

Spatial distribution of bovine TB in two different areas in Spain

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Bovine tuberculosis (bTB), caused by members of *Mycobacterium tuberculosis* complex (mainly *M. bovis*) is an important zoonotic disease of worldwide distribution. In Spain, although a large reduction in the prevalence of the disease has been achieved in the last 15 years (from 5.9% in 1993 to 1.6% in 2009) progress has not been homogeneous throughout the country (1).

Objective: Here, the spatial distribution of infected farms/most prevalent strains was evaluated in 2 regions of high prevalence but different size (Madrid and Guijuelo) to identify clusters of higher risk potentially associated with common risk factors and/or local transmission events.

Materials and Methods

The autonomous community of Madrid (ACM) and the Guijuelo region in the autonomous community of Castilla y León were selected due to their high prevalence (5.45% and 8.35% respectively in 2010) and the presence of several significant risk factors associated with bTB in Spain in spite of different sizes. Data from the years 2010-2012 were collected from the National Eradication Program for Bovine Tuberculosis at the herd-level. Herds were classified as positive if 1 or more reactors at the skin test/IFN- γ test were detected. Location of herds was provided by the OVS. 127 and 169 positive farms were detected in Guijuelo and ACM respectively (Fig. 1). Positive, incident (positive herds negative in the previous year) and persistent (positive herds also positive in the previous year) herds in which *M. bovis* was isolated per year are shown in Table 1.

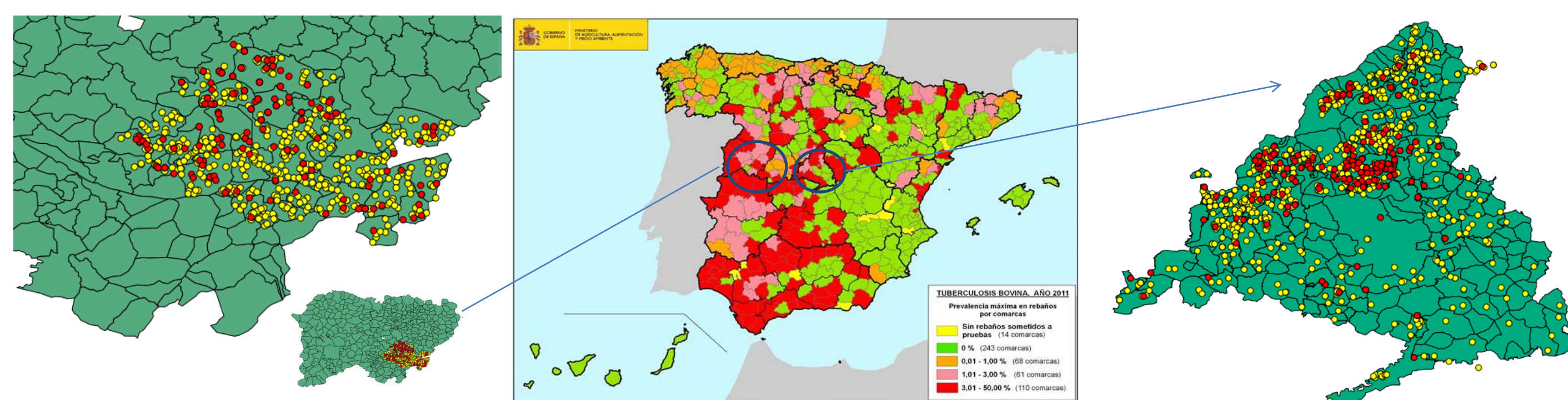


Fig. 1. bTB-positive (red) and negative (yellow) herds tested in ACM and Guijuelo in 2010-12

Table 1. Positive, incident and persistent bTB-infected herds in 2010-2012

YEAR	ACM			GUIJUELO		
	PREVALENTS	INCIDENTS	PERSISTENTS	PREVALENTS	INCIDENTS	PERSISTENTS
2010	75	44		47	35	
2011	97	74	29	44	29	21
2012	80	47	38	47	36	13

In addition, clustering of the most prevalent spoligotypes was assessed in all bTB-infected herds detected in 2010-2012 in which *M. bovis* had been isolated and subjected to spoligotyping (2) (ACM, n=98, and Guijuelo, n=65).

Presence of clusters with significantly ($p<0.05$) higher probability of including positive farms /certain spoligotypes was assessed using the spatial scan (SaTScan 9.0) based on Bernoulli model, and genetic heterogeneity of isolates was evaluated using Simpson's Diversity Index (DI) (3). Maps were obtained using Quantum GIS 1.8.0.

Results

Significant clusters of positive, incident and persistent bTB-infected herds were detected in 2010-2012 in ACM (Figs 2A-C) and Guijuelo (Figs 3A-C), although there was almost a complete overlap between all clusters in the former, and this overlap was less evident in the latter.

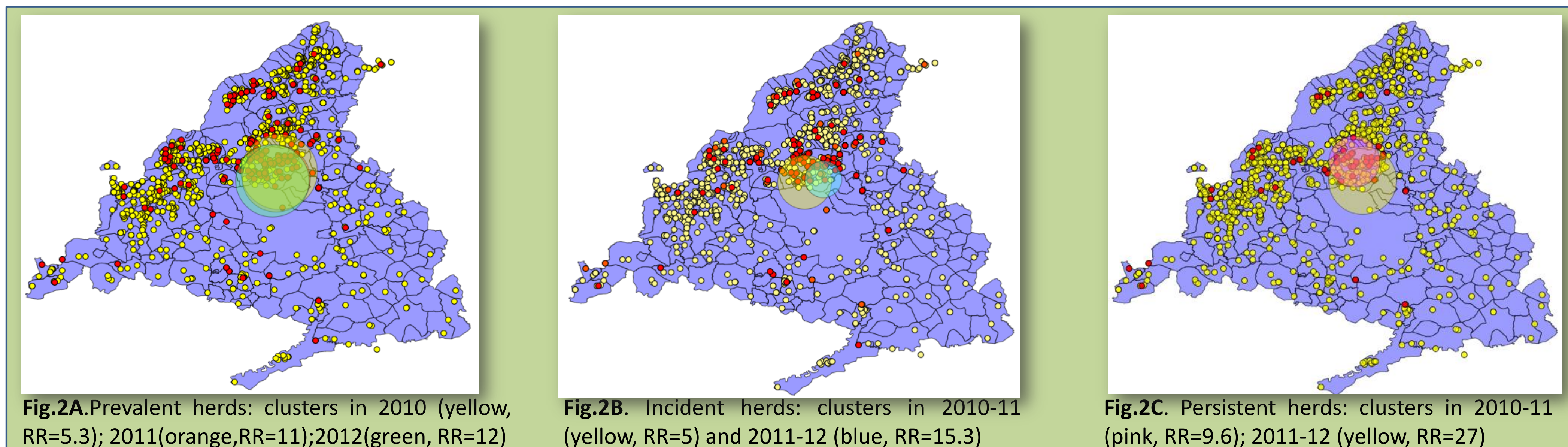


Fig.2A.Prevalent herds: clusters in 2010 (yellow, RR=5.3); 2011(orange,RR=11);2012(green, RR=12)

Fig.2B. Incident herds: clusters in 2010-11 (yellow, RR=5) and 2011-12 (blue, RR=15.3)

Fig.2C. Persistent herds: clusters in 2010-11 (pink, RR=9.6); 2011-12 (yellow, RR=27)

Table 2. Frequencies and %* of the most prevalent (>7%) spoligotypes in ACM and Guijuelo

Spoligotype	ACM	Guijuelo
SB0339	52 (34.4%)	3 (4.6%)
SB0121	27 (17.9%)	17 (26.2%)
SB1142	27 (17.9%)	1 (1.5%)
SB0134	4 (2.6%)	5 (7.7%)
Simpson's DI	0.818	0.901

*From the sum of all different spoligotypes found in each infected herd (ACM=151; Guijuelo=65)

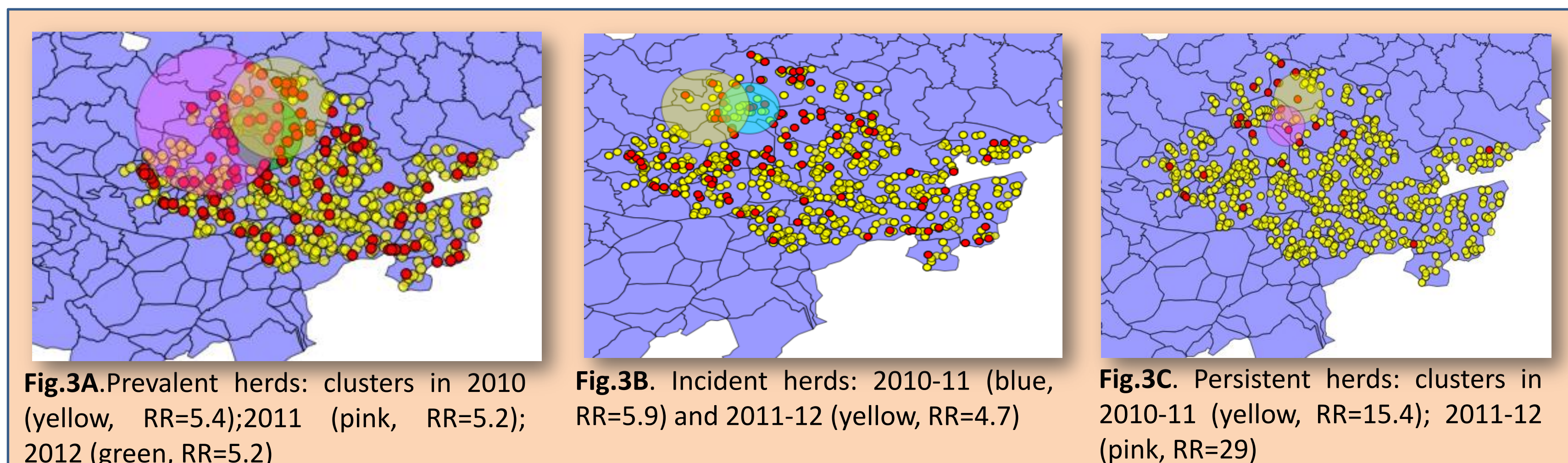
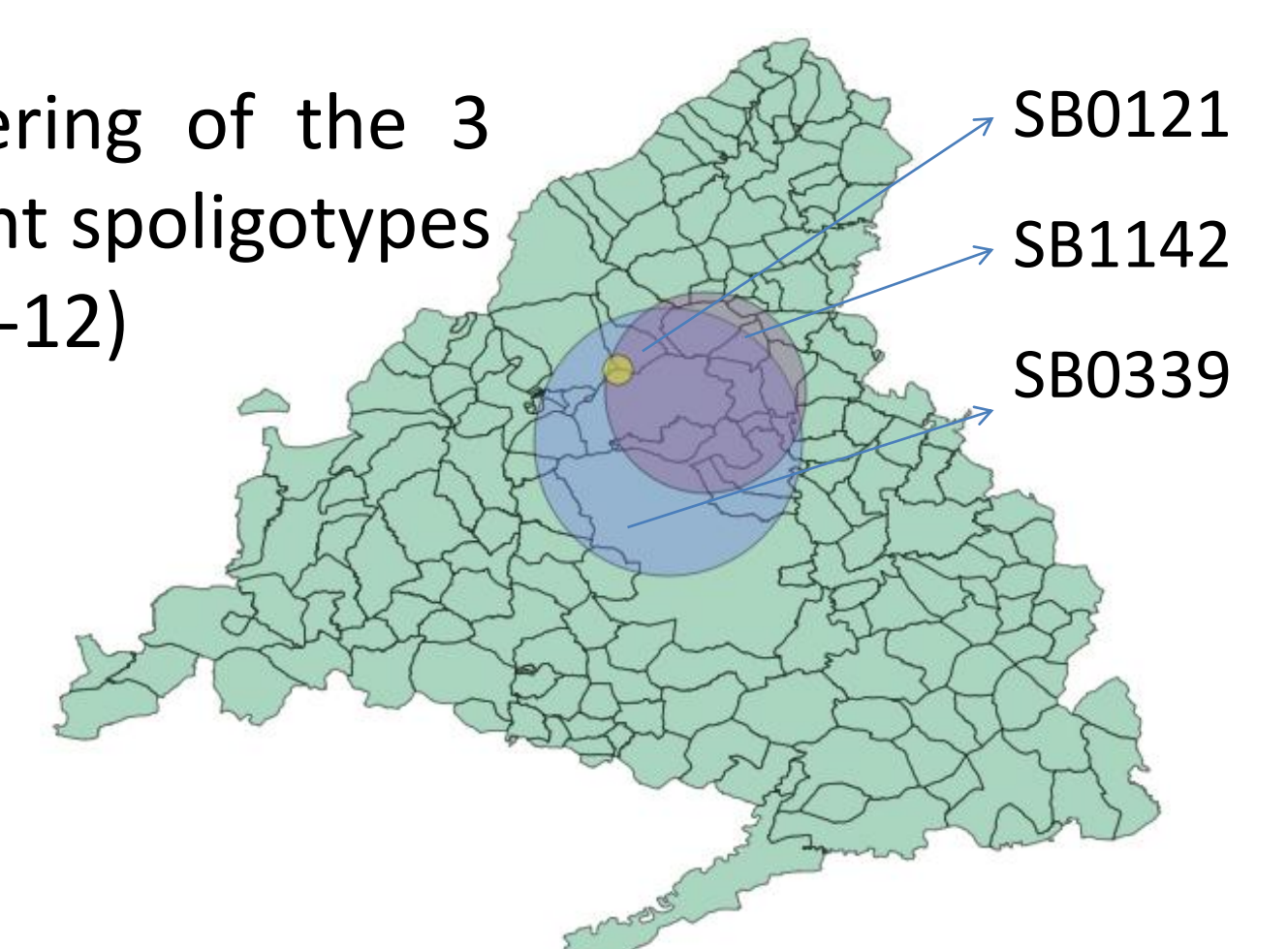


Fig.3A.Prevalent herds: clusters in 2010 (yellow, RR=5.4);2011 (pink, RR=5.2); 2012 (green, RR=5.2)

Fig.3B. Incident herds: 2010-11 (blue, RR=5.9) and 2011-12 (yellow, RR=4.7)

Fig.3C. Persistent herds: clusters in 2010-11 (yellow, RR=15.4); 2011-12 (pink, RR=29)

Fig. 4. Clustering of the 3 most prevalent spoligotypes in ACM (2010-12)



Up to 29 and 25 different spoligotypes were identified in ACM and Guijuelo respectively, with a higher distribution of certain profiles in ACM compared to Guijuelo in spite of having several bTB episodes with more than one spoligotype (Table 2). Significant clusters were identified for the three most prevalent spoligotypes in ACM, while spatial analyses in Guijuelo was hampered by the much higher heterogeneity of profiles (Simpson's DI ACM=0.818; DI Guijuelo=0.901).

Conclusions

- In ACM positive, incident and persistent bTB-infected herds clustered around the same area, as well as three of the four most prevalent spoligotypes in the region, suggesting local transmission events or exposure to a common source
- A more limited overlapping of clusters of positive, incident and persistent herds was observed in Guijuelo, with a much higher variability of spoligotypes in spite of its lower surface, pointing at a more complex epidemiological situation

References

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