# The neglected navigating web of incomprehensibly emerging and re-emerging Sarcoptes mite



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Review

**The neglected navigating web of the incomprehensibly emerging and re-emerging Sarcoptes mite**

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Abstract

Parasite presence in any ecosystem generates complex navigating webs (Parasite-NW) within the system, through which parasites move from one to another host. The appropriate assimilation of parasite navigating web is pivotal for a better understanding of pathogen flow in the ecosystem, with implications for disease control. Sarcoptes mite has been approached from medical, veterinary, entomological, physiological and, recently, molecular sides, to understand its epidemiological navigating web between isolates from different hosts and geographical regions. The obtained conclusions are still a matter of debate. Sarcoptes navigating web (Sarcoptes-NW) is intricate and uncertain, with unexplainable pathogenic flow. In this review we summarize by which routes, under what conditions and at what levels the Sarcoptes mite moves among its hosts.

Keywords

Sarcoptes scabiei; Scabies; Sarcoptes mite; Parasite navigating web (Parasite-NW); Parasite flow; Emerging and re-emerging disease

## 1. Introduction

The neglected parasite Sarcoptes scabiei affects humans and a wide range of mammalian hosts worldwide ( Bornstein et al., 2001, Pence and Ueckermann, 2002, Walton et al., 2004b and Alasaad et al., 2011a), entailing significant mortality in both wild and domestic animals, with considerable economic losses ( Bornstein, 1995, Pence and Ueckermann, 2002, Heukelbach and Feldmeier, 2006 and Dagleish et al., 2007), and ravages in human populations ( Walton et al., 2004b and Hay et al., 2012).

There are no accurate estimates of the prevalence of Sarcoptes mite in the many animal populations worldwide, particularly in sylvatic animals. In humans, estimations indicate that hundreds of million people are infested with scabies worldwide ( WHO, 2009). The prevalence of scabies in African children can be as high as 40–80%, and in remote indigenous communities in northern Australia, up to 50% of children and 25% of adults were found to be infested ( Kristensen, 1991, Carapetis et al., 1997 and Terry et al., 2001). Considering increasing resistance of topical chemotherapy, there is an urgent need to develop new control strategies ( Currie et al., 2004, Bradberry et al., 2005 and Sanderson et al., 2007), and the increasing need of sensitive and reliable diagnostic tests for humans and many domestic and wild animals ( Haas et al., 2005 and Heukelbach and Feldmeier, 2006).

Sarcoptes mite has been approached from morphological ( Fain, 1978), medical ( Carapetis et al., 1997 and Feldmeier et al., 2009), veterinary ( Bornstein, 1995), entomological ( Fain, 1978), physiological ( Arlian, 1989, Arlian et al., 1996 and Haas et al., 2005) and, recently, molecular points of view ( Zahler et al., 1999, Walton et al., 1997, Walton et al., 1999, Walton et al., 2004a, Alasaad et al., 2008b, Alasaad et al., 2009a, Alasaad et al., 2009b, Alasaad et al., 2011b, Alasaad et al., 2012c, Rasero et al., 2010 and Gakuya et al., 2011) aiming to understand its epidemiology between isolates from different hosts and geographical regions, but this issue is still a matter of vivid debate.

The objective of the present review is to summarize available evidence on Sarcoptes movement among hosts, in order to further elucidate transmission dynamics and provide an evidence-based rationale for sustainable control.

## 2. Emerging and re-emerging Sarcoptes scabiei

Parasite navigating webs (Parasite-NW) are the complex webs through which zoonotic parasites move from one host to another within the ecosystem (Polley, 2005). Pivotal to an appreciation of the function of parasite webs is an understanding of parasite flow: by which routes, under what conditions and at what levels the parasite flows among its various hosts, of the same or different species (including vectors where applicable), and between the hosts and the environment (Daszak et al., 2000).

Based on the definition of emergence and re-emergence of diseases by Lederberg et al. (1992), Sarcoptes mite emergence could be the result of the spread of Sarcoptes mites in one human/animal population from an infectious origin, or simply the realization that an infection has been present in a population but undetected for several reasons. The re-emergence of Sarcoptes is defined as the reappearance of Sarcoptes after a decline in incidence. Accordingly:

(i) A Sarcoptes mite mange outbreak can be ‘genuine’ emergence of an infestation, which is new to that particular and naive animal/human population. In this case, other infested hosts (humans, domestic and/or wild animals) sharing space with the non-infected population are suspected to be the reservoir and source of the mites through cross-infestation. In ruminants, the possibility that mites, adapted to a “main” reservoir host, may infest other sympatric species has been documented in mange foci in Europe ( León-Vizcaíno et al., 1999, Rossi et al., 2007 and Oleaga et al., 2008), and field evidence has been supported by the results of experimental infestations ( Meneguz and Rossi, 1995 and Lavín et al., 2000). Migration of human populations may also be a driving force for genuine emergence of scabies.

(ii) A Sarcoptes mite outbreak can be 'apparent' emergence/re-emergence, where Sarcoptes infestation is pre-existing, and the newly recognition is a result of increased detection opportunities ( Kutz et al., 2003 and Oleaga et al., 2008) and/or the modification of a pre-existing host-parasite equilibrium ( Pence et al., 1983 and Lloyd, 1995). In this second case, destabilizing modifications may have occurred on the host side, e.g. a diminished herd resistance, and/or the parasite side, e.g. the selection or of a more pathogenic strain or drug resistance ( Pence and Windberg, 1994 and Leung and Grenfell, 2003).

Further epidemiological studies should consider a third category, which is a mixture of genuine and apparent emergence of Sarcoptes mite outbreaks. Such mixture category can be revealed using both epidemiological and population genetic approaches.

## 3. Sarcoptes transmissions

It is thought that Sarcoptes mite originated from a human ancestor and then spread to domestic and then free-living animals ( Fain, 1968 and Walton et al., 2004b). Sarcoptes mites lack free-living stages, and individual hosts, depending on their susceptibility and behaviour, are essentially ephemeral habitats providing patchy environments that hamper random mating ( Price, 1980 and Criscione et al., 2005). All mites on an individual host may in fact form an 'infrapopulation' ( Bush et al., 1997 and Alasaad et al., 2008b) that has a number of recurrent generations. The number of generations is influenced by the short generation interval of this parasite (about three weeks), as well as by the infected host's life expectancy and susceptibility ( Bornstein et al., 2001).

Transmission of S. scabiei may occur by direct or indirect contact. Larvae and nymphs of S. scabiei frequently leave their burrows and wander on the skin ( Arlian and Vyszenski-Moher, 1988), which may, in the case of crusted scabies, harbour hundreds to several thousands of mites/cm2 ( Zeh, 1974, Arlian et al., 1988 and Pérez et al., 2011). Some may become dislodged from the host and fall off ( Arlian and Vyszenski-Moher, 1988). In controlled environments, mites may survive up until a few weeks if conditions (microclimate) are optimal ( Arlian, 1989). Cooler temperatures and high humidy prolong off-host survival of S. scabiei, presumably because under these conditions mite metabolism is reduced ( Davis and Moon, 1987 and Arlian et al., 1989).

However, Sarcoptes navigating web (Sarcoptes-NW) is intricate and uncertain with fragility of parasite flow, and consequently transmission dynamics are not clear. For example, the mode of scabies transmission in humans is still discussed-whereas some authors define scabies as a sexually-transmitted disease, others suggest close body contact between children and their mothers to be the main route of transmission in endemic communities ( Jackson et al., 2007). Clearly, these aspects depend on many interacting factors and differ from setting to setting.

The time needed for S. scabiei var. hominis, immediately transferred from one host to another, to initiate penetration into the stratum corneum was ∼10 min ( Arlian et al., 1984), and it took the mites ∼35 min to become completely submerged into the epidermis. The time required for complete penetration into the stratum corneum increased as a function of the time the mites had been off their host. Experiments indicate that mites remain infective at least one-half to two-thirds of their survival time when dislodged from their host ( Arlian, 1989). In historical but classical studies, Mellanby (1944) believed that the stage responsible for transmission was the young, newly fertilised adult female, which wandered around on the skin surface before burrowing. His studies on transmission of scabies determined that patients with a high parasite load in excess of 100 adult female mites are more likely to spread the disease than those harbouring a lower number of parasites.

Additional studies on Sarcoptes transmission and off-host survival under different host species, climatic conditions and fomite materials are still needed ( Arlian, 1989).

From the other side, the co-infection between Sarcoptes mite and other ecto- and endo-parasites still not well-understood and need further studies ( Alasaad et al., 2008a, Alasaad et al., 2008b and Ryser-Degiorgis et al., 2002). The better understanding of mixed infection, involving S. scabiei, is of pivotal interest for the better understanding of Sarcoptes epidemiology, diagnosis and treatment

### 3.1. Intra-mammalian groups transmission

#### 3.1.1. Intra-humans transmission

Epidemics of human scabies have been hypothesised to occur on a worldwide basis in 15–25 year cycles (Falk, 1982, Arlian, 1989 and Lassa et al., 2011). Nonetheless, this possible “fluctuations” of disease occurrence is not corroborated by appropriate data (Orkin and Maibach, 1978).

Estimations indicate that 300 million people, especially children, are affected (WHO, 2009). Prevalence of scabies in African children can be as high as 40–80% (Kristensen, 1991 and Terry et al., 2001). In low and middle income countries, scabies is a significant public health problem because it is highly prevalent and complications are frequent (Heukelbach et al., 2005, Hay et al., 2012 and Heukelbach et al., 2012). Presence and severity of scabies are associated with young age, presence of many children in the household, illiteracy, low family income, poor housing, sharing clothes and towels, and irregular use of shower (Feldmeier et al., 2009). The high association with sharing clothes and towels points to a substantial contribution of fomites in the transmission of mites between humans, at least in certain settings (Zeh, 1974). However, in practice (and in endemic communities) it is not possible to quantify the importance of each single factor in epidemiological studies. Crusted scabies (also called Norwegian scabies), which is a scabies mite hyper-infection with hundreds of thousands of parasites on a single host, is rarely diagnosed in healthy individuals, but sometimes is seen in elderly, immune-suppressed patients with chronic disease, or patients suffering from malnutrition. These high transmitter individuals, who because of behaviours or mite load or some other factor, may provide a much higher risk of transmitting infestations (de Almeida Barbosa et al., 1996).

In an urban slum in Bangladesh, the incidence of scabies in children younger than 5 years was 952/1000 per year, which means that almost all children experienced at least one infestation per year (Stanton et al., 1987). This is in contrast to the situation in industrialized countries, where the disease occurs sporadically in all age groups, particularly in sexually active adults, or causes epidemics in institutions and nursing homes (Andersen et al., 2000, Heukelbach et al., 2005 and Ariza et al., 2012).

### 3.1.2. Intra-domestic animals transmission

In Africa, mites from sheep were successfully transferred to goats (Abu-Samra et al., 1984), and transmission of mites from goats to sheep was also achieved (Ibrahim and Abu-Samra, 1987). In both cases, infested goats and sheep developed severe lesions, particularly in moistened areas, and observation of skin scrapings revealed large numbers of mites belonging to all developmental stages, which demonstrated active reproduction of transferred mites in the new host. Similar results were obtained with experimental cross-infection between camels and goats (Nayel and Abu-Samra, 1986). Conversely, other attempts to transfer Sarcoptes mites between domestic species failed, like those involving dogs, sheep, goats, cattle and cats ( Arlian et al., 1988) ( Table 1).

Table 1.

Experimental cross-transmission of Sarcoptes scabiei, host species and outcomes.

| Host of origin | Receiver host | Outcome | Citation |
|---|---|---|---|
| Man | Macacus rhesus | Not successful | Ruch (1959) |
| Man | Domestic sheep | Not successful | Pirilä et al. (1967) |
| Man | Cattle | Not successful | Pirilä et al. (1967) |
| Domestic goat | Northern chamois | Successful | Fiebiger (1917) and Kerschagl (1955) |
| Domestic goat | Camel | Successful | Nayel and Abu-Samra (1986) |
| Domestic goat | Domestic sheep | Successful | Ibrahim and Abu-Samra (1987) |
| Domestic goat | Southern chamois | Successful | Lavín et al. (2000) |
| Domestic goat | Donkey | Successful | Abu-Samra et al. (1984) |
| Northern chamois | Domestic goat | Successful | Meneguz and Rossi (1995) |
| Southern chamois | Cattle | Not successful | Lavín et al. (2000) |
| Southern chamois | Domestic sheep | Not successful | Lavín et al. (2000) |
| One humped camel | Domestic goat | Successful | Navel and Abu-Samra (1986) |
| Dog | Domestic sheep | Not successful | Arlian et al. (1988) |

| | | | |
|---|---|---|---|
| Dog | Domestic goat | Not successful | Arlian et al. (1988) |
| Dog | Cattle | Not successful | Arlian et al. (1988) |
| Dog | Cat | Not successful | Arlian et al. (1988) |
| Dog | Rabbit | Successful | Arlian et al. (1984) |
| Dog | Guinea pig | Not successful | Arlian et al. (1984) |
| Dog | House mouse | Not successful | Arlian et al. (1984) |
| Dog | Pig | Not successful | Arlian et al. (1984) |
| Dog | Rat | Not successful | Arlian et al. (1984) |
| Dog | Man | Not successful | Kutzer and Grunberg (1970) |
| Coyote | Dog | Not successful | Samuel (1981) |
| Coyote x dog hybrid | Red fox | Successful | Stone et al. (1972) |
| Wolf | Dog | Not successful | Samuel (1981) |
| Red fox | Dog | Not successful | Samuel (1981) |
| Red fox | Dog | Successful | Stone et al. (1972) and Bornstein (1991) |
| Red fox | Coyote x dog hybrid | Successful | Stone et al. (1972) |
| Red fox | Coyote | Successful | Samuel (1981) |
| Red fox | Man | Not successful | Kutzer and Grunberg (1970) |
| Tapir | Man | Not successful | Kutzer and Grunberg (1970) |

Table options

3.1.3. Intra-wild animals transmission

Mange, caused by S. scabiei, has been reported from many species of wild mammals worldwide. Some of the most remarkable hosts include (1) canids in North America ( Pence et al., 1983 and Little et al., 1998); (2) red foxes and other canids in Europe ( Mörner, 1992, Ippen et al., 1995 and Gortazar et al., 1998); (3) red foxes and dingoes in Australia ( McCarthy, 1960); (4) chamois, ibex and a variety of other ungulates in Europe ( Ippen et al., 1995, Fernández Morán et al., 1997 and Rossi et al., 2007); (5) felids in Europe ( Mörner, 1992) and Africa ( Young, 1975); (6) wild boar in Europe ( Ippen et al., 1995); (7) wombats in Australia ( Skerratt et al., 1998); and (8) a range of ungulates, primates, and canids in Africa ( Young, 1975, Kalema et al., 1998, Munang'andu et al., 2010 and Gakuya et al., 2012b). New outbreaks in wildlife are being continually reported worldwide ( Alasaad et al., 2012a).

The molecular analyses of sympatric wild animals in Europe show unambiguously that there has been a lack of gene flow or recent admixture between carnivore-, herbivore-, and omnivore-derived Sarcoptes populations ( Rasero et al., 2010). Host-taxon-derived effect seems stronger driver of intra-specific differentiation than geographical separation, and it seems temporally stable ( Alasaad et al., 2011b). The existence of host-taxon-derived Sarcoptes mites could explain why mange-free populations can live in sympatry with mangy animals, as is the case of the mange-free Capra ibex and Rupicapra rupicapra of the western Italian Alps that live in close proximity with the endemically mangy population of red fox Vulpes vulpes, and wild boar Sus scrofa ( Rasero et al., 2010). Vice versa, this effect could be the immediate reason why cross-transmission easily occurs, in Europe, between foxes, dogs and other canids, as well as felids including domestic European cats, when these hosts are exposed to the same vulpine-derived strain ( Bornstein 1995) ( Table 1).

The studied wild animals in Europe (from which the host-taxon was coined) lacked of clear predator–prey interaction and putative inter-specific transmission models. Recent epidemiological and molecular studies revealed potential prey-to-predator gene flow between wild animals from Africa. Cheetahs were infected from both wildebeest and Thomson's gazelle, while lions were only infected from wildebeest. In a predator/prey ecosystem, like Masai Mara in Kenya, it seems that Sarcoptes infestation is from prey-to-predator, in relation to the predator's "favourite prey", which could be attributed to the direct skin-to-skin prolonged contact between the predator and the prey during hunting process ( Gakuya et al., 2011 and Gakuya et al., 2012a).

### 3.2. Inter-mammalian groups transmission

#### 3.2.1. Humans-wild/domestic animals transmission

Humans are occasionally infected with S. scabiei of animal origin ( Arlian, 1989). This includes human infection from camel, cat, chamois, coyote, dog, ferret, fox, wombat, gazelle, goat, horse, llama, pig, sheep, water buffalo and cattle ( Kutzer, 1970, Fain, 1978, Chakrabarti et al., 1981, Samuel, 1981, Folz, 1984, Chakrabarti, 1990, Mitra et al., 1993, Morsy et al., 1995, Skerratt and Beveridge, 1999, Menzano et al., 2004 and Bazargani et al., 2007). Those infected include farmers, personnel working in slaughterhouses researchers, veterinarians, wildlife biologist, and pet owners.

Most human infections from animal sources involve only topographically circumscribed body regions, are short-lived and self-limiting, lasting from a few days to several weeks (Arlian, 1989). As infestation is less severe and clinical features are different from infestation with Sarcoptes scabiei var. hominis, this condition is usually referred in the medical literature as "pseudoscabies". Lesions are frequently seen on the trunk, arms, and abdomen and rarely on the fingerwebs and genitalia. In addition, the incubation period is markedly shorter, and mite burrows are not regularly seen ( Orkin and Maibach, 1991). Pruritus may be as intensive as in classical scabies, but symptoms usually wane within a maximum of 2–4 weeks. The human host is a not a source of infection to other humans. Reportedly, nonhuman mites most frequently originate from dogs infested with S. scabiei var. canis (30–50% of cases) ( Thomsett, 1968, Folz, 1984 and Aydıngöz and Mansur, 2011).

The short-life and self-limiting infection of Sarcoptes mites of animal origin when transmitted to humans was confirmed by molecular analysis. Walton et al., 1999 and Walton et al., 2004a used multi-locus genotyping applied to microsatellite markers to substantiate previous findings that gene flow between human- and dog-derived mite populations is extremely rare in scabies-endemic Aboriginal communities in Australia.

### 3.2.2. Domestic animals-wildlife transmission

Considering the increasing deforestation and changing ecosystems worldwide, there has been more and more contact of domestic animals with sylvatic animals. In fact, the introduction of infected domestic animals and the success of the Sarcoptes mite in adapting to new highly susceptible wild hosts have been proposed as the origin of Sarcoptes mite epizootics in previously mange-free wildlife populations ( Arlian, 1989). This scenario was also proposed for a Sarcoptes mite outbreak in Iberian ibex in Sierra Nevada mountain range, Spain in the 1970s, possibly from domestic infected goats ( Pérez et al., 1997).

Molecular studies have been carried out to understand Sarcoptes transmission between humans and animals, and between wild host species, but never between domestic and wild animals, and hence effort should be made in this direction. We know very little of interspecific transmission between (putative) domestic reservoirs and wildlife, while we know much more on wildlife to wildlife transmission.

In the Sierras de Cazorla, Segura y Las Villas Natural Park (southern Spain) mange has become an endemic disease. At the end of the 1980s, it firstly affected Iberian ibex (Capra pyrenaica) causing devastating mortality rates with a reduction of the population by 95%. Then, the disease reached other sympatric wild ungulate species: European mouflon (Ovis aries), red deer (Cervus elaphus) and fallow deer (Dama dama). The origin of this epizooty is attributed to infested domestic goat herds (see, for instance, León-Vizcaíno et al., 1999). Regarding this situation, an attempt to experimentally infect chamois (Rupicapra rupicapra) with Sarcoptes mites derived from naturally-infested domestic goats was successful ( Lavín et al., 2000). The opposite route of transmission was also previously demonstrated under experimental conditions ( Meneguz and Rossi, 1995). A recent outbreak of Sarcoptes mite in domestic goats from northern Italy has been attributed to presumable contact with wild animals under natural conditions ( Menzano et al., 2007).

Domestic-wild animals transmission usually produce high mortality and morbidity rates, probably because of insufficient management actions.

## 4. Predictions of emergence and re-emergence

Sarcoptes emergence and re-emergence could be predicted by different approaches, such as (i) endemic cycles, (ii) increasing agglomeration of people, wild and domestic animals, and increasing contact between human-wildlife-livestock. Notwithstanding, the prediction of Sarcoptes emergence and re-emergence could be affected by (a) the emerging of resistant against some acaricides ( Currie et al., 2004), (b) the lack of effective diagnosis method for many host species especially the wild ones ( Alasaad et al., 2012b), and (c) the totally neglected role of fomites in Sarcoptes transmission.

Better prediction of scabies and mange emergence and re-emergence could be achieved through better understanding of inter-specific transmission patterns, which requires further studies including the effect of (i) travelling, sexual and familiar contact, biomedical manipulation and migration in intra-humans transmission; (ii) agricultural intensification and animal translocation in intra-domestic animals transmission; (iii) translocation and animal stress in intra-wild animals transmission; (iv) technology and industry manipulation in humans-domestic animals transmission; (v) human encroachment, tourism, and ecological manipulation in humans-wild animals transmission; and (vi) animal encroachment and animal introduction in domestic animals-wildlife transmission (Fig. 1).

Full-size image (80 K)

Fig. 1.

The neglected Sarcoptes navigating web (Sarcoptes-NW), including multiple putative routes of parasite flow between mammalian hosts, following authors' criteria. Dotted lines: flow through fomites. Solid lines: flow through direct contact (host-to-host). Circular arrow: flow within animal group. Question mark: questionable parasite flow. Curved lines: flow between groups.

Figure options

5. Public awareness

A better understanding of Sarcoptes navigating web is of pivotal interest for the public health. Unfortunately many facets of Sarcoptes navigating web regarding humans are not yet clear, including human-to-human transmission, especially the sexually transmission and family care, and wild and domestic animals to humans transmission. Integral programs should be carried out including epidemiological and genetic studies of Sarcoptes navigating web between humans and wild/domestic animals, and review of knowledge and practices regarding Sarcoptes infection in humans ( Gakuya et al., 2012b). Effective and operator-friendly methods for direct and indirect diagnosis of scabies are still missing and the resistance of Sarcoptes to drugs is now becoming of major concern.

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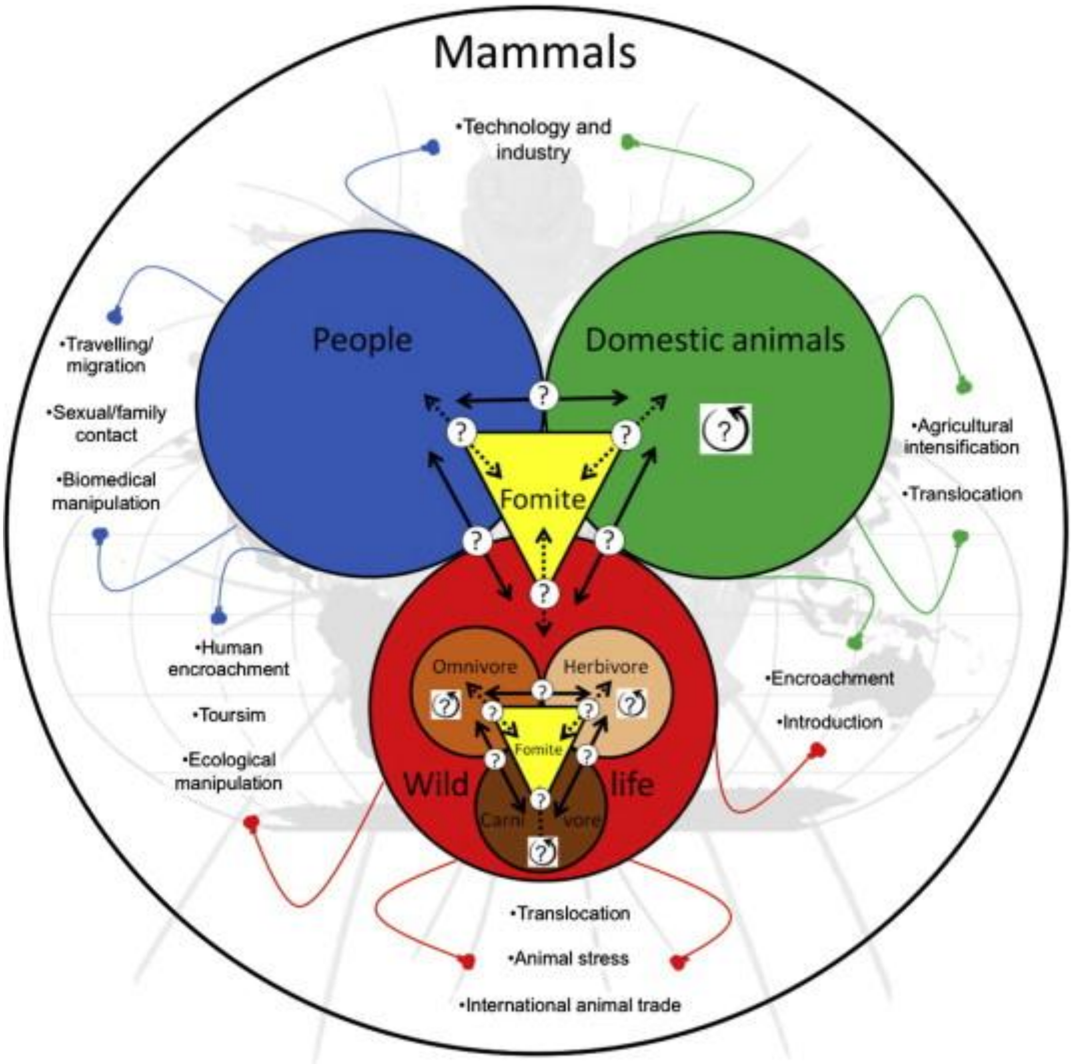
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•Ecological manipulation
Omnivore
Herbivore
Fomite
Wild
life
Carni
vore
•Encroachment
•Introduction
•Translocation
•Animal stress
•International animal trade