

APPROVED: 05 January 2020

doi:10.2903/sp.efsa.2020.EN-1800

RVF vector spatial distribution models: Probability of presence

William Wint¹, Wim Van Bortel², Francis Schaffner³

1. Ergo – Environmental Research Group Oxford, Oxford, United Kingdom
2. Institute of Tropical Medicine, Antwerp, Belgium
3. Francis Schaffner Consultancy, Riehen, Switzerland

Abstract

EFSA has requested the Vextornet consortium to undertake a series of spatial distribution models for seven potential mosquito vectors of Rift Valley fever virus, namely *Aedes albopictus*, *Aedes caspius*, *Aedes detritus*, *Aedes japonicus*, *Aedes vexans*, *Culex pipiens* and *Culex theileri*. The modelling used the distribution data held within the VectorNet archive (as at September 2018), updated by literature searches to acquire new records available since 2016. The modelling has been implemented in three phases: (i) data collection, collation and standardisation; (ii) spatial modelling for presence and absence, and the calculation of presence metrics at the country level to be compatible with the MintRisk utilities; and (iii) the spatial modelling of vector abundance, dependent on the data available. This document briefly summarises the results of the data collection, and presence and absence modelling due for delivery in December 2020. Sufficient data were amassed to produce statistically reliable spatial models of the probability of presence of all species except *Ae. detritus*. The models were implemented at 1 km resolution covering the whole of continental Europe, using standard modelling techniques (Boosted Regression Trees and Random Forest) implemented through the VECMAP software suite. The distribution data for the period 2016 onward will be added to the VectorNet archive when its migration to a new data warehouse within ECDC has been completed. All spatial data in the form of an ARCMAP ‘package’ containing summaries of the vector distribution data collected, and all model outputs have been made available online to Vectornet partners, EFSA and ECDC. This interim report will be followed by a more complete document which also includes the results of the abundance modelling, due in March 2020.

© European Food Safety Authority, 2020

Key words: Rift Valley fever virus, probability of presence, spatial distribution model, mosquito vectors, Europe

Question number: EFSA-Q-2020-00131

Correspondence: ALPHA@efsa.europa.eu

Disclaimer: The present document has been produced and adopted by the bodies identified above as author(s). This task has been carried out exclusively by the author(s) in the context of a contract between the European Food Safety Authority and the author(s), awarded following a tender procedure. The present document is published complying with the transparency principle to which the Authority is subject. It may not be considered as an output adopted by the Authority. The European Food Safety Authority reserves its rights, view and position as regards the issues addressed and the conclusions reached in the present document, without prejudice to the rights of the authors.

Acknowledgements: We thank the VectorNet consortium and our counterparts with the VectorNet funding agencies for their support and input. We thank Marijn van der Gaag and Renate Smallegange from Wageningen Academic Publishers for editing this report.

Suggested citation: Wint W, Van Bortel W, Schaffner F, 2020. RVF vector spatial distribution models: Probability of presence. EFSA supporting publication 2020:EN-1800. 30 pp.
doi:10.2903/sp.efsa.2020.EN-1800

ISSN: 2397-8325

© European Food Safety Authority, 2020

Reproduction is authorised provided the source is acknowledged.

Summary

The VectorNet consortium received an ad hoc request for technical support from the European Food Safety Authority (EFSA) to quantify the risk of Rift Valley fever (RVF) virus to the European Union in September 2019. One of the activities required to contribute to the risk assessment is an estimation of the distribution of the main RVF arthropod vectors within each member state. The vectors specified are *Aedes albopictus*, *Aedes vexans*, *Aedes japonicus*, *Culex pipiens*, *Culex theileri*, *Aedes (Ochlerotatus) caspius* and *Aedes (Ochlerotatus) detritus*.

This first phase of distribution modelling focuses only on presence and absence assessment. Sufficient data were available for all species except *Ae. detritus*.

Table of contents

Abstract.....	1
Summary	3
1. Introduction.....	5
1.1. Background and Terms of Reference as provided by the requestor	5
1.2. Interpretation of the Terms of Reference.....	5
1.3. Additional information	5
2. Data and Methodologies	5
2.1. Data.....	5
2.2. Methodologies	5
3. Results	7
4. Conclusions	10
Appendix A- Habitat masks used to define absences.....	11
Appendix B- File list	17
Appendix C- Available point and polygon data	19
Appendix D- Masked and unmasked predictions.....	25
Appendix E- Spreadsheet column list	30

1. Introduction

1.1. Background and Terms of Reference as provided by the requestor

This contract/grant was awarded by EFSA to: VectorNet

Contractor/Beneficiary: VectorNet

Contract/Grant title: RVF vector spatial distribution models: Probability of presence

Contract/Grant number: SPECIFIC CONTRACT No 01/EFSA implementing framework contract NO ECDC/2019/020

1.2. Interpretation of the Terms of Reference

The overall aim of this scientific report is to model the probability of presence of Rift Valley fever (RVF) arthropod vectors in Europe using spatial distribution models.

RVF is a mosquito-borne viral disease affecting mainly ruminants. It causes abortion in pregnant susceptible ruminants and high mortality in new-borne animals. During epidemics, it can have a high impact on public health and the economy in the affected regions. The disease is caused by the RVF virus, a virus of the family Bunyaviridae and genus *Phlebovirus*. The virus has been isolated from more than 30 mosquito species. Mosquitoes belonging to the *Aedes* and *Culex* genera are considered to be the main vectors. The disease is widespread in Africa and it spread to the Arabian Peninsula in 2000-2001.

1.3. Additional information

The VectorNet consortium received an ad hoc request for technical support from the European Food Safety Authority (EFSA) to quantify the risk of RVF virus to the European Union in September 2019. One of the activities required to contribute to the risk assessment is an estimation of the distribution of the main RVF arthropod vectors within each member state. The vectors specified are *Aedes albopictus*, *Aedes vexans*, *Aedes japonicus*, *Culex pipiens*, *Culex theileri*, *Aedes (Ochlerotatus) caspius* and *Aedes (Ochlerotatus) detritus*. This first phase of distribution modelling focuses only on presence and absence assessment.

2. Data and Methodologies

2.1. Data

The methods thus depend heavily on the availability of known observations (training data). For these RVF vectors, training data were available from a number of sources, namely the VectorNet archive, as of September 2019; a series of previous studies by Avia-GIS on RVF vector distribution produced for EFSA in 2013, and data collated from and extensive literature review for all specified species from 2016 to date. These data consist of georeferenced point data and records of distribution status within a polygon (Present, Absent, Introduced, Established) for administrative units ("polygon data").

2.2. Methodologies

The method specified to provide distribution of the main RVF arthropod vectors within each member state was to provide spatial distribution models of the vectors based on the methodologies outlined in the recent European Centre for Disease Prevention and Control Technical Report entitled "A spatial modelling method for vector surveillance, namely Boosted Regression Trees and/or Random Forest modelling". These methods estimate statistical relationships between known georeferenced observations of presence, absence or abundance and a series of predictor covariates at a series of sample locations. These relationships are then used to calculate the predicted probability of presence (or abundance) for the whole area of interest at a fixed resolution, in this case 1 kilometre.

This first phase of distribution modelling focuses only on presence and absence assessment. The majority of both polygon and point data collated are for vector presence – absence records are relatively few and far between. The methods used rely on training data that is comprised of roughly equal numbers of presence and absence data points. This means that absence points had to be defined. This is often done by assuming that vectors are absent in all areas more than a certain distance from known locations of presence (pseudo-absence). This is not, however particularly effective if the distribution of known presences is patchy or only available for a part of the vector's likely range – as is the case for most of the species modelled in this exercise. An alternative is to define absence based on known ecological preferences for habitat type, climate or environment (or indeed any other known limiting factor), i.e. the suitable habitat. Known flight ranges can be added as buffers to the suitable habitat. Absences can then be allocated to locations defined as unsuitable and beyond the flight range from suitable habitats.

To define the habitat suitabilities, the land cover categories for two land cover surfaces (Corine and the ESA CCI) were defined as primary, secondary or unsuitable. These were assessed against the available distribution records, and unsuitable habitat defined using primary or primary plus secondary habitat scores accordingly. To these, known climate limits and flight ranges were added. The resulting layers are shown in Appendix A. Absences were then allocated throughout the area of interest – even if distribution status is otherwise unknown – as well as within unsuitable locations of polygons of known presence and throughout polygons of known absence.

Presences were obtained from the point location records, and were also defined within habitat suitable areas of the polygons where the distribution status was defined as present. All presences and absences other than those from known point records were allocated randomly within designated areas. The numbers allocated were set so that the final numbers of presence and absence records were approximately equal.

For some species, the point location records were heavily clustered or records for a single location were available for several dates. In an attempt to remove contradictions this produced – records were aggregated by location and the maximum value calculated for each aggregated point. Absences (0) were thus superseded by presences (1). Three levels of aggregation were performed – the precise coordinate, 0.1 degree (approx. 10 km), and 0.01 degree (approx. 1 km). Each aggregated dataset was 'balanced' using random selection of the largest category so that the numbers of presence and absence points were approximately equal.

Though the core of the final datasets is the existing VectorNet archive, substantial amounts of data were available from the 2013 Avia-GIS datasets – significant numbers of point data and limited polygon only data for *Ae. vexans*, *Cx. pipiens*, and *Cx. theileri*, and some polygon data were available for *Ae. caspius*. The recent literature review provided large numbers of point records and relatively few polygon level records for all species. The polygon level records with no precise sample coordinates have been added to the data entry VectorNet polygon map file supplied with this preliminary report and are identified by the date in the species *dat columns (see file list in Appendix B). The polygons have NOT been updated with the new point data, which are too extensive to be processed within the resources available. It is envisaged that these will be added to the VectorNet archive once the ongoing migration to ECDC's new data warehouse has been finalised. Both the points and the polygon status of each species is however illustrated in Appendix C.

Spatial modelling requires the training data to be fairly evenly spread throughout the potential range of each target species. If the records are too clustered or too sparse then modelling is not possible. Sufficient data were available for all species except *Ae. detritus*.

As indicated above, spatial modelling was implemented with Boosted Regression Trees and Random Forest Techniques, executed through the VECMAP software suite. Models were only accepted with a minimum AUC metric of 0.85, and outputs for each method were ensembled to provide a mean prediction. These consensus predictions were then partially masked using the least constrained habitat suitability surfaces, i.e. those using primary and secondary habitats in their definition. The unmasked outputs for 'unsuitable' areas were reduced by a quarter. In this way the models were 'allowed' to

predict presence in unsuitable areas, but only those where the modelled probability was highest. Both masked and unmasked predictions are illustrated in Appendix D.

The final masked outputs were converted to binary presence or absence using a threshold of 0.5 and these files then used to calculate the proportion of each EU Member State with each vector species predicted to be present. Two combination measures have also been provided: the proportion of each member state where the sum of predicted probabilities for all species exceeds 80%; and the proportion of each Member State where at least one species is predicted to be present (i.e. where the predicted probability of presence of least one species is more than 0.5). These tables are both provided individually and summarised in the spreadsheet that accompanies this report. The summary table is presented in Table 1 and illustrated in Figure 1 below, and the worksheets are listed in Appendix E.

3. Results

All geographic data – predicted surfaces, updated point and polygon data, and habitat suitability surfaces are provided in an ArcMap 10.4 ‘package’ *vnrvfvectormodelsdec19.mpk* which is available for download at the following link:

https://drive.google.com/open?id=1SK8tObt50Su6b_Pus1BUDwSvNyeorfDK.

This dataset also includes a surface for the distribution of vector hosts, provided for a previous EFSA study, to allow for the calculation of the overlap between hosts and predicted vector presence. The package includes an ArcMap document (*vnrvfvectormodelsdec19.mpk.mxd*) file which displays all layers with an explanatory legend and simplified file label. Actual filenames to which these file label refer are given in the file list in Appendix B, and can be accessed through the source tab in the layer properties dialogue box.

Table 1: Proportion of each country with predicted presence of RVF vectors.

Country	EU	ALL Spp.	Sum prob >0.8	albo	casp	japo	pip	thei	vexa
Austria	YES	0.805	1.000	0.455	0.003	0.609	0.261	0.000	0.524
Belgium	YES	0.998	1.000	0.592	0.263	0.572	0.980	0.000	0.924
Bulgaria	YES	0.905	1.000	0.468	0.219	0.009	0.367	0.004	0.633
Croatia	YES	0.988	1.000	0.897	0.142	0.721	0.690	0.004	0.701
Cyprus	YES	0.741	1.000	0.332	0.393	0.000	0.064	0.563	0.003
Czechia	YES	0.413	0.996	0.053	0.001	0.098	0.067	0.000	0.303
Denmark	YES	0.473	1.000	0.000	0.075	0.000	0.130	0.000	0.444
Estonia	YES	0.471	0.694	0.000	0.000	0.000	0.021	0.000	0.477
Finland	YES	0.050	0.286	0.000	0.001	0.000	0.096	0.000	0.048
France	YES	0.846	0.996	0.639	0.142	0.267	0.414	0.025	0.485
Germany	YES	0.888	1.000	0.333	0.033	0.589	0.260	0.000	0.598
Greece	YES	0.899	1.000	0.697	0.355	0.000	0.527	0.327	0.194
Hungary	YES	0.998	1.000	0.140	0.042	0.157	0.162	0.000	0.994
Ireland	YES	0.156	1.000	0.000	0.154	0.002	0.358	0.000	0.001
Italy	YES	0.862	0.989	0.734	0.354	0.149	0.502	0.135	0.376
Latvia	YES	0.663	0.778	0.000	0.000	0.000	0.009	0.000	0.669
Lithuania	YES	0.963	0.975	0.000	0.000	0.000	0.003	0.000	0.963
Luxembourg	YES	1.000	1.000	0.875	0.000	1.000	0.987	0.000	0.745
Malta	YES	1.000	1.000	0.846	0.989	0.000	0.939	0.783	0.133
Netherlands	YES	0.984	1.000	0.208	0.325	0.226	0.667	0.000	0.972
Poland	YES	0.798	0.977	0.012	0.001	0.005	0.026	0.000	0.792
Portugal	YES	0.917	1.000	0.741	0.378	0.008	0.746	0.776	0.079
Romania	YES	0.869	1.000	0.160	0.172	0.093	0.132	0.000	0.802
Slovakia	YES	0.713	1.000	0.151	0.004	0.130	0.085	0.000	0.608
Spain	YES	0.474	0.993	0.294	0.142	0.060	0.224	0.213	0.043
Sweden	YES	0.122	0.339	0.000	0.001	0.000	0.036	0.000	0.122
United Kingdom	YES	0.290	0.999	0.004	0.258	0.019	0.497	0.000	0.113
Albania	NO	0.942	1.000	0.858	0.278	0.035	0.793	0.102	0.476
Andorra	NO	0.350	0.950	0.150	0.000	0.007	0.279	0.000	0.248
Bosnia and Herzegovina	NO	0.951	1.000	0.880	0.035	0.647	0.880	0.010	0.751
Faroe Islands	NO	0.031	0.990	0.000	0.004	0.010	0.047	0.000	0.010
Iceland	NO	0.003	0.090	0.000	0.000	0.000	0.000	0.000	0.000
Kosovo*	NO	0.944	1.000	0.785	0.124	0.265	0.804	0.000	0.813
Liechtenstein	NO	1.000	1.000	0.571	0.000	0.938	0.636	0.000	0.669
North Macedonia	NO	0.809	1.000	0.448	0.202	0.011	0.554	0.001	0.544
Moldova	NO	0.926	0.999	0.000	0.384	0.000	0.035	0.000	0.921
Monaco	NO	0.000	1.000	0.000	0.235	0.000	1.000	0.000	0.000
Montenegro	NO	0.985	1.000	0.672	0.100	0.102	0.763	0.014	0.852
Norway	NO	0.023	0.171	0.000	0.006	0.001	0.026	0.000	0.016
San Marino	NO	1.000	1.000	1.000	0.105	0.000	0.848	0.010	0.362
Serbia	NO	0.949	1.000	0.538	0.067	0.404	0.573	0.000	0.845
Slovenia	NO	0.988	1.000	0.947	0.015	0.980	0.838	0.000	0.676
Switzerland	NO	0.679	0.982	0.443	0.002	0.554	0.483	0.000	0.536
Turkey	NO	0.836	0.998	0.185	0.152	0.001	0.208	0.666	0.313

albo = *Aedes albopictus*; casp = *Aedes caspius*; japo = *Aedes japonicus*; pip = *Culex pipiens*; thei = *Culex theileri*; vexa = *Aedes vexans*. EU = EU Member State; All Spp. = Any vector present; Sum prob >0.8 = Sum of predicted probabilities for all species >0.8.

* This designation is without prejudice to positions on status and is in line with UNSCR 1244 and the ICJ Opinion on the Kosovo Declaration of Independence. This footnote applies all the time Kosovo is mentioned in this document

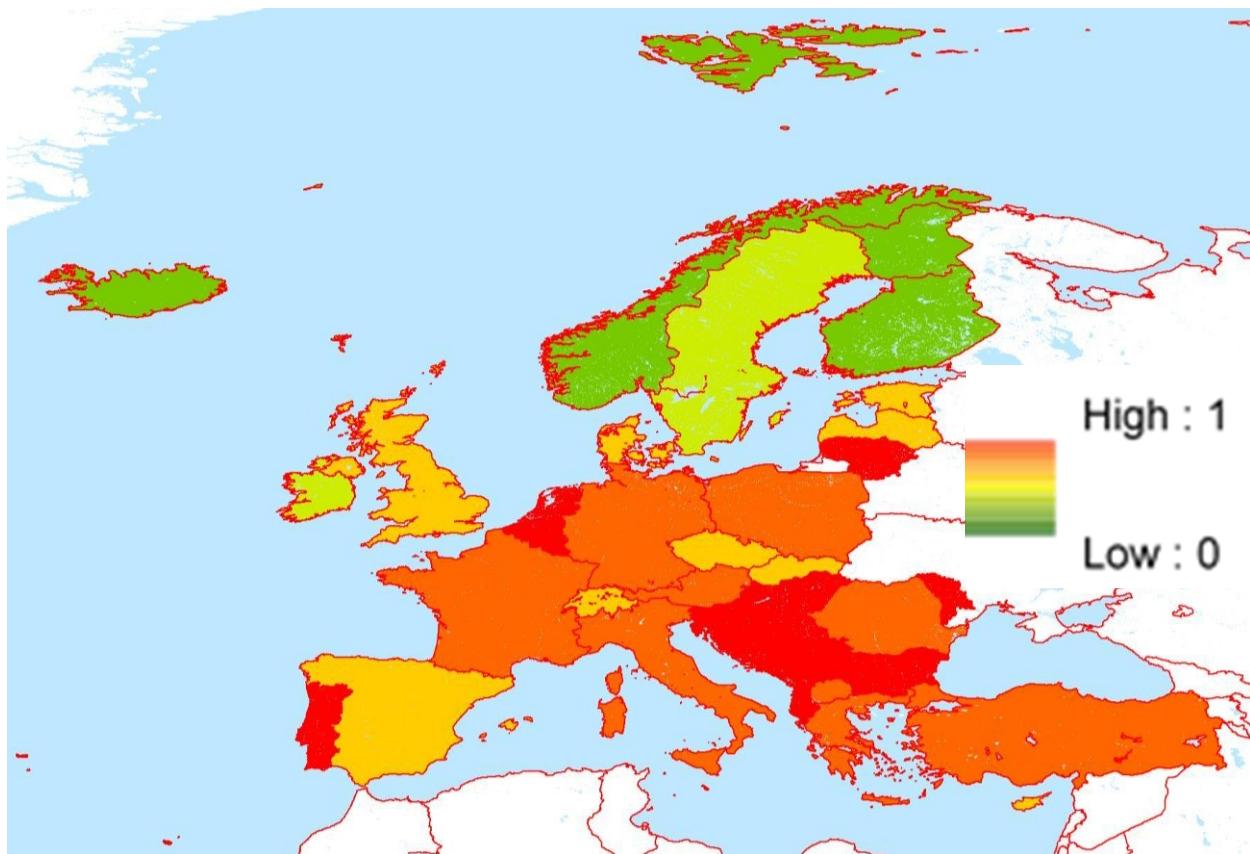
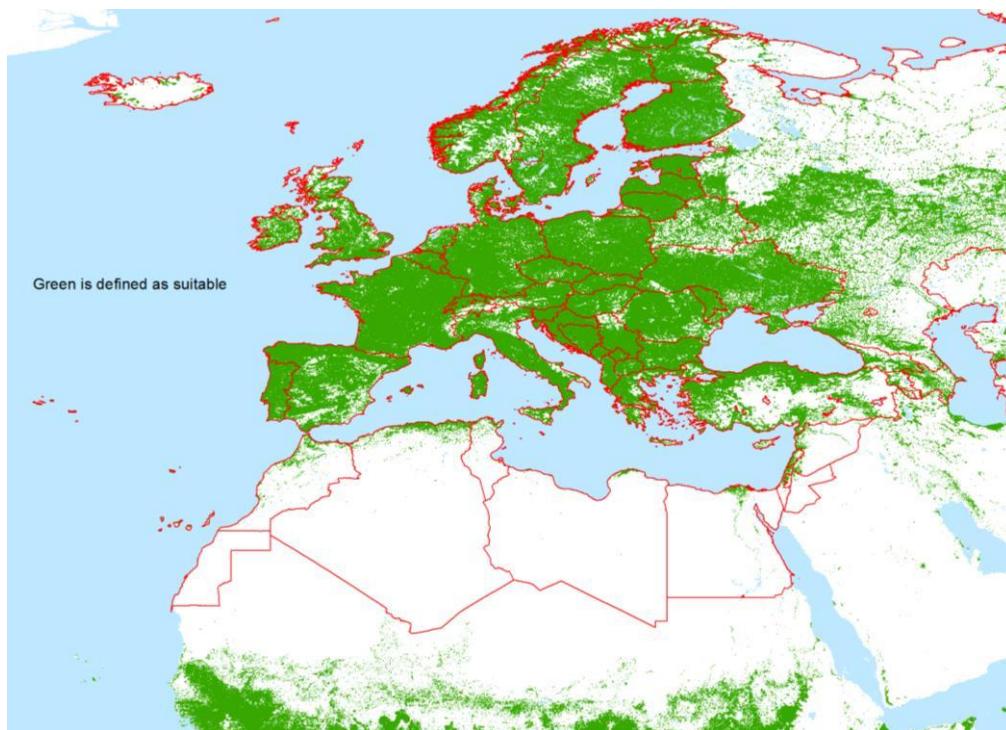


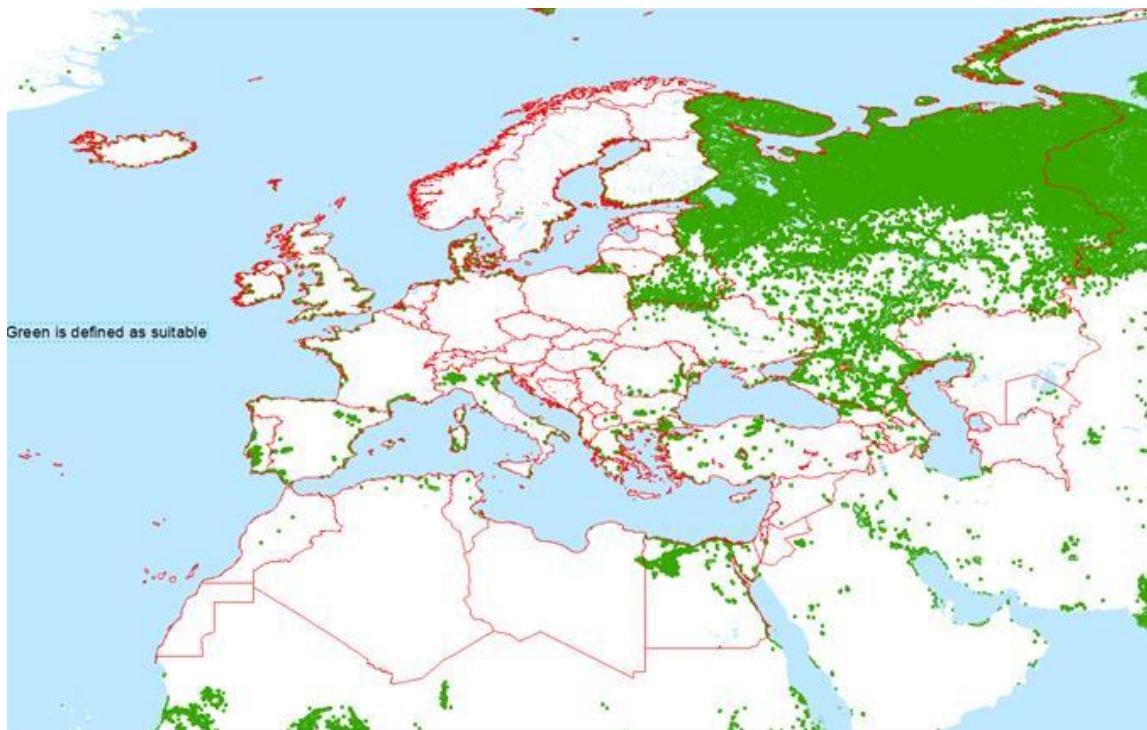
Figure 1: Proportion of each country with predicted presence of RVF vectors.

4. Conclusions

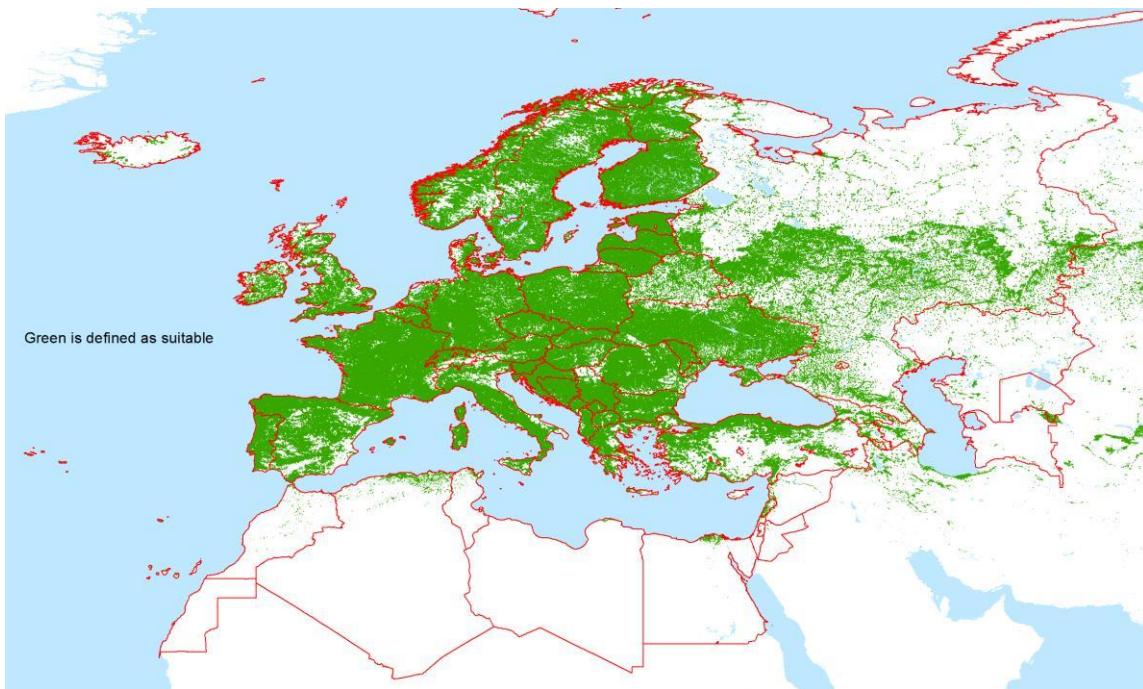
This first phase of distribution modelling focuses only on presence and absence assessment. Sufficient data were available for all species except *Ae. detritus*.

Appendix A- Habitat masks used to define absences

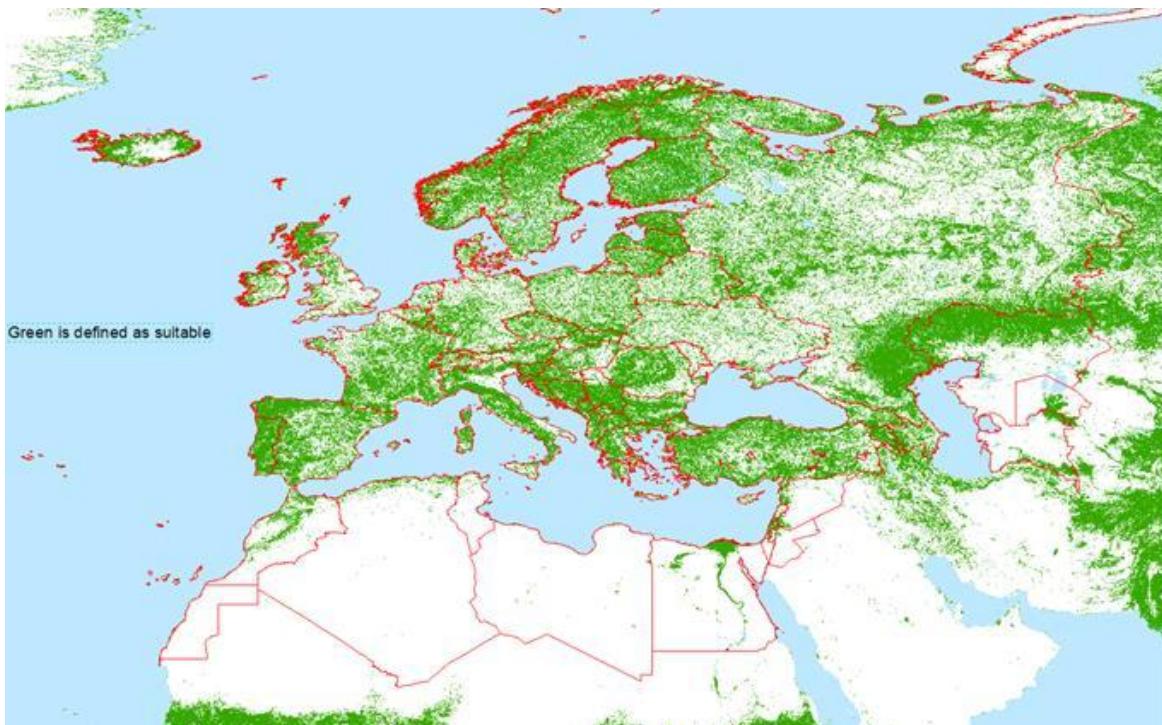
Habitat masks used to define absences for *Ae. albopictus* (primary and secondary).



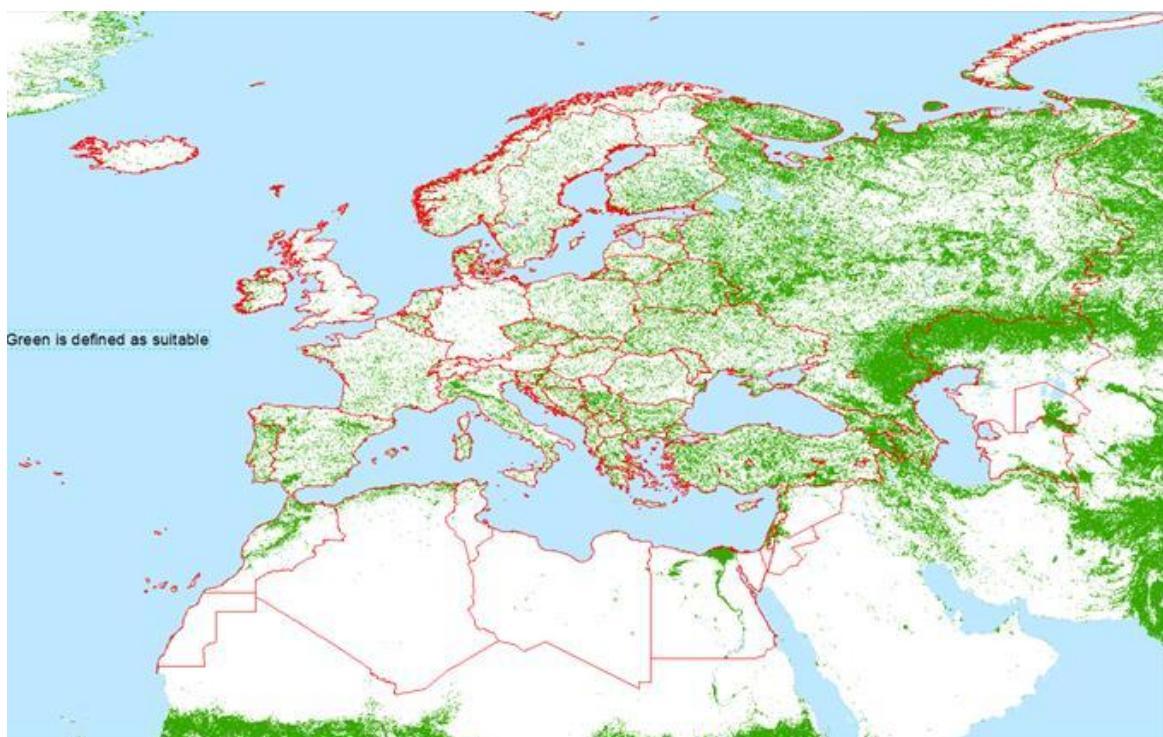
Habitat masks used to define absences for *Ae. caspius* (primary).



Habitat masks used to define absences for *Ae. japonicus* (primary).



Habitat masks used to define absences for *Cx. pipiens* (primary and secondary).



Habitat masks used to define absences for *Cx. theileri* (primary and secondary).



Habitat masks used to define absences for *Ae. vexans* (primary).

Appendix B- File list

Table 2. All GIS data are provided as an ARCMAP 10.4.1 'package' vnrvfvectormodelsdec19.mpk , visualised using the ARC Document file supplied (vnrvfvectormodelsdec19.mxd). The package can be downloaded from the following link

https://drive.google.com/open?id=1SK8tObt50Su6b_Pus1BUDwSvNyeorfDK.

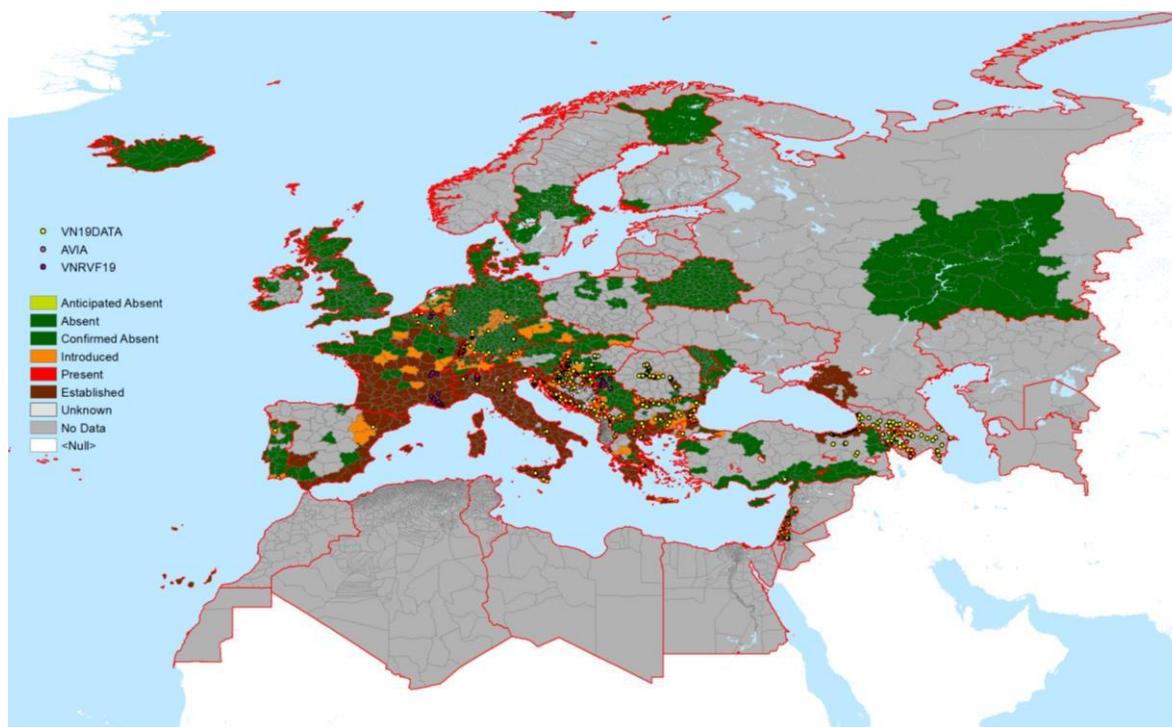
Probability Presence file	Masked	Unmasked
Albopictus	albo10xyPABALBRTRFMEANmsk2y3qunsuit.tif	albo10xyPABALBRTRFMEAN.tif
Caspius	caspious10xyPABALBRTRFMEANmsk2y3qunsuit.tif	casp10xyPABALBRTRFMEAN.tif
Japonicus	jap10xyPABALBRTRFMEANmsk2y3qunsuit.tif	jap10xyPABALBRTRFMEAN.tif
Pipiens	pip10xyPABALBRTRFMEANmsk2y3qunsuit.tif	pip10xyPABALBRTRFMEAN.tif
Theileri	the10xyPABALBRTRFMEANmsk2y3qunsuit.tif	the10xyPABALBRTRFMEAN.tif
Vexans	vex10xyPABALBRTRFMEANmsk2y3qunsuit.tif	vex10xyPABALBRTRFMEAN.tif
Binary PA files from Masked Predictions		
All vectors	ALLRVFVECTORS10xyMEANBinaryPres.tif	
Sum vector probabilities gt 0.8	sumRVF19vectprhighRVF.tif	
Albopictus	albo10xyMEANBinaryPres.tif	
Caspius	caspious10xyMEANBinaryPres.tif	
Japonicus	japonicus10xyMEANBinaryPres.tif	
Pipiens	pipiens10xyMEANBinaryPres.tif	
Theileri	theileri10xyMEANBinaryPres.tif	
Vexans	vexans10xyMEANBinaryPres.tif	
High host density from previous study	any90hosthighCCHV.tif	
Habitat mask files	Primary	Secondary
Albopictus	ALBOunsuitallP2.tif	ALBOunsuitall2.tif
Caspius	caspiusLUunsuitbuff1k01P.TIF	caspiusLUunsuitbuff1k01.TIF
Japonicus	Japunsuitall.tif	JapunsuitallP.tif
Pipiens	pipiensLUunsuit1k01P.TIF	pipiensLUunsuit1k01.TIF
Theileri	theileriLUunsuit1k01P.tif	theileriLUunsuit1k01.tif
Vexans	vexansLUunsuitbuff1k01P.TIF	vexansLUunsuitbuff1k01.TIF

Updated Vectornet Point Data	Filename	
Albopictus	newandoldalbopictuspointnov19.shp	
Caspious	newandoldcaspiusspointnov19.shp	
Japonicus	newandoldjaponicuspointnov19.shp	
Pipiens	newandoldpipienspointnov19.shp	
Theileri	newandoldtheileripointnov19.shp	
Vexans	newandoldvexanspointnov19.shp	

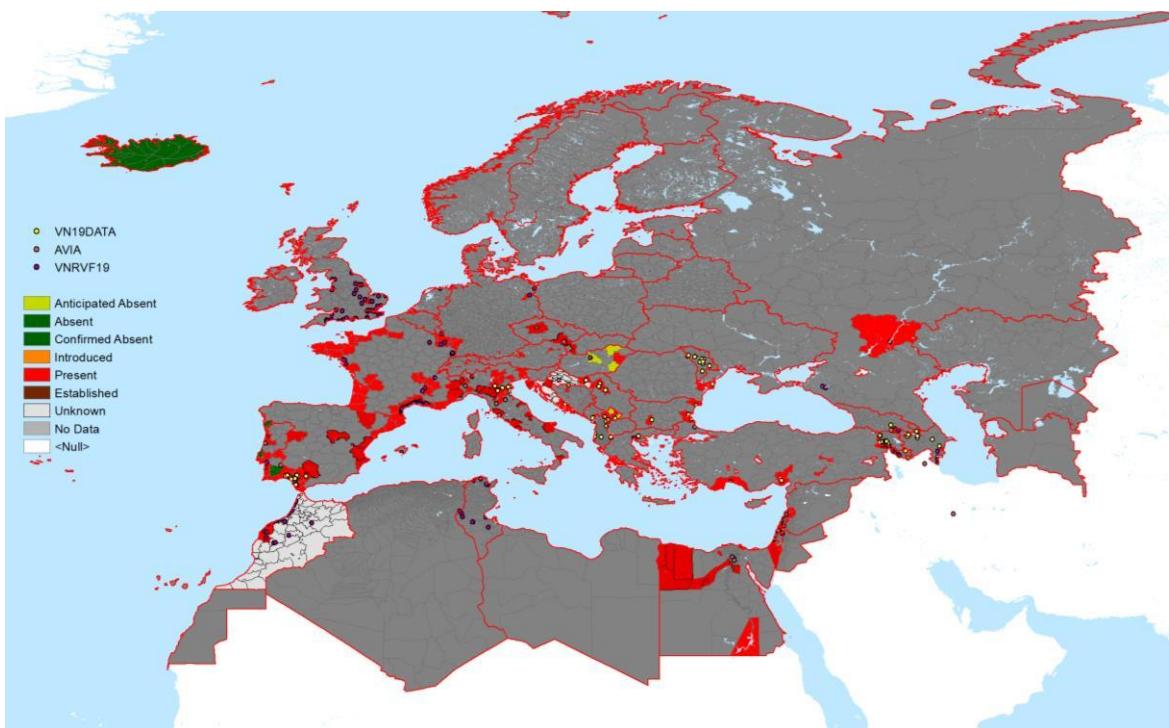
Columns:
 Rowid, sourcerow: File row number, rownumber from source data files.
 Latitude and longitude - recorded laitude and longitude
 *.pa and *.rfpa, presence or absence coded for BRT and RF moelling
 Lat10k,lon10k: latitude and Longitude rounded to 1 decimal place
 lat1k, lon1k :latitude and Longitude rounded to 2 decimal places
 studysampl : sample size or number trap nights
 collmeth, traptyle: collections method and trap type
 number, Innum, numcat: recoded number, In (number +1), abundance category
 numbersamp, Innumpsamp, numpsamCAT: Number per sample or trapnight, In (number per sample +1), number per sample category
 Country

NOTE: the number related files are working data which will be adapted and used in attempts to model abundance

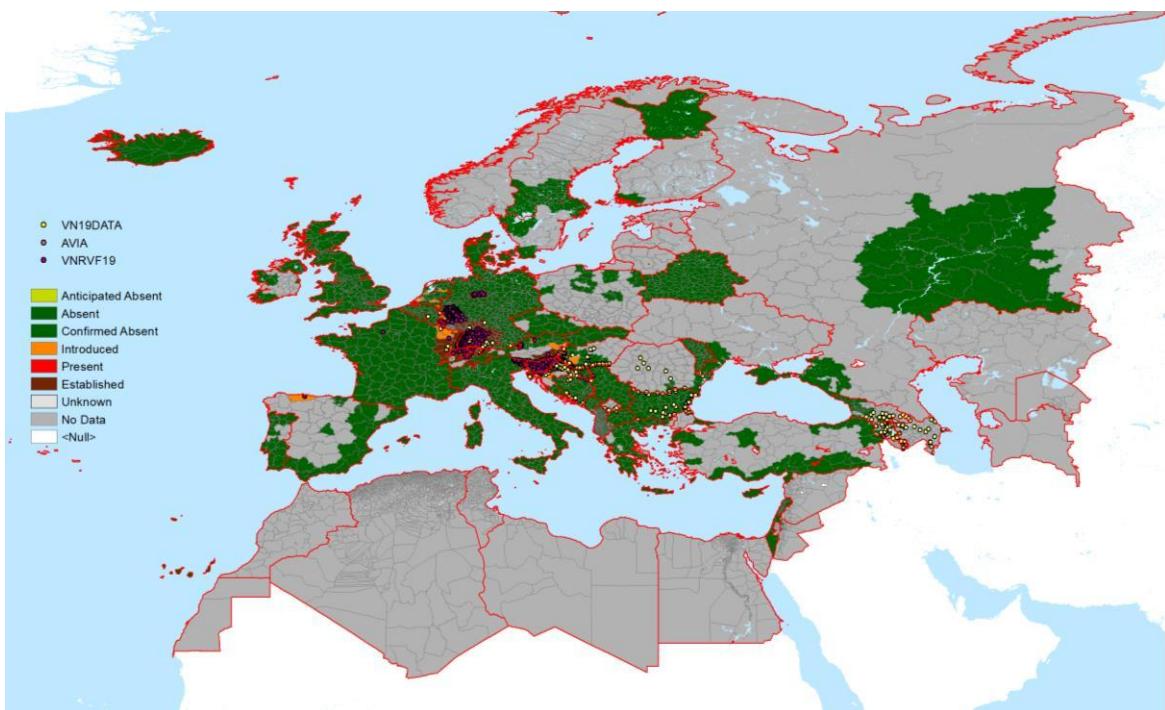
Updated Vectornet Polygon Data	Filename	Status and status date columns (Nov and Dec 2019 dates indicate date of update)
Albopictus	vnmapnov19rvfmosq.shp	albstat, albdat
Caspious	vnmapnov19rvfmosq.shp	casstat, casdat
Japonicus	vnmapnov19rvfmosq.shp	japstat, japdat
Pipiens	vnmapnov19rvfmosq.shp	pipstat, pipdat
Theileri	vnmapnov19rvfmosq.shp	thestat, thedat
Vexans	vnmapnov19rvfmosq.shp	vexstat, vexdat
Additional Files		
mintriskrvf19vectorsby country.xls	Excel with extracted vector data per country, suitability tables, files and column lists,	
Draft RVFVector modelling V2.docx	This document file	

Appendix C- Available point and polygon data

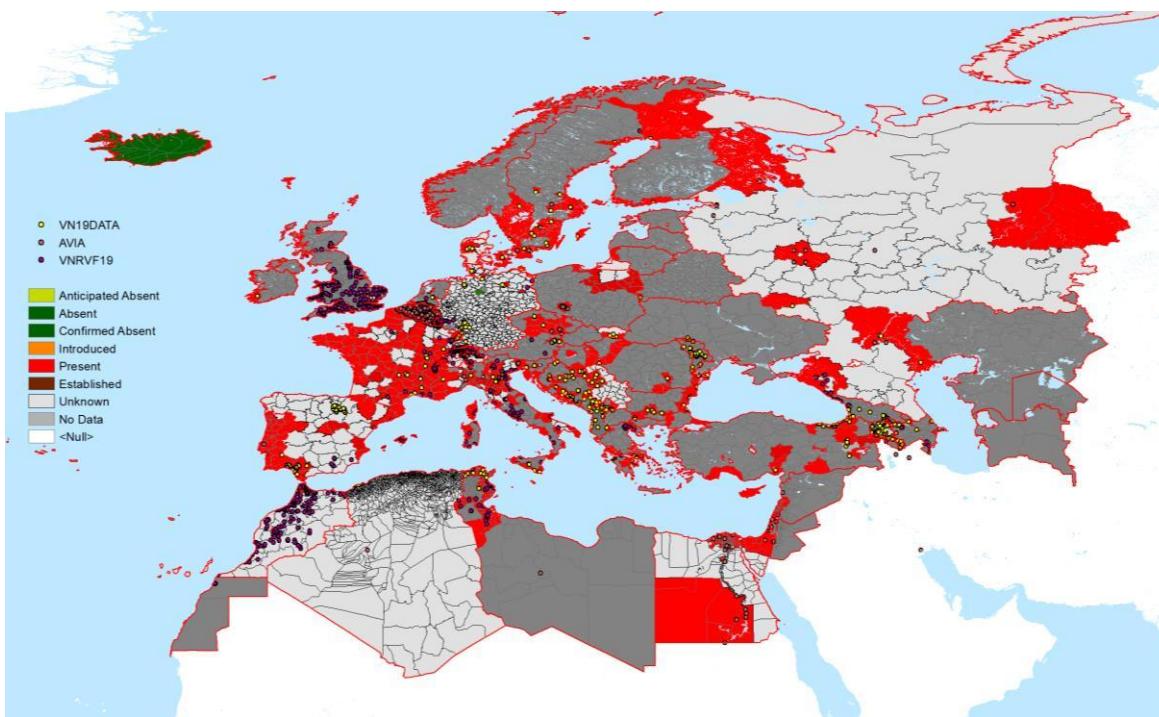
Available point and polygon data for *Ae. albopictus*.



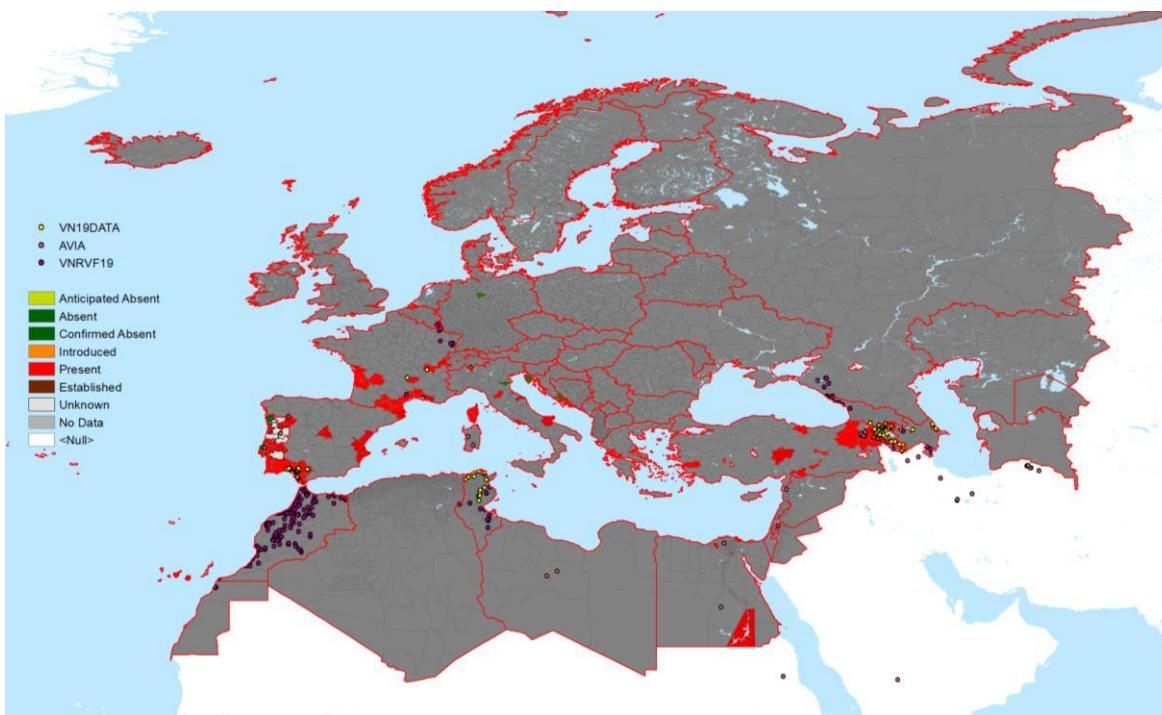
Available point and polygon data for *Ae. caspius*.



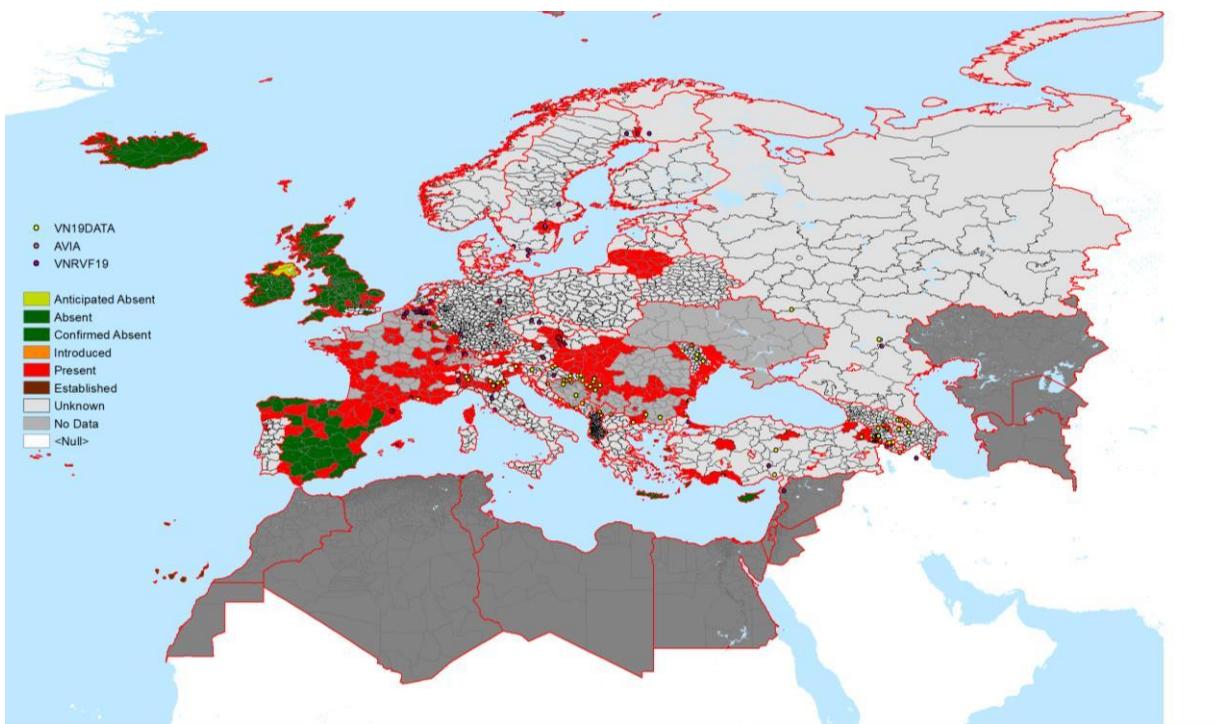
Available point and polygon data for *Ae. japonicus*.



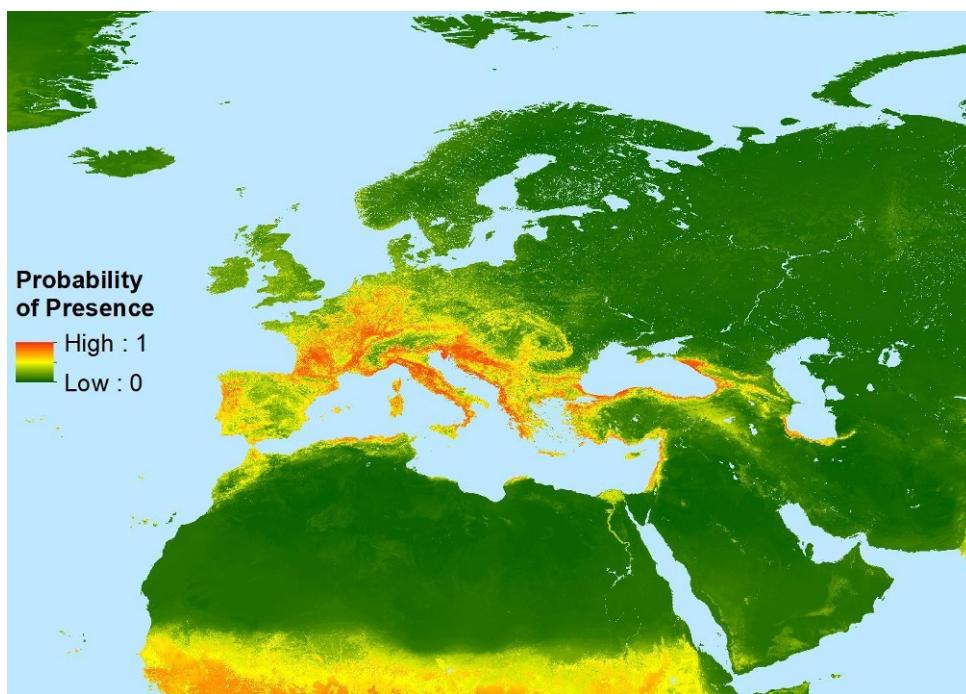
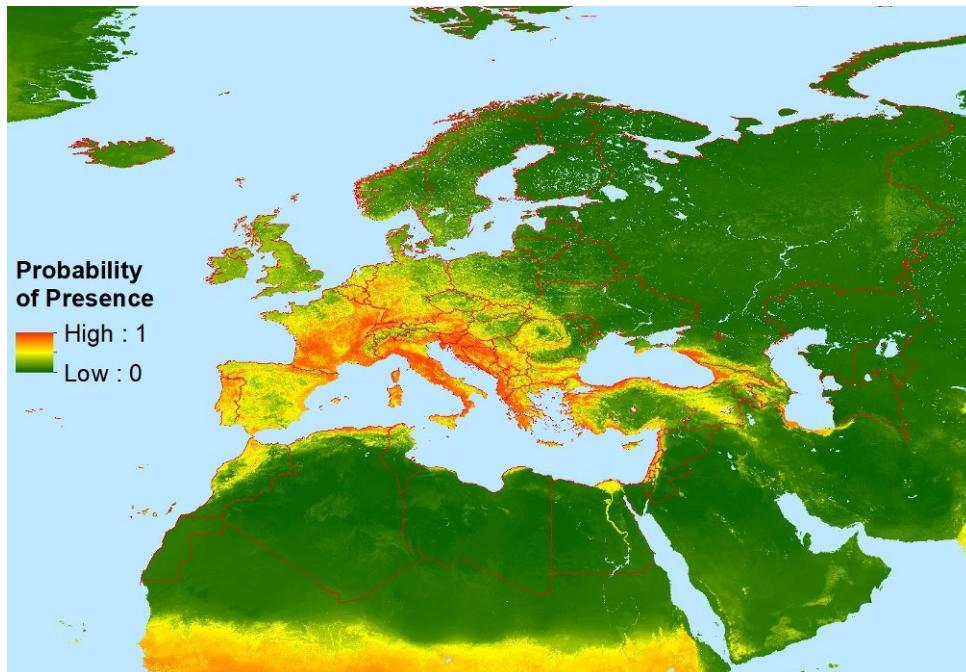
Available point and polygon data for *Cx. pipiens*.

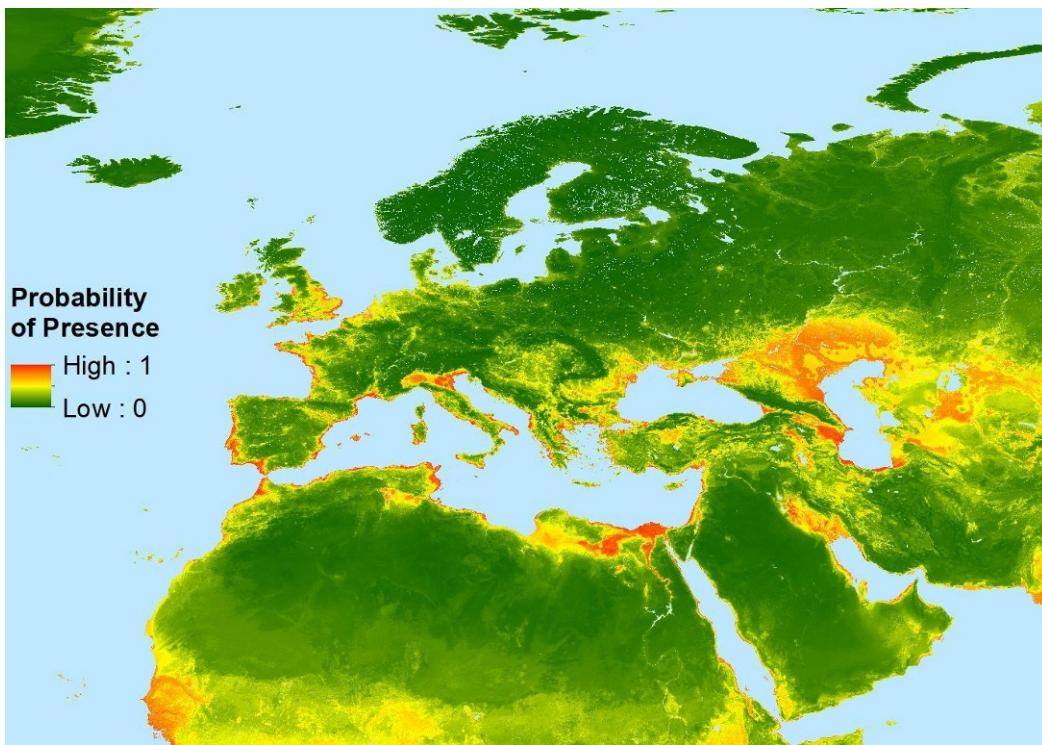
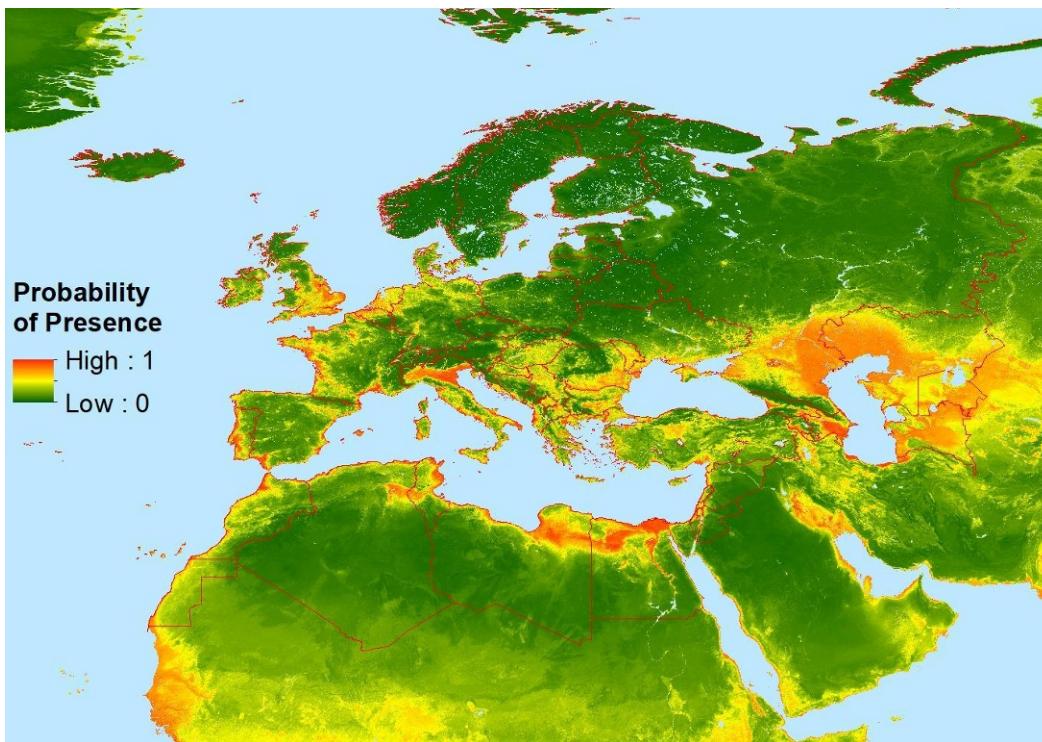


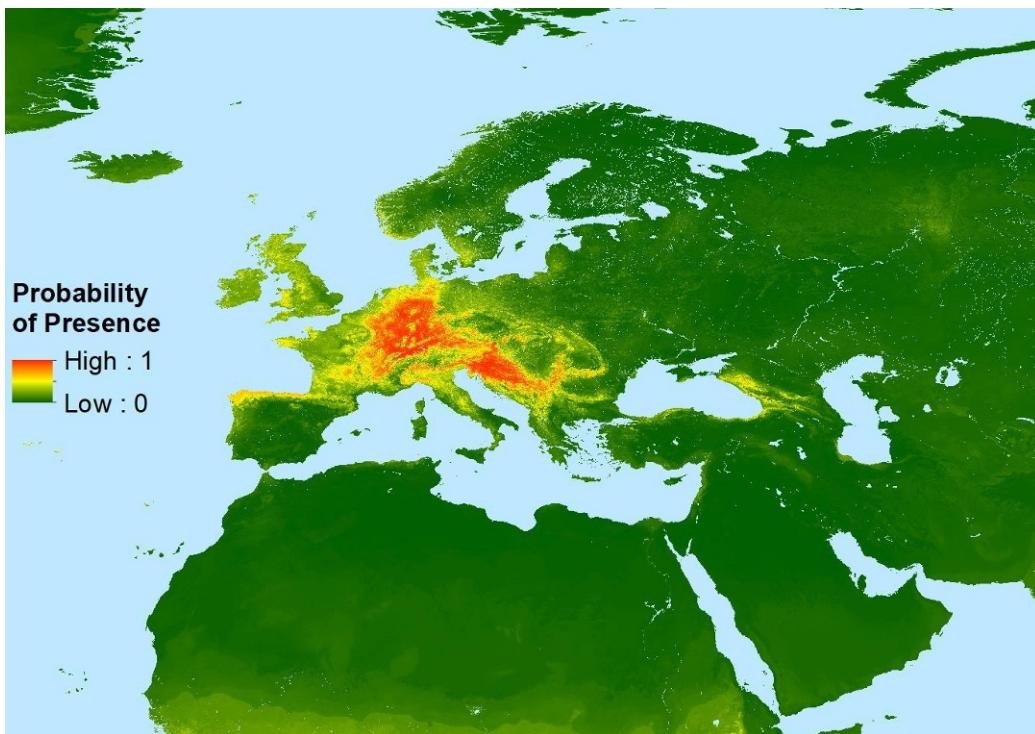
Available point and polygon data for *Cx. theileri*.



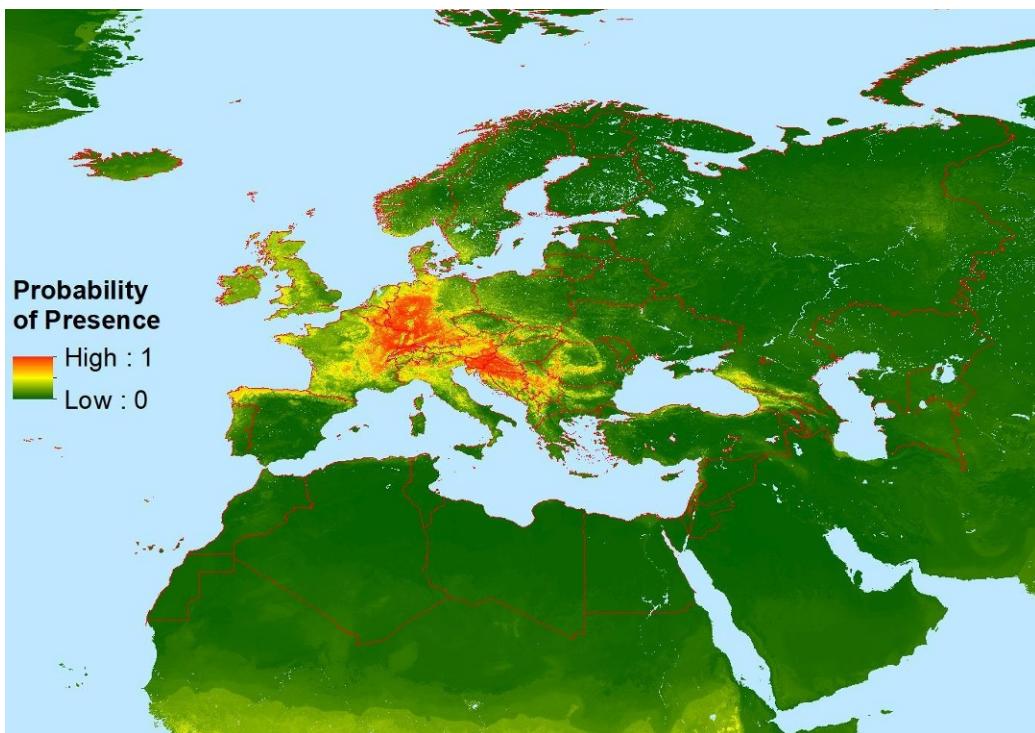
Available point and polygon data for *Ae. vexans*.

Appendix D- Masked and unmasked predictionsMasked predictions for *Ae. albopictus*.Unmasked predictions for *Ae. albopictus*.

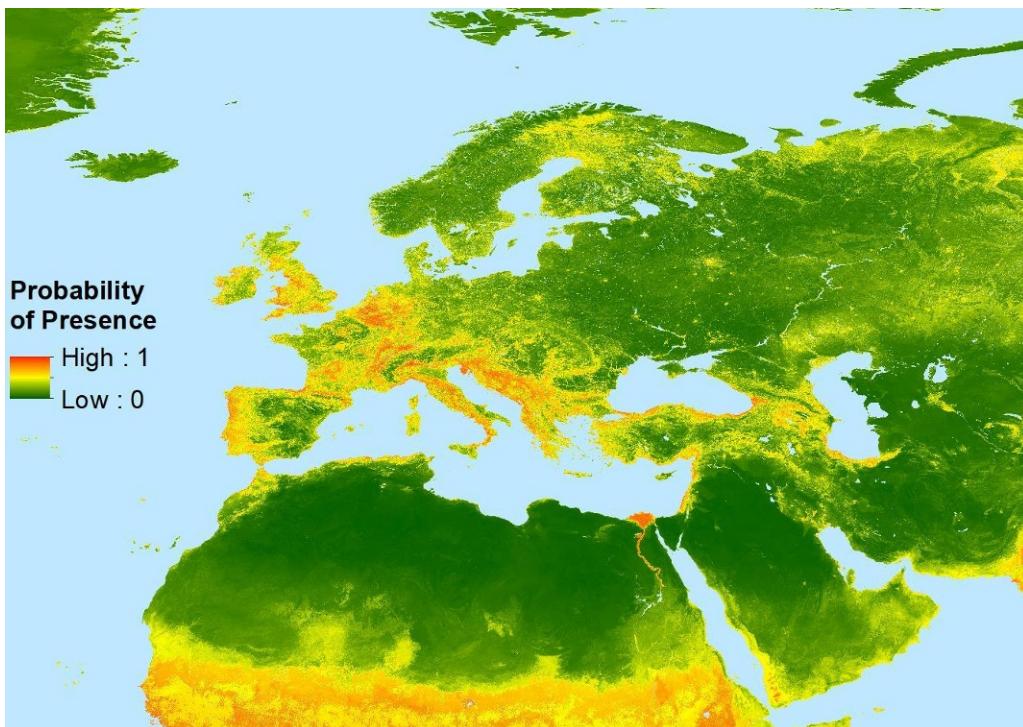
Masked predictions for *Ae. caspius*.Unmasked predictions for *Ae. caspius*.



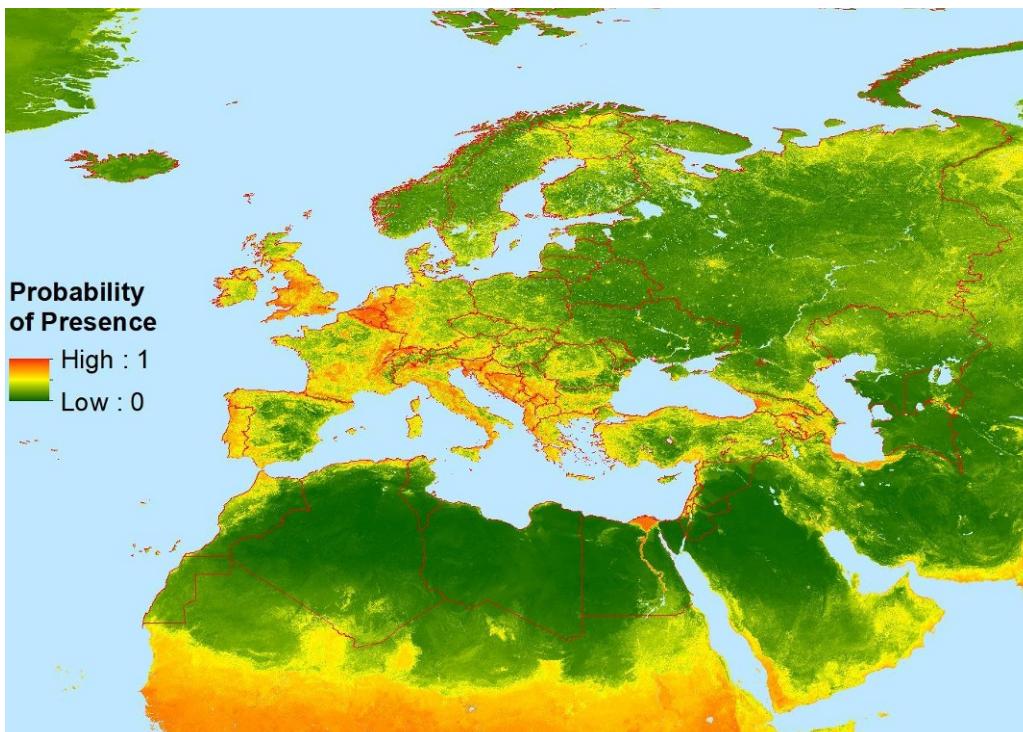
Masked predictions for *Ae. japonicus*.



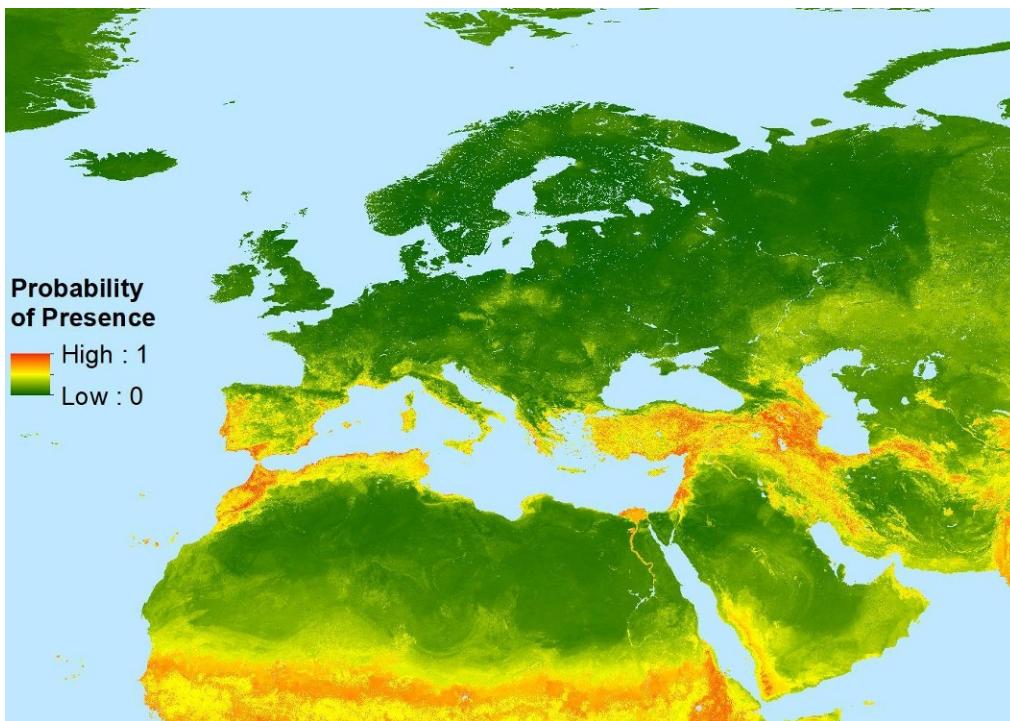
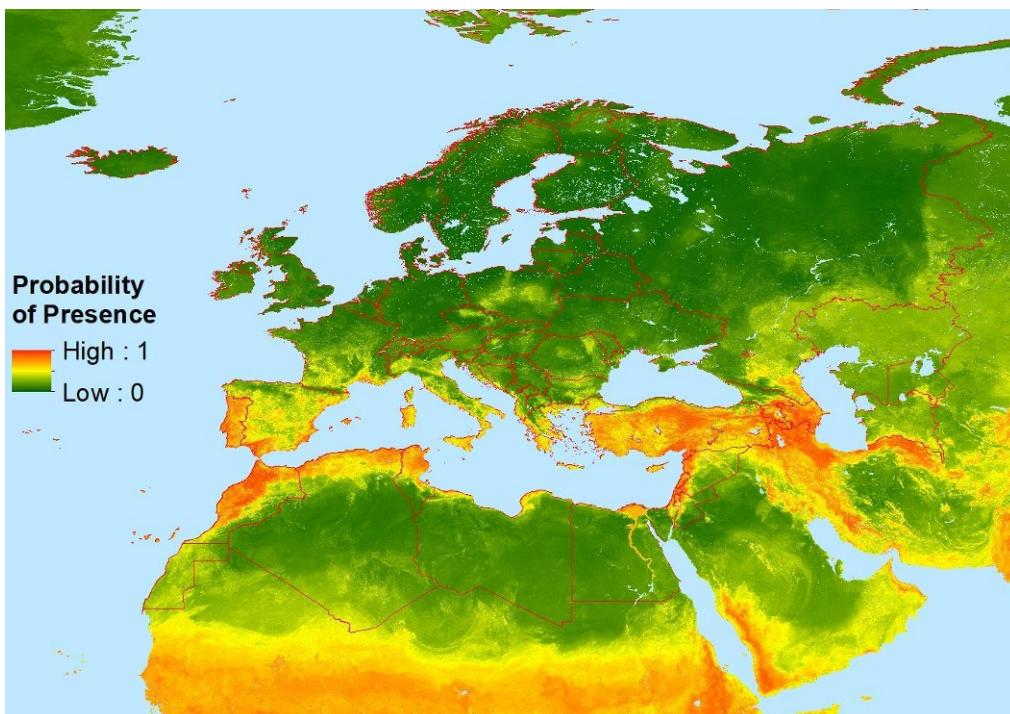
Unmasked predictions for *Ae. japonicus*.



Masked predictions for *Cx. pipiens*.



Unmasked predictions for *Cx. pipiens*.

Masked predictions for *Cx. theileri*.Unmasked predictions for *Cx. theileri*.

Appendix E- Spreadsheet column list
File name: mintriskrvf19vectorsbycountry.xls

Worksheet	Summary COLUMN	Variable	worksheet Column
	euhn	EU or Not: 1 = yes, 2 continental Europe, Non EU	
ALLRVFBINARYPRESABSFCOUNTRY	allvecPA	proportion of country with any RVF vector presence	MEAN
sumrvf19hostvetoroverlapCOUNTRY	sumvecgt80	proportion of country with sum of all vector Probability >0.8	MEAN
ALboRVF19vecBinaryPACOUNTRY	albopa	proportion of country with vector present: Albopictus	MEAN
CASPRVF19vecBinaryPACOUNTRY	caspa	proportion of country with vector present: Caspius	MEAN
japRVF19vecBinaryPACOUNTRY	jappa	proportion of country with vector present: Japonicus	MEAN
pieniensRVF19vecBinaryPACOUNTRY	pippa	proportion of country with vector present: Pieniens	MEAN
theiRVF19vecBinaryPACOUNTRY	thepa	proportion of country with vector present: theileri	MEAN
vexRVF19vecBinaryPACOUNTRY	vexpa	proportion of country with vector present: Vexans	MEAN
any90hosthighRVFCOUNTRY	anyhosthi	proportion of country with any host high density or probability: if sum density for sheep+goats+cattle >50, or if any of three deer species (roe, red, fallow) >90% probability of presence	MEAN
habitat score Corine	as labelled	Corine Habitat Suitability scores for each species	
habitat score ESA CCI	as labelled	ESA CCI Habitat Suitability Scores for each vector species	
Env limits	as labelled	environmental limits extracted from literature for each species	