PALE-Blu work package 4, deliverable report (May 2018)

D4.2 Spatial data base of vector distributions due M12

Introduction and WP4 overview

One of the PALE-Blu activities is to identify pathways and mechanisms for BTV spread into and within regions covered by the project, including Europe, Maghreb and Western Africa. This will be achieved by the definition and the mapping of spatial epi-zones for BTV circulation, which should correspond to phylogeographic structure in the virus populations. These epi-zones could be connected, i.e. virus could be introduced from one to another epi-zone, by national and international animal movements or by the movements of infected *Culicoides*, which could be active or driven by winds.

Within the project, Work Package 4 is dedicated to the study of *Culicoides* populations. Their structure may contribute to the definition of epi-zones and their movements are involved in the connectivity of epi-zones. The WP4 aims to establish the structure of *Culicoides* populations at two levels: at the species community and at the population, and to assess the ability of *Culicoides* dispersal using mainly indirect methods (population genetics or modelling for wind transportation).

These analyses require an assessment of the factors driving these processes, using multivariate analysis for species community and microbiome data, population genetic tools for data on population structure and modelling approaches for *Culicoides* wind dispersal. The multivariate analyses will be applied on an extensive dataset of abundance data focusing on the most common *Culicoides* species. The applicable deliverable is D4.2 (*Spatial data base of vector distributions*) due in project month 12. This database will be used in a second step to describe and map the composition of species communities across a long geographical gradient (from Senegal to Scandinavia).

These activities are a core element of task 4.1 (*To characterise the environmental factors determining distribution of* Culicoides *species along a transect crossing different biomes*), as follows:

- a) share and adapt existing databases to provide an extensive dataset for the project (D4.2);
- b) describe and map species community composition along a long south/northern gradient;
- c) identify ecological factors responsible for community composition.

Deliverable Activities

The composition of species communities could be assessed using presence/absence data or using an index of the relative abundance. *Culicoides* are widespread species present in a large range of latitudes. The present dataset will thus focus on abundance data, as presence/absence data will not be sufficiently informative.

The UV-light trap collections remain the most time efficient and widespread method to assess *Culicoides* abundance at a wide scale. Several publications have highlighted the discrepancy of *Culicoides* composition recorded by UV-light trap and by host-baited trap collections (Carpenter *et al.* 2008; Viennet *et al.* 2011; Meiswinkel *et al.* 2016), meaning that UV-light abundance could not be directly used as a direct estimation

of aggressive density which is the abundance parameter used in the reproductive number (R_0). However, Viennet et~al. (2012 and 2013) showed that UV-light trap collections were linearly correlated to aggressive density on animals for several *Culicoides* species meaning that abundance assessed by UV-light trap collections may be useful for risk assessment. It could thus be considered that abundance assessed by light traps was likely to be broadly representative of aggressive density (in identifying orders of magnitude differences in population size according to spatial or temporal variation) but may be misleading at a fine scale. It is worth to highlight that abundances assessed by UV-light traps have been used for more than a decade to manage animal movements under EU regulations, and that this system has demonstrated its utility.

The *Culicoides* abundance will change across the year and may change from one year to another depending on the climatic conditions. Longitudinal follow-ups, ideally during several years, are thus necessary to be able to estimate the *Culicoides* abundance at a location. Moreover, adverse meteorological conditions may limit the active fraction of the *Culicoides* population, and thus underestimate the abundance collected by light-traps. Carry out collections during several consecutive nights helps to overcome adverse meteorological conditions. Finally, *Culicoides* abundance may be highly heterogeneous at a local scale (Kluiters *et al.* 2013). It is hypothesised that the changes in the species composition (assessed as a relative abundance) at the continental scale will dominate the local variations.

To build the abundance dataset, we used as long as possible longitudinal *Culicoides* follow-ups carried out with UV light-traps. The yearly maximum abundance (i.e. the largest single night trap catch in the collecting period) was used to aggregate data against time and to produce an index of the species abundance. If the collection period covers several years, then we used the average of the yearly maxima of abundance.

We considered the most common *Culicoides* species potentially involved in the bluetongue virus transmission:

- Culicoides (Avaritia) obsoletus/Culicoides (Avaritia) scoticus, females of these species could not be reliably distinguished using morphological routine identifications and are thus considered together;
- Culicoides (Avaritia) imicola;
- Culicoides (Avaritia) chiopterus;
- Culicoides (Avaritia) dewulfi;
- Culicoides (Culicoides) punctatus;
- Culicoides (Culicoides) newsteadi;
- Culicoides (Culicoides) pulicaris/Culicoides (Culicoides) lupicaris, the wing patterns used to distinguish females of these species may present intermediary forms and lead the identification difficult; these species are thus considered together;

Moreover, we included *Culicoides (Remmia) kingi* in the dataset. This species was not, up-to-now, involved in the bluetongue virus transmission, however it is very abundant in Northern Africa.

The gathered data may have been shared by National surveillance systems or have been produced by the VectorNet initiative, using retrospective identifications (to obtain species level data) on stored collections from National surveillance system or carrying out prospective field work (mostly longitudinal surveys). VectorNet is a joint initiative of the European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC), which started in May 2014. The project supports the collection of data on vectors and pathogens in vectors, related to both animal and human health, with the objective to

map the presence/absence of vectors in Europe (in the geographical sense) and around the Mediterranean basin. The VectorNet data were obtained by a formal request to ECDC (reference number 18-1421).

The final dataset contains a total of 639 sites (see Table 1 for details) from 30 countries (Fig 1).

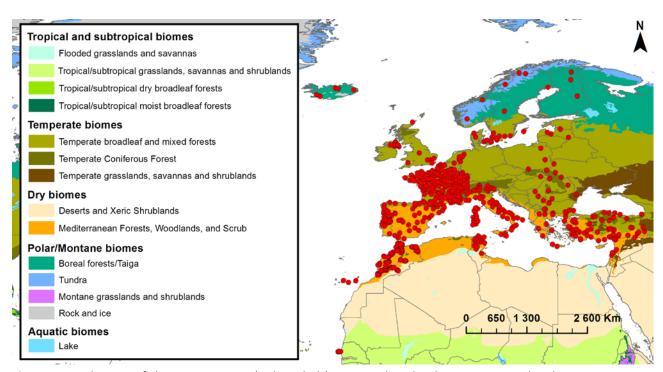


Figure 1. Localisation of the trapping sites (red symbols) contained in the dataset compared to biomes present in Europe, in the Mediterranean basin and in Senegal.

References

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Table 1. Description of the origin of gathered *Culicoides* abundance data.

| Country Belgium | No. sites | Data origin National surveillance | Contributors to data collections Sohier C, De Deken R, Deblauwe I, Madder M, Fassotte C, Losson B, De Regge N | Referent Nick De Regge (CODA-CERVA) Nick.DeRegge@coda-cerva.be |
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| Slovakia | 1 | VectorNet activities | Petric D Kocišová A, Komorová P, Sarvašová A, Halán M, Mathieu B | dusanp@polj.uns.ac.rs Alica Kocisova (Univ. of Veterinary Medicine) |
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