, Paweska JT, McMullan LK, et al. Genetic detection and characterization of Lujo virus, a new hemorrhagic fever-associated arenavirus from southern Africa. *PLoS Pathog* 2009; **5**(5): e1000455.
5. Armstrong C, Lillie RD. Experimental Lymphocytic Choriomeningitis of Monkeys and Mice Produced by a Virus Encountered in Studies of the 1933 St. Louis Encephalitis Epidemic. *Public Health Reports (1896-1970)* 1934; **49**(35): 1019-27.
6. Georges AJ, Gonzalez JP, Abdul-Wahid S, Saluzzo JF, Meunier DM, McCormick JB. Antibodies to Lassa and Lassa-like viruses in man and mammals in the Central African Republic. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1985; **79**(1): 78-9.
7. Enserink M. Emerging diseases. New arenavirus blamed for recent deaths in California. *Science* 2000; **289**(5481): 842-3.
8. Oshiro LS, Haley CE, Roberto RR, et al. A 27-nm virus isolated during an outbreak of acute infectious nonbacterial gastroenteritis in a convalescent hospital: a possible new serotype. *Journal of Infectious Diseases* 1981; **143**(6): 791-5.
9. Xu AY, Pang QF, Qiu FX. Detection of astrovirus in faeces of infants with gastroenteritis in autumn [Article in Chinese]. *Journal of Medical Research* 1981; (06): 32.
10. Dowling JM, Wynne H. Role of Enteric Adenoviruses and Rotaviruses in Infantile Gastroenteritis. *Lancet* 1981; **2**(8241): 305-6.
11. Finkbeiner SR, Le BM, Holtz LR, Storch GA, Wang D. Detection of Newly Described Astrovirus MLB1 in Stool Samples from Children. *Emerging Infectious Diseases* 2009; **15**(3): 441-4.
12. Chu DK, Chin AW, Smith GJ, et al. Detection of novel astroviruses in urban brown rats and previously known astroviruses in humans. *The Journal of general virology* 2010; **91**(Pt 10): 2457-62.
13. Kapoor A, Li L, Victoria J, et al. Multiple novel astrovirus species in human stool. *Journal of General Virology* 2009; **90**: 2965-72.
14. Finkbeiner SR, Holtz LR, Jiang Y, et al. Human stool contains a previously unrecognized diversity of novel astroviruses. *Virology journal* 2009; **6**: 161.
15. Wang Y, Li Y, Jin Y, Li DD, Li X, Duan ZJ. Recently identified novel human astroviruses in children with diarrhea, China. *Emerg Infect Dis* 2013; **19**(8): 1333-5.
16. Finkbeiner SR, Li Y, Ruone S, et al. Identification of a novel astrovirus (astrovirus VA1) associated with an outbreak of acute gastroenteritis. *Journal of virology* 2009; **83**(20): 10836-9.
17. Tao Z, Wang H, Zhang W, Xu A. Novel astrovirus types circulating in Shandong Province (Eastern China) during 2016: A clinical and environmental surveillance. *J Clin Virol* 2019; **116**: 69-73.
18. Rott R, Herzog S, Fleischer B, et al. Detection of serum antibodies to Borna disease virus in patients with psychiatric disorders. *Science* 1985; **228**(4700): 755-6.
19. Chen CH, Chiu YL, Wei FC, et al. High seroprevalence of Borna virus infection in schizophrenic patients, family members and mental health workers in Taiwan. *Molecular psychiatry* 1999; **4**(1): 33-8.
20. Bode L, Riegel S, Lange W, Ludwig H. Human infections with Borna disease virus: Seroprevalence in patients with chronic diseases and healthy individuals. *Journal of medical virology* 1992; **36**(4): 309-15.
21. Kapikian AZ, Wyatt RG, Dolin R, Thornhill TS, Kalica AR, Chanock RM. Visualization by immune electron microscopy of a 27-nm particle associated with acute infectious nonbacterial gastroenteritis. *Journal of virology* 1972; **10**(5): 1075-81.
22. Fang ZY, Wen LY, Jin SJ, Zhao ZH. Norwalk-like virus infection found in diarrhea patients in China [Article in Chinese]. *Chinese Journal of Virology* 1995; **11**(03): 215-9.
23. Taylor MB, Schildhauer CI, Parker S, et al. Two successive outbreaks of SRSV-associated gastroenteritis in South Africa. *Journal of medical virology* 1993; **41**(1): 18-23.
24. Nakata S, Estes MK, Chiba S. Detection of Human Calicivirus Antigen and Antibody by Enzyme-Linked Immunosorbent Assays. *J Clin Microbiol* 1988; **26**(10): 2001-5.
25. Wolfaardt M, Taylor MB, Booysen HF, Engelbrecht L, Grabow WO, Jiang X. Incidence of human calicivirus and rotavirus infection in patients with gastroenteritis in South Africa. *Journal of medical virology* 1997; **51**(4): 290-6.
26. Smith AW, Berry ES, Skilling DE, et al. In vitro isolation and characterization of a calicivirus causing a vesicular disease of the hands and feet. *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America* 1998; **26**(2): 434-9.

27. Hamre D, Procknow JJ. A new virus isolated from the human respiratory tract. *Proceedings of the Society for Experimental Biology and Medicine Society for Experimental Biology and Medicine* 1966; **121**(1): 190-3.
28. Virus Research Group of Kun Number 323 Unit TCPsLA. Isolation, identification and serological studies of a coronavirus strain [Article in Chinese]. *Acta Microbiologica Sinica* 1975; **15**(03): 231-5+62.
29. Hays JP, Myint SH. PCR sequencing of the spike genes of geographically and chronologically distinct human coronaviruses 229E. *J Virol Methods* 1998; **75**(2): 179-93.
30. Esper F, Weibel C, Ferguson D, Landry ML, Kahn JS. Evidence of a novel human coronavirus that is associated with respiratory tract disease in infants and young children. *J Infect Dis* 2005; **191**(4): 492-8.
31. Chan KH, Cheng VC, Woo PC, et al. Serological responses in patients with severe acute respiratory syndrome coronavirus infection and cross-reactivity with human coronaviruses 229E, OC43, and NL63. *Clinical and diagnostic laboratory immunology* 2005; **12**(11): 1317-21.
32. Smuts H, Workman L, Zar HJ. Role of human metapneumovirus, human coronavirus NL63 and human bocavirus in infants and young children with acute wheezing. *Journal of medical virology* 2008; **80**(5): 906-12.
33. McIntosh K, Dees JH, Becker WB, Kapikian AZ, Chanock RM. Recovery in tracheal organ cultures of novel viruses from patients with respiratory disease. *Proc Natl Acad Sci U S A* 1967; **57**(4): 933-40.
34. Venter M, Lassauniere R, Kresfelder TL, Westerberg Y, Visser A. Contribution of Common and Recently Described Respiratory Viruses to Annual Hospitalizations in Children in South Africa. *Journal of medical virology* 2011; **83**(8): 1458-68.
35. Esper F, Weibel C, Ferguson D, Landry ML, Kahn JS. Coronavirus HKU1 infection in the United States. *Emerging Infectious Diseases* 2006; **12**(5): 775-9.
36. Woo PC, Lau SK, Chu CM, et al. Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia. *Journal of virology* 2005; **79**(2): 884-95.
37. Bialek SR, Allen D, Alvarado-Ramy F, et al. First Confirmed Cases of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Infection in the United States, Updated Information on the Epidemiology of MERS-CoV Infection, and Guidance for the Public, Clinicians, and Public Health Authorities - May 2014. *Mmwr-Morbid Mortal W* 2014; **63**(19): 431-6.
38. Gao J, Song P. China upgrades surveillance and control measures of Middle East respiratory syndrome (MERS). *Bioscience trends* 2015; **9**(3): 203-4.
39. Abroug F, Slim A, Ouanes-Besbes L, et al. Family Cluster of Middle East Respiratory Syndrome Coronavirus Infections, Tunisia, 2013. *Emerging infectious diseases* 2014; **20**(9): 1527-30.
40. Charles M, Cdc. Severe acute respiratory syndrome (SARS) and coronavirus testing - United States, 2003 (Reprinted from MMWR, vol 52, pg 297-302, 2003). *Jama-J Am Med Assoc* 2003; **289**(17): 2203-6.
41. Peiris JS, Lai ST, Poon LL, et al. Coronavirus as a possible cause of severe acute respiratory syndrome. *Lancet* 2003; **361**(9366): 1319-25.
42. Chiu W-T, Huang J-S, Ho Y-S. Bibliometric analysis of Severe Acute Respiratory Syndrome-related research in the beginning stage. *Scientometrics* 2004; **61**(1): 69-77.
43. Miranda ME, White ME, Dayrit MM, Hayes CG, Ksiazek TG, Burans JP. Seroepidemiological study of filovirus related to Ebola in the Philippines. *Lancet* 1991; **337**(8738): 425-6.
44. Bowen ET, Lloyd G, Harris WJ, Platt GS, Baskerville A, Vella EE. Viral haemorrhagic fever in southern Sudan and northern Zaire. Preliminary studies on the aetiological agent. *Lancet* 1977; **1**(8011): 571-3.
45. Le Guenno B, Formenty P, Wyers M, Gounon P, Walker F, Boesch C. Isolation and partial characterisation of a new strain of Ebola virus. *Lancet* 1995; **345**(8960): 1271-4.
46. Johnson KM, Lange JV, Webb PA, Murphy FA. Isolation and partial characterisation of a new virus causing acute haemorrhagic fever in Zaire. *Lancet* 1977; **1**(8011): 569-71.
47. CDC. Imported case of Marburg hemorrhagic fever - Colorado, 2008. *MMWR Morb Mortal Wkly Rep* 2009; **58**(49): 1377-81.
48. Gear JS, Cassel GA, Gear AJ, et al. Outbreak of Marburg virus disease in Johannesburg. *British medical journal* 1975; **4**(5995): 489-93.
49. Smithburn KC, Paterson HE, Heymann CS, Winter PA. An agent related to Uganda S virus from man and mosquitoes in South Africa. *South African medical journal = Suid-Afrikaanse tydskrif vir geneeskunde* 1959; **33**: 959-62.
50. Lavinder CH, Francis E. The Etiology of Dengue. An Attempt to Produce the Disease in the Rhesus Monkey by the Inoculation of Defibrinated Blood. *The Journal of Infectious Diseases* 1914; **15**(2): 341-6.
51. Clarke EJ, Jr., Sutor EC, Jr., Jenkin HM. A serologic survey for arbovirus antibodies in inhabitants of a southwest Taiwan village. *Tropical and geographical medicine* 1967; **19**(4): 326-32.
52. Edington AD. "Dengue " as seen in the Recent Epidemic in Durban. *J Med Assoc S Africa* 1927; **1**(17): 446-8.
53. Pina FP, Merikangas UR. Japanese B-Encephalitis in an American Soldier Returning from Korea. *New England Journal of Medicine* 1953; **249**(13): 531-2.

54. Yen CH. Isolation of a Virus from an Acute Encephalitis Case in Peiping. *Proceedings of the Society for Experimental Biology and Medicine* 1941; **46**(4): 609-11.
55. Simon-Loriere E, Sall AA. Autochthonous Japanese Encephalitis with Yellow Fever Coinfection in Africa. *New England Journal of Medicine* 2017; **376**(15): 1483-5.
56. Wang J, Zhang H, Fu S, et al. Isolation of kysanur forest disease virus from febrile patient, yunnan, china. *Emerg Infect Dis* 2009; **15**(2): 326-8.
57. Andayi F, Charrel RN, Kieffer A, et al. A Sero-epidemiological Study of Arboviral Fevers in Djibouti, Horn of Africa. *PLoS neglected tropical diseases* 2014; **8**(12).
58. Rivers TM, Schwentker FF. Louping Ill in Man. *The Journal of experimental medicine* 1934; **59**(5): 669-85.
59. Smithburn KC. Neutralizing antibodies against certain recently isolated viruses in the sera of human beings residing in East Africa. *Journal of immunology* 1952; **69**(2): 223-34.
60. Goldfield M, Austin SM, Black HC, Taylor BF, Altman R. A non-fatal human case of Powassan virus encephalitis. *Am J Trop Med Hyg* 1973; **22**(1): 78-81.
61. Sulkin SE, Burns KF, Shelton DF, Wallis C. Bat salivary gland virus: infections of man and monkey. *Texas reports on biology and medicine* 1962; **20**: 113-27.
62. Webster LT, Fite GL. A Virus Encountered in the Study of Material from Cases of Encephalitis N the St. Louis and Kansas City Epidemics of 1933. *Science* 1933; **78**(2029): 463-5.
63. Tang Y, Gao X, Diao Y, et al. Tembusu virus in human, China. *Transboundary and emerging diseases* 2013; **60**(3): 193-6.
64. Cruse RP, Rothner AD, Erenberg G, Calisher CH. Central European tick-borne encephalitis: an Ohio case with a history of foreign travel. *American journal of diseases of children (1960)* 1979; **133**(10): 1070-1.
65. Wang WS, Zhao CL. Isolation and identification of forest encephalitis virus [Article in Chinese]. *Journal of Harbin Medical University* 1956; (02): 44-9.
66. Dick GW, Haddow AJ. Uganda S virus; a hitherto unrecorded virus isolated from mosquitoes in Uganda. I. Isolation and pathogenicity. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1952; **46**(6): 600-18.
67. Smithburn KC, Kokernot RH, Weinbren MP, De Meillon B. Studies on arthropod-borne viruses of Tongaland. IX. Isolation of Wesselsbron virus from a naturally infected human being and from Aedes (Banksinella) circumluteolus Theo. *The South African journal of medical sciences* 1957; **22**(2-3): 113-20.
68. Nash D, Mostashari F, Fine A, et al. The outbreak of West Nile virus infection in the New York City area in 1999. *New Engl J Med* 2001; **344**(24): 1807-14.
69. Li XL, Fu SH, Liu WB, et al. West nile virus infection in Xinjiang, China. *Vector Borne Zoonotic Dis* 2013; **13**(2): 131-3.
70. Smithburn KC, Hughes TP, Burke AW, Paul JH. A Neurotropic Virus Isolated from the Blood of a Native of Uganda. *The American Journal of Tropical Medicine and Hygiene* 1940 **s1-20**(4): 471 - 92.
71. GUITERAS GM. THE YELLOW FEVER EPIDEMIC OF 1903 AT LAREDO, TEXAS. *Jama* 1904; **XLIII**(2): 115-21.
72. Chen J, Lu H. Yellow fever in China is still an imported disease. *Bioscience trends* 2016; **10**(2): 158-62.
73. Stokes A, Bauer JH, Hudson NP. THE TRANSMISSION OF YELLOW FEVER TO MACACUS RHESUS: PRELIMINARY NOTE. *Journal of the American Medical Association* 1928; **90**(4): 253-4.
74. Foy BD, Kobylinski KC, Chilson Foy JL, et al. Probable non-vector-borne transmission of Zika virus, Colorado, USA. *Emerg Infect Dis* 2011; **17**(5): 880-2.
75. Sun H, Jia FJ, Huang BC. Research progress and epidemic situation of the Zika Virus [Article in Chinese]. *Chin J Diagnostics (Electronic Edition)* 2016; **04**(01): 66-9.
76. Dick GW. Zika virus. II. Pathogenicity and physical properties. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1952; **46**(5): 521-34.
77. Choo QL, Kuo G, Weiner AJ, Overby LR, Bradley DW, Houghton M. Isolation of a cDNA clone derived from a blood-borne non-A, non-B viral hepatitis genome. *Science* 1989; **244**(4902): 359-62.
78. Xu Z, Shen FM, Xu ZY, Huang QS. HCV infection and primary liver cell cancer [Article in Chinese]. *Tumor (Shanghai)* 1990; **10**(03): 115-05.
79. Kew MC, Houghton M, Choo QL, Kuo G. Hepatitis C virus antibodies in southern African blacks with hepatocellular carcinoma. *Lancet* 1990; **335**(8694): 873-4.
80. Simons JN, Leary TP, Dawson GJ, et al. Isolation of Novel Virus-Like Sequences Associated with Human Hepatitis. *Nat Med* 1995; **1**(6): 564-9.
81. Wang Y, Okamoto H, An P, Chen HS, Liu YL, Wang FS. Infection of hepatitis G virus among blood donors in China [Article in Chinese]. *Journal of Beijing Medical University* 1996; **28**(02): 97.
82. Kapoor A, Kumar A, Simmonds P, et al. Virome Analysis of Transfusion Recipients Reveals a Novel Human Virus That Shares Genomic Features with Hepaciviruses and Pegiviruses. *mBio* 2015; **6**(5): e01466-15.

83. Wang H, Wan Z, Xu R, et al. A Novel Human Pegivirus, HPgV-2 (HHpgV-1), Is Tightly Associated With Hepatitis C Virus (HCV) Infection and HCV/Human Immunodeficiency Virus Type 1 Coinfection. *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America* 2018; **66**(1): 29-35.
84. Rodgers MA, Holzmayer V, Vallari A, et al. Hepatitis C virus surveillance and identification of human pegivirus 2 in a large Cameroonian cohort. *Journal of viral hepatitis* 2019; **26**(1): 30-7.
85. Yolken R, Dubovi E, Leister F, Reid R, Almeida J, Santosh M. Infantile Gastroenteritis Associated with Excretion of Pestivirus Antigens. *Lancet* 1989; **1**(8637): 517-20.
86. Giangaspero M, Wellemans G, Vanopdenbosch E, Belloli A, Verhulst A. Bovine viral diarrhoea. *Lancet* 1988; **2**(8602): 110.
87. Morzunov SP, Feldmann H, Spiropoulou CF, et al. A newly recognized virus associated with a fatal case of hantavirus pulmonary syndrome in Louisiana. *Journal of virology* 1995; **69**(3): 1980-3.
88. Ravkov EV, Rollin PE, Ksiazek TG, Peters CJ, Nichol ST. Genetic and serologic analysis of Black Creek Canal virus and its association with human disease and Sigmodon hispidus infection. *Virology* 1995; **210**(2): 482-9.
89. Lee PW, Gajdusek DC, Gibbs CJ, Xu ZY. Aetiological relation between Korean haemorrhagic fever with renal syndrome in People's Republic of China. *Lancet* 1980; **1**(8172): 819-20.
90. Klempa B, Koivogui L, Sylla O, et al. Serological evidence of human hantavirus infections in Guinea, West Africa. *J Infect Dis* 2010; **201**(7): 1031-4.
91. Forthal DN, Bauer SP, McCormick JB. Antibody to hemorrhagic fever with renal syndrome viruses (Hantaviruses) in the United States. *American journal of epidemiology* 1987; **126**(6): 1210-3.
92. Song G, Qiu XZ, Ni DS, Zhao JN, Kong BX. Etiological studies of epidemic hemorrhagic fever. I. Virus isolation in Apodemus agrarius from non-endemic area and its antigenic characterization [Article in Chinese]. *Zhongguo yi xue ke xue yuan xue bao Acta Academiae Medicinae Sinicae* 1982; **4**(2): 73-7.
93. Tomori O, Morikawa S, Matsuura Y, Kitamura T. Antibody to Japanese strain of haemorrhagic fever with renal syndrome (HFRS) virus in Nigerian sera. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1986; **80**(6): 1008-9.
94. Nichol ST, Spiropoulou CF, Morzunov S, et al. Genetic identification of a hantavirus associated with an outbreak of acute respiratory illness. *Science* 1993; **262**(5135): 914-7.
95. Decock KM, Bradley DW, Sandford NL, Govindarajan S, Maynard JE, Redeker AG. Epidemic Non-a, Non-B Hepatitis in Patients from Pakistan. *Ann Intern Med* 1987; **106**(2): 227-30.
96. Huang RT, Wei J, Tian X, Li DR, Yin SR. Isolation of a small RNA virus from feces of a patient with enterically transmitted Non-A Non-B hepatitis in China [Article in Chinese]. *Journal of Academy of Military Medical Sciences* 1989; **13**(04): 273-7.
97. Belabbes EH, Bouguermouh A, Benatallah A, Illoul G. Epidemic Non-a, Non-B Viral-Hepatitis in Algeria - Strong Evidence for Its Spreading by Water. *Journal of medical virology* 1985; **16**(3): 257-63.
98. Sridhar S, Yip CCY, Wu S, et al. Rat Hepatitis E Virus as Cause of Persistent Hepatitis after Liver Transplant. *Emerg Infect Dis* 2018; **24**(12): 2241-50.
99. Yen YC, Kong LX, Lee L, et al. Characteristics of Crimean-Congo hemorrhagic fever virus (Xinjiang strain) in China. *Am J Trop Med Hyg* 1985; **34**(6): 1179-82.
100. Simpson DI, Knight EM, Courtois G, Williams MC, Weinbren MP, Kibukamusoke JW. Congo virus: a hitherto undescribed virus occurring in Africa. I. Human isolations--clinical notes. *East African medical journal* 1967; **44**(2): 86-92.
101. Causey OR, Kemp GE, Madbouly MH, Lee VH. Arbovirus surveillance in Nigeria, 1964-1967. *Bulletin de la Societe de pathologie exotique et de ses filiales* 1969; **62**(2): 249-53.
102. Morrill JC, Johnson BK, Hyams C, et al. Serological evidence of arboviral infections among humans of coastal Kenya. *The Journal of tropical medicine and hygiene* 1991; **94**(3): 166-8.
103. Francis T, Magill TP. IMMUNOLOGICAL STUDIES WITH THE VIRUS OF INFLUENZA. *The Journal of experimental medicine* 1935; **62**(4): 505-16.
104. Chang HT, Chiang YT. Studies on an epidemic of influenza in Peking. *Chin Med J* 1950; **68**(7-8): 185-92.
105. Isaacs A, Andrewes CH. The Spread of Influenza. Evidence from, 1950-1951. *British medical journal* 1951: 921-7.
106. Thomas Francis J. Differentiation of Influenza A and Influenza B by the Complement-Fixation Reaction. *Proceedings of the Society for Experimental Biology and Medicine* 1940; **45**(3): 861-3.
107. Wen C-Cü, Chu C-M. Survey of Influenza Antibodies in Normal Human Sera in Peking. *Chinese Medical Journal* 1957; **75**(10): 792-801.
108. Montefiore D, Drozdov SG, Kafuko GW, Fayinka OA, Soneji A. Influenza in East Africa, 1969-70. *Bulletin of the World Health Organization* 1970; **43**(2): 269-73.

109. Francis T, Jr., Quilligan JJ, Jr., Minuse E. Identification of another epidemic respiratory disease. *Science* 1950; **112**(2913): 495-7.
110. Zhang Q. Process of isolating influenza virus in 1956 [Article in Chinese]. *Biological Products Newsletter* 1957; **2**(1): 80.
111. Joosting AC, Head B, Bynoe ML, Tyrrell DA. Production of common colds in human volunteers by influenza C virus. *British medical journal* 1968; **4**(5624): 153-4.
112. Burnet FM. Human infection with the virus of Newcastle disease of fowls. *The Medical Journal of Australia* 1943; **30**(6): 313-4.
113. Karzon DT. Studies on a neutralizing antibody against canine distemper virus found in man. *Pediatrics* 1955; **16**(6): 809-18.
114. Goldberger J, Anderson JF. The nature of the virus of measles. *Journal of the American Medical Association* 1911; **LVI**(12): 971-2.
115. Tang FF, Wu SY, Huang YT, Wen ZQ. Research on the isolation of measles virus [Article in Chinese]. *Chinese Science Bulletin* 1958; (10): 314-5.
116. Baylet R, Schluep R, Cantrelle DS, Rey M. Age-Grouping in Measles in an Urban Environment (A Serological Study). *Bulletin de la Societe Medicale d'Afrique Noire de Langue Francaise* 1963; **8**(6): 771-8.
117. Chanock RM, Parrott RH, Cook K, et al. Newly recognized myxoviruses from children with respiratory disease. *The New England journal of medicine* 1958; **258**(5): 207-13.
118. Chen ZH, Zhang EH, Zhang XZ, He NX. Isolation of parainfluenza type I virus by tissue culture and adsorption-hemagglutination test [Article in Chinese]. *Journal of Zhejiang University [Medical Sciences]* 1964; (03): 9-14+49.
119. Taylor-Robinson D, Tyrrell DA. Virus diseases on Tristan da Cunha. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1963; **57**: 19-22.
120. Yu JQ, Chang RX, He CJ, Guan QH, Xie JP. Serological study of 722 infants with viral pneumonia [Article in Chinese]. *Guangdong Medical Journal* 1987; **08**(04): 32-4.
121. Baker KS, Todd S, Marsh GA, et al. Novel, potentially zoonotic paramyxoviruses from the African straw-colored fruit bat *Eidolon helvum*. *Journal of virology* 2013; **87**(3): 1348-58.
122. Chanock RM. Association of a new type of cytopathogenic myxovirus with infantile croup. *The Journal of experimental medicine* 1956; **104**(4): 555-76.
123. Pathogen biology research group Jnmc. Virus isolation in 535 elderly patients with chronic bronchitis and other respiratory infections and antibody tests in some cases [Article in Chinese]. *Jiangsu Medical Journal* 1975; (01): 47-53.
124. Balestrieri A, Russo V, D'Arrigo C. Serum haemagglutination-inhibiting antibodies for haemadsorbing viruses types 1 and 3 and croup-associated in persons in Accra, Ghana. *Arch Ital Sci Med Trop e Parassit* 1967; **48**(11/12): 299-306.
125. Johnson KM, Chanock RM, Cook MK, Huebner RJ. Studies of a new human hemadsorption virus. I. Isolation, properties and characterization. *American journal of hygiene* 1960; **71**: 81-92.
126. Lau SK, To WK, Tse PW, et al. Human parainfluenza virus 4 outbreak and the role of diagnostic tests. *Journal of clinical microbiology* 2005; **43**(9): 4515-21.
127. Niang MN, Diop OM, Sarr FD, et al. Viral etiology of respiratory infections in children under 5 years old living in tropical rural areas of Senegal: The EVIRA project. *Journal of medical virology* 2010; **82**(5): 866-72.
128. Schultz EW, Habel K. SA virus; a new member of the myxovirus group. *Journal of immunology* 1959; **82**(3): 274-8.
129. Johnson CD, Goodpasture EW. An Investigation of the Etiology of Mumps. *The Journal of experimental medicine* 1934; **59**(1): 1-19.
130. Wang TJ, Sun WC, Fang Z, Du SM. Etiology of Mumps in Beijing [Article in Chinese]. *National Medical Journal of China* 1958; **44**(01): 18-29.
131. Bayer P, Gear J. Virus meningo-encephalitis in South Africa; a study of the cases admitted to the Johannesburg Fever Hospital. *South African journal of laboratory and clinical medicine Suid-Afrikaanse tydskrif vir laboratorium- en kliniekwerk* 1955; **1**(1): 22-35.
132. Albarino CG, Foltzer M, Towner JS, et al. Novel paramyxovirus associated with severe acute febrile disease, South Sudan and Uganda, 2012. *Emerg Infect Dis* 2014; **20**(2): 211-6.
133. Work TH. Serological evidence of arbovirus infection in the Seminole Indians of southern Florida. *Science* 1964; **145**(3629): 270-2.
134. Smithburn KC, Haddow AJ, Mahaffy AF. A neurotropic virus isolated from Aedes mosquitoes caught in the Semliki forest. *Am J Trop Med Hyg* 1946; **26**: 189-208.
135. Smithburn KC, Mahaffy AF, Paul JH. Bwamba Fever and Its Causative Virus. *The American Journal of Tropical Medicine and Hygiene* 1941; **s1-21**(1): 75 - 90.

136. Hammon WM, Reeves WC. California encephalitis virus, a newly described agent. *California medicine* 1952; **77**(5): 303-9.
137. Gu HX, Spence L, Artsob H, Chia WK, Th'ng C, Lampotang V. Serological evidence of infection with California serogroup viruses (family Bunyaviridae) in residents of Long Hua, suburb of Shanghai, People's Republic of China. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1984; **78**(6): 780-1.
138. Bardos V, Sefcovicova L. The Presence of Antibodies neutralizing Tahyna Virus in the Sera of Inhabitants of some European, Asian, African and Australian Countries. *Journal of Hygiene, Epidemiology, Microbiology and Immunology* 1961; **5**(4): 501-4.
139. Williams MC, Woodall JP, Corbet PS. Nyando Virus: A Hitherto Undescribed Virus Isolated from Anopheles Funestus Giles Collected in Kenya. *Archiv fur die gesamte Virusforschung* 1965; **15**: 422-7.
140. Moore DL, Causey OR, Carey DE, et al. Arthropod-borne viral infections of man in Nigeria, 1964-1970. *Annals of tropical medicine and parasitology* 1975; **69**(1): 49-64.
141. Liu W, Sun FJ, Tong YG, Zhang SQ, Cao WC. Rift Valley fever virus imported into China from Angola. *Lancet Infect Dis* 2016; **16**(11): 1226.
142. Daubney R, Hudson JR, Garnham PC. Enzootic hepatitis or rift valley fever. An undescribed virus disease of sheep cattle and man from east africa. *The Journal of Pathology and Bacteriology* 1931; **34**(4): 545-79.
143. Sabin AB. Experimental studies on Phlebotomus (pappataci, sandfly) fever during World War II. *Archiv fur die gesamte Virusforschung* 1951; **4**(4): 367-410.
144. McMullan LK, Folk SM, Kelly AJ, et al. A new phlebovirus associated with severe febrile illness in Missouri. *The New England journal of medicine* 2012; **367**(9): 834-41.
145. Zhang YZ, Zhou DJ, Xiong Y, et al. Hemorrhagic fever caused by a novel tick-borne Bunyavirus in Huaiyangshan, China. *Zhonghua liu xing bing xue za zhi = Zhonghua liuxingbingxue zazhi* 2011; **32**(3): 209-20.
146. Grohmann GS, Glass RI, Pereira HG, et al. Enteric viruses and diarrhea in HIV-infected patients. Enteric Opportunistic Infections Working Group. *The New England journal of medicine* 1993; **329**(1): 14-20.
147. Rosen BI, Fang ZY, Glass RI, Monroe SS. Cloning of human picobirnavirus genomic segments and development of an RT-PCR detection assay. *Virology* 2000; **277**(2): 316-29.
148. Luo RH, Xie JQ, Chen YM, Yang SJ. Report of one case of hand-foot-mouth disease in human [Article in Chinese]. *New Medicine* 1999; **30**(03): 37-8.
149. Donia HA, Youssef BZ. Foot and mouth disease (FMD): serological investigation in some farms of Alexandria Governorate of Egypt. *The Journal of the Egyptian Public Health Association* 2002; **77**(3-4): 371-82.
150. Jonkers AH. Serosurvey of encephalomyocarditis virus neutralizing antibodies in southern Louisiana and Peruvian Indian populations. *Am J Trop Med Hyg* 1961; **10**: 593-8.
151. Feng R, Wei J, Zhang H, et al. National serosurvey of encephalomyocarditis virus in healthy people and pigs in China. *Archives of virology* 2015; **160**(12): 2957-64.
152. Dick GW, Best AM, et al. Mengo encephalomyelitis; a hitherto unknown virus affecting man. *Lancet* 1948; **2**(6521): 286-9.
153. Jones MS, Lukashov VV, Ganac RD, Schnurr DP. Discovery of a novel human picornavirus in a stool sample from a pediatric patient presenting with fever of unknown origin. *Journal of clinical microbiology* 2007; **45**(7): 2144-50.
154. Xu ZQ, Cheng WX, Qi HM, Cui SX, Jin Y, Duan ZJ. New Saffold cardiovirus in children, China. *Emerg Infect Dis* 2009; **15**(6): 993-4.
155. Zoll J, Erkens Hulshof S, Lanke K, et al. Saffold virus, a human Theiler's-like cardiovirus, is ubiquitous and causes infection early in life. *PLoS Pathog* 2009; **5**(5): e1000416.
156. Dai XQ, Hua XG, Shan TL, Delwart E, Zhao W. Human cosavirus infections in children in China. *J Clin Virol* 2010; **48**(3): 228-9.
157. Kapusinszky B, Phan TG, Kapoor A, Delwart E. Genetic diversity of the genus Cosavirus in the family Picornaviridae: a new species, recombination, and 26 new genotypes. *PLoS One* 2012; **7**(5): e36685.
158. Yang Y, Ju A, Xu X, Cao X, Tao Y. A novel type of cosavirus from children with nonpolio acute flaccid paralysis. *Virology journal* 2016; **13**(1): 169.
159. Sickles GM, Dalldorf G. Serologic differences among strains of the Cocksackie group of viruses. *Proceedings of the Society for Experimental Biology and Medicine Society for Experimental Biology and Medicine* 1949; **72**(1): 30.
160. Xiao MH, Ye ZZ, Zhang ZL, Tian XQ, Zheng JM, Liu ZY. An epidemic of hand-foot-and-mouth disease due to Cocksackie A16 in Tianjin City [Article in Chinese]. *Tianjin Medical Journal* 1985; **06**(02): 355-7+2.
161. Wu JR, Che JL, Wu GQ, Lin SQ. Investigation on Cocksackie Virus Disease in Fujian Province [Article in Chinese]. *National Medical Journal of China* 1960; **46**(01): 40-8.

162. Patz IM, Measroch V, Gear J. Bornholm disease, pleurodynia or epidemic myalgia; an outbreak in the Transvaal associated with Cocksackie virus infection. *South African medical journal = Suid-Afrikaanse tydskrif vir geneeskunde* 1953; **27**(19): 397-402.
163. Flexner S, Lewis PA. The transmission of acute poliomyelitis to monkeys. *Journal of the American Medical Association* 1909; **LIII**(20): 1639-.
164. Hudson NP, Lennette EH. The Neutralization of Poliomyelitis Virus by the Serum of Liberian Negroes. *American journal of hygiene* 1933; **17**: 581-6.
165. Schieble JH, Fox VL, Lennette EH. A probable new human picornavirus associated with respiratory diseases. *American journal of epidemiology* 1967; **85**(2): 297-310.
166. Institute SEaSDPaT. Isolation and identification of acute hemorrhagic conjunctivitis virus in 1975 [Article in Chinese]. *Chinese Journal of Ophthalmology* 1979; **15**(2): 90.
167. Mirkovic RR, Kono R, Yin-Murphy M, Sohler R, Schmidt NJ, Melnick JL. Enterovirus type 70: the etiologic agent of pandemic acute haemorrhagic conjunctivitis. *Bulletin of the World Health Organization* 1973; **49**(4): 341-6.
168. Moscovici C, Laplaca M, Maisel J, Kempe H. Studies of bovine enteroviruses. *American journal of veterinary research* 1961; **22**: 852-63.
169. Price WH. The isolation of a new virus associated with respiratory clinical disease in humans. *Proc Natl Acad Sci U S A* 1956; **42**(12): 892-6.
170. Health GIoMa. Investigation report on virus types in patients with cold in Guangzhou [Article in Chinese]. *Guangdong Medical Journal* 1975; (03): 2-6.
171. Taylor-Robinson D. Studies on some viruses (rhinoviruses) isolated from common colds. *Archiv fur die gesamte Virusforschung* 1963; **13**: 281-93.
172. Hamre D, Procknow JJ. Viruses isolated from natural common colds in the U.S.A. *British medical journal* 1961; **2**(5264): 1382-5.
173. Xiang Z, Gonzalez R, Xie Z, et al. Human rhinovirus group C infection in children with lower respiratory tract infection. *Emerg Infect Dis* 2008; **14**(10): 1665-7.
174. Briese T, Renwick N, Venter M, et al. Global distribution of novel rhinovirus genotype. *Emerg Infect Dis* 2008; **14**(6): 944-7.
175. Lamson D, Renwick N, Kapoor V, et al. MassTag polymerase-chain-reaction detection of respiratory pathogens, including a new rhinovirus genotype, that caused influenza-like illness in New York State during 2004-2005. *J Infect Dis* 2006; **194**(10): 1398-402.
176. Lau SK, Yip CC, Tsoi HW, et al. Clinical features and complete genome characterization of a distinct human rhinovirus (HRV) genetic cluster, probably representing a previously undetected HRV species, HRV-C, associated with acute respiratory illness in children. *Journal of clinical microbiology* 2007; **45**(11): 3655-64.
177. Feinstone SM, Kapikian AZ, Purceli RH. Hepatitis A: detection by immune electron microscopy of a viruslike antigen associated with acute illness. *Science* 1973; **182**(4116): 1026-8.
178. College MRGoSFM, Hospital LoSSPs. Preliminary report on the examination of hepatitis A antigen particles by immunoelectron microscopy [Article in Chinese]. *Shanghai Medical Journal* 1978; (10): 13-5+65.
179. Szmunes W, Dienstag JL, Purcell RH, et al. The prevalence of antibody to hepatitis A antigen in various parts of the world: a pilot study. *American journal of epidemiology* 1977; **106**(5): 392-8.
180. Chhabra P, Payne DC, Szilagyi PG, et al. Etiology of viral gastroenteritis in children <5 years of age in the United States, 2008-2009. *J Infect Dis* 2013; **208**(5): 790-800.
181. Yang S, Zhang W, Shen Q, et al. Aichi virus strains in children with gastroenteritis, China. *Emerg Infect Dis* 2009; **15**(10): 1703-5.
182. Sdiri-Loulizi K, Gharbi-Khelifi H, de Rougemont A, et al. Acute infantile gastroenteritis associated with human enteric viruses in Tunisia. *Journal of clinical microbiology* 2008; **46**(4): 1349-55.
183. Ramos-Alvarez M, Sabin AB. Enteropathogenic viruses and bacteria; role in summer diarrheal diseases of infancy and early childhood. *Journal of the American Medical Association* 1958; **167**(2): 147-56.
184. Shan TL, Guo W, Cui L, et al. The first detection of human parechovirus infections in China. *J Clin Virol* 2009; **45**(4): 371-2.
185. Greninger AL, Runckel C, Chiu CY, et al. The complete genome of klassevirus - a novel picornavirus in pediatric stool. *Virology journal* 2009; **6**: 82.
186. Shan T, Wang C, Cui L, et al. Picornavirus salivirus/klassevirus in children with diarrhea, China. *Emerg Infect Dis* 2010; **16**(8): 1303-5.
187. Li L, Victoria J, Kapoor A, et al. A novel picornavirus associated with gastroenteritis. *Journal of virology* 2009; **83**(22): 12002-6.
188. Kayali G, Ortiz EJ, Chorazy ML, et al. Serologic evidence of avian metapneumovirus infection among adults occupationally exposed to turkeys. *Vector Borne Zoonotic Dis* 2011; **11**(11): 1453-8.
189. Falsey AR, Erdman D, Anderson LJ, Walsh EE. Human metapneumovirus infections in young and elderly adults. *J Infect Dis* 2003; **187**(5): 785-90.

190. Peiris JS, Tang WH, Chan KH, et al. Children with respiratory disease associated with metapneumovirus in Hong Kong. *Emerg Infect Dis* 2003; **9**(6): 628-33.
191. Madhi SA, Ludewick H, Abed Y, Klugman KP, Boivin G. Human metapneumovirus-associated lower respiratory tract infections among hospitalized human immunodeficiency virus type 1 (HIV-1)-infected and HIV-1-uninfected African infants. *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America* 2003; **37**(12): 1705-10.
192. Chanock R, Roizman B, Myers R. Recovery from infants with respiratory illness of a virus related to chimpanzee coryza agent (CCA). I. Isolation, properties and characterization. *American journal of hygiene* 1957; **66**(3): 281-90.
193. Kun Number 323 Unit tCPsLA. Studies on the isolation and growth characteristics of respiratory syncytial virus [Article in Chinese]. *Acta Microbiologica Sinica* 1975; **15**(02): 125-32.
194. Doggett JE. Antibodies to respiratory syncytial virus in human sera from different regions of the world. *Bulletin of the World Health Organization* 1965; **32**(6): 849-53.
195. Florio L, Stewart MO, Mugrage ER. The Etiology of Colorado Tick Fever. *The Journal of experimental medicine* 1946; **83**(1): 1-10.
196. Yang JM, Yin GQ, Feng YH, Luo ZY, F. JJ, Zhang ZQ. Superinfection of colti virus and Japanese encephalitis virus [Article in Chinese]. *Journal of Nanjing Railway Medical college* 1996; **15**(03): 29.
197. Tomori O, Fabiyi A, Murphy F. Characterization of Orungo virus, an orbivirus from Uganda and Nigeria. *Archives of virology* 1976; **51**(4): 285-98.
198. Ramos-Alvarez M, Sabin AB. Characteristics of poliomyelitis and other enteric viruses recovered in tissue culture from healthy American children. *Proceedings of the Society for Experimental Biology and Medicine Society for Experimental Biology and Medicine* 1954; **87**(3): 655-61.
199. Zhao JM, Qiang BQ, Zhao TX, et al. Detection of diarrhoea viruses in children with acute gastroenteritis. *Chinese Journal of Experimental and Clinical Virology* 1995; (01): 45-9.
200. Malherbe H, Roux P, Kahn E. THE ROLE OF ENTEROPATHOGENIC BACTERIA AND VIRUSES IN ACUTE DIARRHOEAL DISORDERS OF INFANCY AND CHILDHOOD IN JOHANNESBURG. II. 'NON-SPECIFIC' GASTRO-ENTERITIS. *South African medical journal = Suid-Afrikaanse tydskrif vir geneeskunde* 1963; **37**: 259-61.
201. Cheng P, Lau CS, Lai A, et al. A novel reovirus isolated from a patient with acute respiratory disease. *J Clin Virol* 2009; **45**(1): 79-80.
202. Kapikian AZ, Kim HW, Wyatt RG, et al. Recent advances in the aetiology of viral gastroenteritis. *Ciba Foundation symposium* 1976; (42): 273-309.
203. Pang QF, Qiu FX, Yu FR, Chen SZ. Rotavirus-the source of acute gastroenteritis in infants in autumn [Article in Chinese]. *Bulletin of Medical Research* 1979; (07): 26-7.
204. Eiden J, Vonderfecht S, Yolken RH. Evidence that a novel rotavirus-like agent of rats can cause gastroenteritis in man. *Lancet* 1985; **2**(8445): 8-11.
205. Hung T, Chen GM, Wang CG, et al. Waterborne outbreak of rotavirus diarrhoea in adults in China caused by a novel rotavirus. *Lancet* 1984; **1**(8387): 1139-42.
206. Nakata S, Estes MK, Graham DY, Wang SS, Gary GW, Melnick JL. Detection of antibody to group B adult diarrhea rotaviruses in humans. *Journal of clinical microbiology* 1987; **25**(5): 812-8.
207. Jiang B, Dennehy PH, Spangenberg S, Gentsch JR, Glass RI. First detection of group C rotavirus in fecal specimens of children with diarrhea in the United States. *J Infect Dis* 1995; **172**(1): 45-50.
208. Qiao H, Nilsson M, Abreu ER, et al. Viral diarrhea in children in Beijing, China. *Journal of medical virology* 1999; **57**(4): 390-6.
209. Sebata T, Steele AD. Human group C rotavirus identified in South Africa. *South African medical journal = Suid-Afrikaanse tydskrif vir geneeskunde* 1999; **89**(10): 1073-4.
210. Wang C, Hu C, Huang F, X. C, Hung T. A novel discovered rotavirus from adult acute diarrhoeal patients in China [Article in Chinese]. *Chinese Journal of Virology* 1987; **03**(04): 321-5+411.
211. Xu PT, Wang YM, Zuo JM, Lin JW, Xu PM. New orbiviruses isolated from patients with unknown fever and encephalitis in Yunnan Province [Article in Chinese]. *Chinese Journal of Virology* 1990; **06**(01): 27-33+100.
212. Poesz BJ, Ruscetti FW, Gazdar AF, Bunn PA, Minna JD, Gallo RC. Detection and isolation of type C retrovirus particles from fresh and cultured lymphocytes of a patient with cutaneous T-cell lymphoma. *Proc Natl Acad Sci U S A* 1980; **77**(12): 7415-9.
213. Williams CK, Alabi GO, Junaid TA, et al. Human T cell leukaemia virus associated lymphoproliferative disease: report of two cases in Nigeria. *British medical journal (Clinical research ed)* 1984; **288**(6429): 1495-6.
214. Kalyanaraman VS, Sarngadharan MG, Robert-Guroff M, Miyoshi I, Golde D, Gallo RC. A new subtype of human T-cell leukemia virus (HTLV-II) associated with a T-cell variant of hairy cell leukemia. *Science* 1982; **218**(4572): 571-3.

215. Ma Y, Zheng S, Wang N, et al. Epidemiological analysis of HTLV-1 and HTLV-2 infection among different population in Central China. *PLoS One* 2013; **8**(6): e66795.
216. Delaporte E, Louwagie J, Peeters M, et al. Evidence of HTLV-II infection in central Africa. *AIDS (London, England)* 1991; **5**(6): 771-2.
217. Calattini S, Chevalier SA, Duprez R, et al. Discovery of a new human T-cell lymphotropic virus (HTLV-3) in Central Africa. *Retrovirology* 2005; **2**: 30.
218. Safai B, Sarngadharan MG, Groopman JE, et al. Seroepidemiological studies of human T-lymphotropic retrovirus type III in acquired immunodeficiency syndrome. *Lancet* 1984; **1**(8392): 1438-40.
219. Chang RS, Chan RC, French GL, et al. HTLV-III antibody testing in Hong Kong. *Jama* 1986; **256**(1): 41.
220. Brun-Vezinet F, Rouzioux C, Montagnier L, et al. Prevalence of antibodies to lymphadenopathy-associated retrovirus in African patients with AIDS. *Science* 1984; **226**(4673): 453-6.
221. (CDC) CfDC. AIDS due to HIV-2 infection--New Jersey. *MMWR Morb Mortal Wkly Rep* 1988; **37**(3): 33-5.
222. Yan YS, Zheng ZS, Chen G, Zheng J, Yan PP, Shao YM. Confirmation of the first HIV-2 case in China [Article in Chinese]. *Journal of Chinese AIDS&STD Prevention and Control* 2000; **06**(01): 16-8.
223. Kanki PJ, Barin F, M'Boup S, et al. New human T-lymphotropic retrovirus related to simian T-lymphotropic virus type III (STLV-IIIAGM). *Science* 1986; **232**(4747): 238-43.
224. Khabbaz RF, Rowe T, Murphey-Corb M, et al. Simian immunodeficiency virus needlestick accident in a laboratory worker. *Lancet* 1992; **340**(8814): 271-3.
225. Rua R, Betsem E, Calattini S, Saib A, Gessain A. Genetic characterization of simian foamy viruses infecting humans. *Journal of virology* 2012; **86**(24): 13350-9.
226. Achong BG, Mansell PW, Epstein MA. A new human virus in cultures from a nasopharyngeal carcinoma. *The Journal of pathology* 1971; **103**(2): P18.
227. Huang F, Wang H, Jing S, Zeng W. Simian foamy virus prevalence in Macaca mulatta and zookeepers. *AIDS research and human retroviruses* 2012; **28**(6): 591-3.
228. Meredith CD, Prossouw AP, Koch H. An unusual case of human rabies thought to be of chiropteran origin. *South African medical journal = Suid-Afrikaanse tydskrif vir geneeskunde* 1971; **45**(28): 767-9.
229. Liu Y, Zhang S, Zhao J, Zhang F, Hu R. Isolation of Irkut virus from a Murina leucogaster bat in China. *PLoS neglected tropical diseases* 2013; **7**(3): e2097.
230. Familusi JB, Osunkoya BO, Moore DL, Kemp GE, Fabiyi A. A fatal human infection with Mokola virus. *Am J Trop Med Hyg* 1972; **21**(6): 959-63.
231. Black SP, Powers LM. History of Rabies in Southern California. *Cal State J Med* 1910; **8**(11): 369-72.
232. Wu BQ. Report of four cases of rabies encephalitis [Article in Chinese]. *New Medicine* 1981; **12**(07): 357-8.
233. Wilhelm N, Alexis T. Rabies in South Africa: Occurrence and Distribution of Cases During 1932. *Onderstepoort Journal of Veterinary Science and Animal Industry* 1933; **1**: 51-6.
234. Grard G, Fair JN, Lee D, et al. A novel rhabdovirus associated with acute hemorrhagic fever in central Africa. *PLoS Pathog* 2012; **8**(9): e1002924.
235. Stremlau MH, Andersen KG, Folarin OA, et al. Discovery of novel rhabdoviruses in the blood of healthy individuals from West Africa. *PLoS neglected tropical diseases* 2015; **9**(3): e0003631.
236. Patterson WC, Mott LO, Jenney EW. A study of vesicular stomatitis in man. *Journal of the American Veterinary Medical Association* 1958; **133**(1): 57-62.
237. Hanson RP, Rasmussen AF, Jr., Brandly CA, Brown JW. Human infection with the virus of vesicular stomatitis. *The Journal of laboratory and clinical medicine* 1950; **36**(5): 754-8.
238. CDC. Chikungunya fever diagnosed among international travelers--United States, 2005-2006. *MMWR Morb Mortal Wkly Rep* 2006; **55**(38): 1040-2.
239. Ross RW. The Newala epidemic. III. The virus: isolation, pathogenic properties and relationship to the epidemic. *The Journal of hygiene* 1956; **54**(2): 177-91.
240. Howitt B. Recovery of the Virus of Equine Encephalomyelitis from the Brain of a Child. *Science* 1938; **88**(2289): 455-6.
241. Ehrenkranz NJ, Sinclair MC, Buff E, Lyman DO. The natural occurrence of Venezuelan equine encephalitis in the United States. *The New England journal of medicine* 1970; **282**(6): 298-302.
242. Li XD, Qiu FX, Yang H, Rao YN, Calisher CH. Isolation of Getah virus from mosquitos collected on Hainan Island, China, and results of a serosurvey. *The Southeast Asian journal of tropical medicine and public health* 1992; **23**(4): 730-4.
243. Meehan PJ, Wells DL, Paul W, et al. Epidemiological features of and public health response to a St. Louis encephalitis epidemic in Florida, 1990-1. *Epidemiology and infection* 2000; **125**(1): 181-8.

244. Tesh RB, Watts DM, Russell KL, et al. Mayaro virus disease: an emerging mosquito-borne zoonosis in tropical South America. *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America* 1999; **28**(1): 67-73.
245. Kokernot RH, McIntosh BM, Worth CB. Ndumu virus, a hitherto unknown agent, isolated from culicine mosquitoes collected in northern Natal. Union of South Africa. *Am J Trop Med Hyg* 1961; **10**: 383-6.
246. Williams MC, Woodall JP. O'nyong-nyong fever: an epidemic virus disease in East Africa. II. Isolation and some properties of the virus. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1961; **55**: 135-41.
247. Xu CH, Peng YF, Bai ZJ, et al. Seroepidemiological survey of arbovirus in Hainan Province in 1998 [Article in Chinese]. *Chinese Journal of Epidemiology* 1999; **20**(04): 20.
248. Mathiot CC, Grimaud G, Garry P, et al. An outbreak of human Semliki Forest virus infections in Central African Republic. *Am J Trop Med Hyg* 1990; **42**(4): 386-93.
249. Taylor RM, Hurlbut HS, Work TH, Kingston JR, Frothingham TE. Sindbis virus: a newly recognized arthropodtransmitted virus. *Am J Trop Med Hyg* 1955; **4**(5): 844-62.
250. Casals J, Curnen EC, Thomas L. Venezuelan Equine Encephalomyelitis in Man. *The Journal of experimental medicine* 1943; **77**(6): 521-30.
251. Habel K. Transmission of Rubella to Macacus mulatta Monkeys. *Public Health Reports (1896-1970)* 1942; **57**(31): 1126-39.
252. He NX, Xu TZ, Ma JY, et al. Isolation of rubella virus [Article in Chinese]. *Journal of Zhejiang University(Medical Sciences)* 1979; **8**(04): 169-72+217.
253. Selzer G. VIRUS ISOLATION, INCLUSION BODIES, AND CHROMOSOMES IN A RUBELLA-INFECTED HUMAN EMBRYO. *Lancet* 1963; **2**(7303): 336-7.
254. Rizzetto M, Shih JW, Gocke DJ, Purcell RH, Verme G, Gerin JL. Incidence and significance of antibodies to delta antigen in hepatitis B virus infection. *Lancet* 1979; **2**(8150): 986-90.
255. Rizzetto M, Purcell RH, Gerin JL. Epidemiology of HBV-associated delta agent: geographical distribution of anti-delta and prevalence in polytransfused HBsAg carriers. *Lancet* 1980; **1**(8180): 1215-8.
256. Crocchiolo PR, Caredda F, D'Arminio Monforte A, et al. The aetiology of acute hepatitis in Zimbabwe. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 1984; **78**(4): 514-8.