Title

A geopositioned, evidence-graded, pan-species compendium of Mayaro Virus occurrence

Authors

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Abstract

Mayaro Virus (MAYV) is an emerging health threat in the Americas that can cause febrile illness as well as debilitating arthralgia or arthritis. To better understand the geographic distribution of MAYV risk, we developed a georeferenced database of MAYV occurrence based on peer-reviewed literature and unpublished reports. Here we present this compendium, which includes both point and polygon locations linked to occurrence data documented from its discovery in 1954 until 2022. We describe all methods used to develop the database including data collection, georeferencing, management and quality-control. We also describe a customized grading system used to assess the quality of each study included in our review. The result is a comprehensive, evidence-graded database of confirmed MAYV occurrence in humans, non-human animals, and arthropods to-date, containing 266 geo-positioned occurrences in total. This database - which can be updated over time - may be useful for local spill-over risk assessment, epidemiological modelling to understand key transmission dynamics and drivers of MAYV spread, as well as identification of major surveillance gaps.

Background & Summary

43
44 First detected in Trinidad in 1954 [1], Mayaro virus (MAYV) is a mosquito-borne *Alphavirus* that causes
45 periodic outbreaks of febrile illness in several Latin American countries [2-5]. Serological surveys conducted
46 in the Americas suggest widespread circulation of the virus throughout the region [6-8]. Although MAYV
47 may cause debilitating arthralgia or arthritis, it often presents with non-specific symptoms that may be
48 clinically indistinguishable from other vector-borne diseases such as dengue or Zika [9]. No licensed
49 vaccine or antiviral treatment currently exists, and the current standard of care for MAYV infections is
50 limited to supportive care [9,10].
51
52 Collating and evaluating the current evidence regarding the distribution of MAYV occurrence is a critical
53 step in characterizing its transmission potential and identifying the communities at greatest risk for
54 MAYV outbreaks. Such compendium databases have proven valuable for the study and prevention of
55 other emerging and re-emerging pathogens and diseases, such as Middle East respiratory syndrome
56 coronavirus (MERS-CoV), leishmaniasis, Crimean-Congo hemorrhagic fever, and dengue viruses [11-14].
57 Previously published reviews have explored MAYV occurrence in the Americas [15,16]. This review seeks to
58 fill gaps in the current literature by providing the highest possible level of geographic resolution for the
59 available MAYV occurrence data across humans, non-human animals, and arthropods, coupled with an
60 evidence-based grading for each of those occurrences. In addition to drawing from occurrences
61 identified in a human systematic review, this compendium database includes occurrences identified in
62 another systematic review [17] evaluating the distribution of MAYV occurrence among non-human animal
63 and arthropod species in the Americas. Collectively, these two systematic reviews provide a
64 comprehensive compendium of MAYV occurrence to permit ecological and epidemiological risk
65 prediction and forecasting. Further, these two systematic reviews put forward joint citable frameworks
66 for the field to evaluate the quality of studies that propose non-human animal, arthropod, and human
67 MAYV occurrence.
68
69 This georeferenced, evidence-graded MAYV database contains 266 unique localities across 15 countries
70 published between 1954 and 2022. The methods described below are adapted from previously
71 published disease occurrence compendiums [11-14].

Methods

73 **Data Collection**
74 Data collection and abstraction for non-human animal and arthropod data was described in a previously
75 published study [17]. We followed a similar data collection strategy for human MAYV occurrence data. We
76 first searched Embase, Web of Science, PubMed/MEDLINE, and SciELO databases for English, Spanish,
77 and Portuguese language articles published between January 1954 and January 2021 using the search
78 term "Mayaro". Furthermore, a PubMed/MEDLINE alert using the search term "Mayaro" captured five
79 additional eligible studies reporting human MAYV occurrence that were published between the initial
80 search and May 2022.
81
82 This database search was extended using the bioRxiv (https://www.biorxiv.org/) and medRxiv
83 (https://www.medrxiv.org/) pre-print databases. We complemented these database search results with
84 'grey literature', including hand-searched bibliographies of the included articles and MAYV review
85 articles (including systematic reviews), the Pan American Health Organization (PAHO) Institutional
86 Repository for Information Sharing database (iris.paho.org), the GIDEON database
87 (https://www.gideononline.com/), and GenBank [29] (https://www.ncbi.nlm.nih.gov/genbank/). We

88 also searched for dissertations from several Brazilian university repositories including Instituto Evandro
89 Chagas (https://patua.iec.gov.br/), Universidade de São Paulo (https://teses.usp.br/), Universidade
90 Federal de Goiás (https://repositorio.bc.ufg.br/), Pontifícia Universidade Católica do Rio Grande do Sul
91 (http://tede2.pucrs.br/), Universidade Federal de Mato Grosso (https://bdm.ufmt.br/), Fundação
92 Oswaldo Cruz (https://portal.fiocruz.br/), and Universidade Federal do Pará
93 (http://repositorio.ufpa.br/). In addition, we searched conference handbooks that are available online
94 (2004-2019) from the American Society of Tropical Medicine and Hygiene
95 (https://www.astmh.org/annual-meeting/past-meetings). Articles were considered for eligibility if they
96 reported original research studies on MAYV occurrence in humans including serological surveys,
97 outbreak investigations, case reports, or surveillance studies. After the initial literature search, we
98 conducted a secondary search to identify any relevant articles describing the occurrence of Uruma virus.
99 Initially described as a novel human pathogen in 1959 [18], Uruma virus is now considered a strain of
100 MAYV [19]. Therefore, it was decided that Uruma virus records would be included in our systematic
101 review.

103 Two reviewers independently screened all titles and abstracts to determine articles that could
104 immediately be discarded based on relevancy and articles that should be included in the second stage of
105 review. Results were compared to reconcile any differences between the reviewers. Each reviewer then
106 independently read the full text of potentially eligible articles identified through screening and identified
107 articles that were candidates for inclusion in the study. Results were compared to reconcile any
108 differences between the two reviewers. A third-party reviewer adjudicated if consensus was not
109 reached between the reviewers. From those studies deemed eligible, data was extracted from articles
110 by one reviewer using a predetermined data abstraction tool in Microsoft Excel. Five percent of entries
111 were randomly selected and reviewed by a second reviewer.

113 Overall, 144 research items (including journal articles, dissertations, news articles, GenBank entries, etc.)
114 were deemed eligible. All eligible articles are included in the Supplementary materials (Data Citation 1).
115 No additional articles were deemed eligible following the secondary search for Uruma virus.

117 **Grading quality of evidence**
118 For human occurrences, we developed a customized grading system to assess the quality of each study
119 included in our review. This followed a similar framework we developed for evaluating the quality of
120 each study included in the published systematic review on MAYV occurrence in non-human animals and
121 arthropods [17]. We assigned each study in our systematic review a grade for each of four quality items:
122 clarity of research question/objective; description of study methods; description of sampling methods;
123 and validity of diagnostic tests. For each quality item, eligible studies were assigned a score of 3 (strong
124 evidence), 2 (moderate evidence), 1 (weak evidence), or unable to judge. Studies were deemed unable
125 to judge if the information provided was insufficient to assign quality scores (e.g., a single GenBank
126 entry, conference abstract, or report). Table 1 refers to a description of the four quality grading
127 domains.

129 Two reviewers independently graded the evidence quality for each study and results were compared to
130 reconcile any differences between the two reviewers. A third-party reviewer adjudicated if the two
131 initial reviewers did not reach consensus.

132

133 **Geo-positioning of the MAYV Occurrence Data**
134 All available location information from each confirmed MAYV case was extracted from each article and
135 added to the database based on methods that have been described previously [11-14]. Each occurrence of
136 MAYV was designated as either a point or polygon location according to the spatial resolution provided
137 in the article. When specific latitude and longitude coordinates were provided, they were verified in
138 Google Maps (https://www.google.com/maps) and added to the database as a point location and
139 coordinates were converted to decimal degrees. If a neighborhood, town, village, or small city was
140 explicitly mentioned in the article and the uncertainty of the location was less than 5 kilometers (km), it
141 was entered into the database as a point location and its centroid coordinates were recorded. An online
142 gazetteer (www.geonames.com) as well as Google Maps or ArcGIS (ESRI 2011. ArcGIS Pro: Release 2.6.0.
143 Redlands, CA: Environmental Systems Research Institute), along with contextual information, were used
144 to verify site locations.
145
146 For studies that reported a less precise spatial resolution such as states or counties, first level (ADM1),
147 second level (ADM2) or third level (ADM3) administrative divisions were recorded as polygons and
148 coded according to the global administrative unit layers (GAUL) from the Food and Agriculture
149 Organization [20]. If the uncertainty of a specific named location was greater than 5 km (e.g., the city of
150 Manaus, Brazil), the occurrence was assigned to a custom polygon created in ArcGIS that encompassed
151 the extent of the city. In the rare case that no specific intra-country location was provided, the record
152 was assigned to its country of occurrence (ADM0). When place names were duplicated (i.e., the ADM1
153 and ADM2 units had the same name), the coarsest spatial resolution was used. For example, if the
154 MAYV case location was reported as "*Cusco, Peru,*" with no additional information provided, the record
155 was assigned to the Cusco ADM1 polygon. However, if the study specified that the case occurred in the
156 "*City of Cusco*", the record was assigned to a custom polygon that encompassed the City of Cusco. The
157 centroid coordinates of ADM1, ADM2, and ADM3 polygons, or custom polygons were retrieved from the
158 GeoNames gazetteer whenever possible. If centroid coordinates were not available in GeoNames, they
159 were estimated using Google Maps. The coordinates for each georeference and the methods and source
160 used to obtain the coordinates were documented in the compendium.
161
162 Uncertainty was measured in kilometers for each MAYV occurrence point or polygon [21]. For polygons,
163 uncertainty was calculated as the distance from the polygon centroid coordinates to the polygon's
164 furthest boundary. For point locations with well-defined boundaries, the same procedure was followed,
165 whereby the uncertainty encompassed the extent of the location's area. When locations did not have
166 well defined boundaries, uncertainty was calculated as half the distance to the nearest named place
167 [21,22]. Calculation of uncertainty was completed using measurements from Google Maps. When authors
168 provided exact coordinates gathered using GPS, uncertainty was calculated using a georeferencing
169 calculator [23]. Exact coordinates were only used if authors provided a high level of precision (e.g.,
170 precision higher than "minutes" in degrees-minutes-seconds format and similarly high precision for
171 coordinates in decimal degrees). When coordinates were provided at a low precision, we georeferenced
172 the named place instead.
173
174 Several articles reported the diagnosis of MAYV in human blood samples at urban hospitals. If no
175 relevant information was provided on the study participants (e.g., place of residence), we georeferenced
176 the ADM2 unit in which the hospital was located.

177 # Data and Metadata Records
178 This database is available in the Supplementary materials (Data Citation 1). Each of the 280 rows
179 represents a unique occurrence of MAYV in a human, non-human animal, or arthropod. Location IDs for

points and polygons were assigned to each unique location. The MAYV occurrence database contains the following fields, following best-practice nomenclature as previously documented in georeferenced compendiums of other pathogens [11-14]:

1) **Location_ID:** A unique identifier was assigned to each georeference. The prefix used in the location ID denoted the georeference type: *ADM 0, 1, 2,* or *3* for administrative units, *CP* for custom polygons, and *P* for point locations. Separate studies with duplicate georeferences were assigned the same Location ID, and duplicates were removed according to the methods described above.

2) **Author_Year:** The first author and publication year for each record.

3) **Ref_Number:** A reference identification number was documented when applicable. A PubMed ID number was recorded for all published studies. If this was not available a DOI, GenBank locus, URL, ProMED identifier, etc., was captured.

4) **Year_MAYV_Start:** The earliest year that MAYV infection was detected within the publication was recorded if available. If studies only included a range of years and did not specify the precise year that MAYV was found, this range was documented. Note that this variable refers to infection detection and doesn't infer the onset of infection (particularly in the case of serological-based occurrence studies).

5) **Year_MAYV_End:** The latest year that MAYV infection was detected within the publication was recorded if available. If studies only included a range of years and did not specify the precise year that MAYV was found, this range was documented. We followed the methods of Hill et al.,[24] when studies did not report any year (i.e., an assumption was made that the case was detected three years before publication) .

6) **Host_Type:** One of three host types was documented for each occurrence: human, non-human animal, or arthropod. If multiple host types were detected with MAYV in the same location, a separate row was included for each host type.

7) **Location_Description:** We documented relevant information related to the location of the occurrence record. This field included the decisions made during the georeferencing process to reach the final determination regarding the location of each record.

8) **Adm0:** The country where MAYV occurrence was detected.

9) **Adm1:** The first level administrative unit where MAYV occurrence was detected (if available).

10) **Adm2:** The second level administrative unit where MAYV occurrence was detected (if available).

11) **GAUL_code:** When a MAYV occurrence was georeferenced as an ADM1 or ADM2 administrative polygon, the GAUL code was included.

12) **Finer_Res:** If finer spatial resolution was documented (e.g., a town, city, or exact coordinates) this was recorded.

13) **Location_Type**: Each occurrence was documented as either a point or polygon location type, depending on the spatial resolution that was provided. Custom polygons are available as shapefiles in the Supplementary materials (Data Citation 1). These can be opened in GIS software or using statistical packages that handle spatial data.

14) **Admin_Level:** The administrative level for each polygon location was recorded as either 0 (country level), 1 (first level administrative division), 2 (second level administrative division), or 3 (third level administrative division) depending on the spatial resolution that is provided. If the occurrence was georeferenced as a point location or custom polygon, -999 was recorded.

15) **Y_Coord:** The longitude coordinate was recorded in decimal degrees. The coordinates were taken verbatim from the article when available. Otherwise, the polygon centroid was recorded.

16) **X_Coord:** The latitude coordinate was recorded in decimal degrees. The coordinates were taken verbatim from the article when available. Otherwise, the polygon centroid was recorded.

227 17) **Coord_Source:** This field describes how the coordinates were determined. Possibilities include
228 the following:
229 a. Exact coordinates provided in the article.
230 b. Polygon centroid coordinates retrieved from GeoNames.
231 c. Location was determined based on the details provided in the article (e.g., a specific
232 neighborhood was mentioned), and centroid coordinates were subsequently
233 determined using Google Maps.
234 18) **Uncertainty_km:** The amount of uncertainty associated with the record, measured in km.
235 19) **Uncertainty_Description:** The method used to calculate uncertainty for each georeference. For
236 example, the uncertainty of polygons was measured as the distance from the polygon centroid
237 to the furthest polygon boundary. For certain point and polygon locations where the boundary
238 was not clear, uncertainty was measured as half the distance to the nearest named place.
239 Uncertainty calculations were based on previously published methods [21,22].
240 20) **Diagnostic_Type:** The specific diagnostic test (e.g., polymerase chain reaction [PCR],
241 neutralization test [NT]; hemagglutination inhibition [HI]; enzyme-linked immunosorbent assay
242 [ELISA]) was documented.
243 21) **Positive_n:** The number of positive MAYV cases that were reported.
244 22) **Denominator:** The total number of humans, non-human animals, or arthropod pools in the
245 study.
246 23) **Language:** The language of the article, either English, Portuguese, or Spanish.

Technical Validation

248 All georeferencing was completed by one study author and validated by a second author. In the case of
249 a disagreement or discrepancy between the two authors, a third author adjudicated. A location
250 identification was assigned to each unique georeference in the dataset. All final georeferences were
251 plotted in ArcGIS for visual inspection. All data points were checked to ensure they fell on land and
252 within the correct country. In the case of duplicate georeferences, we retained the record with the
253 highest quality score; if quality scores were identical, we retained the more recent record.

Usage Notes

255 We identified 144 eligible references for inclusion in our study (see flowchart in Fig 1). The resulting
256 database 266 unique geo-positioned MAYV locations worldwide, including 96 unique points and 170
257 unique polygons. Therefore, each row in the database represents a unique location where MAYV was
258 detected in humans, non-human animals, or arthropods. Duplicate georeferences from the same host
259 type were removed from the main database (see the Duplicates table in Supplementary material in Data
260 Citation 1) following the approach specified in the methods section. Some duplicate georeferences were
261 included if multiple host types (e.g., human and arthropod) were found with MAYV at the same location.
262 For example, Hoch et al., 1981 [25] detected MAYV in both humans and arthropods in the ADM2 unit of
263 Belterra, Brazil. Two separate rows (one row for humans and one for arthropods) are included in the
264 compendium with the same georeference.; therefore, the database includes 280 rows, each
265 representing a unique occurrence of MAYV in a human, non-human animal, or arthropod. Of these 280
266 rows, 222 (79%) were in humans, 34 (12%) were in non-human animals, and 24 (9%) were in arthropods.
267 MAYV was reported in 15 countries overall, with the majority occurring in Brazil (n = 135). According to
268 our review, MAYV occurrences are limited to the region between latitude 35S and 12N of tropical South
269 America. One article [26] reported MAYV occurrence in Zambia; this occurence was not included in our
270 georeferenced database due to the lack of evidence supporting MAYV circulation outside of the
271 Americas and the potential cross-reactivity with antibodies of other alphaviruses in the Semliki Forest
272 serocomplex [27].

273
274   Studies were included in our systematic review if they reported testing for MAYV occurrence, even if
275   MAYV was not detected. These negative results are not included in the georeferenced compendium, but
276   they can be found in the Supplementary materials (Data Citation 1). Many machine-learning models that
277   are common in the ecological literature are presence-only or presence-background algorithms that rely
278   on "pseudoabsence" data in lieu of true absences. For this reason, the true absence data presented here
279   are potentially valuable for disease modelling. However, any reports of disease absence must be
280   considered carefully as true absence is difficult to establish and false absence data can result in
281   miscalibration of distribution models [28]. Ideally, representative country-wide surveys should be used to
282   ascertain "true" absence locations that can be used in subsequent modelling efforts [29,30].

283
284   As with other published compendiums [11], these curated data derived from published sources are
285   expected to complement and augment other survellance data used by public health agencies, thereby
286   increasing our understanding of the distribution of MAYV in the Americas across multiple host types
287   with a high spatial resolution. These data may also assist in identifying under-sampled regions, and may
288   assist in identifying priority regions for surveillance. The georeferences can also serve as the basis for
289   development of epidemiological models or risk maps that characterize the potential suitability for MAYV
290   occurrence, including the risk of spillover into human populations and the potential influence of climate
291   change on MAYV distribution. For example, the 2013 compendium of dengue virus (DENV) occurrence [12]
292   was used as the basis for a highly cited modelling study that estimated the global distribution of DENV
293   risk [31]. Finally, leveraging the methods and data presented here, this open access database can be
294   updated as additional studies are published that report MAYV in the Americas.

295
296   There are several important limitations that must be considered when using this dataset. One significant
297   limitation is the impact of sampling bias on the detection and public reporting of MAYV occurrence.
298   Heterogeneity of public health arboviral survellance systems (including variability in surveillance
299   infrastructure and competing public health demands) and MAYV research activity may skew MAYV
300   detection and reporting by geographic region. Therefore, the absence of MAYV occurrence in some
301   settings may not represent true disease absence, but rather ascertainment bias. This important
302   limitation must be addressed in subsequent modeling studies in order to reduce the effects of sampling
303   bias on model accuracy [32]. Some published studies have proposed an evidence consensus score which
304   quantifies the evidence supporting the presence or absence of a pathogen in a given region [33]. This score
305   can be calculated using multiple evidence categories (e.g., health organization reporting status or health
306   expenditure) which may provide useful evidence of disease presence or absence in areas, including
307   those with more limited arboviral surveillance.

308
309   Another limitation of our study is the lack of geographic precision associated with MAYV occurrence
310   records. Many articles did not provide sufficient geographic detail to georeference MAYV records with a
311   high level of precision. We attempted to capture this uncertainty by assigning polygon locations to these
312   records. When a greater level of geographic detail was provided by study authors, we were able to
313   georeference some records as point locations (i.e., locations of MAYV occurrence with less than 5 km of
314   uncertainty).

315
316   Finally, an additional limitation is associated with the variable assay validity used to detect MAYV. Some
317   studies reported MAYV presence based only on positive serological assays such as hemagglutination
318   inhibition (HI) tests while other studies provided stronger evidence of MAYV occurrence based on
319   reference neutralization assays or PCR testing. We estimated the strength of evidence of MAYV
320   occurrence using a custom evidence grade which could be used in other studies. The strength of

321 evidence annotated in these data can be considered in future modeling efforts, with certain low-
322 evidence records potentially excluded from models as part of sensitivity analyses. Moreover, the
323 variability of evidence for MAYV occurrence demonstrated here prompts study design considerations for
324 future MAYV research and public health surveillance.
325
326 In addition to the main comma-delimited database, three Supplementary Files are included as part of
327 the file set which can be found online (Data Citation 1). These files include: (i) a document containing
328 the quality score and a citation for each of the references included in our review, (ii) a list of duplicate
329 georeferences that were excluded from the database, and (iii) a shapefile of the custom polygons. The
330 studies that described only negative MAYV results (i.e., those that are not included in the georeferenced
331 compendium) are indicated by an asterisk in the S2 File.
332

Acknowledgements

348

Author Contributions

350 M.C., B.A.H, A.A., and S.P. drafted the data collation protocol. M.C., A.P., B.F., J.D., G.R., N.K.M.M., E.L.L,
351 R.K., I.C.S, K.P, R.C.M, and S.P. assisted with article review, evidence grading, and data extraction. M.C.,
352 A.P., N.K.M.M, E.L.L, R.K., and I.C.S contributed to georeferencing. C.L.M. checked all extracted data.
353 M.C. and S.P. wrote the first draft, and all authors contributed to the manuscript.

Data Citation

355 To download data click the following link:
356 https://datadryad.org/stash/share/2EY752eZN2Rfh8LXL6QHXfU6bxHPEjWQcchikr61ImM

Competing Interests

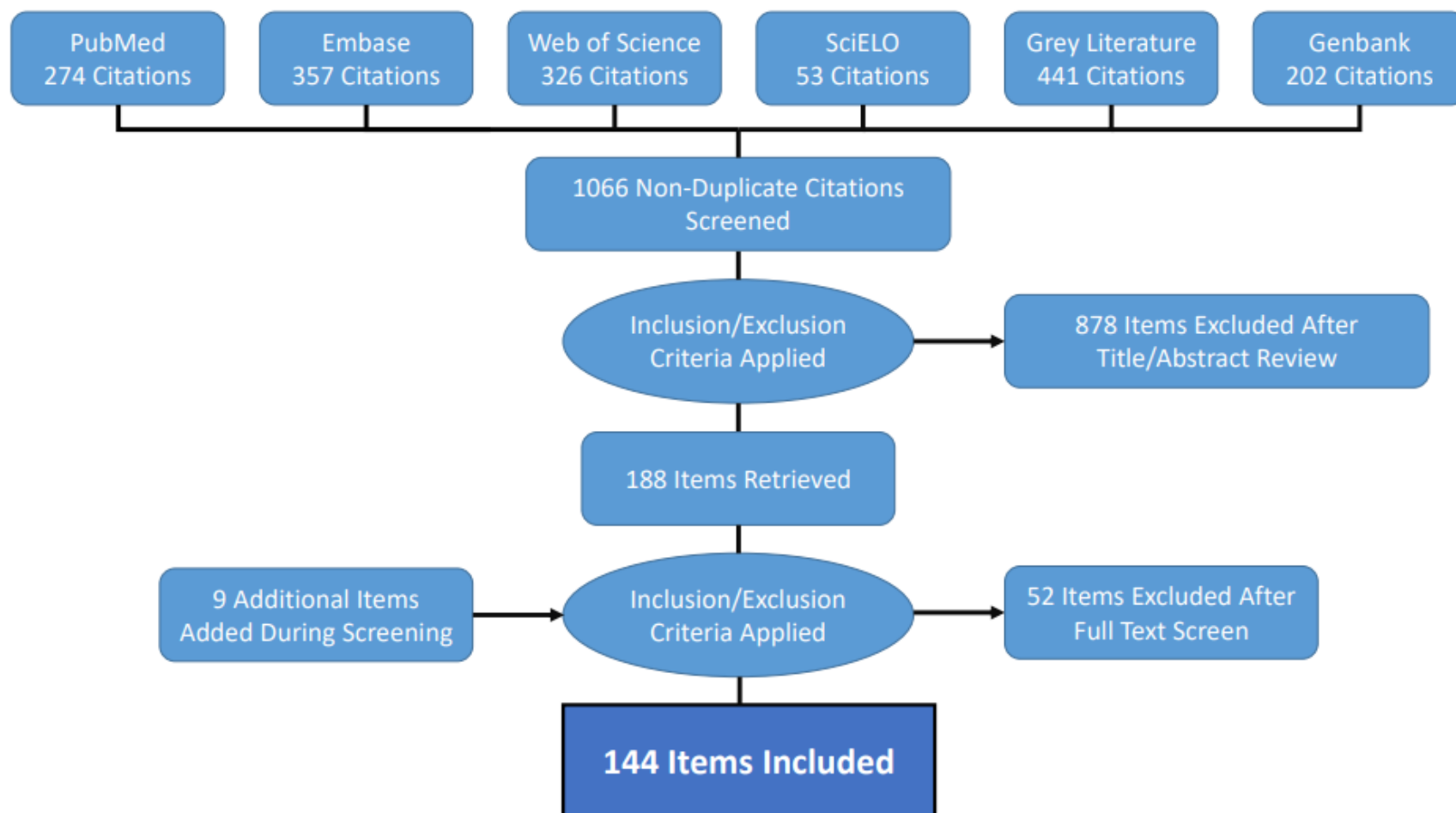358 The authors declare no competing financial interests.

359

Figure 1. MAYV literature extraction flowchart for human occurrence. The flowchart for non-human animal and arthropod occurrence is provided in the previously published systematic review [17].
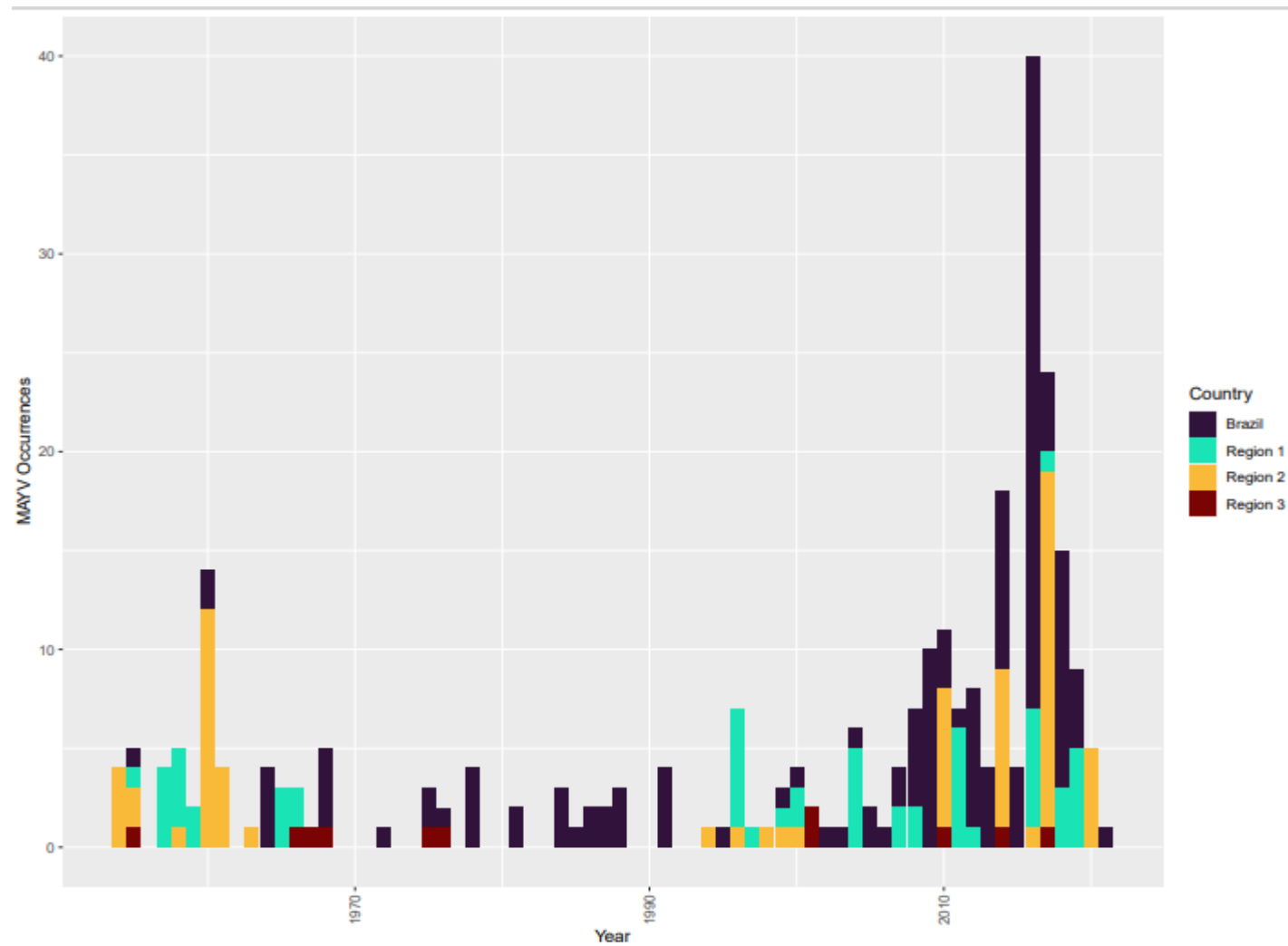
365

Figure 2. MAYV occurrence (all host types) by year and region. All countries except Brazil were grouped according to geographic region. Region 1 includes Peru, Bolivia, Ecuador, and Colombia. Region 2 includes French Guiana, Guiana, Suriname, Venezuela, and Trinidad & Tobago. Region 3 includes Panama, Costa Rica, Mexico, Haiti and Antigua.
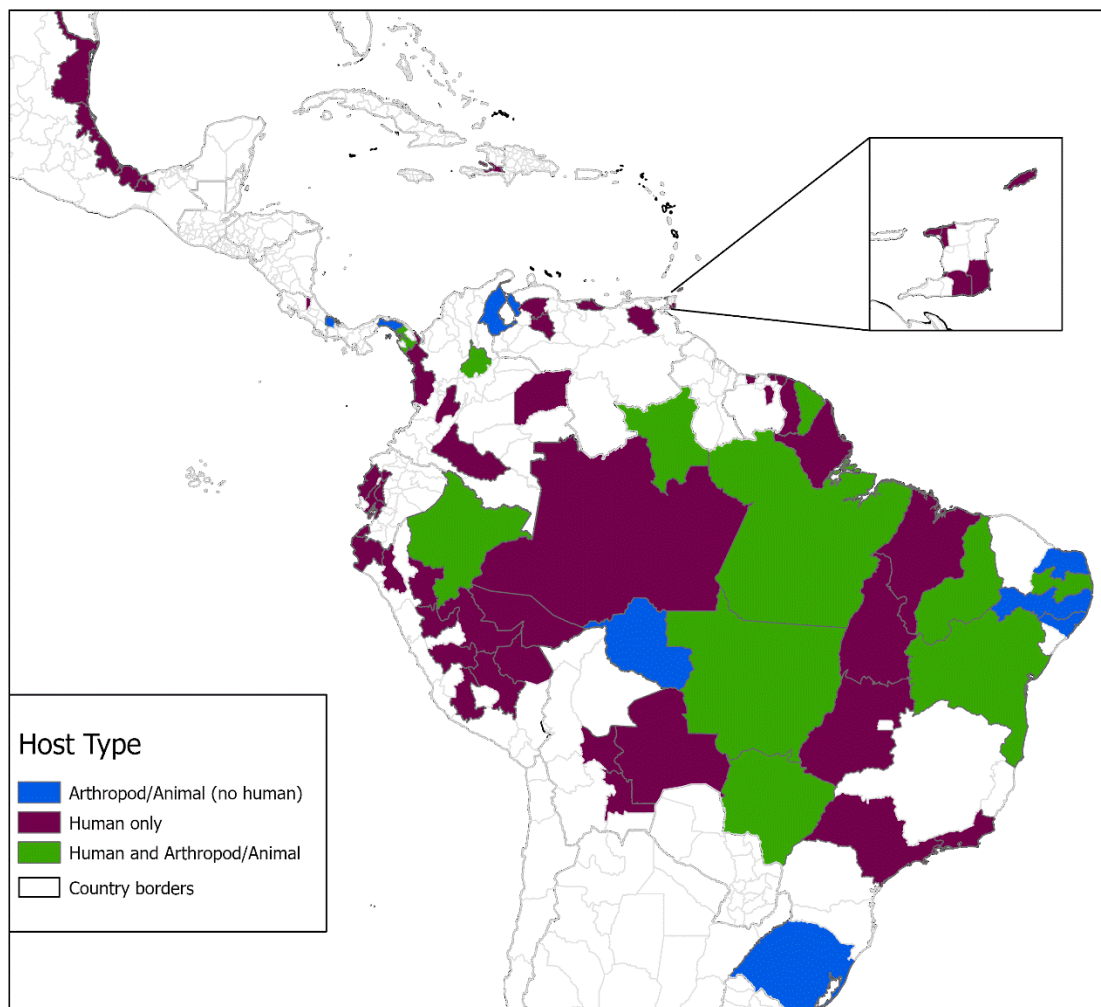
Figure 3. Distribution of MAYV occurrence by first level administrative division. MAYV occurrences are aggregated to the ADM1 level and presented by host type. Host types include human only, reservoir only (non-human animal, arthropod, or both), or human and reservoir (human and non-human animal or arthropod, or all three host types). The inset map shows Trinidad and Tobago.

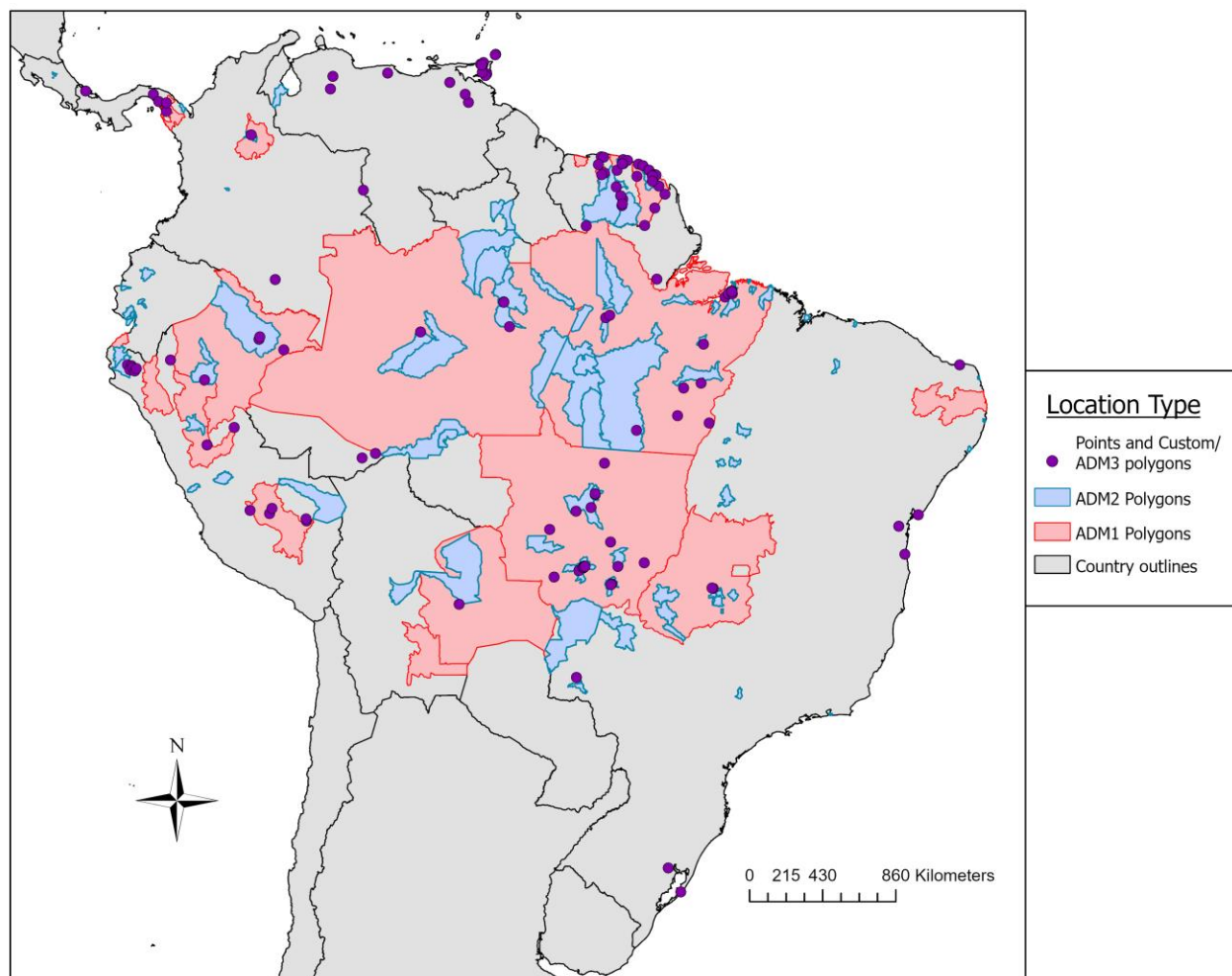**Figure 4. Distribution map of MAYV occurrence by location type.** All unique MAYV occurrences are presented according to the precision of the georeference. Red outlines represent first-level administrative units and blue outlines represent second-level administrative units. Both point locations and custom polygons are represented as purple points. Not visible on the map are two ADM2 polygons in Mexico and one ADM2 polygon in Haiti.

Tables

Table 1: Evidence quality grading scheme – Human infection

Quality item	3-Strong	2- Moderate	1- Weak	Unable to judge
Was the research question/objective clearly described and stated?	Described in full detail	Described in moderate detail (neither strong nor weak evidence)	Not described at all	Unable to judge based on the information presented
Were the study design (including location and year of study) and participant recruitment presented in a reproducible way?	Described in full detail	Described in moderate detail (neither strong nor weak evidence)	Not described at all	Unable to judge based on the information presented
Was relevant information collected on participants, including travel history, occupation, location of residence, etc.?	Described in full detail	Described in moderate detail (neither strong nor weak evidence)	Not described at all	Unable to judge based on the information presented
Was MAYV exposure positivity measured in a valid way?[1]	PCR or viral culture or high-specificity serological method (e.g., PRNT)	Lower -specificity serological assay (i.e., HI and ELISA) without exclusion of sero-cross-reactivity	No confirmatory assay, presumptive exposure only	Unable to judge based on the information presented[2]

MAYV: Mayaro virus; PCR: polymerase chain reaction; PRNT: plaque-reduction neutralization test; HI:
hemagglutination inhibition; ELISA: enzyme-linked immunosorbent assay
[1]When multiple methods were used with varying validity (e.g., HI and PCR), we assigned a score to the most valid
assay that detected MAYV positivity.
[2]When no MAYV-positive results were found, we assigned a score of N/A.

Table 2. Unique occurrences by country and location type

Country	Point	Polygon	Total
Brazil	35	100	135
Peru	10	24	34
French Guiana	23	8	31
Suriname	5	9	14
Trinidad & Tobago	11	2	13
Colombia	3	6	9
Venezuela	4	3	7
Panama	4	2	6
Bolivia	1	5	6
Ecuador	0	5	5
Mexico	0	2	2
Haiti	0	1	1
Costa Rica	0	1	1

Antigua	0	1	1
Guyana	0	1	1
TOTALS	**96**	**170**	**266**

410

411 **Table 3. Mayaro virus occurences by host type and spatial resolution**

	Points	Custom	Admin3	Admin2	Admin1	Admin0
Human	74	24	7	88	19	10
Non-human animal	7	2	0	20	4	1
Arthropod	15	3	1	2	1	2

412

413 **Code Availability**

414 No custom code was used to generate or process the data described in the manuscript.

References

1   Anderson, C. R., Downs, W. G., Wattley, G. H., Ahin, N. W. & Reese, A. A. Mayaro virus: a new human disease agent. II. Isolation from blood of patients in Trinidad, B.W.I. *Am J Trop Med Hyg* **6**, 1012-1016, doi:10.4269/ajtmh.1957.6.1012 (1957).

2   Causey, O. R. & Maroja, O. M. Mayaro virus: a new human disease agent. III. Investigation of an epidemic of acute febrile illness on the river Guama in Para, Brazil, and isolation of Mayaro virus as causative agent. *Am J Trop Med Hyg* **6**, 1017-1023 (1957).

3   LeDuc, J. W., Pinheiro, F. P. & Travassos da Rosa, A. P. An outbreak of Mayaro virus disease in Belterra, Brazil. II. Epidemiology. *Am J Trop Med Hyg* **30**, 682-688, doi:10.4269/ajtmh.1981.30.682 (1981).

4   Schaeffer, M., Gajdusek, D. C., Lema, A. B. & Eichenwald, H. Epidemic jungle fevers among Okinawan colonists in the Bolivian rain forest. I. Epidemiology. *Am J Trop Med Hyg* **8**, 372-396, doi:10.4269/ajtmh.1959.8.372 (1959).

5   Auguste, A. J. *et al.* Evolutionary and Ecological Characterization of Mayaro Virus Strains Isolated during an Outbreak, Venezuela, 2010. *Emerg Infect Dis* **21**, 1742-1750, doi:10.3201/eid2110.141660 (2015).

6   Forshey, B. M. *et al.* Arboviral etiologies of acute febrile illnesses in Western South America, 2000-2007. *PLoS Negl Trop Dis* **4**, e787, doi:10.1371/journal.pntd.0000787 (2010).

7   Jonkers, A. H., Spence, L. & Karbaat, J. Arbovirus infections in Dutch military personnel stationed in Surinam. Further studies. *Trop Geogr Med* **20**, 251-256 (1968).

8   Talarmin, A. *et al.* Mayaro virus fever in French Guiana: isolation, identification, and seroprevalence. *Am J Trop Med Hyg* **59**, 452-456, doi:10.4269/ajtmh.1998.59.452 (1998).

9   Suhrbier, A., Jaffar-Bandjee, M. C. & Gasque, P. Arthritogenic alphaviruses--an overview. *Nat Rev Rheumatol* **8**, 420-429, doi:10.1038/nrrheum.2012.64 (2012).

10   Pan American Health Organization / World Health Organization. Epidemiological Alert: Mayaro Fever. (2019).

11   Ramshaw, R. E. *et al.* A database of geopositioned Middle East Respiratory Syndrome Coronavirus occurrences. *Sci Data* **6**, 318, doi:10.1038/s41597-019-0330-0 (2019).

12   Messina, J. P. *et al.* A global compendium of human dengue virus occurrence. *Sci Data* **1**, 140004, doi:10.1038/sdata.2014.4 (2014).

13   Messina, J. P. *et al.* A global compendium of human Crimean-Congo haemorrhagic fever virus occurrence. *Sci Data* **2**, 150016, doi:10.1038/sdata.2015.16 (2015).

14   Pigott, D. M. *et al.* Global database of leishmaniasis occurrence locations, 1960-2012. *Sci Data* **1**, 140036, doi:10.1038/sdata.2014.36 (2014).

15   Caicedo, E. Y. *et al.* The epidemiology of Mayaro virus in the Americas: A systematic review and key parameter estimates for outbreak modelling. *PLoS Negl Trop Dis* **15**, e0009418, doi:10.1371/journal.pntd.0009418 (2021).

453   16   Ganjian, N. & Riviere-Cinnamond, A. Mayaro virus in Latin America and the Caribbean. *Revista*
454   *Panamericana de Salud Pública* **44**, doi:10.26633/rpsp.2020.14 (2020).

455   17   Celone, M. *et al.* A systematic review and meta-analysis of the potential non-human animal
456   reservoirs and arthropod vectors of the Mayaro virus. *PLoS Negl Trop Dis* **15**, e0010016,
457   doi:10.1371/journal.pntd.0010016 (2021).

458   18   Schmidt, J. R., Gajdusek, D. C., Schaffer, M. & Gorrie, R. H. Epidemic jungle fever among
459   Okinawan colonists in the Bolivian rain forest. II. Isolation and characterization of Uruma virus, a newly
460   recognized human pathogen. *Am J Trop Med Hyg* **8**, 479-487, doi:10.4269/ajtmh.1959.8.479 (1959).

461   19   U.S. Centers for Disease Control and Prevention. *Arbovirus Catalog. ,*
462   <https://wwwn.cdc.gov/arbocat/VirusDetails.aspx?ID=293&SID=5> (

463   20   Food and Agricultural Organization of the United Nations. The global administrative unit layers
464   (GAUL): technical aspects. . (FAO, 2008).

465   21   Wieczorek, J., Guo, Q. & Hijmans, R. The point-radius method for georeferencing locality
466   descriptions and calculating associated uncertainty. *Int. J. Geogr. Inf. Sci* **18**, 745-767 (2004).

467   22   Chapman, A. D. & Wieczorek, J. *Guide to Best Practices for Georeferencing*. (Global Biodiversity
468   Information Facility. Available at: http://www.gbif.org/resource/80536, 2006).

469   23   Wieczorek, C. & Wieczorek, J. *Georeferencing Calculator*,
470   <http://georeferencing.org/georefcalculator/gc.html> (2021).

471   24   Hill, E. *et al.* A database of geopositioned onchocerciasis prevalence data. *Sci Data* **6**, 67,
472   doi:10.1038/s41597-019-0079-5 (2019).

473   25   Hoch, A. L., Peterson, N. E., LeDuc, J. W. & Pinheiro, F. P. An outbreak of Mayaro virus disease in
474   Belterra, Brazil. III. Entomological and ecological studies. *Am J Trop Med Hyg* **30**, 689-698,
475   doi:10.4269/ajtmh.1981.30.689 (1981).

476   26   Chisenga, C. C. *et al.* Sero-prevalence of arthropod-borne viral infections among Lukanga swamp
477   residents in Zambia. *PloS One* **15**, e0235322, doi:10.1371/journal.pone.0235322 (2020).

478   27   Hassing, R. J., Leparc-Goffart, I., Tolou, H., van Doornum, G. & van Genderen, P. J. Cross-
479   reactivity of antibodies to viruses belonging to the Semliki forest serocomplex. *Euro Surveill.* **15** (2010).

480   28   Escobar, L. E. & Craft, M. E. Advances and Limitations of Disease Biogeography Using Ecological
481   Niche Modeling. *Front. Microbiol.* **7**, doi:10.3389/fmicb.2016.01174 (2016).

482   29   Deribe, K. *et al.* Mapping the global distribution of podoconiosis: Applying an evidence
483   consensus approach. *PLoS Negl Trop Dis* **13**, e0007925, doi:10.1371/journal.pntd.0007925 (2019).

484   30   Deribe, K. *et al.* Predicting the environmental suitability and population at risk of podoconiosis in
485   Africa. *PLoS Negl Trop Dis* **14**, e0008616, doi:10.1371/journal.pntd.0008616 (2020).

486   31   Bhatt, S. *et al.* The global distribution and burden of dengue. *Nature* **496**, 504-507,
487   doi:10.1038/nature12060 (2013).

488   32   Kramer-Schadt, S. *et al.* The importance of correcting for sampling bias in MaxEnt species
489   distribution models. *Divers. Distrib.* **19**, 1366-1379, doi:10.1111/ddi.12096 (2013).

490   33   Nsoesie, E. O. *et al.* Global distribution and environmental suitability for chikungunya virus, 1952
491   to 2015. *Euro Surveill* **21**, doi:10.2807/1560-7917.Es.2016.21.20.30234 (2016).
492