

G Bongiorno¹, R Bianchi¹, T Di Muccio¹, C De Liberato², M Calzolari³, A Michelutti⁴, F Montarsi⁴, C Foxi⁵, M Dottori³, G Satta⁵, L Gradoni¹, P Angelini⁶

¹Istituto Superiore di Sanità, DMI, Unit of Vector-borne Diseases, Rome; ²Istituto Zooprofilattico Sperimentale del Lazio e della Toscana “M. Aleandri”, Via Appia Nuova 1411, Rome; ³Istituto Zooprofilattico Sperimentale della Lombardia e dell’Emilia Romagna (IZSLER) “B. Ubertini”, Via Bianchi 9, 25124 Brescia; ⁴Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro (Padua); ⁵ Istituto Zooprofilattico Sperimentale della Sardegna, Sassari; ⁶Servizio Prevenzione collettiva e Sanità pubblica - Regione Emilia-Romagna, Italy.

INTRODUCTION. Diseases transmitted by sand flies, in particular those caused by *Leishmania* and Phlebovirus, are currently considered to be expanding both in terms of incidence and territory. The factors involved are many, starting with the abandonment of agricultural use of hilly areas and the impact of climate change. The assessment of the historical and geographical dynamics is complex due to the lack of systematicity and standardization in the reporting sand fly data (Busani et al., 2012 Rapporti ISTISAN 12/22). Under the patronage of the Italian Ministry of Health, entomological surveys have been conducted in six Italian regions in the frame of West Nile virus surveillance. Phlebotomine sand flies were collected along with others hematophagous insects and kept frozen. In this study, we report the results of sand fly identification and their distribution in the investigated regions, pending examination for specific pathogens.

MATERIALS AND METHODS. Attractive traps were set every two weeks, from May till October 2020 (2017 in Latium) near animal shelters. Morphological identification using fresh samples of the last abdomen segments (3 for females and 4 for males) was performed at the stereo microscope. During the dissection, the insect body was kept refrigerated on ice to avoid deterioration of possible pathogens’ genetic material necessary for the subsequent molecular analyses, which is in progress. Real-time PCR and nested-PCR are being used for preliminary screening of TOSV and *Leishmania*, respectively, to detect natural sand fly infections, further analysis is planned, also for *Leishmania* detection a Real-time is planned to be performed.

RESULTS AND CONCLUSIONS. The putative *Leishmania* and Phlebovirus vectors were differently represented in the investigated sites with markedly different densities, ranging from 2 sand flies/site in Veneto region, to 196 sand flies/site in Emilia-Romagna (Tab. 1). The species prevalence by territory was also different, being 100% *Ph. perniciosus* collected in Friuli Venezia Giulia (7 sites), in contrast to 96-99% *Ph. perfiliewi* collected in Tuscany and Emilia-Romagna (15 sites) (Fig. 1).

Numerous specimens from Tuscany were from 2017, 2018 and 2019 collections, which will be identified and examined in the next future.

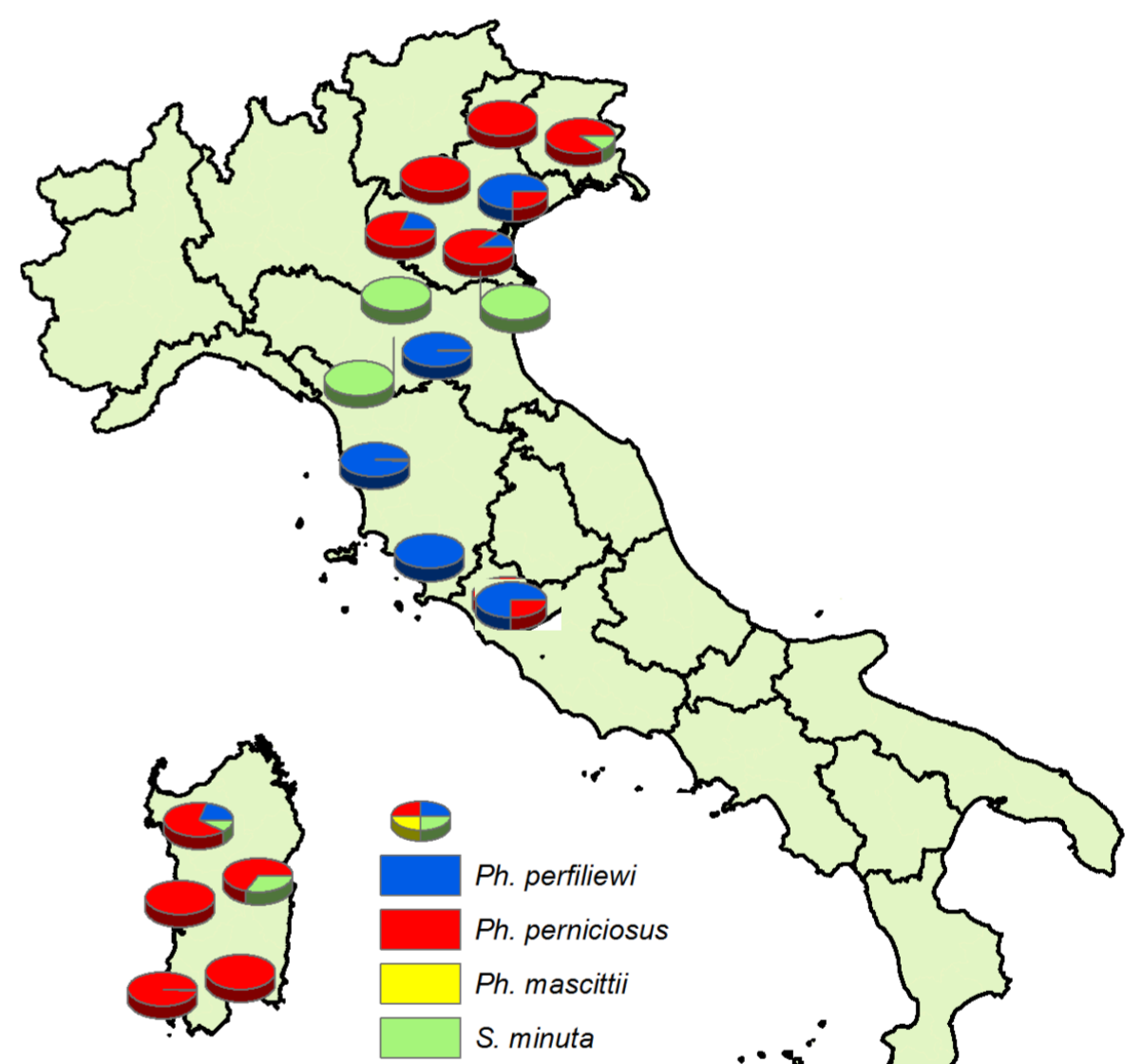


Fig. 1 Prevalence of sand fly species by territory

Table 1 Prevalent sand fly species identified by Region pending examination for pathogens

| REGION | No. of sites | No. of sand flies | % <i>Ph. perfiliewi</i> | % <i>Ph. perniciosus</i> |
|-----------------------|--------------|-------------------|-------------------------|--------------------------|
| Friuli Venezia Giulia | 7 | 39 | 0.0 | 100.0 |
| Veneto | 9 | 20 | 26.3 | 73.7 |
| Emilia-Romagna | 6 | 1174 | 98.6 | 1.2 |
| Tuscany | 9 | 661 | 96.2 | 3.8 |
| Latium | 1 | 200* | 70.0 | 30.0 |
| Sardinia | 16 | 364 | 11.7 | 88.3 |

*Samples collected in 2017