Preliminary distribution maps of sandflies in Emilia-Romagna region, Italy (2003-2013)

Keywords: sandfly, distribution, *Phlebotomus perfiliewi*, *Phlebotomus perniciosus*

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Introduction

Sandflies can transmit a variety of pathogens, from parasites (as Leishmania) to viruses (as Toscana, Sicilian and Naples fever viruses), that have a wide health impact. Burden of sandfly transmitted diseases are heavily increasing worldwide, but the biology of sandflies is largely enigmatic, as for the clear characterization of breeding sites and border of their distribution. This is partially due to the focal distribution of these insects, which shows also sharp peaks of abundance, characteristics that hampered their quantitative sampling.

With the aim to characterize the distribution of sandflies in the Emilia-Romagna region, data obtained by sampling campaigns from 2003 to 2013 were integrated in a database and analyzed by GIS approach.

Methods and Results

More than 160,000 sandflies were collected in the study period, by surveillance plans targeting different sandflies borne diseases (Toscana virus and Leishmania) and mosquito borne diseases (as West Nile Virus). Different locations (kennels, natural environments, surroundings of houses of affected persons or infected dogs) were surveyed with different trap models (sticky traps, ST; CDC light traps, CDC; carbon dioxide traps, CO_2) ad sampling frequencies (point 1). Sub-samples of collected sandflies were identified to species according to morphological characters and two species were mainly detected, *Phlebotomus perfiliewi* (21,429 specimens-97.4% of identified specimens) and *Phlebotomus perniciosus* (563 specimens-2.6% of identified specimens); also 6 specimens of *Sergentomyia minuta* were collected (point 1). Data from parallel samplings, performed in the same day with different trap models, were used to determine possible linear correlations between number of sandfly sampled by different trap models (point 2). These correlations were utilized to transform data from different trap model in comparable values; then an average value of collected sandflies were obtained for every monitored site, considering only samples in which sandflies were collected (point 3). Sandflies spatial occurrence and abundance were modelled using Random Forest (RF) approach and two maps at 1 km resolution were created (point 4). Analyses of these data with other models, to possibly extrapolate results to a larger area are in progress.

Final considerations

The sand flies abundance maps could be very useful in the risk assessments of sandflies transmitted pathogens, especially if, as recently hypothesized, the link between circulation of these diseases and sandflies abundance will be confirmed.

1) Sampling.
Sandflies were trapped over the region in different locations and by different trap model from 2003 to 2013.

Number of collected specimens and number of samplings (specimens/samplings) for different locations and trap models
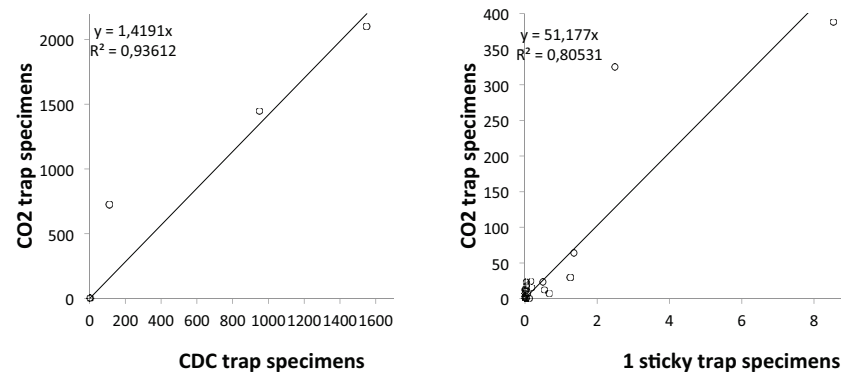
	Kennels	Dwellings	Natural loc.	Total
CO_2	2834/135	11540/210	126763/380	141137/725
CDC	662/649	17783/134	1/1	18446/784
ST	679/603	129/5	-	808/608
Total	4175/1387	29452/349	126764/381	160391/2117

Sub-samples of collected sandflies were identified to species level

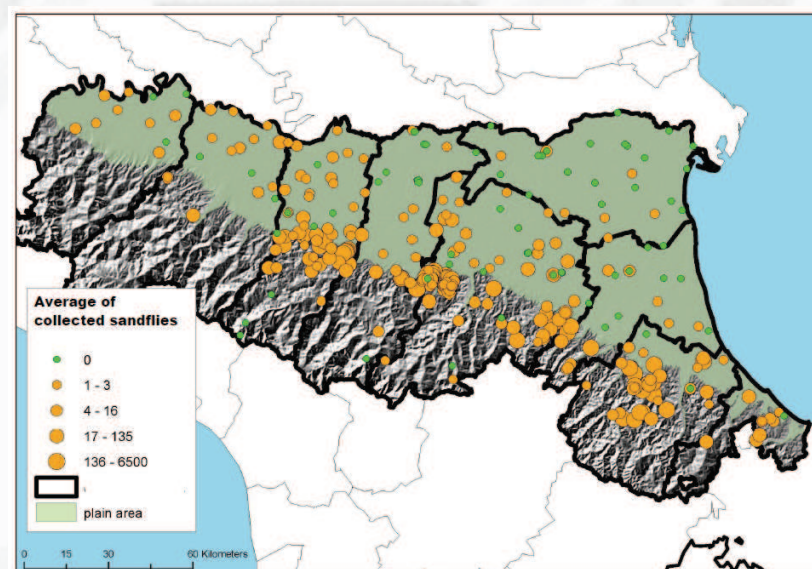|	Number
Ph. perfiliewi	21429
Ph. perniciosus	563
S.minuta	6
Sandflies	138393
Total	160391

2) Correlation.
Data from parallel samplings were utilized to obtain comparable value between different trap model performance.
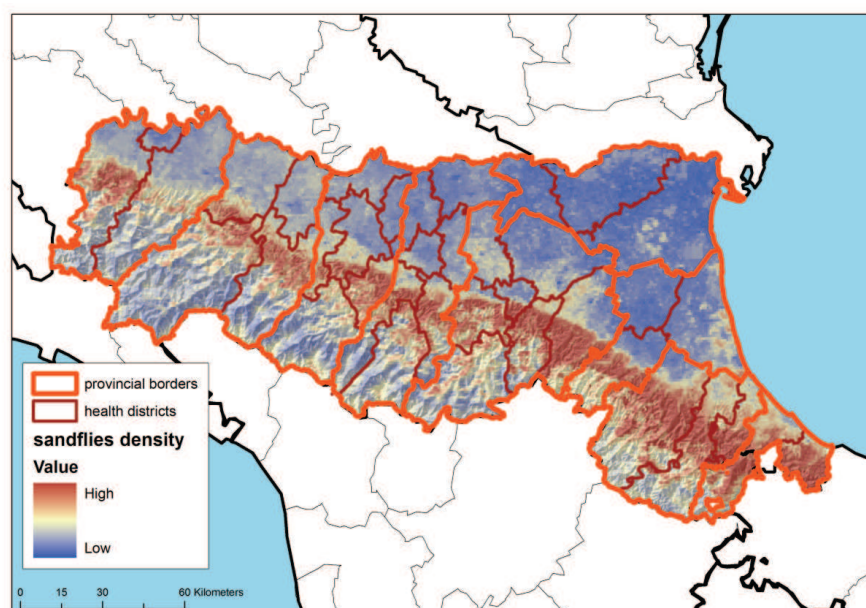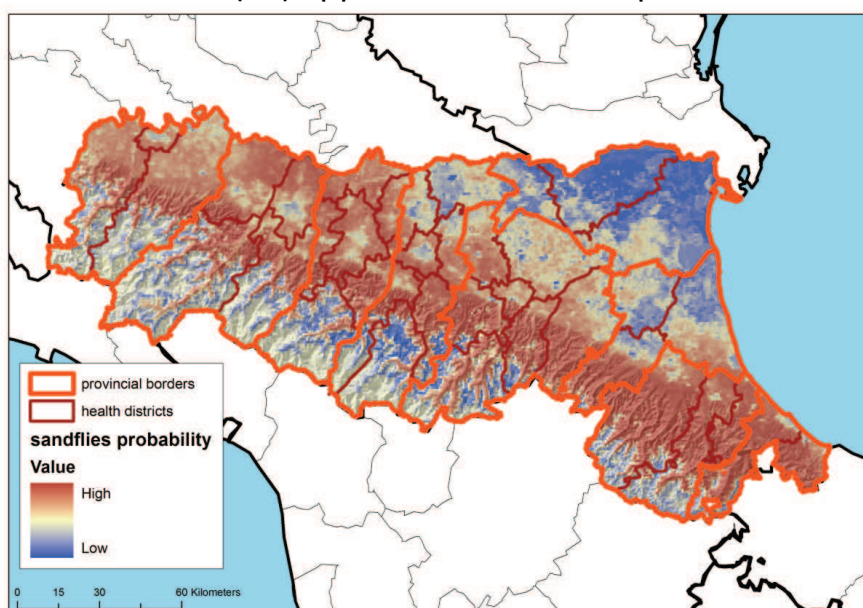

3) Site abundance.
Average value of collected sandflies were obtained for every monitored site.

4) Occurrence and abundance modelling.
Sandflies spatial occurrence and abundance were modelled using Random Forest (RF) approach and two maps at 1 km resolution were created.