CHAMOIS INTERNATIONAL CONGRESS
PROCEEDINGS

Lama dei Peligni - Majella National Park - Italy
17-19 June 2014

CONGRESS ORGANIZED BY THE MAJELLA NATIONAL PARK
DURING THE LIFE09/NAT/IT/000183 COORNATA PROJECT
Development of coordinated protection measures
for Apennine Chamois (*Rupicapra pyrenaica ornata*)

DISEASES OF RUPICAPRA SPP.
AT THE INTERFACE WITH LIVESTOCK AND OTHER UNGULATES

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Diseases and parasites have long been recognized as drivers of evolution in free-ranging wildlife, domestic animals and man (Combes 2001). In recent years, evidence is accumulating that the demographic impact of selected transmissible diseases may result in substantial modifications of the structure and genetics of affected wild targets (Lachish et al. 2011), similarly as weather constraints and the presence of predators. Accordingly, views of scientists and resource managers are changing regarding the opportunity to interfere, and if this is feasible, with wildlife disease dynamics (Wobeser 2002). Amongst ruminants in the Holartic, wild *Caprinae* are by far the most frequently exposed to a range of transmissible diseases with remarkable demographic impact in the short term (Gavier-Widen et al. 2012). However, current evidence shows that large-sized and well connected populations of wild *Caprinae* (eg, Northern chamois in the Alps) are not threatened, at least in the long term, by any known disease-related emergencies. Oppositely, from a conservation perspective there is strong and justified concern on the effects that transmissible diseases may cause in small-sized and isolated populations (eg, transmissible pneumonias in Desert bighorn sheep in the Rocky Mountains, or in Flare-horned markhor in Hindukush). Noteworthy, such concerns has been the rationale of the successful redistribution program of the Apennine chamois from the sole population survived (Herrero et al. 2008).

Several diseases and parasites of wild *Caprinae* are in common with domestic ruminants, particularly with the so called small ruminants (sheep and goats) due to closer zoological relationships. In the mountain ranges in Europe, wild and domestic *Caprinae* are used to share range on a seasonal basis, when transhumant flocks are allowed access to the montane, sub-alpine and alpine meadows, usually not earlier than late May and not later than early November. Under these circumstances, wild and domestic *Caprinae* may get in direct or indirect contact (Ruttiman et al. 2008), permitting the inter-specific transmission of pathogens. For several reasons – amongst them the obvious increase in number of wild *Caprinae* throughout Europe – the fore mentioned contacts have become closer in the last decades, and reports of outbreaks have raised in parallel, suggesting emergence of a specific two-ways management problem at the livestock/wildlife interface (Richomme et al. 2006). In this contribution we will review the main epidemic and endemic diseases of *Rupicapra* spp. in Western and Central Europe, and try to give an answer to the following two questions: Q1) are domestic ruminants the actual origin and the reservoir of these diseases in the major outbreak areas?; Q2) in this case, are there any tools and/or strategies available that are meaningful to control and prevent the cross-transmission of the agents between domestic flocks and sympatric chamois?

There are four transmissible diseases known to have major demographic effects in chamois: infectious kerato-conjunctivitis (IKC), pestivirosis (PV), scabies or sarcoptic mange (SM) and the "transmissible pneumonias" (TPs). However, since inconclusive results have been obtained so far on the complex etiology of TPs (Citterio et al. 2003), little can be inferred on the cross-transmission of candidate pathogens at the livestock/chamois interface. Accordingly, this contribution will deal with the remaining three diseases.

Outbreaks of IKC are due to virulent strains of *Mycoplasma conjunctivae*, an atypical bacteria (class Mollicutes) lacking a cell wall, hence having extremely poor off-host environmental persistence. Transmission occurs via direct contact and the mechanical eye-to-eye transport operated by flies over short distances. In the frame of a long-term study, Crampe et al. (2008) have shown clear connections between the spread of IKC and the space use by different social units of the investigated chamois.

Onset of a novel IKC outbreak in unaffected chamois areas is usually perceived as a problem that occurs during the summer, characterized by high incidence, relatively low mortality and lethality and the biased distribution of clinical cases (significantly more often in females than in males, and in adult females compared with kids). The symptoms and behavior of affected chamois and the presence of orphan kids have a strong emotional impact on mountain visitors, that are especially numerous and active in this season. In contrast, spread of IKC during winter is characterized by lower incidence, higher mortality and lethality and lower visibility by a large public. Overall, decrease rates may range, locally, from approximately 5 to more than 30% (Giacometti et al. 2002a).

A striking characteristic of IKC outbreaks is the rapid spreading potential over large areas, at the speed of over 15 km/year from the index case (Degiorgis et al. 2000). Since the last decades of the past century, IKC outbreaks involving large areas (e.g., of above ten thousand hectares) have been reported in the Alps, Pyrenees and Cantabrians though not in the Apennines. In recent years, outbreaks with a particularly large spatial extension – the largest ever known – have occurred in the Western Alps and in the Central Pyrenees (Arnal et al. 2013). However, also sporadic cases and small foci with limited spatial spread are known to wildlife professionals and resource managers in the Alps. On the other hand, IKC does not persist endemically in the same area and, at the small scale (eg, some hundred or a few thousand hectares), the epidemic wave is used to vanish within a few months, suggesting little role for herd immunity.

M. conjunctivae is frequently isolated from the eyes of sheep and goats, and IKC is a well known condition amongst small

ruminant farmers worldwide. Sheep to chamois transmission has been observed (Giacometti et al. 2002a). It is a largely accepted view that: a) domestic flocks are reservoir of *M. conjunctivae*; b) IKC outbreaks in chamois originate, most frequently, from occasional spill-over of virulent strains from the domestic reservoir; c) chamois IKC is not maintained in chamois (nor any wild *Caprinae*) populations (Giacometti et al. 2002b). Amongst other evidence, a strong argument in favor of this "classic" view is the rare and timely spaced occurrence of IKC outbreaks in large chamois herds monitored over long time-series (eg, within National Parks and Hunting Reserves), and the first occurrence of epidemic IKC in chamois in New Zealand, some 40 years after the introduction of only 8 individuals from the Austrian Alps. However, the "classic" view is being put in question by the molecular-based isolation of *M. conjunctivae* in the eyes of healthy chamois in Switzerland (Mavrot et al. 2012). Although it is not clear if positive asymptomatic animals are true healthy carriers or are in an incubation phase or not yet cleared of a previous infection, such recent findings suggest "that an endemic presence of *M. conjunctivae* in wild mountain ungulates cannot be excluded on large territories used by interconnected subgroups of wild ungulates, although this would not rule out sheep as a potential source of infection" (Mavrot et al., 2012). Interestingly, however, the Alpine ibex (*Capra ibex*) seems better candidate than chamois to a reservoir role complementary to domestic flocks (Ryser-Degiorgis et al. 2009). More epidemiological studies are needed to define if cohabitation with ibex is a risk factor for occurrence of IKC outbreaks in chamois.

At the interface with livestock, little can be done for the benefit of unaffected chamois provided that: i) healthy carriers of *M. conjunctivae* are frequent amongst transhumant sheep and goats; ii) no vaccines are available; iii) no mass chemoprophylactic protocols have been evaluated for efficacy, economic sustainability and compatibility with the consumer-friendly production of valuable meat and cheese. As a result, enhanced clinical surveillance of sheep and goat flocks about to move to chamois land and the isolation and treatment of clinically affected individuals remains the only feasible (though weak) option at the moment.

In the early years of the current century, a novel Pestivirus (Fam. *Flaviviridae*) of the "Border Disease Virus" (BDV) group was isolated from sick chamois in the Central and Eastern Pyrenees. The agent of Pestivirosis (PV) in chamois is described as a specific variant belonging to the BDV4 genotype, which is the same genotype as the BDV circulating in sheep in Spain (Marco et al. 2009).

PV in chamois is clinically characterized by variable degrees of cachexia, alopecia (often associated with skin hyperpigmentation) and neurological disorders (eg, depression, weakness and difficulty in moving) prior to death. The signs of secondary infections magnified by the immunosuppressive effects of BDV4 infection (eg, dyspnoea due to bacterial bronchopneumonia) are also frequent findings (Gavier-Widen et al. 2012).

The demographic effects of PV are extremely variable, from a mild impact on reproductive performance to severe die-offs with mortality rates between 40 and 85%, as observed in the Eastern Pyrenees (Marco et al. 2009). The reasons of such variability, though still to be fully elucidated, include the viral strains involved, the epidemiological phase of the infection (epidemic vs. endemic), the herd immunity eventually influenced by contacts with related viral strains of domestic origin, the social and spatial structure of the affected host populations, and their genetic variability (Fernandez-Sirera et al. 2012, Cavallero et al. 2012). Nevertheless, it is estimated that the whole chamois population of the Central and Western Pyrenees has decreased of approximately one third since 2001 (Gavier-Widen et al. 2012).

Persistence of BDV4 infection after a first PV outbreak has been demonstrated, as well as the opposite scenario of viral extinction. Interestingly, recovery of the affected chamois population was weak in the first case and rapid in the second, though return to a viral and serological naive status of the second population is now a matter of concern for resource managers, since BDV4 infected chamois are still present in neighboring chamois herds (Fernandez-Sirera et al. 2012).

As to the origin of this emerging conservation problem, an innovative phylogenetic study of available viral sequences suggests that: i) the chamois clade originated from sheep BDV4, generating a founder effect; ii) the "capture" by the new sylvatic host was recent event, that can be dated back to approximately two decades ago. In addition, the study shows that intra-specific subclading of the BD "chamois" variant is already detectable along the Pyrenees (Luzzago et al. this volume).

Based on available information, it seems that sheep (and goats) have no role in maintaining the circulation of the BD "chamois strain" within the infected range in the Pyrenees. Accordingly, control of BD in livestock (if feasible, in the absence of an effective and safe vaccine) would be of no help for control in current outbreak areas. As opposite, it is tempting to figure out that contact with flocks endemically infected by "their" BD strains may result in a sort of natural and beneficial cross-vaccination of sympatric chamois, enhancing herd immunity against the "chamois strain" or other putative novel "chamois" strains, in future. If that is the case (more field studies are necessary to confirm), sympatry with such flocks would be desirable, in contrast with traditional views by resource managers. Similarly, implementation of active sero-surveillance schemes in managed chamois populations is warranted to check the herd immunity in front of any variants of the BDV, and design management according to the epidemiological status, without inappropriate generalizations. Outside Pyrenees, seroreactors to Pestiviruses of livestock origin have been frequently found amongst chamois surveyed in the Western Alps (Riekerink et al. 2005, Martin et al. 2011) and, to a lesser extent, in the Central Alps and Cantabrians (Gaffuri et al. 2006, Falconi et al. 2009), while no seroreactors were found in an isolated chamois herd in the Apennines (Fernandez-Sirera et al. unpublished).

Scabies or Sarcoptic mange (SM) is caused by the burrowing mite, *Sarcoptes scabiei*. Several varieties of the mite are traditionally described, each of them able to successfully infect a limited range of related hosts. For example, mites infecting the Northern chamois in the Alps, usually referred as *S. scabiei* var. *rupicaprae*, are naturally or experimentally cross-transmissible to the Alpine ibex and the domestic goat, and more unfrequently, to domestic sheep, mouflons (*Ovis aries musimon*), roe deer (*Capreolus capreolus*) and red deer (*Cervus elaphus*) (Alasaad et al. 2013).

As of May 1993, there was a single SM outbreak area affecting chamois in the Eastern Alps (across Austria, Germany, Slovenija and Italy) eastbound of a line connecting two large rivers, Inn and Adige (Miller 1986). Since then, a new outbreak area established in the Cantabrians, involving the Eastern population of *R. pyrenaica parva* (Fernandez-Moran et al. 1997). Evidence shows that chamois living in the Pyrenees and in the Western and Central Alps are SM-free.

Persistence (for centuries in the case of the Austrian Alps) and relatively low spread (3-6 km/year on average) are well known characteristics of SM in chamois. Seasonality is another feature, since the majority of deadly cases are reported in winter and spring, suggesting interaction of the disease with natural factors (eg, winter starvation and other climate constraints) (Rossi et al. 2007).

On a large scale, mortality is mainly related to the life history of affected populations, namely to previous contacts (or absence of contact) with the disease. In the case of a first epidemic wave of SM in previously unaffected areas, the demographic impact is remarkable, eg. in the recently affected Dolomite Alps and Cantabrians, it is estimated that population size has decreased of approximately two thirds (Rossi et al. 2007, Perez-Barberia & Palacios 2009), with maxima well above 80%. As opposite, in the case of successive contacts, usually occurring in form of minor waves at 10-15 years intervals, mortality is rarely exceeding maxima of 25% (Rossi et al. 1995). In the Cantabrians (though not as clearly in the Alps), a new equilibrium characterized by a lower population size of approximately two thirds the pre-outbreak one was reached as the cumulative effect of the epidemic and the subsequent endemic phase of SM (Perez-Barberia & Palacios 2009). However, other factors may influence the outcome of SM at a smaller scale, namely the host genetic structure and variability, which are currently the object of stimulating studies (Mona et al. 2007, Schaschl et al. 2012).

Though suspected, the responsibility of infected livestock (domestic goats and less likely sheep) in triggering SM in naive chamois in the Eastern Alps and the Cantabrians has never been unambiguously demonstrated. Experimental infection trials have been successfully carried out in both directions (Lavin et al. 2000), and a spontaneous SM outbreak in domestic goats originating from naturally infected chamois has been reported (Menzano et al. 2007). Actually, however, livestock does not play any significant role in the dynamics of SM in the two recognized endemic areas. Finally, chamois are more likely to infect other sympatric wildlife than the opposite occurring, as in the case of the several colonies of Alpine ibex in the Eastern Alps (Rossi et al. 2007), and a single isolated colony of Iberian ibex (*Capra pyrenaica*) in the Cantabrians.

From a conservation perspective, attention to the livestock/wildlife interface should be focused on preventing that infected goats may turn into long distance carriers of *Sarcoptes mites* (eg., to the large SM-free chamois land which still exist across Europe). Awareness on this neglected trade related risk should be raised primarily at the institutional (international and national) level.

Back to questions Q1 and Q2, that prompted this contribution, we conclude that:

a) there is evidence or plausibility that pathogens transmitted to chamois by domestic sheep and/or goats may have been at the origin of IKC, PV and SM in the major outbreak areas known in Central and Western Europe;

b) in these areas, it is recognized that transhumant sheep and goats represent the main reservoir of *M. conjunctivae*, whereas chamois themselves are the exclusive reservoir of *S. scabiei* and the specific BDV4 variant;

c) little can be done at the livestock/chamois interface to control running emergencies. As an exception, cohabitation with BDV endemically infected flocks should be encouraged in order to strenghten the herd immunity of chamois against PV;

d) prevention of IKC outbreaks seems unlikely, and little can be done to anticipate that new BDV strains may adapt to chamois, as occurred in the Central Pyrenees. In contrast, active surveillance of caprine flocks about to move to chamois land (and their mass treatments of with injectable miticide drugs, if appropriate) is pivotal to contrast the risk that SM may spread to unaffected chamois, namely entire subspecies (*pyrenaica* and *ornata*, amongst other) and the subpopulations of *R. rupicapra rupicapra* and *R. pyrenaica parva* so far protected by natural and artificial barriers. Europe wide eradication of SM in domestic goats should be the optimal standard to achieve in the near future;

e) with rare exceptions, no specific guidelines can be given at the regional scale to optimize the conservation-oriented management of livestock health. However, since the priority is for early detection of emerging/re-emerging diseases which may potentially impact on the demography of chamois, focus and resources should target the effective and sustained (passive and active) surveillance of selected disease in livestock and the sympatric chamois.

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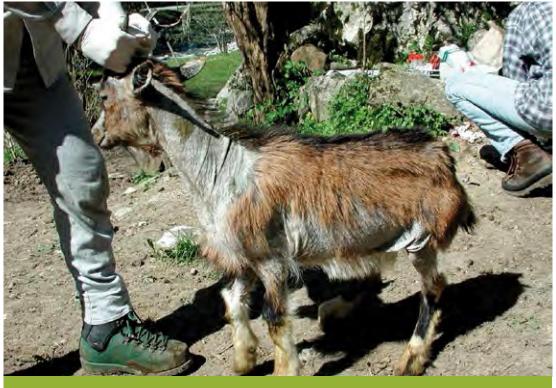Wobeser G. 2002. Disease management strategies for wildlife. Scientific and Technical Review 21(1): 159-178.

Picture 1. Severe presentation of Infectious Kerato-conjunctivitis (IKC) caused by *Mycoplasma conjunctivae*. Corneal ulceration and vascularisation can be observed in addition to abundant ocular discharge. Obvious signs of blindness (circling amongst them) were visible from distance.

Picture 2. Generalised scabies in a parva buck from the Cordillera Cantabrica, Spain. Severely affected individuals are often attracted by water and may even drown, as in this case. Saponification of crusty lesions is visible.

Picture 3. Dry crusty lesions caused by Sarcoptes scabiei are frequently localized in the head and neck. In this yearling, contrast between the dark and bright parts of the face has vanished. Condition of the affected individuals rapidly deteriorates when lesions involve the mouth parts.

Picture 4. Scabies may be croos transmitted between domestic goats and their wild counterparts. In this case, recorded in the Eastern Alps, Italy, spill-over occurred from the traditional chamois reservoir. The opposite has likely occurred in the early Nineties of the past century in the Cordillera Cantabrica, Spain.