Modeling the Distribution of Buffalo Populations in Africa
Summary of the Buffalo Meeting held 7 June to 8 June in Rome at FAO Headquarters

Background

In sub-Saharan Africa, where disease pathogens have co-evolved with their natural, wild hosts for millennia, wildlife are still relatively abundant and widely distributed. Increasing pressure on the land has, however, reduced the availability of rangeland for free-ranging, grassland-based production systems and has forced livestock, wildlife and people into closer vicinity as they compete for decreasing resources. This, in turn, increases the probability of transfer of pathogens among the different groups. In this context, many disease pathogens have made the passage from their original wild hosts to livestock and, in some cases, eventually into people. One such pathogen, *Trypanosoma brucei rhodesiense*, has made the transition from wild ungulates into ruminant livestock and hence into humans, who now contract the disease from tsetse flies infected primarily from livestock. Other livestock pathogens have undergone similar transitions, or parts thereof; East Coast Fever (ECF), Foot-and-Mouth Disease Virus (FMD) serotypes SAT1-3 and Lumpy Skin Disease (LSD), for example.

If we can gain an understanding of the processes underlying these transitions, and the risk factors associated with them, this offers the possibility not only to locate the interfaces where diseases of livestock are likely to persist in wild populations, many of which are zoonotic in nature, but also areas where novel pathogens may emerge at the interface of wildlife, ecosystems and farming systems. Disease surveillance activities can be targeted towards and intensified in areas of high risk. This will require maps of the distribution and abundance, and possibly seasonal movements, of wild hosts to be explored in relation to livestock and the ecological settings and production systems in which they are raised.

The distribution of the African buffalo, *Syncerus caffer*, has been taken as an example with which to develop and evaluate a methodology that takes reported statistics on the numbers of wildlife species, most of which come from protected areas, and to combine these with environmental data in multivariate statistical models that predict their distribution and abundance in areas where no data are available. For a number of reasons the African buffalo presents itself as a model candidate to evaluate the methodology proposed below. First, on account of its size, it is one of the most accurately reported wildlife species, the 'total count' census approach usually being adopted in estimates. Second, it is widespread in protected areas. And third, it is similar in its grazing requirements to domestic cattle, for which the modelling techniques use here have been tried and tested. Whilst the buffalo is not necessarily the optimal host for some disease pathogens, such as trypanosomes, it is of direct and primary importance in the ecology of other diseases; FMD in particular.

Buffalo are in the family bovidae, subfamily bovidae and tribe bovini. Other bovidae in the same tribe are cattle, yaks, bison and the Asian buffalo, to which the African buffalo is most similar genetically [1]. There are four subspecies of buffalo. The southern African savanna buffalo, also known as Cape buffalo (*Syncerus caffer caffer*), lives in the savanna of eastern and southern Africa from the south of Ethiopia and the upper White Nile as far as the Cape reaching the west coast south of Zaire. It is the largest buffalo subspecies and lives in larger herds with a mean size of 350 generally but can be up to 2,000[3,6,9]. The red or dwarf buffalo, also known as the forest buffalo (*Syncerus caffer nanus*), is the smallest subspecies of Western and Central Africa, utilizing the equatorial rain forests. It is a smaller and less gregarious animal; typically living in herds of less than thirty. Also in West Africa is the West African savanna buffalo, also known as Sudanese buffalo (*Syncerus caffer brachyceros*) [2,3]. A fourth subspecies proposed by Sinclair (1977) is the central African savanna buffalo or Nile buffalo (*Syncerus caffer aequinoctialis*) and it lives In the savanna of Ethiopia, the Sudan and Chad, northeast of the central African rain forest. It is similar to the Cape buffalo but smaller and lighter in colour [3]. Although, these subspecies are distinct, interrelationships most likely occur where the distributions of the subspecies come in to close proximity or overlap (figure 1).

The species' distribution and numbers have been greatly reduced by habitat loss and poaching. It is a favourite target of meat and trophy hunters in many countries, and poaching has been a major contributor to the recent decline of buffalo populations in many protected areas, e.g., Ivory Coast, Congo and Tanzania. It is also susceptible to drought, which has caused substantial declines in some populations during the 1990s, alone, or in combination with diseases such as anthrax or rinderpest, e.g., in Tsavo, Serengeti, Masai Mara, Gonarezhou and Kruger National Parks [4] . Rinderpest and other diseases such as anthrax have continued to result in localized declines and extinctions of populations throughout the 20th century, as rinderpest has spread from cattle to wildlife. East (1999) produced a total population estimate for the forest buffalo of about 60,000. This estimate is probably very conservative, but forest buffalo populations are in decline over most of the subspecies' remaining range.

In the past, numbers of African Buffalo suffered their most severe collapse during the great rinderpest epidemic of the 1890s, which, coupled with pleuropneumonia, caused mortalities as high as 95% among livestock and wild ungulates. Virtually all livestock, ruminant wildlife and, indirectly, species closely associated with these such as large carnivores and tsetse flies were all but eradicated. The current distribution and dynamics of disease pathogens has been shaped by these changing host-reservoir (and sometimes vector) population distributions and interactions. If we can gain insights as to how these changes may have influenced ecology and distribution of livestock diseases, this may help us to understand future disease threats that may emerge in association with increasingly restricted wildlife populations and increasing populations of livestock. These trends are on-going as a result of population growth, which places increasing pressure on the land and is likely to push wildlife and livestock into closer vicinity as they compete for grazing and water resources.

A meeting was organized by EuFMD and FAO EMPRES-i Wildlife Health and Ecology Unit to gather experts in buffalo ecology to review efforts at FAO to predict the densities of buffalo in Africa and to get feedback on the validity of the results. This was the second in a series of 3 workshops that focused on understanding wildlife and livestock dynamics. The first covered FMD and wild boar, and was held in Berlin in April 2011, and the third will review the role of Eurasian wild ungulates and FMD transmission to livestock, and will be held in September in Kazakhstan. The objectives of the meeting were to assess the validity of the buffalo distribution mapping efforts, to discuss risk factors for FMD transmission between buffalo and livestock, and to identify where to focus surveillance efforts for FMD.

Participants

Daniel Cornélis (La Recherche Agronomique Pour Le Développment, CIRAD), Richard Kock (Royal Veterinary College), Nick Knowles (Pirbright Laboratory), Mario Melletti (Biologist, independent researcher), Iacopo Sinibaldi (biologist for protected areas in the Lazio Region) and the following from the Food and Agriculture Organization (FAO) Headquarters: Scott Newman, Keith Sumption, Tim Robinson, Jan Slingenbergh, Jennifer Siembieda

Presentations and discussions (Annex 1)

1. Mapping African buffalo distributions, in relation to livestock disease risk - *Tim Robinson and Jennifer Siembieda*
2. Ecology and social organization of forest buffalo - *Mario Melletti*
3. Spatiotemporal dynamics of West African savanna buffalo - *Daniel Cornélis*
4. Patterns of contacts between African buffalo and cattle : an investigation using telemetry tools - *Daniel Cornélis*
5. Group discussion to review buffalo maps
6. Spatial distribution of Foot-and-Mouth Disease viral lineages in African buffalo - *Nick Knowles*
7. Livestock vs. wildlife economy: the importance of avoiding disease control fencing and sustaining viable rangeland ecosystems - *Richard Kock*

8. Group discussion on identifying priorities for FMD surveillance

Summary of discussions

Validity of the general approach and Evaluation of results

The experts (Daniel Cornélis, Richard Kock, and Mario Melletti) provided information on the actual densities in many of the protected areas. A few obvious problems with the predictions according to the experts are the following: in Kenya, the model predicted low densities of buffalo in Tsavo East and Boni Dodori National Parks east of the Tana river but in fact there are high densities in these areas. Another problem noted was that in Sudan, where habitat is suitable for buffalo the model predicted high buffalo densities, all the wildlife populations including buffalo have been decimated due to illegal poaching. Another concern was that the vegetative indexes reflect photosynthetic activity. Buffalo are grazers and they would choose grass even in dense tropical forest (e.g. in natural forest clearings). To support this, the lowest buffalo populations are in the central and western, forested regions of Africa but the model predicted high buffalo densities here. It was proposed that this may be due to the normalized difference vegetative index (NDVI) not reflecting habitat quality by adequately distinguishing tree cover from grass cover (the main food source for buffalo). The experts also stressed that woodland systems can go from no vegetation to lush vegetation in 24 hours (and thus show NDVI responses to rainfall similar to grassland). The African vegetative map produced by the Joint Research Centre at Ispra was recommended as an alternative indicator of habitat suitability compared to NDVI variables. Water, cattle and buffalo are the most important variables but food (i.e. grass) limits buffalo distribution and abundance mainly in the rainforest regions where this resource is patchy distributed[7]. It was suggested that areas outside of protected areas could mostly be masked out because buffalo are conservation dependent. A prediction agreed by all was that in the next 20 years, 95% of the buffalo would be restricted to protected areas.

Other additional factors to analyze

Additional factors such as poaching and social conflict could be added as variables to the model or as a map layer. Quantify poaching may be important; Tsavo park has 60 incursions per night, for example. Another idea was to mask out areas that are known to have no buffalo such as in Sudan the majority of the buffalo in Boma and Southern so-called protected areas have been poached although substantial numbers ~ millon of other species such as White eared kob persist in eastern Equatoria and around the Nile. To better predict areas of habitat suitability for buffalo, hydrology maps were considered potentially useful, because water is a major factor in limiting savanna buffalo populations, particularly in the dry season. On the contrary in the rainforest areas, where water is available throughout the year, grass is the limiting factor[8]. For this meeting, areas that had a high human footprint were masked out as unsuitable for buffalo.

Input data of buffalo mapping

It was agreed that total buffalo counts, where available, were better to use than line transects. Total buffalo counts are the preferred method for estimating buffalo populations nowadays compared to 10 to 20 years ago when line transect sampling was used. For this mapping analysis, the total number of buffalo per area sampled was used. It was stressed that total buffalo counts are only used for savannah species and not forest buffalo because forest buffalo prefer the dense forest and are therefore more difficult to count. The big debate was what the sampling window should be and whether you take an average over the years or the most recent count. The latter was used for this analysis. Using an average would not represent the data accurately because of the huge disparities in buffalo counts seasonally. Nigel Hunger who works with MIKE, Monitoring Illegal Killing of Elephants, may have updated numbers on buffalo.

Social Behaviour

Research conducted by Mario Melletti and Daniel Cornélis estimated the movement patterns by using satellite telemetry to track forest and savanna buffalo herds, respectively. Savanna buffalo were found to be water dependent and there was overlap of the land used between herds. In general, buffalo stayed close to water sources during the dry season. The home range during the wet season is established by the availability of perennial grasses and appears to not overlap. Potentially, this could be due to the species being territorial; however, during his study he observed no territorial activity. During the dry season, when resources are scarce, only 2 out 6 herds had 20 % overlap further suggesting that herds do not generally share space. Forest buffalo herds show little or no overlapping during the whole year and home range remains stable for years[5,7]. Other researchers have found that they maintain the same home range for up to 15 years. The herd size is around 45 individuals. Mean herd size is an indicator of habitat quality. In really lush areas (e.g. Manyara in Tanzania) there can be up to 2,000 individuals per herd. In W park in Burkina Faso, herd sizes are limited by the habitat or rather size of the park. Another review found that in the Chobe river the buffalo undertake the same movements during the dry season. The main limitation of this study was that the radio collars were only on female buffalos because the bull buffalos would break the collars off within one month. These data suggest that spatial and demographic expansion is heavily dependent on water and forage. Forest buffalo form smaller herds of about 3-24 individuals, and spend most of their time in the forest clearings[7]. It was suggested that a potential way to estimate forest buffalo habitat suitability was to identify such clearings via satellite remote sensing.

Disease transmission

Most disease occurs during dry seasons which supports the notion that certain times of the year favour disease transmission. Buffalo and cattle interactions however indirect occur mainly in the protected areas and in the buffer areas surrounding them. It was suggested strongly that transmission of FMD from buffalo to cattle is a rare event. Buffalo herds can carry the disease non-symptomatically for 5 years but virus excretion may be low or intermittent. In areas where there is lots of FMD in cattle then buffalo are not as important in the persistence or emergence the transmission of disease (for example in West and East Africa). Evidence from five collars that were placed on buffalo at the edge of a protected area in West and Southern Africa suggested there to be no direct contact with livestock and minimal sharing of habitat spatially or temporally. The cattle come in to the protected areas mainly in dry season because there is food and water during the dry season which increases the chance of contact and at times buffalo will seek pasture and water in the periphery of protected areas. These are also the times of the highest level of residency and density of both cattle and buffalo who are dependent on daily water availability. During the dry season the parks tend to be better monitored compared to the wet season, when they are difficult to patrol the park because the rains make it difficult to move around.

In the natural environment, there is compartmentalization but when humans get involved then there is more interaction i.e. placing watering holes. Buffalo have separate herding behaviours according to sex and age. As an example, bulls leave the group during the wet season but return to breed at the beginning of the dry season. The experts observed very few contacts between cattle and buffalo. In one month, all cattle had indirect contact with very few buffalos and in instances when cattle did share the same environment the cattle came to where buffalo were after 5 hours. A comparison was drawn with observations in Amboseli, where herders release the cattle to use the watering points in the middle of the park and. Here, wildlife and cattle will not share the water at the same time. In general, unless they are hand reared, buffalo will not share space with cattle so pathogens are more likely to be transferred via fomites, water or biting flies, than by direct contact.

There is anecdotal data to support FMD transmission from buffalo to cattle. For example, in North Zimbabwe where cattle and buffalo shared the same water source and both had the same serotype and where buffalo bulls associated with cows in oestrus. The concentration of buffalo and cattle in these fenced systems probably also intensifies the interface and opportunity for transmission. From serological studies iIt appears that all SAT types occur in buffalo across Africa with some gaps in Central and West Africa for SAT 1 and with SAT 3 relatively rare. Sserology suggests mainly SATat 1 & 23 in East African buffalo but it is notable that there have not been few if any confirmed outbreaks in cattle with these serotypes, with most reported outbreaks A or O. In East and West Central Afirca the lack of virus isolates to confirm prevalence of different viruses and serology is a major problem. Prevalence of FMD antibody in buffalo populations has been reported to be above 60% in East Central African populations with positive infections predominately in the 1-3 age group and few infections less than 9 months of age but data is deficient from this age group. There is no prevalence correlation with sex. It is important to note that 75% of the buffalo populations occur in protected areas. For this reason, it is speculated that the most common interaction occurs when cattle enter the parks for grazing. It was noted that FMD might not sustain itself in isolated buffalo populations with numbers less than 50 based on serology but this would need to be confirmed epidemiologically.

Environment

The possibility of environmental persistence being the source of infection was discussed. Disturbances caused by poaching, predation and disease could also be important. Fusion and fission patterns suggested the possible importance of predation i.e. more predation occurs at the beginning of the night. During rinderpest outbreaks of high mortality, animals were observed moving out of the location of mortalities perhaps another example of adaptation.

Genetics

There are 4 subspecies recognised on morphological criteria; the most recent was *Syncerus caffer aequinoctialis*, proposed by Sinclair in 1977. This is only based on morphology. The genetic distance is 2.5% between forest and cape buffalo (Randi and Melletti, unpublished data). Savanna buffalo more frequently split into smaller herds, herd-switching is more common and they have a large home range. There are many isolated populations of forest buffalo where they have been for 100's of years. Colleagues of Daniel Cornélis are looking at the genetic structure of all the African buffalo populations by using mitochondrial DNA. The species appears to cluster in two groups along the rift valley, though the results are, as yet, inconclusive. In populations where there are savanna and forest buffalos next to each other it would be interesting to study for gene flow among buffalos and genetic viral changes of FMD.

At the end of the 1800's, the rinderpest pandemic killed 90-95% susceptible species. This affected FMD diversity in Africa by severely reducing the numbers of susceptible hosts. Prior to the pandemic African buffalo ranged almost continuously from southern Sudan to the Cape. Afterwards only isolated herds were left, some of which harboured the SAT serotypes of FMD. The early introductions of FMD into Kenya and Nigeria most likely originated from Europe. There are 5 African serotypes (A, O, SAT1, SAT2, SAT3) and the SAT types were present in buffalo populations well before the rinderpest outbreak. SAT 1 was first observed in Zimbabwe in 1937 and there are 9 topotypes. SAT 2 is more wide spread with 14 topotypes. SAT 3 is the most limited serotype geographically and has only 5 topotypes. In Kruger National Park, there is evidence to support the spread of FMD by cattle and not by buffalo. SAT 2 is the serotype in buffalo only and present in southern African countries. The last outbreak in South Africa in buffalo was in 2006 and the buffalo herd had not been in contact with cattle, suggesting that the virus can persist for long periods of time in buffalo. Serology of SAT 3 supports this as well as it was detected in two male buffalos following an outbreak in cattle. Buffalos can be infected with all 3 serotypes and they can maintain the infection for at least 5 years and perhaps longer, but long term sampling would be needed to confirm this. Currently there is a funded project in Kruger National Park, to determine how FMD is maintained and how antigenic diversity is generated in African buffalo. Overall, the goal is to improve the security of the people and integrate wildlife and livestock systems.

Conclusions and Next Steps

Identifying priorities for FMD surveillance

Areas that should be prioritised for FMD surveillance were identified per region throughout Africa. In Africa, the cattle used for dairy production are generally a crossbreeds between FMD-susceptible high-yielding breeds (e.g. Holstein) and local, FMD-resistent African breeds. It was suggested that surveillance efforts should be focussed on are areas with high dairy production. These areas are concentrated in Ethiopia, Uganda, Kenya and Tanzania specifically the protected areas in the Rift valley system (Abedare, Masai Mara, Tsavo and Shimba Hills National Parks and any area east of Tsava National Park), western Uganda (Lake Mburu, Queen Elizabeth) and a few protected areas in the north (i.e. Murchinson Falls and Kadepo National Parks). In addition, this would aid in identifying areas that might need to be compartmentalized (e.g. by fencing).

The difference in the risk between the pastoral systems compared to the mixed, high production systems, especially dairy production should be acknowledged. Pastoral systems are at risk from disease introduction but to a lesser extent than the intensive dairy production systems. Improved mapping to identify areas where agriculture and wildlife are present, where they interface and where to conduct surveillance we considered important. The extreme importance of Africa, because of the diversity of wildlife and the explosive growth of human population, was noted, as was the need to create solutions that would work both for agriculture and wildlife. Specific interfaces between cattle and buffalo and listed below (Table 1).

Table 1: Protected areas considered to be of importance for FMD transmission in Africa by country, with notes on buffalo and cattle populations and their potential interactions.

Country	Protected Areas	Buffalo/cattle populations and interactions
West Africa		
Senegal	Niokolo Koba NP (10, 000 km^2)	- N and E of park about 58 buffalo and 957 +/- 800 transhumance (13O photographed in 2004 R Kock in one herd in the East) - Cattle populations in the W and N - Buffalo highest in the E but small numbers in the central - Poaching in the W - Human footprint is the lowest to the E
Burkina Faso/Niger	W park (32,000 km^2)	- 2,300 buffalo (aerial survey)
Burkina Faso	Nazinga GR (100 km^2)	- 145 buffalos
Burkina Faso	W Arly Panjari NPs (32,000 km^2)	- 10,000 buffalo - This is an area for high transhumance - Also a high human population and in certain areas there is hunting (therefore easy access to samples)
Cameroon	Campo Maán NP	- Forest and savanna buffalo present - Large population of cattle outside protected areas
Ivory coast	Comoe NP	- Unknown
Nigeria	Yankari GR	- 28 buffalo and 8,228 cattle - FMD occurs at the end of dry season
Central/East Africa		
Angola		- No information
Burundi	Rumubu NP	- May be important for cattle interaction also
Central African Republic	St. Floris NP	- Important place to monitor for FMD - 4,000 buffalo and transhumance (Felani)
	Bamingui-Bangoran	- Not very many buffalo - Major corridor for wildlife in N
	Andre felix NP	- Not many buffalo
Chad	Zakouma NP	- 4,000 buffalo isolated (2006) - North cattle present - Cattle do enter the park
Congo		
	Garamba	- ~1 000 buffalo - Few cattle to the east
	Upemba, Salonga Kundaludu, Lubudi	- Lots of buffalo
Ethiopia	Gambela NP	- Lots of cattle in Ethiopia - Big pastoral populations - Big dairy and beef in the mountains - Few bufflo
	Omo Mago Tama	- ~1 000 buffalo
Kenya	Boni-Dodori NR[1]	- North coast near Lamu there are many buffalo ~10 000
	Tsavo E and W[1]	- Masai and Somali trade here some come from Ethiopia ~10 000 buffalo
	Masai Mara[1]	- Borana and Somali pastoral groups - Massive wildlife die-off due to drought in 1990s now ~1 000 buffalo
	Northern rangeland [1]	- Between Samburu and Losai ~5 000 buffalo
	Laikipia[1]	- ~5 000 buffalo mixed cattle east side of the Rift Valley

		- In white highlands cattle ranching replaced by wildlife - Very interesting to study for FMD
	Abadare[1]	- Lots of buffalo (more than 850) - Buffalo being moved in from Laikipia
	Nakuru[1]	- FMD capital - 1 000+ buffalo in the national park **Note:** Kenya has plenty of buffalo pops and there is a WRL and therefore should be a priority for surveillance.
Sudan	Southern Park	- Buffalo present but they have been heavily poached - Remaining buffalo in SE corner next to Tedo (Ethiopia) - Follow up with Mike Kock for numbers
	Dinder and Borana	- Very few buffalo
Rwanda	Akagera NP	- < 1 000? Buffalo important for the likely development of dairy industry
Tanzania	Rungwa	- Almost of the buffalo have been shot
	Ruaha NP	- Significant populations still exist
	Selous NP	- Not many cattle because of tsetse fly but many buffalo
	Tarangire NP	- 3 000 to 4 000 single herds of 2 000 seen at times
	Ngorngoro CA	- Few hundred buffalo and many cattle
	Maswa HR	- Lots of buffalo
	Mkomazi	- Seasonally get lots of buffalo and lots of cattle cross the border between Kenya and Tanzania
	Tsavo	- 10 000? buffalo
	Manyara	- Few buffalo and they are concentrated by the Lake **Note:** Tanzania is an important area because there are lots of buffalo, cattle and FMD but not a priority because there is already a lot of research being done there.
Uganda	Kidepo Valley	- Buffalo interaction with pastoralists Sudanese cattle 2 000? buffalo
	Pian Upe	- Small population of buffalo
	Murchison falls NP	- Large pop of buffalo in the S and SW - An important area because 2 subpopulations, 1 in the N and 1 S of river.
	Bugungu	- Lots of cattle
	Queen Elizabeth NP	- Forest and savanna buffalos present 5 000+
	Kibale (E. of QE)	- Savanna buffalo few hundred
	Rwenzori (W of QE)	- Forest buffalo and few savanna buffalos
	Semiliki	- Lots of cattle and buffalo interaction seasonally especially during the dry season
	Lake Mburo	- Largest population of cattle and buffalo interacting - Very densely populated in and around protected area
Southern Africa		
Botswana	Kafue[1]	- Many cattle to the SE - TB transmission occurs - FMD surveillance priority **Note:** There are fences and many buffalo and cattle but little interaction.
Mozambique	Niassa[1]	- This is a large area - Important area in the north for FMD
	Limpopo NP[1]	- Important area in the south for FMD - In the great Limpopo transfrontier conservation area TB present in adjacent cattle herds but no interaction

Zambia	Luwanga Valley	- North and south there are lots of buffalo - Lots of poaching
Zimbabwe	Hwange NP	- Many buffalo but there are zones that prevent movement and interaction with cattle - Many buffalo in NW protected areas that are isolated from cattle populations - Cattle and buffalo interaction occurs in the protected areas to the south - FMD present but work being done and not priority
	Mana Pools NP	-Many buffaloes into the NP and in the contiguous hunting areas. No interaction with cattle in these areas of Zambezi valley. Still the tsetse control along the main road crossing the Zambezi Escarpment.
	Gonarezhou NO	- Many buffalo and cattle to the NE

NP = National Park, NR = Nature Reserve, GR = Game Reserve, CA = Conservation Area, N = North, E = East, S = South, W = West

[1] = important park for FMD surveillance

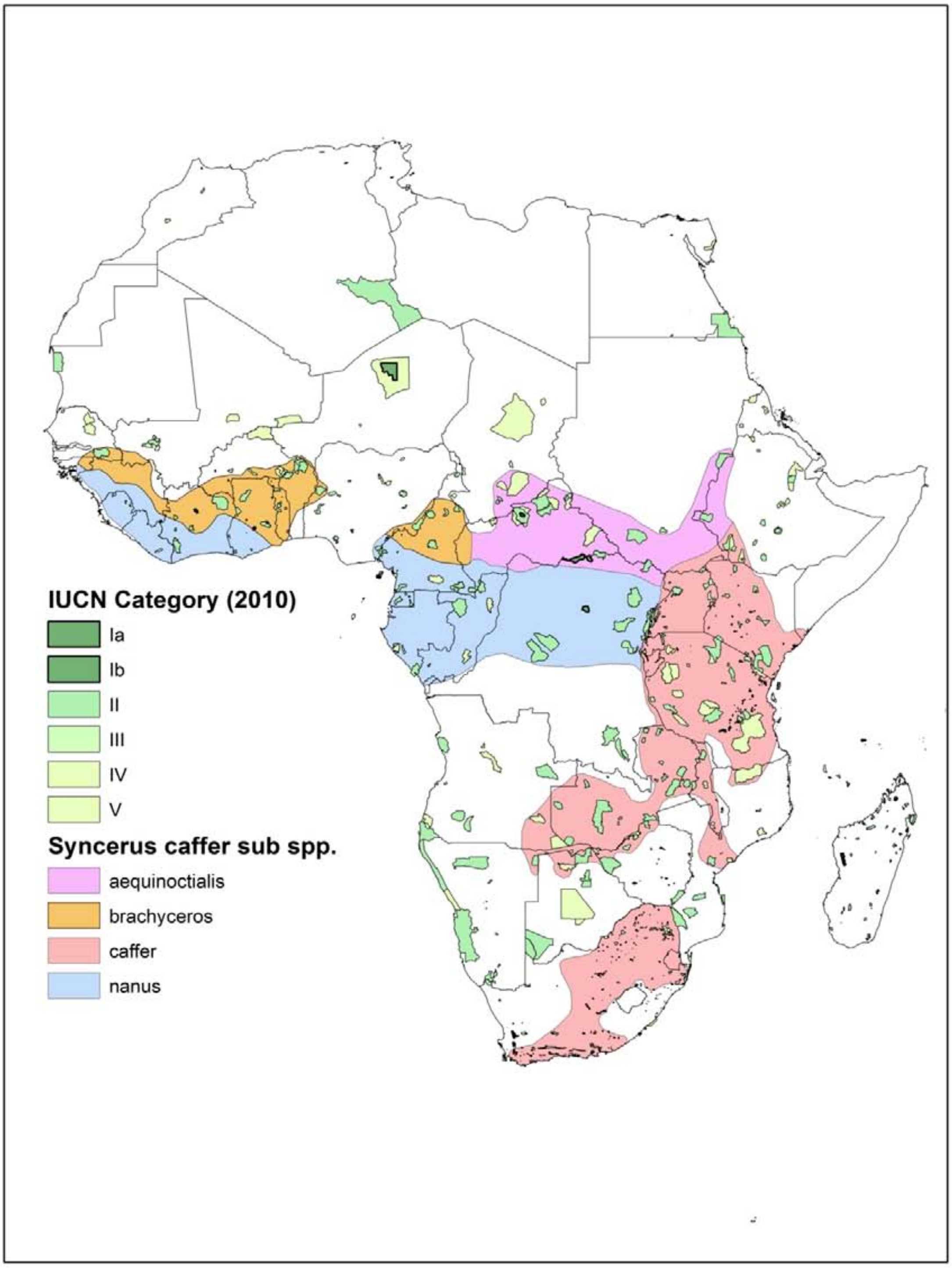

Figure 1. Distribution of protected areas (IUCN levels I-V) in Africa (Source: IUCN 2010a), superimposed on the distributional extents of the four subspecies of buffalo (*Syncerus caffer*) on the continent (Source: IUCN 2010b).

Annex 1: Agenda for buffalo meeting held 7-8 June, Rome-FAO Headquarters

Date		Presentation	Presenter
June 7		Welcome	S.Newman J. Slingenbergh
	A. Mapping of African buffalo populations	- Methodology to predict African buffalo densities	J. Siembieda
		- Using cattle and production system information to identify the buffalo-cattle interfaces	T. Robinson
	B. Buffalo ecology	- Ecology and social organization of forest buffalo	M. Melletti
		- Spatiotemporal dynamics of West African savanna buffalo	D. Cornélis
		- Patterns of contacts between African buffalo and cattle : an investigation using telemetry tools	D. Cornélis
	C. Putting it all together	- Group work to peer review buffalo maps: Objectives: (i) validity of the general approach; (ii) input data; (iii) evaluation of results; (iv) suggestions for improvements.	T. Robinson J. Siembieda
	C. Putting it all together	continue	
June 8	**D. Disease ecology**	- Spatial distribution of Foot-and-Mouth Disease viral lineages in African buffalo	N.Knowles
		- African buffalo and Foot-and-Mouth Disease	K. Sumption
		- Livestock vs. wildlife economy: the importance of avoiding disease control fencing and sustaining viable rangeland ecosystems.	R. Kock
		- Modelling the risk of Foot and Mouth Disease transmission at the wildlife/livestock interface of Kruger National Park	K. Sumption
	E. Future directions	- Group work on what to do next (i) identify priorities for advancing the science (ii) data needs? (iii) additional approaches? (iv) additional partners?	
		- Summary - Conclusions/recommendations	S.Newman K. Sumption

Annex 2: Specific comments on objectives and scope of the buffalo density mapping efforts and FMD (I. Sinibadli)

Objectives and scope of the buffalo density mapping effort:
Part of the discussion was focused on the methodology, approach to, and purpose of the buffalo density mapping exercise. Based on my experience, continental scale species distribution mapping can be very useful for the following: information and communication (to public and decision makers), assessment (of species status, trends, etc.), and broad scale strategic planning (e.g. to decide where to concentrate surveillance and monitoring, or to select areas or regions that should be allocated funding). Apart from these objectives, however, or from more research-oriented objectives, continental scale mapping is often of very limited practical application. This is because the uncertainties, assumptions and compromises required to take into account the variability of ecological conditions and preferences of widely distributed species such as buffalo, coupled with the need to assemble and use data sets of different quality, make continental-scale maps, even if produced at rather detailed resolution, not accurate enough to be used, with sufficient reliability, for more applied management needs (e.g. planning, prioritization of interventions, etc.). Conversely very detailed mapping at local scale, e.g. that at the level of single parks or groups of protected areas, is often very useful for researching and understanding ecological patterns and mechanisms, but can be of less value in terms of planning actions and interventions to be implemented over larger areas.

In my opinion, it could be worth directing further efforts in the future not only to refining buffalo distribution and densities mapping at continental scale (as it could provide useful insights into the main patterns of the species presence and distribution) but also to explore the feasibility of medium-scale mapping, i.e. at the level of regional or sub-regional groups of countries, if not of single countries, which may also represent a more useful tool for concerned government agencies. Further updating and improvement of data sets (e.g. on protected areas, but also for example on country wide aerial census data) in order to refine continental scale modelling could provide initial data for such finer scale mapping. Moreover, beside exploring other approaches and statistical models, it would be important to give attention also to validation of the distribution models.

FMD control vs. conservation: During the discussion, I was interested in a comment made about the perceived difficulties in engaging with the conservation community (in particular when approaching members of the IUCN specialist group). In my opinion however, the long-term risk of increasing conflicts and negative attitudes towards wildlife species, and consequently towards conservation areas, because of their possible role as reservoirs of livestock diseases, and the possible conservation benefits of pursuing specific approaches to disease prevention and control in wildlife-rich areas, should not be underestimated. For example in central Italy, we have huge problems with wild boars damaging crops, or with predators attacking livestock (even though damage levels are often exaggerated). These conflicts, in addition to draining huge sums of government money from protected areas budgets (thus reducing funds for other management activities) to provide compensation to farmers, already result in the development of negative attitudes towards protected areas and wildlife, which may be further exacerbated if coupled with real or perceived disease risks (as it occasionally happens). The African protected areas context is obviously very different, but in the long term increasing pressure against wildlife and conservation may anyway pose a threat to conservation areas, at least where wildlife resources do not provide obvious economic benefits (e.g. for tourism). Moreover, livestock diseases could negatively affect and pose a threat to other, more endangered wildlife species.

To this end, finer scale modelling and mapping of distribution and density of species such as the buffalo, and of the risk of FMD transmission between livestock and wildlife, could provide a useful tool to highlight and prioritize areas, at the level of single countries or groups of countries, where approaches to fight the disease may be applied that could help in avoiding or reducing the risk of conflict between livestock and wildlife conservation (e.g. increased surveillance, rapid response measures, incentives to adopt preventive measures, intensive vaccination in specific areas surrounding protected areas), which may be of interest to conservationists as well. Regional or country-wide scale modelling and mapping of distribution or densities species such as buffalo could also provide insights on patterns and processes which are difficult to take into account or explore at continental scale (i.e. migration and movements of wildlife, connectivity between sub-populations, presence of significant populations outside parks), and could be applied to other species. Such analyses could even provide the background data to plan, or could represent specific components of, sets of more applied interventions or programs that may be of interest also to funding channels more specifically dedicated to conservation.

Literature cited

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