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# Mapping of VBDs: A cartography model using questionnaire-based surveys and diagnosed cases in veterinary clinics with the example of Canine Leishmaniosis in France

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**Background**

Vector-borne diseases (VBDs) are increasingly relevant, often perceived as expanding due to climate changes and increased animal travel. The concept of risk is important for implementing preventive measures and is highly dependent on the presence of the disease (both agents and vectors) in both endemic (E) and non-endemic (NE) areas. This is particularly relevant in the context of zoonosis, emphasizing a One Health approach. Even though the distribution of the disease using cartography methods, sick animals as "sentinels", and potential sources or reservoirs, has been explored through several studies, some introduced methodological bias or were not representative enough. Therefore, this study aims to introduce a model, applied here to Canine Generalized Leishmaniosis (CanGL) caused by *L. infantum*, using a questionnaire-based survey conducted at repeated intervals.

**Material and methods**

This study analyses two surveys covering two periods (A) 2005 to 2010 and (B) 2011 to 2017. Similar questionnaires were mailed to veterinary clinics in France, with one questionnaire sent per clinic. Among the questions, the collected information for cartography included the following: postal code for geolocation and clinic activity type; origin of dogs visiting the clinic (expressed as a range in kilometres for 90% of cases); number of dogs seen per year (with proposed intervals) and experience in CanGL, indicated by the number of annual cases (with proposed intervals); origin of infection (autochthonous, considered acquired around the clinic, versus imported); techniques used for diagnosis.

The mapping process was based on the previous postulate of "epidemiologic continuity at a low scale," as presented in the EVPC meeting in Dublin in 2014. The territory was divided into multiple surface units, each with a side length of 15 kilometres. A colour was assigned to each unit based on the epidemiological situation, ranging from blue to dark red. This colour scheme was applied for each clinic and its related surface of activity (Figure 1). Additionally, the prevalence of the disease in owned dogs could be calculated by dividing the number of cases by the total number of dogs. Minimal, average, and maximal prevalence values were applied at different levels, including departmental, regional, and national levels. It was postulated that for the data to be considered significant, the participation of at least 10% of veterinary clinics, evenly distributed across the national level, was required.

**Results**

For period A (2005 to 2010), information was obtained from 23.2% (1334/5760) of veterinary clinics in France, whereas for period B (2011 to 2017) data was obtained from 10% (650/6500) of them. The results and comments are presented in Figure 1, and the estimated prevalence of the disease in medicalized companion dogs is indicated in Table 1

**Conclusions**

The estimated distribution of endemic areas increased from (A)11.3 to (B)18.5 % of the territory, encompassing not only previously known endemic regions but also expanding into fringe zones, particularly in the South-East and Northward. Additionally, a growing portion of non-endemic territories now harbours sick and infected dogs, potentially serving as sources of infection through non-vectorial transmission routes.

Despite being detailed, this representation still has some limitations. For example, clinics that did not participate may have cases affecting the non-endemic and fringe areas.

Furthermore, it is important to remember that the prevalence of infected asymptomatic dogs is much higher, with each autochthonous case serving as a sentinel of the “tip of the iceberg” of an area. Additionally, there's the possibility that the relative percentage of infected dogs that become sick could decrease in the future, in parallel with improvements in overall health, as seen in humans.

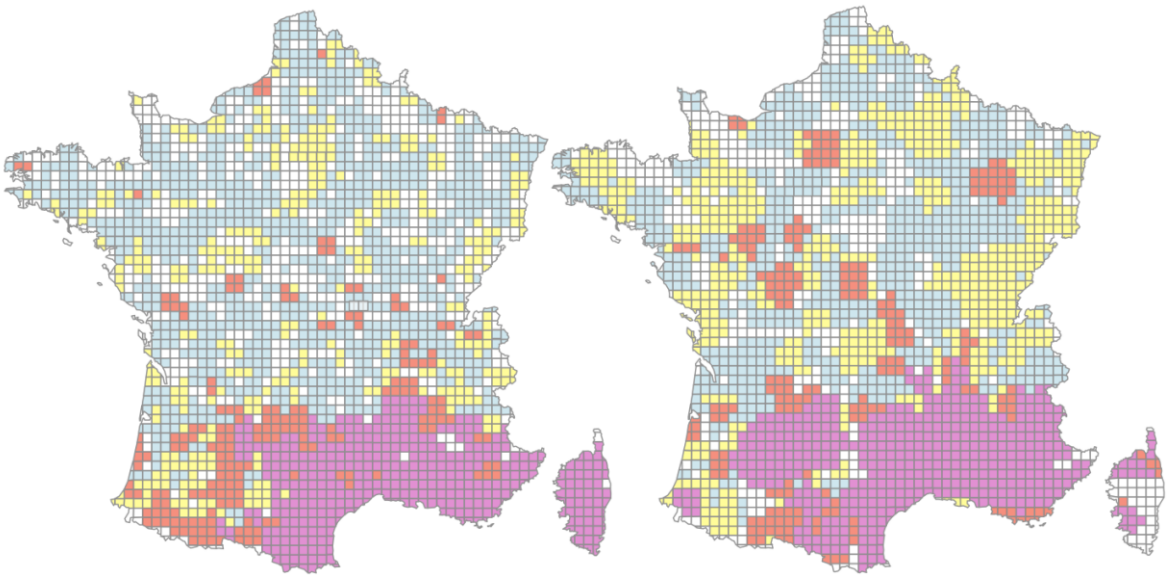
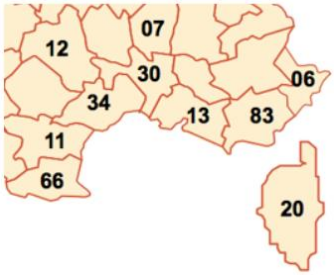


**Figure 1:** Distribution and evolution of CanGL in France. Left (Period A: 2005-2010). Right (Period B: 2011-2017). Colour codes: White: areas not covered by the survey; Blue: no case of CanGL diagnosed during the period by participating clinics; Yellow: imported cases only; Red: autochthonous cases <5/ year (sporadic or moderately endemic); Violet: autochthonous cases: >5/year (highly endemic).

**Table 1:** Calculated prevalences (‰) of CanGL and evolution from 2005 to 2017 in France (National and in some endemic departments).

| | 2005 - 2010 | | 2012 -2017 | |
|---|---|---|---|---|
| | **Average (‰)** | **Range (‰)** | **Average (‰)** | **Range (‰)** |
| **National** | 4.1 | 1.3-9.7 | 1.3 | 0.9-1.6 |
| 06 - Alpes- Maritimes | 12.2 | 3.6-30.4 | 3.7 | 2.8-4.6 |
| 07- Ardèche | 16.2 | 5.4-40.2 | 10.9 | 8.2-13.5 |
| 11- Aude | 14.7 | 4.2-35.1 | 1.3 | 0.8-1.8 |
| 12 - Aveyron | 12.1 | 4.2-30.1 | 3.2 | 2.7-3.7 |
| 13 - Bouches-du- Rhône | 10.6 | 3.9-24.5 | 4.3 | 3.2-5.3 |
| 20 - Corse | 27.2 | 3.5-69.5 | 6.5 | 5.2-7.8 |
| 30 - Gard | 1.8 | 0.53-4.5 | 3.1 | 2.2-4.0 |
| 34 - Hérault | 0.9 | 0.3-2.2 | 3.4 | 2.3-4.5 |
| 66 - Pyrénées-Orientales | 1.7 | 0.5-4.2 | 5.4 | 3.6-7.1 |
| 83 - Var | 1.1 | 0.3-2.5 | 4.7 | 3.6-5.8 |




Red: potential increase; Blue: potential decrease.
Most of the intervals of prevalence (range) overlap (except Herault and Var).

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