

Red foxes as a source of zoonotic scabies in a rural area of Piedmont, Italy

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Introduction

Sarcoptes scabiei is an obligate parasitic mite affecting more than 100 mammal species worldwide. Whether host specificity, genetic strain or geographical occurrence of *Sarcoptes scabiei* might influence the transmission of this parasitic mite between animals and humans is still an ongoing and open debate.

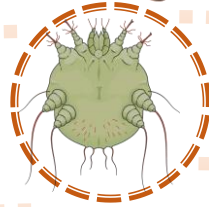


Aim

The aim of this study was to describe a severe episode of human scabies in two patients with no travel history tracing the source of the infection using microsatellites as molecular markers.

Materials & Methods

In November 2019 a woman and her daughter were referred to a local health unit in Piedmont (Italy) for severe pruritus appeared overnight after rescuing a red fox (*Vulpes vulpes*) showing crusty lesions all over the body. Ten *Sarcoptes* microsatellite markers were used to characterize the genetic structure of mites obtained by dermoscopy of the two human patients and skin scrapings of the fox (four and two mites, respectively). All mites were identified as *Sarcoptes scabiei* following morphological criteria. The genetic profiles of mites isolated in the present study were compared with mites collected from sympatric foxes and Spanish ibexes as outgroup.

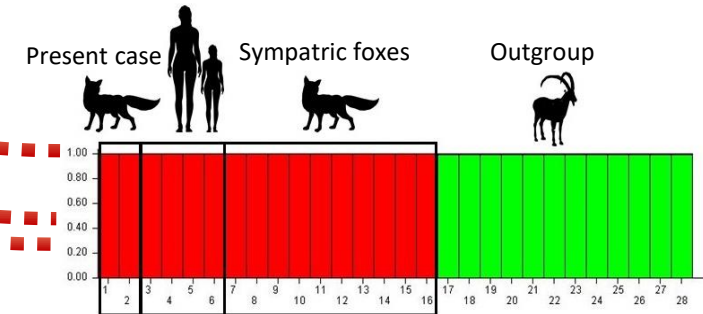


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Results & Conclusions

Dermoscopy from two human patients revealed the presence of *Sarcoptes* eggs, mites of all stages and skin burrows, which imply that the mites transmitted from foxes to humans were able to actively replicate. The Bayesian assignment test revealed the presence of two different *Sarcoptes*-derived clusters (Figure 1), consisting of mites from two human patients, the rescued fox and sympatric foxes, and mites from Spanish ibex.



The results demonstrate a clear origin of the human outbreak identifiable in the red fox rescued by the women. Foxes are well-known wildlife hosts for sarcoptic mange in Europe, and previous genetic studies identified them as one of the most common carnivores spreading mange among different wildlife species, and humans as well. To the best of our knowledge, this is the first genetic report of fox-derived transmission to humans.