Deliverable 4.6: Model wind-borne introduction of flying insects into Europe to estimate the risk under specific climate conditions

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BACKGROUND/ DELIVERABLE DESCRIPTION

The introduction of infectious diseases into a region can cause severe harm to the animal health of susceptible populations and the economy there, and such is the case with bluetongue (BT). There are several ways a vector-borne disease, for instance BT, might be introduced in a new region, such as legal and illegal movements of susceptible hosts, transportation of the vector in vehicles or by wind currents, and by semen and/or embryos. Advection of infected vectors by wind currents is one route of introduction that cannot be prevented (1). However, analyzing and predicting the risk of wind-borne introduction of an infectious disease can result in an improvement of surveillance and reduce the impact of the introduction of the disease.

Three main routes of introduction of BT into Europe have been described based on historical data: from Morocco and Algeria to the Iberian Peninsula and the Balearic Islands, from Algeria and Tunisia to Sardinia and Sicily and, from Turkey to Greece and Bulgaria (1). Insects, such as *Culicoides* spp., can be transported long distances (2), even as far as 700 km under certain climatologic conditions when wind speed is sufficient (3) and orographic barriers are absent (4). In Europe, the wind-borne introduction of BT has been extensively documented (5, 6).

Therefore, the purpose of this task was to develop a tool that could model the aerial transportation of *Culicoides* spp. from a given region where a strain of BTV was present into a free region. The model is fully functional and has been applied exclusively for wind-borne transportation through large water bodies (7, 8).

DELIVERABLE ACTIVITIES

We fully developed a wind model that estimates the risk of wind-borne introduction of potentially infected (engorged) *Culicoides* spp., with suitable temperatures and wind currents, into a country which can end in the introduction or re-introduction of BTV serotypes. Briefly, the advection-deposition-survival (ADS) model predicts the number density of introduced insects over space and time based on three different processes: wind advection, vertical deposition, and the survival rate of *Culicoides* spp. The model assumes that the movement of small insects in the air shows similar behavior to wind-borne small particles.

1. In the advection step *Culicoides* spp. trajectories and movement are calculated based on wind directions and velocities. The advection process is computed using an advection partial differential equation.
2. In the deposition process, particles are deposited into the ground, based on particles' sedimentation and flotation theory, and *Culicoides* spp. physical features are taken into account.

3. Mortality rate is given by the probability of survival which is associated with temperature. This is an important feature since the arrival of dead insects does not pose a threat to the dissemination of arbovirus.

At the beginning of the process, the work area is determined, generating a grid from whose centroid the necessary climatological data (temperature, speed, and wind direction) are obtained with an hourly temporal resolution (**Figure 1**). Next, the user can determine the region of origin of the midges and the destination territory (where it is interesting to determine the risk of introduction).

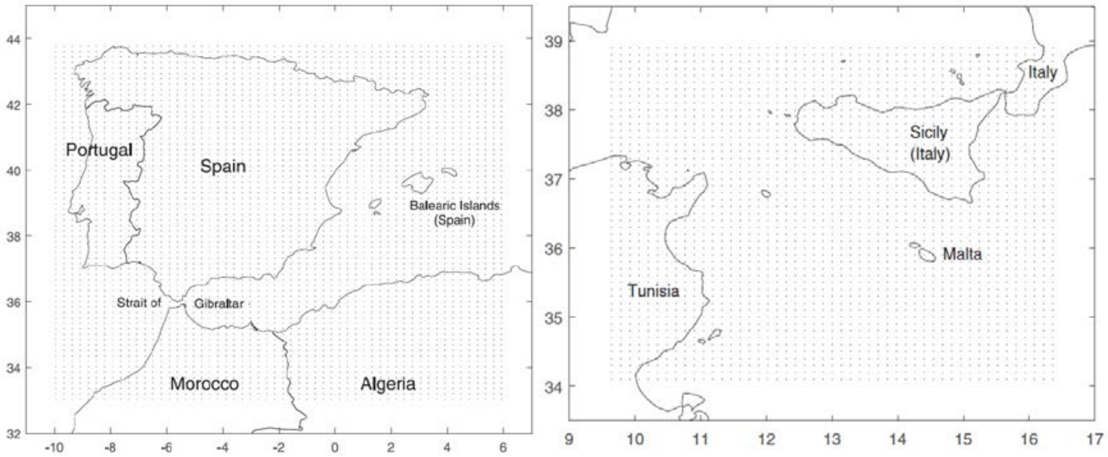


Figure 1. Example of study domain. Axes show the latitude and longitude, and dots indicate the centroid of each grid´s cell. Images obtained from Fernández-Carrión et al., 2018 and Aguilar-Vega et al., 2019 (7, 8).

Wind speed must be sufficient for the advection process to start and be maintained, while the wind direction determines where the particles are directed. When the wind speed is not enough to maintain the advection of the insects, those that have survived the transport based on the temperature-dependent mortality rate, are deposited in the cell of the grid in which they are found; although it will only be indicated if it takes place on land. The model will execute all the aforementioned processes at intervals of one hour in the study period that the user considers necessary. The model will predict the risk of introduction into the destination territory based on the density of insects deposited in each cell in this territory. Apart from generating the introduction risk map (**Figure 2**), the model provides the temporal development of the advection and deposition of the insects, in such a way that it is possible to determine at the time of entry (**Figure 3**).

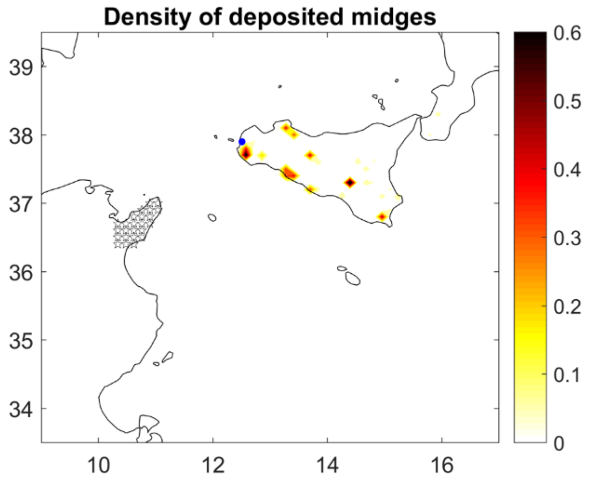
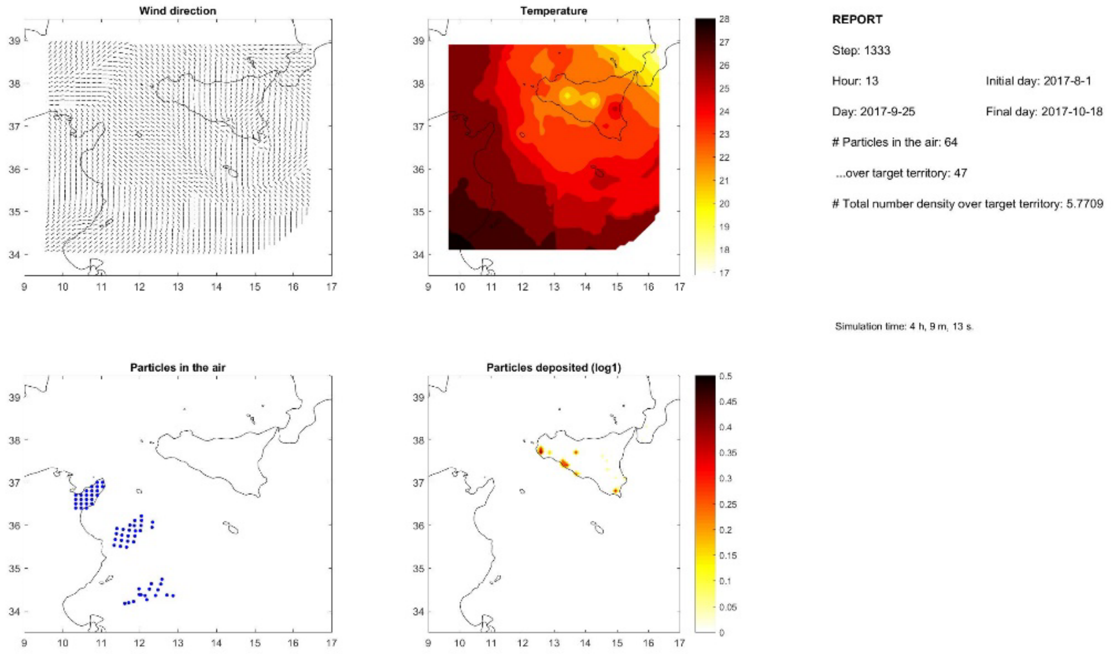


Figure 2. Number density of deposited midges in the target territory for the study period (1 August–18 October, 2017) according to the ADS model. The blue dot shows the location of the Sicilian outbreak of BTV-3. Stars represent the source of midges in the Cape Bon peninsula. Number densities were plotted in logarithmic scale, *log(C + 1)*. Image from Aguilar-Vega et al., 2019 (8).



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REPORT

Step: 1333

Hour: 13                    Initial day: 2017-8-1

Day: 2017-9-25              Final day: 2017-10-18

# Particles in the air: 64

...over target territory: 47

# Total number density over target territory: 5.7709


Simulation time: 4 h, 9 m, 13 s.
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Figure 3. Hourly output of the ADS model. Top left panel shows the direction of the wind for every grid's centroid and right panel the temperature for the area of study. In the bottom left panel, the origin of the particles is shown (blue dots in the origin territory –Tunisia in this example) and particles being transported in the air. Bottom right panel shows the accumulative deposited particles during the study period in the target territory (Sicily).

Initially, hourly meteorological data was retrieved from forecast.io. The early and published studies used this source of climatic data. However, this platform has joined a private company and climatic data is no longer provided for the general public. Therefore, the model has also been adapted for Copernicus's ERA5. ERA5 provides hourly global reanalysis data with a spatial horizontal resolution of 0.25° x 0.25° (9). Using ERA5, it is not possible to modify the spatial resolution of the model, however, there is no need to interpolate when missing data appears in any grid cell.

Some of the key parameters for the advection and deposition processes are gathered in **Table 1**. Parameters were specifically adapted to *Culicoides* physical properties, based on data obtained from a literature review, and some of them were modified in order to better adjust them to Mediterranean Basin's *Culicoides* species.

Table 1. Parameters of the ADS model.

Parameter acronym	Parameter description	Values	Reference
Mc	*Culicoides'* weight (kg)	$5.77 \cdot 10^{-7}$	(7, 8)
Rc	*Culicoides'* radius (m)	$1.01 \cdot 10^{-3}$	(8)
ρ	*Culicoides'* density (kg/m³)	$\rho = M/(4/3\pi R^3)$ 800.34	(7) (8)
Re	*Culicoides'* Reynolds number	100 120	(7) (8)
α_1	Hellmann exponent above open water surfaces	0.10	(7, 8)
α_2	Hellmann exponent above land surfaces	0.16 0.30	(7) (8)

In addition, the model is versatile since despite being designed for midges of the genus *Culicoides*, it can be adapted to other flying insects by modifying the parameters related to the mortality rate, morphology and physical properties of each insect, such as weight, radius, density, and Reynolds number. Additionally, it would be possible to adapt the model to other blood-sucking insects from other families or genera if deemed necessary. In that sense, it would be possible to model the risk of the introduction of other vector-borne diseases.

The model has been applied to several BT introduction events in retrospective studies. First of all, it was used to study the risk of wind-borne introduction of potentially infected *Culicoides* during 2004 from northern African countries to Spain. In this study, we assessed the monthly risk of introduction (**Figure 4**), and we found different patterns of deposition when the source was Morocco and Algeria. This study was published along with the mathematical description of the model (7).

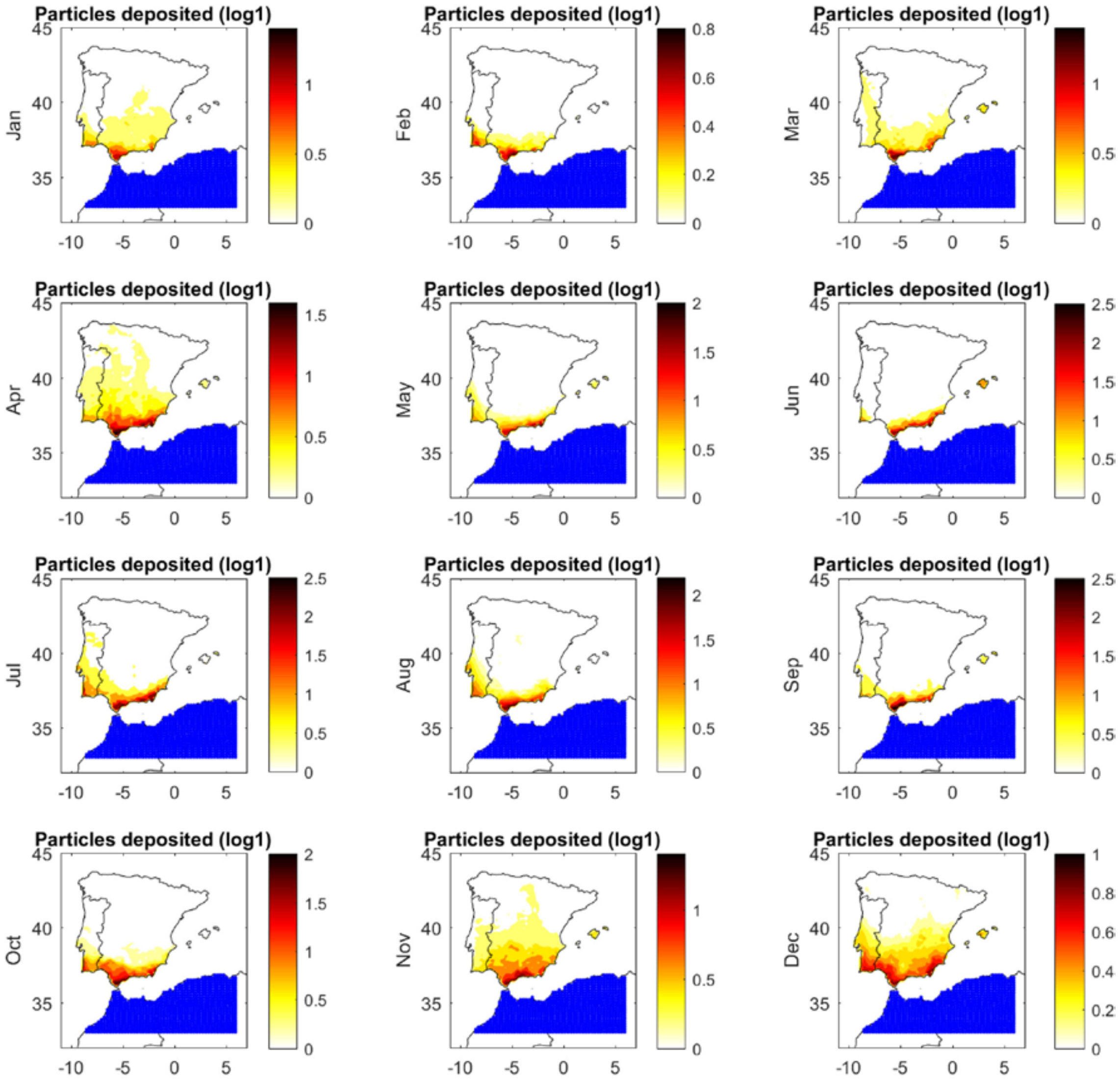

Figure 4. Simulated spatial distribution of the number density of *Culicoides* spp. deposited on Spanish territory for each month of 2004, when the midge source was both Morocco and Algeria. Number densities were plotted in logarithmic scale, *log(C + 1)*. Image from Fernández-Carrión et al., 2018 (7).

The model was also used to assess the possible introduction of the BTV strain BTV-3 TUN2016 into Sicily in 2017. Specific days were identified as possible days of infected *Culicoides* spp. introduction. In this work, we also compared ADS results with the output of the HYSPLIT model, to assess the similarity of both models' outputs for the possible days of introduction (**Figure 5**). Both models, which have methodological differences, yielded similar predictions. Although more retrospective studies are needed to fully validate the model, our results support the quality of the model.

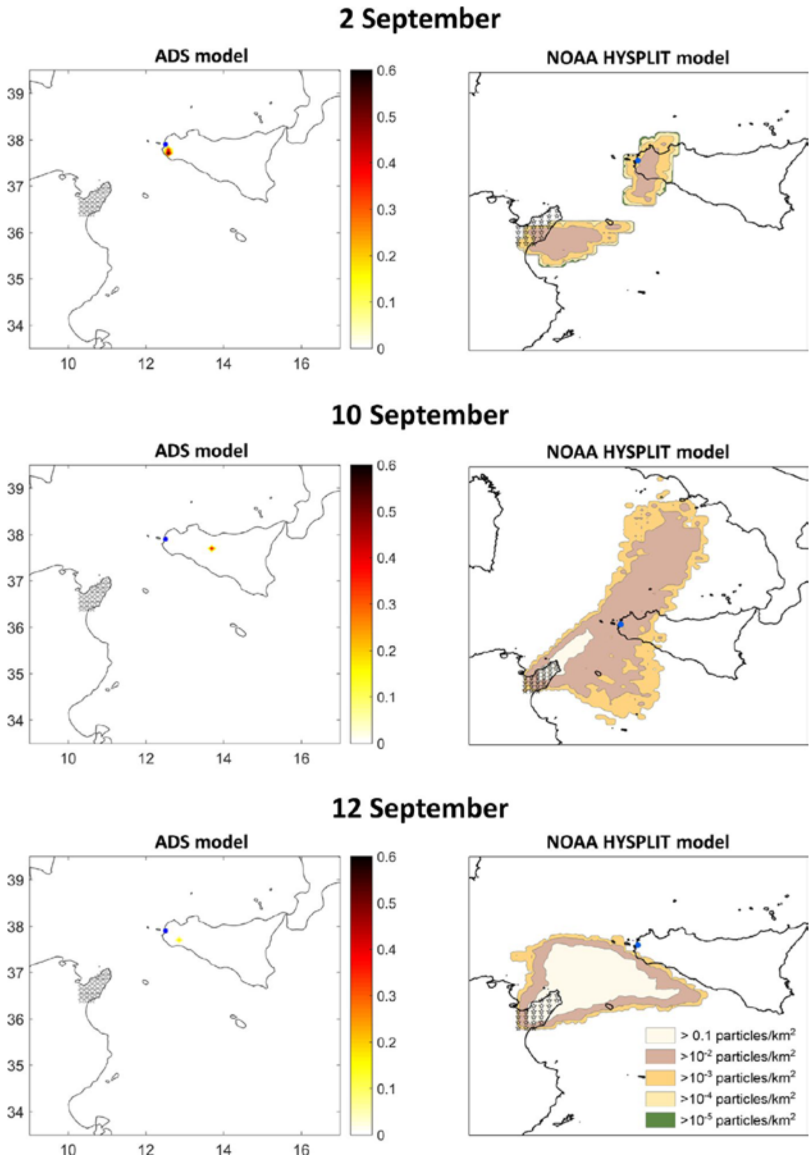

Figure 5. Particle deposition according to ADS and HYSPLIT models for the potential days of introduction. The blue dot shows the location of the Sicilian outbreak of BTV-3. Stars represent the source of midges and particles in the Cape Bon peninsula. Image from Aguilar-Vega et al., 2019 (8).

PUBLICATIONS RELATED TO THIS DELIVERABLE

- Fernández-Carrión E, Ivorra B, Ramos AM, Martínez-López B, Aguilar-Vega C, Sánchez-Vizcaíno JM. An advection-deposition-survival model to assess the risk of introduction of vector-borne diseases through the wind: Application to bluetongue outbreaks in Spain. PloS ONE. 2018;13(3):e0194573.
- Aguilar-Vega C, Fernández-Carrión E, Sánchez-Vizcaíno JM. The possible route of introduction of bluetongue virus serotype 3 into Sicily by windborne transportation of infected *Culicoides* spp. Transboundary and emerging diseases. 2019;66(4):1665-73.

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2. Reynolds DR, Chapman JW, Harrington R. The migration of insect vectors of plant and animal viruses. Advances in virus research. 2006;67:453-517.

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4. Hendrickx G, Gilbert M, Staubach C, Elbers A, Mintiens K, Gerbier G, et al. A wind density model to quantify the airborne spread of *Culicoides* species during north-western Europe bluetongue epidemic, 2006. Preventive Veterinary Medicine. 2008;87(1-2):162-81.

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8. Aguilar-Vega C, Fernández-Carrión E, Sánchez-Vizcaíno JM. The possible route of introduction of bluetongue virus serotype 3 into Sicily by windborne transportation of infected Culicoides spp. Transboundary and emerging diseases. 2019;66(4):1665-73.

9. Hersbach H, Bell B, Berrisford P, Biavati G, Horányi A, Muñoz Sabater J, et al. ERA5 hourly data on pressure levels from 1979 to present. In: Copernicus Climate Change Service (C3S) Climate Data Store (CDS), editor. 2018.