



Genetic epidemiology of *Sarcoptes scabiei* in the Iberian wolf in Asturias, Spain



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ABSTRACT

Background: During the last decades, attempts have been made to understand the molecular epidemiology of *Sarcoptes scabiei*, and to detect and clarify the differences between isolates from different hosts and geographic regions. Two main phenomena have been described: (i) host-taxon derived-*Sarcoptes* mite infection in European wild animals (revealing the presence of three separate clusters, namely herbivore-, carnivore- and omnivore-derived *Sarcoptes* populations in Europe) and (ii) prey-to-predator *Sarcoptes* mite infection in the Masai Mara ecosystem.

Results: Using one multiplex of 9 microsatellite markers and *Sarcoptes* mite samples from sympatric Pyrenean chamois, red deer, red fox and Iberian wolf, different population structure analyses revealed concordance with the host-taxon law described for wild animals in Europe, with two main host-derived *Sarcoptes* mite populations, herbivore- and carnivore-derived. Surprisingly, Iberian wolf derived *Sarcoptes* populations had the highest genetic diversity among the other populations, including two different subpopulations: one similar to the herbivore-derived *Sarcoptes* populations, and another similar to carnivore (fox)-derived *Sarcoptes* mite population.

Conclusions: The host-taxon effect in wild animals is still supported with the maintenance of carnivore- and herbivore-derived *Sarcoptes* clusters' separation in analyzed mites. However, this phenomenon could be modified with the inclusion of a large predator as wolf in the present work, revealing prey-to-predator *Sarcoptes* mite infection between the studied host-taxa and suggesting the importance of wolf's immune system for explaining the high variability reported in *C. lupus* derived mites. Further studies of host diet, behavior and movement, and regarding the role played by its immune system, would be of great help to clarify interactions between the two hypotheses, host-taxon and prey-to-predator.

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1. Introduction

Despite representing the first human illness with a known etiologic agent (Montesu et al., 1991; Gakuya et al., 2012a) and affecting more than 100 mammal species

all over the world (Bornstein et al., 2001; Pence and Ueckerman, 2002), the taxonomical status of the ectoparasitic burrowing mite *Sarcoptes scabiei* has been the subject of continuous debate for decades (Pence et al., 1975; Fain, 1978; Andrews, 1983). The development of molecular techniques has provided new approaches and novel data on this subject (Zahler et al., 1999; Walton et al., 2004a; Gu and Yang, 2008); in particular, microsatellites are a valuable technique for the analysis of *S. scabiei* and the relationship between hosts. Microsatellite analysis supports the standing of *S. scabiei* as a single highly variable species with different strains manifesting physiological host-specificity (Walton et al., 2004b; Alasaad et al., 2008b, 2011b, 2012).

A mange epizootic first detected in 1993 in the southern border of Asturias severely affected Southern chamois (*Rupicapra pyrenaica parva*) from the area (Fernández-Moran et al., 1997), leading to an overall 61.3% reduction of their population during the first years after the outbreak (González-Quirós et al., 2002). Although the origin of the outbreak could not be demonstrated, it has been attributed to many domestic goats sharing pastures with chamois in the study area, and subsequent cross-infection (Lavín et al., 2000; Menzano et al., 2007). The epizootic is still expanding eastwards today with sporadic cases of sarcoptic mange in chamois, red deer (*Cervus elaphus*) and roe deer (*Capreolus capreolus* – Oleaga et al., 2008a,b) from the area. Red foxes (*Vulpes vulpes*) and wolves (*Canis lupus*) have also been diagnosed with sarcoptic mange in Western, Central and Eastern Regions of Asturias, and disease is now considered endemic in red foxes.

Three main groups of *S. scabiei* mites have been genetically identified in European wildlife studied so far, namely herbivore, carnivore and omnivore-derived *Sarcoptes* clusters (Rasero et al., 2010). These mite “strains” occur in sympatric as well as geographically distant populations, including Southern chamois, red deer, roe deer and red fox in our study area in Asturias, Northern Spain (Alasaad et al., 2011b). In sympatric mammals, differentiation of mites into “strains” may result from null or limited interspecific transmission, due to low frequency of direct contacts among hosts, low densities of one or more hosts, or different immunological response to the invading mites, limiting their population size, hence their number on the skin surface and their transmissibility to other individuals of the same or a different species. On the other hand, genetically based preference for a particular host (leading to host-associated mating) or the evolution of higher performance or viability on that host (usually entailing a worse performance on the others, Kassen, 2002) have been proposed as possible mite-dependent mechanisms limiting gene flow (Magalhães et al., 2007). The apparent lack of gene flow or recent admixture between carnivore-, herbivore-, and omnivore-derived *Sarcoptes* populations reported in European studied species, including sympatric animals, led to the so called “host-taxon law” formulation (Rasero et al., 2010; Alasaad et al., 2011b).

Parasites are of pivotal importance in food webs. Moreover food webs are very incomplete without parasites (Lafferty et al., 2006), with endo-parasites (Sukhdeo, 2012) as the most frequently described trophically transmitted

parasites (Luong et al., 2013). The only report, to our knowledge, about ecto-parasites transmission was on *Sarcoptes* mite transmission in Masai Mara ecosystem (Gakuya et al., 2011). Theoretically, the higher frequency of direct contacts among hosts within trophic chains (especially when acting as predator, considering that prey are not a “long-lasting available habitat” after predation for ectoparasitic mites) should favor a more efficient gene flow between different mite “strains”. Nevertheless, the study of *S. scabiei* molecular features in a predator/prey ecosystem has not been carried out in any European model, so far. Recently, molecular and epidemiological studies including wild felids and ungulates in Africa have signaled the existence of a potential predator/prey bond in sarcoptic mange transmission, the so called prey-to-predator parasitic infection (Gakuya et al., 2011, 2012b).

The recent isolation of *S. scabiei* mites in 9 out of 12 wolves bearing skin lesion in Asturias (Northern Spain) suggested an increase in morbidity of sarcoptic mange in this wild canid population (Domínguez et al., 2008; Oleaga et al., 2011) and allowed a genetic study of mites in this host for the first time. This work aims to study the genetic structure of *S. scabiei* mites affecting wolves in Northern Spain, and to genetically compare them with mites originating from sympatric wild herbivores (red deer and Southern chamois) and carnivores (red fox). Both wild and domestic ungulates are common prey of the wolf in the study area (Meriggi and Lovari, 1996; Barja, 2009), whereas predation and scavenging on many foxes have been suspected as a source of infection in this top chain carnivore (Bornstein et al., 1995; Mörner et al., 2005; Domínguez et al., 2008). Such molecular analyses could help in determining the extent to which sarcoptic mites may be interspecifically transmitted in one of the few available large predator-prey food chains in Europe.

2. Materials and methods

2.1. Study area

The study was carried out in the Principality of Asturias, a 10,603 km² autonomous region located in North-Western Spain. The area, with a mixture of open pastures and meadows with deciduous and mixed forests, is home of many different wildlife species, including carnivores like the endangered brown bear (*Ursus arctos*), wolf and red fox, and several wild ungulates (red deer, roe deer, wild boar – *Sus scrofa* – and Cantabrian chamois) that represent a high percentage of the diet of wolves (Llaneza et al., 1996).

2.2. Sampling and mite isolation

The study of wolves submitted for necropsy in Asturias (Northern Spain) as part of a wildlife diseases surveillance program allowed the confirmation of sarcoptic mange by mite isolation in 9 out of 47 wolves from 2008 to 2010 (Oleaga et al., 2011), and the extraction of genetic material from mites belonging to 8 of these 9 many wolves (seven of them were collected in population control hunts carried out by wildlife officers, while one wolf died as a consequence of vehicle collision). Acari were collected after

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