

les dossiers d'**AGROPOLIS** INTERNATIONAL

Expertise of the scientific community



Biodiversity

Science for humans
and nature

Animal movements and the emergence of livestock diseases

The African buffalo (*Syncerus caffer*), an emblematic large African wildlife species, is found in the main protected areas of Africa. This species shares a broad range of pathogens with cattle and humans, including the causal agents of foot-and-mouth disease, brucellosis, tuberculosis, etc. The buffalo-cattle model is being studied by UPR AGIRs (CIRAD) to gain insight into epidemiological interactions between domesticated and wild animals. Several studies have been carried out since 2007 by team members within and around protected areas in western (VW Regional Park) and southern (Limpopo Transfrontier Park) Africa. The risks of interaction between wildlife, cattle and humans are especially high along the edges of protected areas, where herding and crop farming are practiced to an increasing extent. In 1960, for instance, contacts between infected cattle and buffaloes led to the dissemination of bovine tuberculosis throughout Kruger National Park (South Africa), and it has recently spread to Zimbabwe.

UPR AGIRs is striving to gain insight into the dynamics of disease transmission between wild and domesticated herds via direct and indirect contact. It is focusing on animal movements and ecological factors or human-related factors that govern sharing of the same resources and areas. Buffaloes and cattle were fitted with GPS collars that recorded their locations continuously

over annual cycles. These data enabled determination of movement patterns, vital sites and the potential for between-herd contacts. They were analysed with respect to explanatory variables such as vegetation, water, season, human presence, etc. These studies contribute to the

assessment of health risks so as to enhance their management, and more generally of risks of conflicts between conservation and development imperatives.



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▲ Attachment of a GPS collar and collection of a sample from a buffalo in Gonarezho National Park, Zimbabwe.

Trypanosoma: identification, genetic variability, host-parasite interactions

Parasitic trypanosomosis diseases—despite initiatives to control them—are still worrisome public health and development issues. Despite the abandonment of mass screening, the lack of medical surveillance of threatened populations, the sharp increase in sandfly-human-cattle contacts associated with factors such as climate and demographic change, as well as the many shortcomings and unknown aspects of the parasite traits such as transmission patterns, human African trypanosomiasis (HAT, sleeping sickness) is a reemerging endemic disease that now ranks as a WHO public health priority. Animal trypanosomiasis (nagana) is also a major stumbling block to the development of livestock production in sub-Saharan Africa, Latin America and Asia.

This fact, in addition to the scant number of studies focused on these ‘vector-borne diseases’, prompted the joint research unit (UMR) *InterTryp* (CIRAD, IRD) to conduct research on interactions established by the parasites in the two hosts vital to their survival:

an insect host (hematophagous vector) and a mammal host (a blood source for the insect) in order to enhance control of these diseases.

Research conducted concomitantly on natural human diseases by IRD and on animal diseases by CIRAD revealed that many questions apply to both disease types in terms of epidemiology and control, especially since the parasites are transmitted by the same vector (sandflies or tsetse flies). By pooling complementary and synergetic expertise in a single UMR, it is possible to develop a joint multidisciplinary approach aimed at fulfilling three research objectives:

- to analyse and identify trypanosomes (in the host and vector), their genetic variability, virulence and/or pathogenicity factors of the parasite strains according to their geographical origins
- to study host-parasite interactions through the identification of markers involved in infection tolerance/susceptibility during disease development
- to clarify the vectorial transmission conditions in order to better target control initiatives.

To fulfil these objectives, the UMR benefits from teams established in several countries where these

diseases are present, and where there are sufficient human and financial resources to: (i) carry out screening, (ii) detect and characterize the parasites in the vectors and hosts, (iii) provide support for therapeutic follow-up and treatment, (iv) determine the genetic structure of sandfly populations, i.e. key elements of their vectorial competence, (v) study the relationships of three participants in these parasitic ecosystems in their environments, and (vi) perform experimental infections (cattle) with parasite populations that differ in terms of their relevant biological criteria.

This set-up in developing countries is supplemented by a joint IRD-CIRAD laboratory hosted on the Montferrier-Baillarguet campus (France). This laboratory features operational infrastructures that enable molecular and cellular analyses of factors underlying the development, or not, of pathogenic processes and an insectarium where five sandfly species and subspecies of medical and veterinary relevance are reared. It is thus possible to determine the different key elements leading to the abortive or, conversely, optimal development of trypanosomes that are transmissible to mammal hosts. ...