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Investigate, evaluate, protect

Towards a better definition of the immuno-proteome in the frame of contagious or vector-borne animal diseases

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Defining the repertoire of antigenic targets is central to better understanding the immune responses against wether contagious pathogens and those transmitted by arthropod vectors. Traditional molecular approaches of antigen discovery have identified many immunodominant antigens, but they afford limited proteome coverage. Advances in proteomic technologies that are based on peptide library and the increase in genome sequencing that enriched molecular databases, allowed the definition of new analytical strategies with interrogation of the entire proteome for antigens. At the same time, improved technologies for antibodies purification for serum as well as antigens immunocapture lead scientists to revisiting the characterisation of immuno-proteomes, particularly in the frame of contagious or vector-borne animal diseases. Here, we propose an analytical workflow to illustrate how to deepen the definition of the immuno-proteomes, and illustrate the proof of concept targeting Mycoplasma mycoïdes, the causative agent of contagious bovine pleuropneumonia (CBPP).

Bovine innate immunity against *Mycobacterium bovis*

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Keywords: Lung, innate immunity, bovine tuberculosis, mycobacteria, cattle

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Bovine tuberculosis (bTB) is a chronic disease of farmed cattle and wildlife, which may also be transmitted to human, presenting a zoonosis risk. The cost of the active abattoir surveillance (13 millions €/year) so far allows the maintaining of a "bTB" status in France since 2001. Nevertheless, this status is fragilized by the increasing incidence of bTB in some regions (Dordogne, Côte d'Or, Camargue). Even thought the circulation of Mycobacterium bovis (Mb) the main agent of bTB is not precisely characterized, the transmission through the respiratory route as been associated with manifestation in the lungs and the associated lymph nodes. The analysis of the cattle alveolar environment and the associated lymphoid tissues will allow us to better understand the critical primary steps of the mycobacteria infection.

Our laboratory "Infection mycobactérienne animale" has a deep expertise on paratuberculosis and the host response to Mycobacterium tuberculosis (Human tuberculosis) and BCG (attenuated Mb used for Human vaccination) and has just starting to study bTB one year ago. Our primary goal is to characterize the cattle lung environment at the basal level and following Mb interaction to evaluate the initial immune response and more globally the tissue signature following Mb infection.

From different sources, we are currently recovering bovine samples: blood, broncho-alveolar lavages (BAL), lung and draining lymph nodes. We have set up a protocol for alveolar macrophages culture from BAL, and now aim to study their response after a co-culture with Mb. We will also use ex vivo approach, with precision cut lung slices (PCLS), to decipher the cross-talk between Mb and the host.