Leptospirosis is a disease with great impact on both human and veterinary public health, caused by members of the genus *Leptospira* and is considered an emergent or re-emergent disease. It has been reported that over 1 million human cases of severe leptospirosis occur worldwide each year, with approximately 60,000 deaths from this disease. It has to be noted that leptospirosis also generates huge economic losses due to reproductive disorders in cattle, sheep, pigs and horses.

There are lot of gnomically distinct *Leptospira* species and over 260 pathogenic serovars differing in the construction of superficial antigens. The ability of *Leptospira* to occupy various ecological niches, inside and outside the host organism, is undoubtedly due to a diversity of mechanisms encoded by its large genome and that allow it to adapt and resist to stressful conditions. Theoretically, any parasitic Leptospira serovars may infect any animal species. However each serovar shows a high degree of parasitic adaptation to natural reservoir. It means that, they can be divided into two categories which are referred to as host-adapted and non-host adapted serovars. There is a clear association of particular serovars with particular maintenance hosts with classic examples of serovar Icterohaemorrhagiae adapted to R*attus norvegicus* and serovar Hardjo adapted to cattle and sheep. Infections of animals by host-adapted strains produce chronic, asymptomatic carriage. But infection of other animals and humans by these strains, which doesn't show any degree of adaptation to these animal species, usually cause accidental infection with severe signs but without long colonization. The host-parasite relation between Leptospira pathogens and animals hosts which act as natural reservoir or accidental hosts has been a conundrum.

In the last 15 years, there has been a great progress in understanding the entire bacterial genomes. Comparative genomics of *Leptospira* pathogens and saprophytes has allowed the identification of more than 900 genes unique to either *Leptospira interrogans* or *Leptospira borgpetersenii*, both species identified as pathogenic. These genes potentially encodes virulence-associated proteins. Genes of unknown function are over-represented in this subset of pathogen-specific genes. This finding, together with the absence of virulence factor homologues among the proteins of known function, suggests that Leptospira possess unique virulence mechanisms. In the light of this knowledge cross-species genomic comparison of Leptospira infectious species, with the goal of identifying genes related to disease pathogenesis and host adaptation, remains a key gap in the field and lags far behind that of many other bacterial pathogens. It is due largely to the lack of appropriate genetic tools which have been available for decades for other bacteria species. In order to identify genes and proteins that are likely to be differentially expressed during infection, we are planning to perform transcriptomics studies using sheep as animal model for these infections.

The main aim of the project is to improve our understanding of *Leptospira* virulence through identification of genes involved in pathogen-host interactions both in natural reservoir and accidental hosts. Host adaptation is a complex and dynamic process that cannot be fully reproduced outside the animal organism. The objectives we want to obtain by using transcriptome sequencing of three Leptospira (two adapted and one not adapted to sheep) cultivated in host organism and outside the animal organism using artificial media. We expect that the transcriptomic comparison might highlight the genetic determinants involved in pathogen-host interactions during infection. The elucidation of such interactions in the host will be important in understanding mechanisms of the disease and may lead to methods of disease prevention.