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Aime, B., L. Lequen, et al. (2012). "M. bovis and M. caprae infections in Aquitaine: A clinico-epidemiologic study of 15 patients." Pathologie Biologie 60(3): 156-159.

The agent of bovine tuberculosis, Mycobacterium bovis, is a zoonosis which can be transmitted to human beings. In France, the prevalence of tuberculosis due to M. bovis has drastically decreased, both for animals and humans, since public health measures were introduced to prevent its transmission. However, a new outbreak of the disease is noted among cattle in several French areas and more particularly in Aquitaine. In 2008, 40% of bovine tuberculosis French cases provided from Aquitaine. From November 2004 to October 2008, 15 cases were registered at Bordeaux's academic hospital (CHU). Thirteen of them were due to M. bovis and two to Mycobacterium caprae. It represents 2.9% of tuberculosis due to tuberculosis complex. An analysis of the 15 patients' medical files showed that it occurred either to old people who reactivated a former infection, or to younger ones who were born in countries with a strong M. bovis endemic disease. Extrapulmonary forms and especially ganglionics ones are the most frequent. M. caprae seems to be an emergent species among animal mycobacteries transmissible to human being. An epidemiological monitoring seems to be necessary to establish a relation between the regional outbreak of bovine tuberculosis and human tuberculosis.

Akbar, H., C. Pincon, et al. (2012). "Characterizing Pneumocystis in the Lungs of Bats: Understanding Pneumocystis Evolution and the Spread of Pneumocystis Organisms in Mammal Populations." Applied and Environmental Microbiology 78(22): 8122-8136.

Bats belong to a wide variety of species and occupy diversified habitats, from cities to the countryside. Their different diets (i.e., nectarivore, frugivore, insectivore, hematophage) lead Chiroptera to colonize a range of ecological niches. These flying mammals exert an undisputable impact on both ecosystems and circulation of pathogens that they harbor. Pneumocystis species are recognized as major opportunistic fungal pathogens which cause life-threatening pneumonia in severely immunocompromised or weakened mammals. Pneumocystis consists of a heterogeneous group of highly adapted host-specific fungal parasites that colonize a wide range of mammalian hosts. In the present study, 216 lungs of 19 bat species, sampled from diverse biotopes in the New and Old Worlds, were examined. Each bat species may be harboring a specific Pneumocystis species. We report 32.9% of Pneumocystis carriage in wild bats (41.9% in Microchiroptera). Ecological and behavioral factors (elevation, crowding, migration) seemed to influence the Pneumocystis carriage. This study suggests that Pneumocystis-host association may yield much information on Pneumocystis transmission, phylogeny, and biology in mammals. Moreover, the link between genetic variability of Pneumocystis isolated from populations of the same bat species and their geographic area could be exploited in terms of phylogeography.

Alanio, A., C. Cordonnier, et al. (2011). "Low prevalence of resistance to azoles in Aspergillus fumigatus in a French cohort of patients treated for haematological malignancies-authors' response." Journal of Antimicrobial Chemotherapy 66(4): 955-955.

Alanio, A., E. Sitterle, et al. (2011). "Low prevalence of resistance to azoles in Aspergillus fumigatus in a French cohort of patients treated for haematological malignancies." Journal of Antimicrobial Chemotherapy 66(2): 371-374.

An increase in invasive aspergillosis (IA) due to azole-resistant Aspergillus fumigatus isolates has been reported for 10 years. Our study aimed to estimate the prevalence of azole resistance in isolates prospectively collected in patients with haematological diseases. One hundred and eighteen isolates were collected from 89 consecutive patients over 4 years. Fifty-one patients had proven or probable IA. Species identification was ascertained based on beta-tubulin gene sequencing. The MICs of azole drugs were determined using Etest((R)), and the cyp51A gene and its promoter were sequenced to detect mutations. All isolates were identified as A. fumigatus and all of them but one had itraconazole and voriconazole MICs of < 2 mg/L and posaconazole MICs of < 0.25 mg/L. An isolate for which the itraconazole MIC was high (itraconazole MIC = 16 mg/L; voriconazole MIC = 0.38 mg/L; and posaconazole MIC = 0.25 mg/L) was recovered from a patient naive to azole treatment and had a new G432S substitution. To establish whether this mutation existed in other isolates, the 1426-2025 bp cyp51A locus was sequenced for all. G432S was not found. In A. fumigatus, the prevalence of azole resistance is currently low in the haematological population in the Paris area. Surveillance programmes for azole resistance to adapt antifungal treatments are warranted for clinical isolates of A. fumigatus.

Aliouat-Denis, C. M., M. Chabe, et al. (2008). "Pneumocystis species, co-evolution and pathogenic power." Infection Genetics and Evolution 8(5): 708-726.

The genus Pneumocystis comprises uncultured, highly diversified microfungal organisms able to attach specifically to type-1 alveolar epithelial cells and to proliferate in pulmonary alveoli provoking severe pneumonitis. The pathogenic potential of Pneumocystis species, especially of the human-associated Pneumocystis jirovecii, has stimulated a growing interest in these peculiar microfungi. However, a comprehensive understanding of basic biology and pathogenic power of Pneumocystis organisms calls for their recognition as natural, complex entities, without reducing them to their pathogenic role. For many years, the entity named "Pneumocystis carinii" was considered like an anecdotal pulmonary pathogen able to cause pneumonia in immunosuppressed hosts. Only for the last years, marked genetic divergence was documented among the Pneumocystis strains of different mammals. Cross-infection experiments showed that Pneumocystis species are stenoxenous parasites. Mainly on the basis of the Phylogenetic Concept of Species, Pneumocystis strains were considered as genuine species. Five species were described: P. carinii and Pneumocystis wakefieldiae in rats, P. jirovecii in humans, Pneumocystis murina in mice, and Pneumocystis oryctolagi in rabbits. They also present distinctive phenotypic features. Molecular techniques have revealed a high prevalence of Pneumocystis colonization in wild mammals, probably resulting from active airborne horizontal and vertical (transplacental or aerial) transmission mechanisms.

Cophylogeny is the evolutionary pattern for Pneumocystis species, which dwelt in the lungs of mammals for more than 100 million years. Consistently, Pneumocystis organisms exhibit successful adaptation to colonize the lungs of both immunocompromised and healthy hosts that can act as infection reservoir. Pneumocystis pneumonia, rarely reported in wild mammals, seems to be a rather unfrequent event. A larger spectrum of Pneumocystis infections related to the heterogeneous level of immune defence found in natural populations, is, however, expected. Pneumocystis infection of immunocompetent hosts emerges therefore as a relevant issue to human as well as animal health.

Aoun, O., S. A. Lacour, et al. (2012). "Screening for Trichinella britovi infection in red fox (Vulpes vulpes) and wild boar (Sus scrofa) in Southeastern France." Journal of Wildlife Diseases 48(1): 223-225.

From 2006 to 2009 we screened 108 red foxes (Vulpes vulpes) and 894 wild boars (Sus scrota) in Haut-Var, France for Trichinella britovi infection. Prevalences were 2.7 and 0% respectively. The fox may be considered a predictive sentinel for Trichinella in the Haut-Var ecosystem.

Azzag, N., N. Haddad, et al. (2012). "Population Structure of Bartonella henselae in Algerian Urban Stray Cats." Plos One 7(8).

Whole blood samples from 211 stray cats from Algiers, Algeria, were cultured to detect the presence of Bartonella species and to evaluate the genetic diversity of B. henselae strains by multiple locus VNTR analysis (MLVA). Bartonella henselae was the only species isolated from 36 (17%) of 211 cats. B. henselae genotype I was the predominant genotype (64%). MLVA typing of 259 strains from 30 bacteremic cats revealed 52 different profiles as compared to only 3 profiles using MLST. Of these 52 profiles, 48 (92.3%) were identified for the first time. One-third of the cats harbored one MLVA profile only. As there was a correlation between the age of cats and the number of MLVA profiles, we hypothesized that the single profile in these cats was the profile of the initial infecting strain. Two-third of the cats harbored 2 to 6 MLVA profiles simultaneously. The similarity of MLVA profiles obtained from the same cat, neighbor-joining clustering and structure-neighbor clustering indicate that such a diversity likely results from two different mechanisms occurring either independently or simultaneously: independent infections and genetic drift from a primary strain.

Bai, X., X. P. Wu, et al. (2012). "Regulation of cytokine expression in murine macrophages stimulated by excretory/secretory products from Trichinella spiralis in vitro." Molecular and Cellular Biochemistry 360(1-2): 79-88.

Trichinella spiralis is a zoonotic nematode and food borne parasite and infection with T. spiralis leads to suppression of the host immune response and other immunopathologies. The excretory/secretory (ES) products of T. spiralis play important roles in the process of immunomodulation. However, the mechanisms and related molecules are unknown. Macrophages, a target for immunomodulation by the helminth parasite, play a critical role in initiating and

modulating the host immune response to parasite infection. In this study, we examined the effect of ES products from different stages of T. spiralis on modulating J774A.1 macrophage activities. ES products from different stages of T. spiralis reduced the capacity of macrophages to express pro-inflammatory cytokines (tumor necrosis factor alpha, interleukin-1 beta , interleukin-6 , and interleukin-12) in response to lipopolysaccharide (LPS) challenge. However, only ES products from 3-day-old adult worms and 5-day-old adult worms/new-born larvae significantly inhibited inducible nitric oxide synthase gene expression in LPS-induced macrophages. In addition, ES products alone boosted the expression of anti-inflammatory cytokines interleukin-10 and transforming growth factor-beta and effector molecule arginase 1 in J774A.1 macrophages. Signal transduction studies showed that ES products significantly inhibited nuclear factor-kappa B translocation into the nucleus and the phosphorylation of both extracellular signal-regulated protein kinase 1/2 and p38 mitogen-activated protein kinase in LPS-stimulated J774A.1 macrophages. These results suggest that ES products regulate host immune response at the macrophage level through inhibition of pro-inflammatory cytokines production and induction of macrophage toward the alternative phenotype, which maybe important for worm survival and host health.

Bai, X., X. P. Wu, et al. (2012). "Inhibition of mammalian muscle differentiation by excretory secretory products of muscle larvae of Trichinella spiralis in vitro." Parasitology Research 110(6): 2481-2490.

The excretory-secretory products (ESP) released by muscle stage of Trichinella spiralis have been suggested to be involved in nurse cell formation. However, the molecular mechanisms by which ESP modulate nurse cell formation remain unclear. In the present study, the ability of ESP of muscle larvae of T. spiralis (ML-ESP) to influence the proliferation and differentiation of murine myoblasts and the mechanisms were evaluated in vitro using C2C12 myoblast cell line, which were incubated for various times under grow or differentiation culture medium containing various concentrations of ML-ESP. The results indicated that ML-ESP promoted myoblast proliferation in a dose-dependent manner and increased the expression of the cell-cycle regulator cyclin D1 as well as that of proliferating cell nuclear antigen (PCNA). Conversely, ML-ESP inhibited the differentiation of these cells, which was evidenced by a reduction in the levels of MHC and MRFs expression (MyoD and myogenin) as well as that of p21. In addition, ML-ESP also inhibited the phosphorylation of p38 MAPK in differentiating C2C12 myoblast. Taken together, these results imply that certain critical mediators contained in ML-ESP inhibit myogenesis through enhancing skeletal myoblasts proliferation and down-regulating the expression of MRFs as well as involving p38 MAPK signalling pathway, which provides insight into the mechanisms utilised by T. spiralis to interfere normal wound repair in infected muscle cells and affect nurse cell formation.

Baroudi, D., D. Khelef, et al. (2013). "Common occurrence of zoonotic pathogen Cryptosporidium meleagridis in broiler chickens and turkeys in Algeria." Veterinary Parasitology 196(3-4): 334-340.

Only a small number of birds have been identified by molecular techniques as having Cryptosporidium meleagridis, the third most important species for human cryptosporidiosis. In this study, using PCR-RFLP analysis of the small subunit (SSU) rRNA gene, we examined the ileum of 90

dead chickens from 23 farms and 57 dead turkeys from 16 farms in Algeria for Cryptosporidium spp. C meleagridis-positive specimens were subtyped by sequence analysis of the 60 kDa glycoprotein gene. Cryptosporidium infection rates were 34% and 44% in chickens and turkeys, respectively, with all positive turkeys (25) and most positive chickens (26/31) having C meleagridis. All C meleagridis specimens belonged to a new subtype family. The frequent occurrence of C meleagridis in chickens and turkeys illustrates the potential for zoonotic transmission of cryptosporidiosis in Algeria. Published by Elsevier B.V.

Bauchet, A. L., C. Joubert, et al. (2013). "Disseminated Sparganosis in a Cynomolgus Macaque (Macaca fascicularis)." Journal of Comparative Pathology 148(4): 294-297.

An adult male cynomolgus macaque (Macaca fascicularis) from Mauritius arrived at our facility in France after a 1-year period of quarantine in Spain. Clinical examination soon after arrival revealed the presence of numerous firm cutaneous and subcutaneous nodules (0.1-0.5 cm diameter) in the scrotal and inguinal areas, and persistent mild eosinophilia. On necropsy examination additional similar nodules were found in the peritoneum and abdominal wall, omentum and mesentery. Microscopical examination revealed disseminated eosinophilic granulomas containing tapeworm larvae identified as Spirometra erinaceieuropaei by direct sequencing of the cox1 gene.

Bellanger, A. P., L. Millon, et al. (2009). "Aspergillus fumigatus germ tube growth and not conidia ingestion induces expression of inflammatory mediator genes in the human lung epithelial cell line A549." Journal of Medical Microbiology 58(2): 174-179.

Inhalation of conidia is the main cause of invasive pulmonary aspergillosis (IPA) and the respiratory epithelium is the first line of defence. To explore the triggering factor for the inflammatory response to Aspergillus fumigatus, the species mainly responsible for IPA, this study analysed the differential expression of three inflammatory genes in A549 cells after challenge with live and killed conidia. The influence of steroids, one of the main risk factors for developing IPA, was also investigated. Quantification of mRNAs of the inflammatory mediator genes encoding interleukin (IL)-8, tumour necrosis factor (TNF)-alpha and granulocyte-monocyte colony-stimulating factor (GM-CSF) was carried out using real-time PCR. Ingestion rates were studied for the conidia of A. fumigatus and Penicillium chrysogenum using a fluorescence brightener. Similar results were obtained for both species, with ingestion rates ranging from 35 to 40 %. Exposure of A549 cells to live A. fumigatus conidia only induced a four- to fivefold increase in the mRNA levels of the three genes, starting 8 h after the initial contact. Both inactivation of live A. fumigatus conidia and treatment by dexamethasone (10(-7) M) prevented the overexpression of TNF-alpha, IL-8 and GM-CSF. Fungal growth, rather than conidia ingestion, appears to be the main stimulus for the production of inflammatory mediators by epithelial cells, and this production is inhibited by steroid therapy. These results underline the role that the epithelium plays in the innate response against IPA.

Bellanger, A. P., L. Millon, et al. (2011). "Variable beta-glucans production by different states of Eurotium amstelodami explains differences in inflammatory responses in airway cells." Apmis 119(9): 605-610.

Bellanger A-P, Millon L, Rognon B, Roussel S, Botterel F, Bretagne S, Reboux G. Variable betaglucans production by different states of Eurotium amstelodami explains differences in inflammatory responses in airway cells. APMIS 2011; 119: 605-10. Eurotium amstelodami, a mold frequently identified in housing and farm air samples, is a suspected cause of respiratory diseases such as allergic alveolitis, atopic asthma, and organic dust toxic syndrome. This fungus is present in the air in three different states (ascospores, conidia, and hyphae). The aim of this study was to test in vitro the differential inflammatory response of airway cells exposed to 1,3 betaglucanase-treated protein extract (BGPE), from E. amstelodami ascospores, conidia, and hyphae. Confluent cells from the A549 cell line were inoculated with calibrated BGPE issued from the three fungal forms. The levels of eight cytokines and chemokines involved in inflammatory responses were measured after 8 h of exposure. Beta-D-glucan (BDG) was quantified in total fungal extract as well as in the BGPE from the three fungal states. Hyphal BGPE were the only ones to induce a marked inflammatory response and they contain higher quantities of BDG. The present study adds to the growing body of evidence that beta-glucan from fungal hyphae play a crucial role in respiratory diseases.

Bellanger, A. P., G. Reboux, et al. (2010). "New evidence of the involvement of Lichtheimia corymbifera in farmer's lung disease." Medical Mycology 48(7): 981-987.

Farmer's lung disease (FLD) is a form of hypersensitivity pneumonitis resulting from recurrent exposure to moldy plant materials. We investigated and compared the initial response of respiratory epithelium after exposure to extracts of Sacharopolyspora rectivirgula, Lichtheimia corymbifera (formerly Absidia corymbifera), Eurotium amstelodami and Wallemia sebi. The two criteria for selection of these species were their high prevalence in the hay handled by FLD patients and the presence of high levels of specific precipitins to these molds in FLD patients' sera. Hydrosoluble extracts were prepared from spores and hyphae grown in culture under optimal conditions for each of the four species. Confluent A549 cells were inoculated with one of the four calibrated soluble extracts. Two mediators, one inflammatory (Interleukin (IL)-8) and one allergic (IL-13), were quantified using real-time PCR and ELISA assay, after four exposure periods (30 min, 2 h, 4 h and 8 h). S. rectivirgula and L. corymbifera extracts were the only ones which induced a marked upregulation of IL-8, as shown by both real-time PCR and ELISA assay 8 h after the initial contact. This study adds to the growing body of evidence that L. corymbifera should be recognized as an etiologic agent of FLD along with S. rectivirgula.

Ben Abdeljelil, J., F. Saghrouni, et al. (2012). "Temporal Similarity Between Candida albicans Genotypes in a Tunisian Neonatal Intensive Care Unit Suggests Several Nosocomial Cross-Contamination Episodes." DNA and Cell Biology 31(7): 1161-1166.

The nosocomial transmission of Candida albicans in neonatal intensive care units (NICUs) is an increasing concern and understanding the route of this transmission is critical for adequate

infection control measures. The aim of our study was to assess the likeliness of nosocomial acquisition of C. albicans in the NICU of Farhat Hached hospital in Sousse (Tunisia). We genotyped 82 isolates from 40 neonates and 7 isolates from 5 health care workers (HCWs) with onychomycosis, by using CDC3 microsatellite length polymorphism (MLP) and the high-resolution melting (HRM) analysis. Combined MLP and HRM CD3 analysis led to the delineation of 12 genotypes. Five temporal clustering caused by five genotypes occurred during the study period. Three of these genotypes were isolated in both neonates and HCWs. The first clustering included 28 isolates obtained between January 2003 and May 2004 from 16 neonates and 2 HCWs. The second clustering included three isolates collected in 2004 from three neonates and two HCWs. The third clustering included 11 isolates obtained from 6 neonates and 1 HCW in 2006. The two remaining clustering could not be associated with any HCW's contamination. These results argue for the nosocomial transmission of C. albicans in our NICU. The combined MLP and HRM analysis is a rapid first approach for tracking cross-contamination.

Benchekroun, G., A. Desmyter, et al. (2009). "Primary Hyperparathyroidism and Monoclonal Gammopathy in a Dog." Journal of Veterinary Internal Medicine 23(1): 211-214.

Blaga, R., C. M. Cretu, et al. (2009). "Trichinella spp. infection in horses of Romania: Serological and parasitological survey." Veterinary Parasitology 159(3-4): 285-289.

Herbivorous animals are usually, by virtue of their diet, outside the major transmission cycles of Trichinella spp. However, since 1975, the year of the first report of human trichinellosis caused by the consumption of infected horse meat, the domestic horse has appeared as a novel vector of Trichinella spp. infection to humans, with 15 outbreaks documented in France and Italy. Romania, one of the main countries exporting horses into the European Union (EU), experienced a dramatic increase of Trichinella sop. infection in both domestic pigs and humans in the 1990s. Some Trichinella spiralis-infected horses were exported to the EU during this period. The aim of this study was to evaluate the prevalence of Trichinella spp. infections in horses from Romania using both direct and indirect tests. Of 3000 serum samples tested in 2001, none were positive by ELISA using three different Trichinella antigens (crude; excretory/secretory, ES: stg-BSA antigens). Of 2992 serum samples tested in 2002, 17 (0.56%) showed optical density values higher than the cut-off in an ELISA using ES antigens and one was confirmed by western blot (WB). Four of the 17 ELISA positive horses, including the horse with a confirmed serology by WB, were subjected for intensive meat examination at slaughter, but no Trichinella spp. larvae were detected. Further, no Trichinella spp. larvae were detected by trichinelloscopy and artificial digestion of 25,838 horses slaughtered in Alexandria and Timisoara between 2001 and 2004. The false positive results obtained by serology confirm the previous work on the unreliability of serology for detection of Trichinella spp. infection in horses. Furthermore, the lack of detection of Trichinella spp. infected horses by artificial digestion, suggests a very low prevalence of infection in horses in Romania.

Blaga, R., B. Durand, et al. (2009). "Animal Trichinella infection in Romania: Geographical heterogeneity for the last 8 years." Veterinary Parasitology 159(3-4): 290-294.

Previous studies in southeastern Europe reported a high incidence of human trichinellosis and a high prevalence of Trichinella infection in animals in countries like Bulgaria, Croatia, Romania and Serbia. The aim of this study was, using routine Trichinella test data in pig and game animals, to investigate the extent of Trichinella infection in slaughtered animals in Romania, over the period of 1997-2004, and to identify possible differences in prevalence among the various regions of Romania. Trichinella infection data were obtained from trichinelloscopic examinations of domestic (backyard and industrial reared pigs) and game species (wild boar and bears). A marked difference between Transylvania and other counties of Romania, observed for human trichinellosis, was taken into account when analyzing Trichinella epidemiological data. A cumulative prevalence of 8 cases/10(4) animals tested for pigs, 9 cases/10(3) animals tested for wild boars, and 13.1 cases/10(2) animals tested for bears was obtained for the 8 years period. Analysis of animal prevalence data demonstrated a geographical heterogeneity: whereas Trichinella prevalence in pigs is much lower in Transylvania than in the other counties, Trichinella prevalence in game animals is similar for the different regions. This observation suggests that, in Romania, rather than the levels of the parasite circulating in domestic and game animals, it was changes in the social and political structure of Romania in the 1990s, combined with inadequate meat inspection practices that were the main contributors to these geographic variations.

Blaga, R., B. Q. Fu, et al. (2009). "Use of mitochondrial RNA genes for the differentiation of four Trichinella species by multiplex PCR amplification." Journal of Helminthology 83(2): 121-128.

Until now, four species of the Trichinella genus have been identified in Europe: Trichinella spiralis, T. nativa, T britovi and T pseudospiralis. The aim of this work was to establish a sound polymerase chain reaction (PCR)-based method to differentiate these four species using mitochondrial rDNA as a reliable genetic marker and to evaluate the sensitivity of this method. Full-length DNA sequences coding for the small and large mitochondrial rRNA (mt-rrnS and mt-rrnL) of the four species are described. A multiplex PCR was designed and successfully tested on 24 European isolates. As few as one larva, or 100 pg of genomic DNA was detected, providing equivalent sensitivity to previously described PCR methods. The PCR-based method of mitochondrial rDNA amplification was thereby established as a sensitive and reproductive diagnostic method for the four European Trichinella species.

Blaga, R., C. Gherman, et al. (2009). "Trichinella species circulating among wild and domestic animals in Romania." Veterinary Parasitology 159(3-4): 218-221.

Trichinellosis is one of the most important zoonotic diseases in Romania. Even though the disease is a serious public health concern, only a limited number of Trichinella isolates have been identified at the species level; in the past, all larvae were assumed to be Trichinella spiralis. The present study was conducted to identify Trichinella spp. circulating among wild and domestic animals in Romania, using PCR-based methods. Trichinella spp. larvae originating from 54 wild and 23

domestic mammals were examined. No Trichinella spp. larvae were detected in muscle samples of 182 birds. T. spiralis and Trichinella britovi were the only two species identified in the 40 isolates that yielded a positive PCR result. Overall, T. britovi was more prevalent (n = 26; 65%) than T. spiralis (n = 14; 35%). T. spiralis was the predominant species found in domestic animals (n = 9; 75%), while T. britovi was more prevalent in wildlife (n = 24; 86%). No mixed infections were found. The highest prevalence of Trichinella infection was detected in wolves (11/35; 31%), in European wild cats (4/28; 14%), and in red foxes (5/71; 7%). The distribution of Trichinella spp. in Romania does not show a species-specific clustering; both of the two species found were present over the entire range of counties studied.

Borba, M. R., E. M. C. Sanches, et al. (2011). "Immunohistochemical and ultra-structural detection of Pneumocystis in wild boars (Sus scrofa) co-infected with porcine circovirus type 2 (PCV2) in Southern Brazil." Medical Mycology 49(2): 172-175.

Pneumocystis spp. are fungi that are able to infect a variety of host species and, occasionally, lead to severe pneumonia. Porcine circovirus type 2 (PCV2) is an important viral pathogen which affects both swine and wild boar herds worldwide. Co-infection between PCV2 and other pathogens has been reported, and the secondary immunodeficiency caused by the virus may predispose to these co-infections. In the present study, postmortem tissue samples obtained from wild boar herds in Southern Brazil were analyzed by histopathology, ultra-structural observation, and immunohistochemistry. Forty-seven out of seventy-eight (60%) wild boars showed clinical signs, gross, and histopathological lesions characteristic of infection by PCV2. Pneumocystis was detected by immunohistochemistry in 39 (50%) lungs and viral antigens of PCV2 were found in 29 (37.2%) samples. Concomitant presence of Pneumocystis and PCV2 were observed in 16 (20.5%) of the wild boars. Cystic and trophic forms of Pneumocystis were similar to previously described ultra-structural observations in other mammals.

Botterel, F., O. Cabaret, et al. (2012). "Clinical Significance of Quantifying Pneumocystis jirovecii DNA by Using Real-Time PCR in Bronchoalveolar Lavage Fluid from Immunocompromised Patients." Journal of Clinical Microbiology 50(2): 227-231.

Quantitative PCR (qPCR) is more sensitive than microscopy for detecting Pneumocystis jirovecii in bronchoalveolar lavage (BAL) fluid. We therefore developed a qPCR assay and compared the results with those of a routine immunofluorescence assay (IFA) and clinical data. The assay included automated DNA extraction, amplification of the mitochondrial large-subunit rRNA gene and an internal control, and quantification of copy numbers with the help of a plasmid clone. We studied 353 consecutive BAL fluids obtained for investigation of unexplained fever and/or pneumonia in 287 immunocompromised patients. No qPCR inhibition was observed. Seventeen (5%) samples were both IFA and qPCR positive, 63 (18%) were IFA negative and qPCR positive, and 273 (77%) were both IFA and qPCR negative. The copy number was significantly higher for IFA-positive/qPCR-positive samples than for IFA-negative/qPCR-positive samples (4.2 +/- 1.2 versus 1.1 +/- 1.1 log(10) copies/mu l; P < 10(-4)). With IFA as the standard, the qPCR assay sensitivity was 100% for >= 2.6 log(10) copies/mu l and the specificity was 100% for >= 4 log(10) copies/mu l. Since qPCR results were not available at

the time of decision-making, these findings did not trigger cotrimoxazole therapy. Patients with systemic inflammatory diseases and IFA-negative/qPCR-positive BAL fluid had a worse 1-year survival rate than those with IFA-negative/qPCR-negative results (P < 10(-3)), in contrast with solid-organ transplant recipients (P = 0.88) and patients with hematological malignancy (P = 0.26). Quantifying P. jirovecii DNA in BAL fluids independently of IFA positivity should be incorporated into the investigation of pneumonia in immunocompromised patients. The relevant threshold remains to be determined and may vary according to the underlying disease.

Botterel, F., F. Foulet, et al. (2010). "Yeast contamination of kidney, liver and cardiac preservation solutions before graft: need for standardisation of microbial evaluation." Journal of Hospital Infection 76(1): 52-55.

Contamination of preservation solution (PS) with yeasts during solid organ recovery can lead to life-threatening complications in the recipients. The prevalence of such a contamination needs to be established. From January 2004 to December 2008, we prospectively investigated the potential fungal contamination of all the PSs collected in our institution using a standardised procedure consisting in centrifugation of 10 mL PS and incubation of the pellet seeded on fungal-specific medium for 15 days at 30 degrees C. During the study period, 728 transplantations (397 kidneys, 262 livers and 69 hearts) were performed for which 659 PSs (90.5%) were available. The yeast contamination rate was 0% (0/62), 3.1% (11/356) and 4.1% (10/241) for heart, kidney and liver transplants, respectively. We identified 10 Candida albicans, five C. glabrata, two C. krusei, one C. tropicalis, one C. valida, one Pichia etchelsii and one Rhodorula sp. Routine bacterial analysis identified only five of these 21 fungal contaminations. Twenty recipients were alive after at least one year of follow-up and one died from meningeal carcinomatosis at seven months. Three patients were found to have the same species of Candida from their surgical drains but did not develop any infection or abnormalities upon ultrasound investigation. Fourteen patients received antifungal drugs. Yeast contamination occurred in 3.4% of all kidney and liver PSs tested. Its clinical consequences and therapeutic management remain to be defined. Our study also suggests that optimisation/standardisation of microbiological procedures is warranted, including analysis of large PS volume, seeding of fungal-specific medium and prolonged incubation.

Botterel, F., F. Foulet, et al. (2012). "Microsporum praecox and Trichophyton bullosum, two equid-related dermatophytes that may be zoonotic." Mycoses 55: 76-76.

Bouchouicha, R., H. J. Boulouis, et al. (2009). "Comparison of the performances of MLVA vs. the main other typing techniques for Bartonella henselae." Clinical Microbiology and Infection 15: 104-105.

Bouhsira, E., Y. Ferrandez, et al. (2013). "Ctenocephalides felis an in vitro potential vector for five Bartonella species." Comparative Immunology Microbiology and Infectious Diseases 36(2): 105-111.

The blood-sucking arthropod Ctenocephalides fells has been confirmed as a vector for Bartonella henselae and is a suspected vector for Bartonella clarridgeiae, Bartonella quintana and Bartonella koehlerae in Bartonella transmission to mammals. To understand the absence of other Bartonella species in the cat flea, we have developed an artificial flea-feeding method with blood infected successively with five different Bartonella species. The results demonstrated the ability of these five Bartonella species to persist in C. felis suggesting an ability of fleas to be a potential vector for several Bartonella species. In addition, we demonstrated a regurgitation of Bartonella DNA in uninfected blood used to feed C. felis thus suggesting a potential horizontal transmission of Bartonella through C. felis saliva. On the contrary, no vertical transmission was detected in these artificial conditions.

Boulouis, P. H. J., G. Marignac, et al. (2008). "Animal reservoirs and primary hosts of Bartonella." Bulletin De L Academie Veterinaire De France 161(3): 211-220.

Bartonella are hemotropic bacteria that infect numerous wild and domestic mammals, and some are directly responsible for zoonotic infections. There are 27 currently known species or subspecies of Bartonella. Wild and domestic animals represent a large reservoir for Bartonellae, but man is the unique reservoir for two species. Reservoirs are characterized by a long-lasting bacteremia, sometimes with recurrences. Cats have long been considered as an asymptomatic reservoir of Bartonella, but direct and indirect (serological) evidence indicate that they too can be affected by Bartonella infection. Dogs are considered as accidental hosts for Bartonella, and clinical features in this species are very similar to those seen in man. The most frequent signs reported in dogs and man include endocarditis, ocular, neurologic, articular, renal, and even skin disorders, as well as systemic manifestations. Endocarditis has also been described in cattle. In reservoir species, the main vectors of Bartonella are hematophagous arthropods, such as cat flea (Ctenocephalides felis), ticks (genus Nodes), or the louse-fly (Hippoboscidae). Blood culture, serology and PCR are used for the diagnosis of Bartonella infection in reservoir hosts. As no vaccines are available, prevention in carnivores relies mostly on appropriate tick and flea control. The outcome of the treatment of these infections remains uncertain and does not result in complete bacterial eradication.

Bretagne, S. and J. M. Costa (2006). "Towards a nucleic acid-based diagnosis in clinical parasitology and mycology." Clinica Chimica Acta 363(1-2): 221-228.

Background: Multiple in-house polymerase chain reaction (PCR) assays for the diagnosis of parasitic and fungal diseases have been reported. Encouraging results have been published to anticipate or improve the diagnosis. However, the absence of standardized methods has led to discrepant results. As a consequence, these tests are not recognized as consensual diagnostic criteria. Methods: The major breakthrough for improving the results of these methods is the emergence of real-time technologies. This markedly improves the reliability of the PCR results by

dramatically decreasing the risk of false positive results due to PCR products carryover. Moreover, the quantitative results provided by these techniques allow to compare rapidly the efficiency of primers, probes, and DNA extraction. Therefore, one can expect a more consensual method to implement comparisons between laboratories. Automated DNA extraction should also be useful to achieve this goal. Whatever sophisticated technology is used, the meaning of detecting nucleic acids in a given clinical sample still needs to be defined. This requires well-designed studies with clinical consensual criteria and PCR techniques that are as similar as possible. Conclusions: The development of real-time technology should improve our knowledge in order to give the clinicians informative clues for decision-making.

Buffet, J. P., M. Kosoy, et al. (2013). "Natural history of Bartonella-infecting rodents in light of new knowledge on genomics, diversity and evolution." Future Microbiology 8(9): 1117-1128.

Among the 33 confirmed Bartonella species to date, more than half are hosted by rodent species, and at least five of them have been involved in human illness causing diverse symptoms including fever, myocarditis, endocarditis, lymphadenitis and hepatitis. In almost all countries, wild rodents are infected by extremely diverse Bartonella strains with a high prevalence. In the present paper, in light of new knowledge on rodent-adapted Bartonella species genomics, we bring together knowledge gained in recent years to have an overview of the impact of rodent-adapted Bartonella infection on humans and to determine how diversity of Bartonella helps to understand their mechanisms of adaptation to rodents and the consequences on human health.

Buffet, J. P., M. Marsot, et al. (2012). "Co-infection of Borrelia afzelii and Bartonella spp. in bank voles from a suburban forest." Comparative Immunology Microbiology and Infectious Diseases 35(6): 583-589.

We report the molecular detection of Borrelia afzelii (11%) and Bartonella spp. (56%) in 447 bank voles trapped in a suburban forest in France. Adult voles were infected by significantly more Borrelia afzelii than juveniles ($p < 0.001$), whereas no significant difference was detected in the prevalence of Bartonella spp. between young and adult individuals ($p = 0.914$). Six percent of the animals were co-infected by both bacteria. Analysis of the bank vole carrier status for either pathogen indicated that co-infections occur randomly ($p = 0.94$, Cl-95 = 10.53; 1.47]). Sequence analysis revealed that bank voles were infected by a single genotype of Borrelia afzelii and by 32 different Bartonella spp. genotypes, related to three known species specific to rodents (B. taylorii, B. grahamii and B. doshiae) and also two as yet unidentified Bartonella species. Our findings confirm that rodents harbor high levels of potential human pathogens; therefore, widespread surveillance should be undertaken in areas where humans may encounter rodents.

Buffet, J. P., B. Pisanu, et al. (2013). "Deciphering Bartonella Diversity, Recombination, and Host Specificity in a Rodent Community." Plos One 8(7).

Host-specificity is an intrinsic feature of many bacterial pathogens, resulting from a long history of co-adaptation between bacteria and their hosts. Alpha-proteobacteria belonging to the genus Bartonella infect the erythrocytes of a wide range of mammal orders, including rodents. In this study, we performed genetic analysis of Bartonella colonizing a rodent community dominated by bank voles (Myodes glareolus) and wood mice (Apodemus sylvaticus) in a French suburban forest to evaluate their diversity, their capacity to recombine and their level of host specificity. Following the analysis of 550 rodents, we detected 63 distinct genotypes related to B. taylorii, B. grahamii, B. doshiae and a new B. rochalimae-like species. Investigating the most highly represented species, we showed that B. taylorii strain diversity was markedly higher than that of B. grahamii, suggesting a possible severe bottleneck for the latter species. The majority of recovered genotypes presented a strong association with either bank voles or wood mice, with the exception of three B. taylorii genotypes which had a broader host range. Despite the physical barriers created by host specificity, we observed lateral gene transfer between Bartonella genotypes associated with wood mice and Bartonella adapted to bank voles, suggesting that those genotypes might co-habit during their life cycle.

Cabaret, O., A. Emirian, et al. (2012). "Epidemiology of respiratory colonization with Aspergillus fumigatus and Stenotrophomonas maltophilia or Pseudomonas aeruginosa: A retrospective study from 2007 to 2011 in a French hospital." Mycoses 55: 172-172.

Cabaret, O., O. Puel, et al. (2011). "Contribution of uniformly C-13-enriched sterigmatocystin to the study of its pulmonary metabolism." Rapid Communications in Mass Spectrometry 25(19): 2704-2710.

Mycotoxins are secondary metabolites of filamentous fungi which can cause a wide range of systemic effects. Human health effects of inhaled mycotoxins remain poorly documented, despite the large amounts present, associated with airborne particles. Among these mycotoxins, sterigmatocystin is one of the most prevalent. Because its chemical structure is close to that of the aflatoxins, we studied its metabolism and its cellular consequences when in contact with the airway epithelium, using the mass spectral signature from the 10% C-13 uniformly enriched sterigmatocystin. The metabolism was studied in vitro, using recombinant cytochrome P450s enzymes, and in porcine tracheal epithelial cell (PTEC) primary cultures at an air-liquid interface. The metabolites were analyzed by high-performance liquid chromatography coupled with tandem mass spectrometry detection. Expressed enzymes and PTECs were exposed to uniformly C-13-enriched sterigmatocystin to confirm the relationship between sterigmatocystin and its metabolites because this isotopic cluster shape is conserved for all metabolites and their product ions. Incubation of sterigmatocystin with recombinant cytochrome P450 1A1 led to the formation of three metabolites identified as monohydroxysterigmatocystin, dihydroxysterigmatocystin and one glutathione adduct, the latter after the formation of a transient intermediate. In the PTEC cultures, sterigmatocystin metabolism resulted in a glucuro-conjugate. Two other products were detected, a sulfo-conjugate and a glucuro-conjugate of hydroxysterigmatocystin upon cytochrome P450 1A1 induction. This is the first study to report sterigmatocystin metabolism in airway epithelium, and it suggests that, contrary to the aflatoxins, sterigmatocystin is mainly detoxified into its conjugates and is unable to

produce significant amounts of reactive metabolites in respiratory cells, at least in pigs. Copyright (C) 2011 John Wiley & Sons, Ltd.

Cabaret, O., O. Puel, et al. (2011). "PULMONARY METABOLISM OF STERIGMATOCYSTIN AND METHOXY-STERIGMATOCYSTIN STUDIES: CONTRIBUTION OF UNIFORMLY C-13-ENRICHED STERIGMATOCYSTIN." Journal of Labelled Compounds & Radiopharmaceuticals 54(5): 287-288.

Cabaret, O., O. Puel, et al. (2010). "Metabolic Detoxication Pathways for Sterigmatocystin in Primary Tracheal Epithelial Cells." Chemical Research in Toxicology 23(11): 1673-1681.

Human health effects of inhaled mycotoxins remain poorly documented, despite the large amounts present in bioaerosols. Among these mycotoxins, sterigmatocystin is one of the most prevalent. Our aim was to study the metabolism and cellular consequences of sterigmatocystin once it is in contact with the airway epithelium. Metabolites were analyzed first in vitro, using recombinant P450 1A1, 1A2, 2A6, 2A13, and 3A4 enzymes, and subsequently in porcine tracheal epithelial cell (PTEC) primary cultures at an air liquid interface. Expressed enzymes and PTECs were exposed to sterigmatocystin, uniformly enriched with C-13 to confirm the relationship between sterigmatocystin and metabolites. Induction of the expression of xenobiotic-metabolizing enzymes upon sterigmatocystin exposure was examined by real-time quantitative real-time polymerase chain reaction. Incubation of 50 mu M sterigmatocystin with recombinant P450 1A1 led to the formation of three metabolites: monohydroxy-sterigmatocystin (M1), dihydroxy-sterigmatocystin (M2), and one glutathione adduct (M3), the latter after the formation of a transient epoxide. Recombinant P450 1A2 also led to M1 and M3. P450 3A4 led to only M3. In PTEC, 1 mu M sterigmatocystin metabolism resulted in a glucuro conjugate (M4) mainly excreted at the basal side of cells. If PTEC were treated with beta-naphthoflavone prior to sterigmatocystin incubation, two other products were detected, i.e., a sulfo conjugate (M5) and a glucoro conjugate (M6) of hydroxysterigmatocystin. Exposure of PTEC for 24 h to 1 mu M sterigmatocystin induced an 18-fold increase in the mRNA levels of P450 1A1, without significantly induced 7-ethoxyresorufin O-deethylation activity. These data suggest that sterigmatocystin is mainly detoxified and is unable to produce significant amounts of reactive epoxide metabolites in respiratory cells. However, sterigmatocystin increases the P450 1A1 mRNA levels with unknown long-term consequences. These in vitro results obtained in the porcine pulmonary tract need to be confirmed in human epithelial cells.

Cabaret, O., G. Toussain, et al. (2011). "Degradation of fungal DNA in formalin-fixed paraffin-embedded sinus fungal balls hampers reliable sequence-based identification of fungi." Medical Mycology 49(3): 329-332.

Identification of the etiologic agent responsible for sinus fungal ball (SFB) is rarely obtained due to either the culture of patient specimens not being ordered or if cultures were inoculated they proved to be negative. Obviously, this has a significant impact on the design of appropriate therapeutic strategies. We investigated whether paraffin-embedded (PE) tissues, the only materials often available, were suitable for the correct identification of the responsible fungi. We obtained PE

tissues of SFB from 16 different patients who had risk factors for invasive fungal infections. DNA was extracted using an automated extractor and the internal transcribed spacer (ITS) sequenced following amplification with two sets of primers designed to amplify >300 bp fragments. This was attempted in parallel with a real-time quantitative PCR assay targeting Aspergillus spp. mitochondrial DNA designed to amplify <150 bp fragments. ITS sequencing succeeded in appropriately identifying the etiologic agents in 10 of the 16 samples (nine Aspergillus fumigatus, one Lewia spp.). In contrast, the <150 bp PCR assay amplified all specimens correctly except the one involving Lewia spp. If fungal identification is warranted to understand the pathophysiology of SFB and guide clinicians, we cannot rely only on ITS sequencing of the DNA obtained from PE tissues. The main reason is probably due to the fact that formalin prevents amplification of long DNA fragments and consequently, frozen or fresh tissues should be employed.

Cadot, P., P. Hensel, et al. (2011). "Masitinib decreases signs of canine atopic dermatitis: a multicentre, randomized, double-blind, placebo-controlled phase3trial." Veterinary Dermatology 22(6): 554-564.

This study investigated the efficacy and safety of masitinib, a selective tyrosine kinase inhibitor capable of downregulating mast cell functions, for treatment of canine atopic dermatitis (CAD). Dogs with confirmed CAD received masitinib at 12.5 mg/kg/day (n = 202) or control (n = 104) for 12 weeks. A reduction in CAD Extent and Severity Index (CADESI-02) score of >= 50% at week 12 was observed in 61% of masitinib-treated dogs versus 35% of control dogs (P < 0.001), according to the modified intent-to-treat population. For dogs resistant to ciclosporin and/or corticosteroids (60% of the study population), CADESI-02 response rates were 60 versus 31%, respectively (P = 0.004). The mean reduction in pruritus score of severely pruritic dogs was 46 versus 29%, respectively (P = 0.045). Furthermore, 65% of owners with severely pruritic dogs assessed masitinib efficacy as good/excellent versus 35% control (P = 0.05). Overall, 63% of investigators assessed masitinib efficacy as good/excellent versus 35% control (P < 0.001). Premature discontinuations from the modified intent-to-treat population (28.2% masitinib versus 26.0% control) were mainly due to adverse events (13.4 versus 4.8%, respectively) or lack of efficacy (12.4 versus 18.3%, respectively). In total, 13.2% dogs presented with severe adverse events (16.0% masitinib versus 7.7% control). Masitinib showed a risk of reversible protein loss, although regular surveillance of blood albumin and proteinuria allowed for discontinuation of treatment while the dog was still clinically asymptomatic. Masitinib proved to be an effective and mostly well-tolerated treatment of CAD, including severe and refractory cases, with medically manageable adverse effects.

Cafarchia, C., M. S. Latrofa, et al. (2011). "Physiological and molecular characterization of atypical lipid-dependent Malassezia yeasts from a dog with skin lesions: adaptation to a new host?" Medical Mycology 49(4): 365-374.

Three lipid-dependent Malassezia isolates (here named 114A, 114B and 114C) recovered from a dog with skin lesions were phenotypically and genotypically characterized. All presented ovoid cells and buds formed on a narrow base. Most of the results from physiological tests were consistent with those of Malassezia furfur. The phylogenetic analysis of ITS-1 and LSU nucleotide

sequences was concordant in placing all three clinical Malassezia isolates close to M. furfur. However, the phylogenetic data on the chs-2 sequence revealed that clinical isolate 114A is distinct from M. furfur and was closely affiliated to the sequence of M. pachydermatis with high nodal support. In particular, lipid-dependent isolates 114A displayed chs-2 sequences similar (100%) to that of the non-lipid dependent species Malassezia pachydermatis. The presence of the genetic and physiological polymorphisms detected in these three isolates of M. furfur could have resulted from a process of adaptation of this anthropophilic species to a new host.

Chauvin, A., E. Moreau, et al. (2009). "Babesia and its hosts: adaptation to long-lasting interactions as a way to achieve efficient transmission." Veterinary Research 40(2).

Babesia, the causal agent of babesiosis, are tick-borne apicomplexan protozoa. True babesiae (Babesia genus sensu stricto) are biologically characterized by direct development in erythrocytes and by transovarial transmission in the tick. A large number of true Babesia species have been described in various vertebrate and tick hosts. This review presents the genus then discusses specific adaptations of Babesia spp. to their hosts to achieve efficient transmission. The main adaptations lead to long-lasting interactions which result in the induction of two reservoirs: in the vertebrate host during low long-term parasitemia and throughout the life cycle of the tick host as a result of transovarial and transstadial transmission. The molecular bases of these adaptations in vertebrate hosts are partially known but few of the tick-host interaction mechanisms have been elucidated.

Chomel, B. B., H. J. Boulouis, et al. (2009). "Ecological fitness and strategies of adaptation of Bartonella species to their hosts and vectors." Veterinary Research 40(2).

Bartonella spp. are facultative intracellular bacteria that cause characteristic host-restricted hemotropic infections in mammals and are typically transmitted by blood-sucking arthropods. In the mammalian reservoir, these bacteria initially infect a yet unrecognized primary niche, which seeds organisms into the blood stream leading to the establishment of a long-lasting intra-erythrocytic bacteremia as the hall-mark of infection. Bacterial type IV secretion systems, which are supra-molecular transporters ancestrally related to bacterial conjugation systems, represent crucial pathogenicity factors that have contributed to a radial expansion of the Bartonella lineage in nature by facilitating adaptation to unique mammalian hosts. On the molecular level, the type IV secretion system VirB/VirD4 is known to translocate a cocktail of different effector proteins into host cells, which subvert multiple cellular functions to the benefit of the infecting pathogen. Furthermore, bacterial adhesins mediate a critical, early step in the pathogenesis of the bartonellae by binding to extracellular matrix components of host cells, which leads to firm bacterial adhesion to the cell surface as a prerequisite for the efficient translocation of type IV secretion effector proteins. The best-studied adhesins in bartonellae are the orthologous trimeric autotransporter adhesins, BadA in B. henselae and the Vomp family in B. quintana. Genetic diversity and strain variability also appear to enhance the ability of bartonellae to invade not only specific reservoir hosts, but also accidental hosts, as shown for B. henselae. Bartonellae have been identified in many different blood-sucking arthropods, in which they are typically found to cause extracellular infections of the mid-gut epithelium. Adaptation to specific vectors and reservoirs seems to be a common strategy of

bartonellae for transmission and host diversity. However, knowledge regarding arthropod specificity/restriction, the mode of transmission, and the bacterial factors involved in arthropod infection and transmission is still limited.

Choukri, F., F. Botterel, et al. (2013). "Prospective evaluation of azole resistance in Aspergillus fumigatus clinical isolates in France." Mycoses 56: 65-66.

Choukri, F., F. Morio, et al. (2013). "Azole resistance in Aspergillus fumigatus isolates from lung transplant recipients with cystic fibrosis: preliminary results." Mycoses 56: 63-64.

Clavaud, C., R. Jourdain, et al. (2013). "Dandruff Is Associated with Disequilibrium in the Proportion of the Major Bacterial and Fungal Populations Colonizing the Scalp." Plos One 8(3).

The bacterial and fungal communities associated with dandruff were investigated using culture-independent methodologies in the French subjects. The major bacterial and fungal species inhabiting the scalp subject's were identified by cloning and sequencing of the conserved ribosomal unit regions (16S for bacterial and 28S-ITS for fungal) and were further quantified by quantitative PCR. The two main bacterial species found on the scalp surface were Propionibacterium acnes and Staphylococcus epidermidis, while Malassezia restricta was the main fungal inhabitant. Dandruff was correlated with a higher incidence of M. restricta and S. epidermidis and a lower incidence of P. acnes compared to the control population ($p < 0.05$). These results suggested for the first time using molecular methods, that dandruff is linked to the balance between bacteria and fungi of the host scalp surface.

Clavaud, C., I. Mouyna, et al. (2012). "Dandruff is associated with changes in the density of Propionibacterium, Staphylococcus and Malassezia populations." Journal of Investigative Dermatology 132: S56-S56.

Cordonnier, C., F. Botterel, et al. (2006). "Galactomannan antigenaemia has a higher diagnostic yield in invasive aspergillosis in deeply neutropenic patients than in others." Bone Marrow Transplantation 37: S167-S168.

Costa, J. M. and S. Bretagne (2012). "Variation of B1 Gene and AF146527 Repeat Element Copy Numbers According to Toxoplasma gondii Strains Assessed Using Real-Time Quantitative PCR." Journal of Clinical Microbiology 50(4): 1452-1454.

Using the multicopy B1 gene and AF146527 element for the amplification of Toxoplasma gondii DNA raises the issue of reliable quantification for clinical diagnosis. We applied relative

quantification to reference strains using the single-copy P30 gene as a reference. According to the parasite type, the copy numbers for the B1 gene and AF146527 element were found to be 5 to 12 and 4 to 8 times lower than the previous estimations of 35 and 230 copies, respectively.

Costa, J. M., O. Cabaret, et al. (2011). "Genotyping of the protozoan pathogen Toxoplasma gondii using high-resolution melting analysis of the repeated B1 gene." Journal of Microbiological Methods 86(3): 357-363.

Genetic studies of the protozoan parasite Toxoplasma gondii have identified three main distinct types according to virulence in some hosts. Several methods have been developed to differentiate genotypes currently dominated by microsatellite markers targeting single-copy loci. We analyzed the possibility of using the 35-fold repetitive B1 gene via high-resolution melting (HRM) curve analysis. Sequencing of the B1 gene of 14 reference strains (four Type I, six Type II, and four Type Ill strains) identified 18 single nucleotide polymorphisms (SNP). Primers were designed to amplify eight of them for HRM analysis and for relative quantification of each nucleotide variation using SNaPshot mini-sequencing. Genotyping with five microsatellite markers was performed for comparison. Two to four HRM profiles were obtained depending on the SNP tested. The differences observed relied on the different ratios of nucleotides at the SNP locus as evidenced via SNaPshot mini-sequencing. The three main lineages could be distinguished by using several HRM profiles. Some HRM profiles proved more informative than the analysis based on five microsatellite markers, showing additional differences in Type land Type II strains. Using HRM analysis, we obtained at least an equally good discrimination of the main lineages than that based on five microsatellite markers.

Costa, J. M., D. Garcia-Hermoso, et al. (2010). "Genotyping of Candida albicans using length fragment and high-resolution melting analyses together with minisequencing of a polymorphic microsatellite locus." Journal of Microbiological Methods 80(3): 306-309.

Microsatellite length polymorphism (MLP) typing is a PCR-based method used for genotyping of the diploid yeast Candida albicans. However, MLP is subject to homoplasia which can hamper the accuracy of the results. We combined fragment length analysis, high-resolution DNA melting (HRM) analysis, and SNaPshot minisequencing after a single amplification of the CDC3 locus to study 95 epidemiologically independent C albicans isolates. HRM analysis for a given electrophoretic group led to a maximum of three different curves due to the presence of a SNP upstream of the tandem repeat which could be characterized using the SNaPshot assay. The combination of the three methods had a discriminatory index of 0.88 in complete congruence with previous MLP typing (Mantel test R = 0.99, P < 10(-4)). HRM is a useful tool of adding resolving power to MLP genotyping in identifying SNPs.

Cotte, V., S. Bonnet, et al. (2010). "Prevalence of Five Pathogenic Agents in Questing Ixodes ricinus Ticks from Western France." Vector-Borne and Zoonotic Diseases 10(8): 723-730.

In Europe, Ixodes ricinus ticks are vectors of many emerging pathogens, including Borrelia burgdorferi sensu lato (sl), Anaplasma phagocytophilum, spotted fever group Rickettsia sp., Babesia sp., and very likely Bartonella sp. In this study, we looked for the presence of DNA of these microorganisms in 572 ticks from two forests in the west of France. DNA extraction and polymerase chain reaction (PCR) amplification were performed on individual nymphal, male, and female I. ricinus ticks. Amplification from 1 tick among the 572 samples (0.2%) resulted in PCR products with Bartonella-specific primers. Sequence analysis of the amplified fragment did not lead to species identification. Two ticks (0.3%) carried A. phagocytophilum-specific DNA. Eight ticks (1.4%) were positive with spotted fever group Rickettsia-specific primers, and all PCR fragments were related to Rickettsia helvetica. Thirty-five ticks (6.1%) were positive with B. burgdorferi sl-specific primers; the sequences were all related to Borrelia garinii or Borrelia afzelii, except one that was related to Borrelia carolinensis, a newly described species never reported in Europe so far. Thirty-five ticks (6.1%) carried Babesia sp. DNA. Female adults were more infected by B. burgdorferi sl than male adults. The prevalence of B. burgdorferi sl and Babesia sp. was significantly different between the two forests, with a higher prevalence of B. burgdorferi sl in ticks from the forest of Prince and a higher prevalence of Babesia sp. in ticks from the forest of Gavre. To our knowledge, this is the first study that has detected all five pathogens in questing I. ricinus in the west of France and the first report of B. carolinensis DNA in ticks in Europe.

Dei-Cas, E., M. Chabe, et al. (2006). "Pneumocystis oryctolagi sp nov., an uncultured fungus causing pneumonia in rabbits at weaning: review of current knowledge, and description of a new taxon on genotypic, phylogenetic and phenotypic bases." Fems Microbiology Reviews 30(6): 853-871.

The genus Pneumocystis comprises noncultivable, highly diversified fungal pathogens dwelling in the lungs of mammals. The genus includes numerous host-species-specific species that are able to induce severe pneumonitis, especially in severely immunocompromised hosts. Pneumocystis organisms attach specifically to type-1 epithelial alveolar cells, showing a high level of subtle and efficient adaptation to the alveolar microenvironment. Pneumocystis species show little difference at the light microscopy level but DNA sequences of Pneumocystis from humans, other primates, rodents, rabbits, insectivores and other mammals present a host-species-related marked divergence. Consistently, selective infectivity could be proven by cross-infection experiments. Furthermore, phylogeny among primate Pneumocystis species was correlated with the phylogeny of their hosts. This observation suggested that cophylogeny could explain both the current distribution of pathogens in their hosts and the speciation. Thus, molecular, ultrastructural and biological differences among organisms from different mammals strengthen the view of multiple species existing within the genus Pneumocystis. The following species were subsequently described: Pneumocystis jirovecii in humans, Pneumocystis carinii and Pneumocystis wakefieldiae in rats, and Pneumocystis murina in mice. The present work focuses on Pneumocystis oryctolagi sp. nov. from Old-World rabbits. This new species has been described on the basis of both biological and phylogenetic species concepts.

Deng, H. K., D. Le Rhun, et al. (2012). "Identification of Bartonella Trw Host-Specific Receptor on Erythrocytes." Plos One 7(7).

Each Bartonella species appears to be highly adapted to one or a limited number of reservoir hosts, in which it establishes long-lasting intraerythrocytic bacteremia as the hallmark of infection. Recently, we identified Trw as the bacterial system involved in recognition of erythrocytes according to their animal origin. The T4SS Trw is characterized by a multiprotein complex that spans the inner and outer bacterial membranes, and possesses a hypothetical pilus structure. TrwJ, I, H and trwL are present in variable copy numbers in different species and the multiple copies of trwL and trwJ in the Bartonella trw locus are considered to encode variant forms of surface-exposed pilus components. We therefore aimed to identify which of the candidate Trw pilus components were located on the bacterial surface and involved in adhesion to erythrocytes, together with their erythrocytic receptor. Using different technologies (electron microscopy, phage display, invasion inhibition assay, far western blot), we found that only TrwJ1 and TrwJ2 were expressed and localized at the cell surface of B. birtlesii and had the ability to bind to mouse erythrocytes, and that their receptor was band3, one of the major outer-membrane glycoproteins of erythrocytes, (anion exchanger). According to these results, we propose that the interaction between TrwJ1, TrwJ2 and band 3 leads to the critical host-specific adherence of Bartonella to its host cells, erythrocytes.

Derouiche, S., M. Deville, et al. (2009). "Pneumocystis diversity as a phylogeographic tool." Memorias Do Instituto Oswaldo Cruz 104(1): 112-117.

Parasites are increasingly used to complement the evolutionary and ecological adaptation history of their hosts. Pneumocystis pathogenic fungi, which are transmitted from host-to-host via an airborne route, have been shown to constitute genuine host markers of evolution. These parasites can also provide valuable information about their host ecology. Here, we suggest that parasites can be used as phylogeographic markers to understand the geographical distribution of intra-specific host genetic variants. To test our hypothesis, we characterised Pneumocystis isolates from wild bats living in different areas. Bats comprise a wide variety of species; some of them are able to migrate. Thus, bat chorology and migration behaviour can be approached using Pneumocystis as phylogeographic markers. In the present work, we find that the genetic polymorphisms of bat-derived Pneumocystis are structured by host chorology. Therefore, Pneumocystis intra-specific genetic diversity may constitute a useful and relevant phylogeographic tool.

Dobigny, G., P. Poirier, et al. (2011). "Molecular survey of rodent-borne Trypanosoma in Niger with special emphasis on T. lewisi imported by invasive black rats." Acta Tropica 117(3): 183-188.

Invading rodent species can harbor parasites with potential transmission to native rodents and/or humans. To investigate trypanosomes prevalence in rodents, the spleen of 76 rodents from Niger identified by their karyotype was used as a DNA source for Trypanosoma detection using a newly developed qPCR assay. Of the invasive black rat, Rattus rattus, 71% (10/14) were PCR positive as well as 6% (4/62) of native African rodents. Sequences of similar to 400 bp of the SSU rDNA gene identified phylogenetically close Trypanosoma lineages. Trypanosoma lewisi was present in all positive black rats and the sequences displayed 100% similarity with T. lewisi-infected humans in Senegal. T. lewisi was also detected in one Acomys johannis, suggesting a possible transmission to native species. In addition to improved knowledge of Trypanosoma diversity in rodents, our data

underscore the introduction of the potentially pathogenic T. lewisi kinetoplastid through the human-mediated invasion of black rats all over West Africa. (C) 2010 Elsevier B.V. All rights reserved.

Dupouy-Camet, J. and I. Vallee (2006). "Trichinella as a modulator of flu-induced pathology?" Trends in Parasitology 22(10): 452-454.

In Trichinella, spiralis and influenza co-infected mice, the influenza virus-induced secretion of the lung-damaging tumour necrosis factor alpha is modulated, as described by Furze et al. in a recent study. However, the immune response induced by T. spiralis is so variable that this modulation could be of limited value to manage clinical cases of influenza. Nevertheless, the concept that parasites can modulate influenza-induced pathology presents an interesting and potentially useful approach to therapeutics. The local perturbations induced by T. spiralis migration, coincident with the site of influenza infection, certainly warrant further studies.

Eloy, O., S. Marque, et al. (2006). "Uniform distribution of three Candida albicans microsatellite markers in two French ICU populations supports a lack of nosocomial cross-contamination." Bmc Infectious Diseases 6.

Background: The nosocomial acquisition of Candida albicans is a growing concern in intensive care units (ICUs) and understanding the route of contamination is relevant for infection control guidelines. Methods: To analyze whether there is a specific ecology for any given hospital, we genotyped C. albicans isolates of the ICU of Versailles hospital (Hospital A) and compared the results with those previously obtained in another ICU in Henri Mondor hospital (Hospital B) using three polymorphic microsatellite markers (PMM). Results: Among 36 patients with at least one positive culture for C. albicans, 26 had a specific multilocus genotype, two shared a common multilocus genotype, and 8 had the most common multilocus genotype found in the general population. The time interval between periods of hospitalization between patients with common genotypes differed by 13 to 78 days, thus supporting a lack of direct contamination. To confirm this hypothesis, the multilocus genotypic distributions of the three PMM were compared between the two hospitals. No statistically significant difference was observed. Multiple correspondences analysis did not indicate the association of a multilocus genotypic distribution with any given hospital. Conclusion: The present epidemiological study supports the conclusions that each patient harbours his/her own isolate, and that nosocomial transmission is not common in any given ICU. This study also supports the usefulness and practicability of PMM for studying the epidemiology of C. albicans.

Even, C., S. Bastuji-Garin, et al. (2011). "Impact of invasive fungal disease on the chemotherapy schedule and event-free survival in acute leukemia patients who survived fungal disease: a case-control study." Haematologica-the Hematology Journal 96(2): 337-341.

Patients with acute leukemia who initially survive invasive fungal disease must receive chemotherapy or go on to transplant. Many centers change subsequent chemotherapy to decrease the risk of fungal reactivation. This case-control study compared acute leukemia patients (n=28) who

developed a proven or probable fungal disease and survived four weeks later, to patients who did not (n=78), and assessed the impact of fungal disease on the chemotherapy regimens, and overall and event-free survival. Chemotherapy changes (i.e: delays, dose-reduction) were more frequent in the fungal (68%) than in the control group (24%) (P<0.001). Although there was no difference in overall and event-free survival between groups, they were both lower for proven fungal disease cases when compared to controls (HR 2.4, 95% CI 1.1-1.5, and HR 2.9, 95% CI 1.4-5.6, respectively). Patients with invasive fungal disease, even though they initially survive, undergo significant changes to their chemotherapy therapy. This impacts on the survival of patients with proven fungal disease.

Fall, E. H., M. Diagne, et al. (2012). "DEVELOPMENT OF TRICHOSOMOIDES NASALIS (NEMATODA: TRICHINELLOIDEA) IN THE MURID HOST: EVIDENCE FOR LARVAL GROWTH IN STRIATED MUSCLE FIBRES." Parasite-Journal De La Societe Francaise De Parasitologie 19(1): 19-29.

Trichosomoides nasalis (Trichinelloidea) is a parasite of Arvicanthis niloticus (Muridae) in Senegal. Female worms that harbour dwarf males in their uteri, occur in the epithelium of the nasal mucosa. Young laboratory-bred A. niloticus were either fed females containing larvated eggs or intraperitoneally injected with motile first-stage larvae recovered from female uteri. Both resulted in successful infection. Organs examined during rodent necropsy were blood and lymphatic circulatory systems (heart, large vessels, lymphnodes), lungs, liver, kidneys, thoracic and abdominal cavities, thoracic and abdominal muscular walls, diaphragm, tongue, and nasal mucosa. Development to adult nasal stages took three weeks. Recovery of newly hatched larvae from the peritoneal fluid at four-eight hours after oral infection suggests a direct passage from the stomach or intestinal wall to the musculature. However, dissemination through the blood, as observed with Trichinella spiralis, cannot be excluded even though newly hatched larvae of T nasalis are twice as thick (15 mu m). Developing larvae were found in histological sections of the striated muscle of the abdominal and thoracic walls, and larvae in fourth moult were dissected from these sites. Adult females were found in the deep nasal mucosa where mating occurred prior to worms settling in the nasal epithelium. The present study shows a remarkable similarity between T nasalis and Trichinella species regarding muscle tropism, but the development of T. nasalis is not arrested at the late first-larval stage and does not induce transformation of infected fibres into nurse cells. T. nasalis seems a potential model to study molecular relations between trichinelloid larvae and infected muscle fibres.

Farrugia, C., O. Cabaret, et al. (2011). "Cytochrome b Gene Quantitative PCR for Diagnosing Plasmodium falciparum Infection in Travelers." Journal of Clinical Microbiology 49(6): 2191-2195.

A cytochrome b (cytb) gene quantitative PCR (qPCR) assay was developed to diagnose malaria in travelers. First, manual and automated DNA extractions were compared and automated DNA extraction of 400 mu l of blood was found to be more efficient. Sensitivity was estimated using the WHO international standard for Plasmodium falciparum DNA and compared to that of a previously published qPCR targeting the 18S rRNA coding gene (18S qPCR). The limit of detection of the cytb qPCR assay was 20 DNA copies (i.e., 1 parasite equivalent) per 400 mu l of extracted whole blood and was comparable for the two qPCR assays. Both qPCR assays were used on blood samples from 265 consecutive patients seen for suspicion of malaria. There were no microscopy-positive and

qPCR-negative samples. Positive cytb qPCR results were observed for 51 samples, and all but 1 were also 18S qPCR positive. Eight (16%) of these 51 samples were negative by microscopic examination. The 8 cytb qPCR-positive and microscopy-negative samples were from African patients, 3 of whom had received antimalarial drugs. Three non-P. falciparum infections were correctly identified using an additional qPCR assay. The absence of PCR inhibitors was tested for by the use of an internal control of mouse DNA to allow reliable quantification of circulating DNA. The high analytical sensitivity of both qPCR assays combined with automated DNA extraction supports its use as a laboratory tool for diagnosis and parasitemia determination in emergencies. Whether to treat qPCR-positive and microscopy-negative patients remains to be determined.

Fauvel, M., C. Farrugia, et al. (2012). "Aerosolized liposomal amphotericin B: Prediction of lung deposition, in vitro uptake and cytotoxicity." International Journal of Pharmaceutics 436(1-2): 106-110.

To predict the efficacy and toxicity of pulmonary administration of liposomal amphotericin B (L-AMB) for the treatment or the prevention of pulmonary invasive aspergillosis, a multistage liquid impinger was used to estimate the concentrations of drug that could be attained in different lung compartments after nebulization. The highest concentration of amphotericin B was found in the alveolar compartment, where it was calculated that the concentration in the lung surfactant could reach 54 mu M or more when 21.6 mu moles of drug as liposomes was nebulized. The uptake and toxicity of L-AMB were studied in vitro using the A549 human lung epithelial cell line. Uptake was time and concentration-dependent and reached intracellular concentrations exceeding the minimal inhibitory concentrations for most Aspergillus species. The toxicity of L-AMB toward these cells, estimated by the MTT reduction assay, was reduced compared with the conventional form, deoxycholate amphotericin B (D-AMB), with an IC50 value of about 120 mu M after 24 h of exposure for D-AMB, but only a 13% reduction in viability for 200 mu M L-AMB at 24 h. These results indicate that aerosol therapy with nebulized L-AMB could be efficient but that doses need to be carefully controlled to avoid toxicity.

Ferreira, R. R., L. Ferreiro, et al. (2011). "Canine Sinonasal Aspergillosis." Acta Scientiae Veterinariae 39(4).

Background: Sinonasal aspergillosis (SNA) is the second most common cause of nasal discharge in dogs. The diagnosis is confirmed through anamnesis, physical and complementary exams. Aspergillus fumigatus is the species most frequently isolated from dogs with fungal involvement of the upper respiratory tract. Canine SNA is a disease with worldwide distribution but, surprisingly, the disease has never been described in Brazil. The prognosis of SNA is usually good. The objective of this report is to describe the first case of canine sinonasal aspergillosis in Brazil. Case: A 18-months old, male, Rottweiler breed dog was referred to the Hospital de Clinicas Veterinarias at the Universidade Federal do Rio Grande do Sul (UFRGS), Porto Alegre, Southern Brazil, for purulent nasal discharge, variably bloody, and sneezing of approximately 6 months duration. During this period, the dog was treated with various antibiotics with no success and lost 10 kg of corporal mass. The alterations found in the physical exam were bilateral sanguinopurulent nasal discharge,

depigmentation of nose and paranasal region, as well as subnutrition. The dog was anesthetized and sinus and chest x-rays were performed (latero-lateral and ventrodorsal positions). In the radiographic analysis, it was verified the lessening of radiolucency on the left nostril, indicating the destruction of the nasal concha. The chest radiographies did not show alterations. A rhinoscopy was carried out showing destruction in the endoturbinate, purulent discharge and presence of a dark color mass in the frontal sinus, which was collected for histopathological and microbiological culture exams. Histopathologic examination revealed the presence of hyaline, branching septate hyphae, consistent with Aspergillus spp. and inflammatory cells. Culture identified Aspergillus fumigatus. Bacteriological culture was negative. Antibodies to Aspergillus fumigatus were detected by counter electrosyneresis. The haemogram showed lymphocytosis and monocytosis. The dog was treated with itraconazole (5 mg/kg of body weight, orally, twice a day for 30 days). After this period, nasal discharge decreased and a good repigmentation was observed with the dog showing improvement of his appetite and energy level. Discussion: The presence of antibodies to Aspergillus spp. does not always confirm canine nasal aspergillosis. Serological tests can yield 5% to 15% false positive results in dogs. Therefore, it is necessary to perform complementary exams such as radiography, rhinoscopy, histopathology and fungal culture in order to confirm the diagnosis. For many years, aspergillosis was considered as an incurable chronic rhinitis characterized by the turbinate destruction, nasal discharge and intermittent epistaxis. The reported prevalence of canine SNA in animals affected by disorders in the upper respiratory may range from 7 to 34%. Consequently, predisposed animals (like dolichocephalic dogs) are serious candidates to develop nasal aspergillosis that, in many cases, may be not diagnosed. This first report of canine sinonasal aspergillosis in Brazil reinforces the importance of consider this disease as a differential diagnosis in cases of nasal disease in dogs with clinical rhinosinusitis mainly in tropical countries.

Filet, H., N. Vachiery, et al. (2012). "A new typing technique for the Rickettsiales Ehrlichia ruminantium: Multiple-locus variable number tandem repeat analysis." Journal of Microbiological Methods 88(2): 205-211.

Ehrlichia ruminantium (ER) is a member of the order Rickettsiales transmitted by Amblyomma ticks. This obligatory intracellular bacterium is the causative agent of a fatal disease in ruminants, named heartwater. It represents a constraint on breeding development in sub-Saharan Africa and in the Caribbean. The genetic diversity of the strains of ER, which could be a limiting factor to obtain effective vaccines, needs to be better characterized. For this purpose, we developed a molecular typing technique based on the polymorphism of variable number tandem repeat (VNTR) sequences, MLVA (multiple locus VNTR analysis). Eight (out of 21) VNTR candidates were validated using 17 samples representing a panel of ER strains from different geographical origins from West, South Africa, and Caribbean areas and in ER infected ticks and goat tissues. This result demonstrated the ability of these VNTRs to type a wide range of strains. The stability of the selected VNTR markers was very good, at the time scale needed for epidemiological purposes: in particular, no difference in the VNTR profiles was observed between virulent and attenuated strains (for Gardel and Senegal strains) and between strains (Gardel and Blonde strains) isolated in the same area 19 years apart. We validated the strong discriminatory power of MLVA for ER and found a high level of polymorphism between the available strains, with 10 different profiles out of 13 ER strains. The MLVA scheme described in this study is a rapid and efficient molecular typing tool for ER, which allows rapid and

direct typing of this intracellular pathogen without preliminary culture and gives reliable results that can be used for further epidemiological studies.

Fogelman, D. R., R. A. Wolff, et al. (2011). "Evidence for the Efficacy of Iniparib, a PARP-1 Inhibitor, in BRCA2-associated Pancreatic Cancer." Anticancer Research 31(4): 1417-1420.

Pancreatic cancer is an aggressive, frequently fatal malignancy that strikes 37,000 patients annually in the U.S.A. It is poorly responsive to standard chemotherapies such as gemcitabine. Approximately 5-10% of pancreatic cancer occurs in the setting of a BRCA2 mutation. Breast and ovarian carcinomas that harbor BRCA2 mutations are susceptible to the effects of an emerging class of targeted agents, namely, poly(ADP-ribose) polymerase (PARP) inhibitors. This report describes the case of a patient with a germline BRCA2 mutation and an associated pancreatic cancer treated with iniparib (BSI-201), a PARP inhibitor, who demonstrated a complete pathologic response to this agent. This case highlights the potential benefit for PARP inhibition in BRCA2-related pancreatic cancer.

Fu, B. Q., W. H. Li, et al. (2013). "Detection of anti-Trichinella antibodies in serum of experimentally-infected swine by immunochromatographic strip." Veterinary Parasitology 194(2-4): 125-127.

An immunochromatographic strip method, developed with the excretory-secretory antigens from muscle larvae (ML) of Trichinella spiralis labeled with colloidal gold, was used for the detection of anti-Trichinella antibodies in serum of experimentally-infected swine. Sera from swine infected with 200, 2000 and 20,000 infective ML were collected at different days post infection (dpi) and used to evaluate the method. The strip method was shown able to detect anti-Trichinella antibodies by 35 dpi, 28 dpi and 21 dpi for the three different infection doses, respectively, and closely correlated with the results of an ELISA test. The strip method is rapid and easy to perform and is suggested as an acceptable alternative for clinical laboratories lacking specialized equipment, and for field diagnosis of trichinellosis.

Fu, B. Q., M. Y. Liu, et al. (2009). "Species identification of Trichinella isolates from China." Veterinary Parasitology 159(3-4): 214-217.

Two species of Trichinella were identified from China by means of PCR amplification of the mitochondrial small subunit ribosomal DNA and the expansion segment V region of the ribosomal DNA. Seven isolates originating from domestic pig and one isolate originating from dog showed identical DNA banding pattern to Trichinella spiralis, and two isolates from dog showed DNA banding pattern identical to Trichinella nativa. Sequence analysis of the 5S rDNA inter-gene spacer region from the ten Trichinella isolates confirmed the existence of only two Trichinella species and revealed the inner species genetic variation within T. spiralis and T. nativa.

Gajadhar, A. A., E. Pozio, et al. (2009). "Trichinella diagnostics and control: Mandatory and best practices for ensuring food safety." Veterinary Parasitology 159(3-4): 197-205.

Because of its role in human disease, there are increasing global requirements for reliable diagnostic and control methods for Trichinella in food animals to ensure meat safety and to facilitate trade. Consequently, there is a need for standardization of methods, programs, and best practices used in the control of Trichinella and trichinellosis. This review article describes the biology and epidemiology of Trichinella, and describes recommended test methods as well as modified and optimized procedures that are used in meat inspection programs. The use of ELISA for monitoring animals for infection in various porcine and equine pre- and post-slaughter programs, including farm or herd certification programs is also discussed. A brief review of the effectiveness of meat processing methods, such as freezing, cooking and preserving is provided. The importance of proper quality assurance and its application in all aspects of a Trichinella diagnostic system is emphasized. It includes the use of international quality standards, test validation and standardization, critical control points, laboratory accreditation, certification of analysts and proficiency testing. Also described, are the roles and locations of international and regional reference laboratories for trichinellosis where expert advice and support on research and diagnostics are available.

Gomez-Morales, M. A., A. Ludovisi, et al. (2012). "A distinctive Western blot pattern to recognize Trichinella infections in humans and pigs." International Journal for Parasitology 42(11): 1017-1023.

Trichinellosis is a zoonotic disease caused by parasites of the genus Trichinella, which have a cosmopolitan distribution. For diagnostic purposes, a confirmatory test for ELISA-positive human and pig sera such as Western blotting is required, due to the high number of ELISA false positive sera. The objective of this study was to identify the Trichinella-specific antigens most frequently recognized by sera from Trichinella-infected humans and pigs, so as to define a distinctive pattern of Trichinella infection in sera from infected hosts using Western blots which allow false positive sera to be distinguished from true positive sera. Using excretory/secretory antigens, 450 human sera were tested by Western blotting: 150 from persons with a confirmed diagnosis of trichinellosis and 300 from persons who did not have trichinellosis but who tested positive by ELISA (i.e., false positives). We also tested 210 pig sera: (i) 30 from pigs experimentally infected with Trichinella (ii) 90 from naturally T. spiralis-infected pigs; and (iii) 90 from pigs not infected with Trichinella, as shown after artificial digestion of the diaphragm pillars, yet which tested positive by ELISA (i.e., false positives). All true positive sera (i.e., sera from persons with confirmed trichinellosis as well as sera from naturally and experimentally infected pigs), reacted with a three-band pattern ranging in size from 48-72 kDa. A distinctive pattern for recognizing Trichinella spp. infections in humans and pigs by Western blots is defined; it shows a sensitivity of 100% and it allows sera from Trichinella-infected humans and pigs to be distinguished from sera from persons and pigs that were not infected with Trichinella spp. (100% specificity).

Guillot, J., B. Vermeulen, et al. (2011). "Nematodes of the genus Oesophagostomum: an emerging risk for humans and apes in Africa?" Bulletin De L Academie Nationale De Medecine 195(8): 1955-1963.

Nematodes of the genus Oesophagostomum are common intestinal parasites found in cattle, pigs and primates. They can cause severe illness, resulting from the formation of granulomas, caseous lesions and abscesses in the intestinal wall. Human oesophagostomosis is endemic in northern Ghana and Togo. In these regions, epidemiological investigations have been conducted to determine the biological characteristics, transmission dynamics and optimal management of clinical cases. Nodular oesophagostomosis has also been described in free-ranging chimpanzees and gorillas. Clinical signs associated with nodules have been observed in great apes raised in sanctuaries, while the health status of their wild counterparts does not seem to be significantly affected. It has been suggested that some nonhuman primates may act as reservoirs for human oesophagostomosis. In Ghana, identification of genetic differences among Oesophagostomum nematodes infecting different primate hosts suggests that oesophagostomosis is a rare zoonosis. In Uganda, where the situation is different, cross-infection is probably more frequent.

Halos, L., G. Baneth, et al. (2012). "Defining the concept of 'tick repellency' in veterinary medicine." Parasitology 139(4): 419-423.

Although widely used, the term repellency needs to be employed with care when applied to ticks and other periodic or permanent ectoparasites. Repellency has classically been used to describe the effects of a substance that causes a flying arthropod to make oriented movements away from its source. However, for crawling arthropods such as ticks, the term commonly subsumes a range of effects that include arthropod irritation and consequent avoiding or leaving the host, failing to attach, to bite, or to feed. The objective of the present article is to highlight the need for clarity, to propose consensus descriptions and methods for the evaluation of various effects on ticks caused by chemical substances.

Halos, L., S. Bord, et al. (2010). "Ecological Factors Characterizing the Prevalence of Bacterial Tick-Borne Pathogens in Ixodes ricinus Ticks in Pastures and Woodlands." Applied and Environmental Microbiology 76(13): 4413-4420.

Ecological changes are recognized as an important driver behind the emergence of infectious diseases. The prevalence of infection in ticks depends upon ecological factors that are rarely taken into account simultaneously. Our objective was to investigate the influences of forest fragmentation, vegetation, adult tick hosts, and habitat on the infection prevalence of three tick-borne bacteria, Borrelia burgdorferi sensu lato, Anaplasma phagocytophilum, and Rickettsia sp. of the spotted fever group, in questing Ixodes ricinus ticks, taking into account tick characteristics. Samples of questing nymphs and adults were taken from 61 pastures and neighboring woodlands in central France. The ticks were tested by PCR of pools of nymphs and individual adults. The individual infection prevalence was modeled using multivariate regression. The highest infection prevalences were found in adult females collected in woodland sites for B. burgdorferi sensu lato and A. phagocytophilum

(16.1% and 10.7%, respectively) and in pasture sites for Rickettsia sp. (8.7%). The infection prevalence in nymphs was lower than 6%. B. burgdorferi sensu lato was more prevalent in woodlands than in pastures. Forest fragmentation favored B. burgdorferi sensu lato and A. phagocytophilum prevalence in woodlands, and in pastures, the B. burgdorferi sensu lato prevalence was favored by shrubby vegetation. Both results are probably because large amounts of edges or shrubs increase the abundance of small vertebrates as reservoir hosts. The Rickettsia sp. prevalence was maximal on pasture with medium forest fragmentation. Female ticks were more infected by B. burgdorferi sensu lato than males and nymphs in woodland sites, which suggests an interaction between the ticks and the bacteria. This study confirms the complexity of the tick-borne pathogen ecology. The findings support the importance of small vertebrates as reservoir hosts and make a case for further studies in Europe on the link between the composition of the reservoir host community and the infection prevalence in ticks.

Halos, L., I. Lebert, et al. (2013). "Questionnaire-based survey on distribution and clinical incidence of canine babesiosis in France." Bmc Veterinary Research 9.

Background: The causative agent of canine babesiosis is the protozoan Babesia canis, transmitted by the tick Dermacentor reticulatus within France. While the parasite can be found everywhere in France however cases of infection are associated with distinct geographical foci. The aim of the study was to evaluate the clinical occurrence of canine babesiosis diagnosed in veterinary clinics in order to propose an updated map of the disease distribution in France. Results: Questionnaires were sent via email to all canine veterinary clinics in continental France. Information collected included the number of babesiosis cases diagnosed in 2010, the number of veterinary practitioners and the location of the clinic. The total number of dogs and practitioners per administrative department were used to define the reference population. The annual incidence rate of canine babesiosis per department was calculated as the ratio between the number of babesiosis cases reported by the clinics and the total number of dogs in the clinics of the same department. Data were geo-referenced for map construction (Quantum GIS version 1.7.4). The overall annual incidence rate of clinical babesiosis among the surveyed population was 1.07% (CI95 1.05-1.09) with geographical variations between departments, ranging from 0.01% to 16.05%. Four enzootic areas were identified: South-West, Center, East and Paris area. The South-West region should be considered as a hyper-enzootic area with the higher incidence rates. Conclusion: Our results confirmed the burden of canine babesiosis in France. In the context of tick-borne disease emergence in Europe, the risk for canine babesiosis may become more significant in other European countries in the coming years.

Halos, L., A. Thebault, et al. (2010). "An innovative survey underlining the significant level of contamination by Toxoplasma gondii of ovine meat consumed in France." International Journal for Parasitology 40(2): 193-200.

Consumption of sheep meat presents a risk of human contamination by Toxoplasma gondii. A nationwide study was conducted in France to evaluate the prevalence of Toxoplasma in fresh ovine meat. A sampling procedure was established to guarantee the representativity of consumption. As is

the case for meat consumed, half of the samples were from France and half were imported from other countries. Animals were selected according to their age, as lamb (<12 months) represents 90% of the meat consumed. Available data for French samples allowed the selection of 16 districts distributed in seven areas according to their density of production. Diaphragms and hearts from 433 sheep were collected. Diaphragms were collected from 398 imported carcasses. Fluids from hearts and diaphragms were tested serologically. All hearts were bioassayed in mice and parasite isolates were genotyped using PCR-restriction fragment length polymorphism and microsatellite markers. Prevalence estimates were calculated, taking into account uneven distribution of production and age. For French meat, the effect of area, age and their interactions was evaluated. The overall estimate of Toxoplasma seroprevalence was 17.7% (11.6-31.5%) for lambs and 89% (73.5-100%) for adults ($P < 0.0001$). No significant difference was observed between imported and French meat. In France, seroprevalence in lambs showed an increasing North-western to Southern gradient. The proportion of French carcasses carrying live parasites according to bioassay results Was estimated at 5.4% (3-7.5%) (45 genotype II; one genotype III). This study offers an accurate drawing of the toxoplasmosis pattern amongst sheep consumed in France and a model for a zoonosis hazard control survey.

Halos, L., G. Vourc'h, et al. (2006). Prevalence of Anaplasma phagocytophilum, Rickettsia sp and Borrelia burgdorferi sensu lato DNA in questing Ixodes ricinus ticks from France. Century of Rickettsiology: Emerging, Reemerging Rickettsioses, Molecular Diagnostics, and Emerging Veterinary Rickettsioses. K. E. Hechemy, J. A. Oteo, D. A. Raoult, D. J. Silverman and J. R. Blanco. 1078: 316-319.

A total of 4701 Ixodes ricinus, collected during the summer of 2003, were analyzed for three pathogens. DNA was detected from the three pathogens. Co-detection of more than one pathogen was observed.

Hugnet, C., B. Marrou, et al. (2009). "Osteomyelitis and discospondylitis due to Scedosporium apiospermum in a dog." Journal of Veterinary Diagnostic Investigation 21(1): 120-123.

A 6-year-old, 30-kg, female German Shepherd Dog, living in a leishmaniasis enzootic area, was presented with a severe rear limb motor disorder and a medical history of acute onset of fever. Routine hematology indicated neutrophilia. Spinal survey radiographs were consistent with osteomyelitis and discospondylitis. Because of the poor clinical prognosis and the painful nature of the lesions, the dog was euthanized at the owners' request. At necropsy, T13-L1 vertebrae had large areas of necrosis within the vertebral bodies. Histopathological findings were consistent with chronic, severe, fungal osteomyelitis and discospondylitis. Polymerase chain reaction identified Scedosporium apiospermum, a eutrophic filamentous fungus now recognized as an emerging agent of severe infections in immunosuppressed human patients.

Inoue, K., H. Kabeya, et al. (2010). "Bartonella japonica sp nov and Bartonella silvatica sp nov., isolated from Apodemus mice." International Journal of Systematic and Evolutionary Microbiology 60: 759-763.

Two bacterial strains, Fuji 18-1(T) and Fuji 23-1(T), were isolated from the blood of the small Japanese field mouse (Apodemus argenteus) and the large Japanese field mouse (Apodemus speciosus), respectively, specimens of which were captured in the forest of Mount Fuji, Japan. Phenotypic characterization (growth conditions, incubation periods, biochemical properties and cell morphologies), DNA G+C contents (40.1 mol% for strain Fuji 18-1(T) and 40.4 mol% for strain Fuji 23-1T) and sequence analyses of the 16S rRNA genes indicated that both strains were members of the genus Bartonella. Using rpoB and gltA sequencing analysis, the highest sequence similarities between strains Fuji 18-1(T), Fuji 23-1(T) and other recognized species of the genus Bartonella showed values considerably lower than 91.4% and 89.9% in the rpoB gene and 89.1% and 90.4% in the gltA gene, respectively. It is known that similarities of 95.4% for the rpoB gene and 96.0% for the gltA gene can be applied as cut-off values for the designation of novel species of the genus Bartonella. In a phylogenetic tree based on the merged set of concatenated sequences of seven loci [16S rRNA, ftsZ, gltA, groEL, ribC and rpoB genes and the intergenic spacer region (ITS)], strains Fuji 18-1(T) and Fuji 23-1(T) formed a distinct clade from other recognized species of the genus Bartonella. These data support the classification of strains Fuji 18-1(T) and Fuji 23-1T as novel species of the genus Bartonella. The names Bartonella japonica sp. nov. and Bartonella silvatica sp. nov. are proposed for these novel species. The type strains of Bartonella japonica sp. nov. and Bartonella silvatica sp. nov. are Fuji 18-1(T) (=JCM 15567(T)=CIP 109861(T)) and Fuji 23-1(T) (=JCM 15566(T)=CIP 109862(T)), respectively.

Khoufache, K., O. Cabaret, et al. (2010). "Primary in vitro culture of porcine tracheal epithelial cells in an air-liquid interface as a model to study airway epithelium and Aspergillus fumigatus interactions." Medical Mycology 48(8): 1049-1055.

Since the airway epithelium is the first tissue encountered by airborne fungal spores, specific models are needed to study this interaction. We developed such a model using primary porcine tracheal epithelial cells (PTEC) as a possible alternative to the use of primary human cells. PTEC were obtained from pigs and were cultivated in an air-liquid interface. Fluorescent brightener was employed to quantify the internalization of Aspergillus fumigatus conidia. Potential differences (Vt) and transepithelial resistances (Rt) after challenge with the mycotoxin, verruculogen, were studied. Primers for porcine inflammatory mediator genes IL-8, TNF-alpha, and GM-CSF were designed for a quantitative real-time PCR procedure to study cellular responses to challenges with A. fumigatus conidia. TEM showed the differentiation of ciliated cells and the PTEC ability to internalize conidia. The internalization rate was 21.9 +/- 1.4% after 8 h of incubation. Verruculogen (10<SU-6</SU M) significantly increased Vt without having an effect on the Rt. Exposure of PTEC to live A. fumigatus conidia for 24 h induced a 10- to 40-fold increase in the mRNA levels of inflammatory mediator genes. PTEC behave similarly to human cells and are therefore a suitable alternative to human cells for studying interaction between airway epithelium and A. fumigatus.</.

Kopetz, S., M. M. Mita, et al. (2008). "First in human phase I study of BSI-201, a small molecule inhibitor of poly ADP-ribose polymerase (PARP) in subjects with advanced solid tumors." Journal of Clinical Oncology 26(15).

Krief, S., A. Jamart, et al. (2008). "Clinical and pathologic manifestation of oesophagostomosis in African great apes: does self-medication in wild apes influence disease progression?" Journal of Medical Primatology 37(4): 188-195.

Nodular worms (Oesophagostomum spp.) are common intestinal parasites found in cattle, pig, and primates including humans. In human, they are responsible for serious clinical disease called oesophagostomosis resulting from the formation of granulomas, caseous lesions or abscesses in intestinal walls. In wild great apes, the fecal prevalence of this parasite is high, but little information is available concerning the clinical signs and lesions associated. In the present study, we describe six cases of multinodular oesophagostomosis in free-ranging and ex-captive chimpanzees and captive gorillas caused by Oesophagostomum stephanostomum. While severe clinical signs associated with this infection were observed in great apes raised in sanctuaries, nodules found in wild chimpanzees do not seem to affect their health status. One hypothesis to explain this difference would be that in wild chimpanzees, access to natural environment and behavior such as rough leaves swallowing combined with ingestion of plants having pharmacological properties would prevent severe infection and decrease potential symptoms.

Krief, S., B. Vermeulen, et al. (2010). "Nodular Worm Infection in Wild Chimpanzees in Western Uganda: A Risk for Human Health?" Plos Neglected Tropical Diseases 4(3).

This study focused on Oeosophagostomum sp., and more especially on O. bifurcum, as a parasite that can be lethal to humans and is widespread among humans and monkeys in endemic regions, but has not yet been documented in apes. Its epidemiology and the role played by non-human primates in its transmission are still poorly understood. O. stephanostomum was the only species diagnosed so far in chimpanzees. Until recently, O. bifurcum was assumed to have a high zoonotic potential, but recent findings tend to demonstrate that O. bifurcum of non-human primates and humans might be genetically distinct. As the closest relative to human beings, and a species living in spatial proximity to humans in the field site studied, Pan troglodytes is thus an interesting host to investigate. Recently, a role for chimpanzees in the emergence of HIV and malaria in humans has been documented. In the framework of our long-term health monitoring of wild chimpanzees from Kibale National Park in Western Uganda, we analysed 311 samples of faeces. Coproscopy revealed that high-ranking males are more infected than other individuals. These chimpanzees are also the more frequent cropraiders. Results from PCR assays conducted on larvae and dried faeces also revealed that O. stephanostomum as well as O. bifurcum are infecting chimpanzees, both species co-existing in the same individuals. Because contacts between humans and great apes are increasing with ecotourism and forest fragmentation in areas of high population density, this paper emphasizes that the presence of potential zoonotic parasites should be viewed as a major concern for public health. Investigations of the parasite status of people living around the park or working inside as well as sympatric non-human primates should be planned, and further research might reveal this as a promising aspect of efforts to reinforce measures against crop-raiding.

Lacour, S. A., A. Heckmann, et al. (2013). "Freeze-tolerance of Trichinella muscle larvae in experimentally infected wild boars." Veterinary Parasitology 194(2-4): 175-178.

Freeze-tolerance of encapsulated Trichinella muscle larvae (ML) is mainly determined by Trichinella species, but is also influenced by host species, the age of the infection and the storage time and temperature of the infected meat. Moreover, the freeze-tolerance of the encapsulated species appears to be correlated to the development of thick capsule walls which increases with age. An extended infection period and the muscle composition in some hosts (e.g. herbivores) may provide freeze-avoiding matrices due to high carbohydrate contents. The present experiment compares freeze-tolerance of Trichinella spiralis and Trichinella britovi ML in wild boar meat 24 weeks post inoculation (wpi). Three groups of four wild boars were infected with 200, 2000 or 20,000 ML of T. britovi (ISS 1575), respectively. Additionally, three wild boars were inoculated with 20,000 ML of T. spiralis (ISS 004) and two animals served as negative controls. All wild boars were sacrificed 24 wpi. Muscle samples of 70 g were stored at -21 degrees C for 19,30 and 56h, and for 1-8 weeks. Larvae were recovered by artificial digestion. Their mobilities were recorded using Saisam (R) image analysis software and their infectivities were evaluated using mouse bioassays. Samples frozen for 19, 30 and 56 h allowed recovery of mobile ML, but samples frozen for 1 or 2 weeks did not. Correspondingly, only T. spiralis and T. britovi larvae isolated from wild boar meat frozen for 19,30 and 56 h established in mice. This study showed that freezing at -21 degrees C for 1 week inactivated T. spiralis and T. britovi ML encapsulated in wild boar meat for24 weeks.

Laloy, E., E. Petit, et al. (2009). "Dynamics of natural infection by Anaplasma phagocytophilum in a dairy cattle herd in Brittany, France." Clinical Microbiology and Infection 15: 24-25.

Laloy, E., E. Petit, et al. (2009). "First detection of Anaplasma phagocytophilum-like DNA in the French izard Rupricapra pyrenaica." Clinical Microbiology and Infection 15: 26-27.

Le Joncour, A., S. A. Lacour, et al. (2012). "Case Report: Molecular Characterization of Ancylostoma braziliense Larvae in a Patient with Hookworm-Related Cutaneous Larva Migrans." American Journal of Tropical Medicine and Hygiene 86(5): 843-845.

We report a case of hookworm-related cutaneous larva migrans diagnosed microscopically. Viable hookworm larvae were found by microscopic examination of a skin scraping from follicular lesions. Amplification and sequencing of the internal transcribed spacer 2 allowed the specific identification of the larvae as Ancylostoma braziliense.

Li, W. H., W. Z. Jia, et al. (2013). "Molecular Characterization of Taenia multiceps Isolates from Gansu Province, China by Sequencing of Mitochondrial Cytochrome C Oxidase Subunit 1." Korean Journal of Parasitology 51(2): 197-201.

A total of 16 Taenia multiceps isolates collected from naturally infected sheep or goats in Gansu Province, China were characterized by sequences of mitochondrial cytochrome c oxidase subunit 1 (cox1) gene. The complete cox1 gene was amplified for individual T multiceps isolates by PCR, ligated to pMD18T vector, and sequenced. Sequence analysis indicated that out of 16 T multiceps isolates 10 unique cox1 gene sequences of 1,623 bp were obtained with sequence variation of 0.12-0.68%. The results showed that the cox1 gene sequences were highly conserved among the examined T multiceps isolates. However, they were quite different from those of the other Taenia species. Phylogenetic analysis based on complete cox1 gene sequences revealed that T. multiceps isolates were composed of 3 genotypes and distinguished from the other Taenia species.

Liu, M. F., E. Bouhsira, et al. (2013). "The Bartonella henselae SitABCD transporter is required for confronting oxidative stress during cell and flea invasion." Research in Microbiology 164(8): 827-837.

Bartonella henselae is a zoonotic pathogen that possesses a flea-cat-flea transmission cycle and causes cat scratch disease in humans via cat scratches and bites. In order to establish infection, B. henselae must overcome oxidative stress damage produced by the mammalian host and arthropod vector. B. henselae encodes for putative Fe2+ and Mn2+ transporter SitABCD. In B. henselae, SitAB knockdown increases sensitivity to hydrogen peroxide. We consistently show that SitAB knockdown decreases the ability of B. henselae to survive in both human endothelial cells and cat fleas, thus demonstrating that the SitABCD transporter plays an important role during the B. henselae infection cycle.

Liu, M. F., H. J. Boulouis, et al. (2012). "Heme Degrading Protein HemS Is Involved in Oxidative Stress Response of Bartonella henselae." Plos One 7(5).

Bartonellae are hemotropic bacteria, agents of emerging zoonoses. These bacteria are heme auxotroph Alphaproteobacteria which must import heme for supporting their growth, as they cannot synthesize it. Therefore, Bartonella genome encodes for a complete heme uptake system allowing the transportation of this compound across the outer membrane, the periplasm and the inner membranes. Heme has been proposed to be used as an iron source for Bartonella since these bacteria do not synthesize a complete system required for iron Fe3+ uptake. Similarly to other bacteria which use heme as an iron source, Bartonellae must transport this compound into the cytoplasm and degrade it to allow the release of iron from the tetrapyrrole ring. For Bartonella, the gene cluster devoted to the synthesis of the complete heme uptake system also contains a gene encoding for a polypeptide that shares homologies with heme trafficking or degrading enzymes. Using complementation of an E. coli mutant strain impaired in heme degradation, we demonstrated that HemS from Bartonella henselae expressed in E. coli allows the release of iron from heme. Purified HemS from B. henselae binds heme and can degrade it in the presence of a suitable electron donor, ascorbate or NADPH-cytochrome P450 reductase. Knocking down the expression of HemS in B. henselae reduces its ability to face H2O2 induced oxidative stress.

Liu, M. F., S. Cescau, et al. (2012). "Identification of a novel nanoRNase in Bartonella." Microbiology-Sgm 158: 886-895.

In Escherichia coli, only one essential oligoribonuclease (Orn) can degrade oligoribonucleotides of five residues and shorter in length (nanoRNA). In Bacillus subtilis, NrnA and NrnB, which do not show any sequence similarity to Orn, have been identified as functional analogues of Orn. Sequence comparisons did not identify orn, nrnA or nrnB homologues in the genomes of the Chlamydia/Cyanobacteria and Alphaproteobacteria family members. Screening a genomic library from Bartonella birtlesii, a member of the Alphaproteobacteria, for genes that can complement a conditional orn mutant. in E. coli, we identified BA0969 (NrnC) as a functional analogue of Orn. NrnC is highly conserved (more than 80% identity) in the Bartonella genomes sequenced to date. Biochemical characterization showed that this protein exhibits oligo RNA degradation activity (nanoRNase activity). Like Orn from E. coli, NrnC is inhibited by micromolar amounts of 3'-phosphoadenosine 5'-phosphate in vitro. NrnC homologues are widely present in genomes of Alphaproteobacteria. Knock down of nrnC decreases the growth ability of Bartonella henselae, demonstrating the importance of nanoRNase activity in this bacterium.

Liu, M. F., Y. Ferrandez, et al. (2012). "Heme Binding Proteins of Bartonella henselae Are Required when Undergoing Oxidative Stress During Cell and Flea Invasion." Plos One 7(10).

Bartonella are hemotropic bacteria responsible for emerging zoonoses. These heme auxotroph alphaproteobacteria must import heme for their growth, since they cannot synthesize it. To import exogenous heme, Bartonella genomes encode for a complete heme uptake system enabling transportation of this compound into the cytoplasm and degrading it to release iron. In addition, these bacteria encode for four or five outer membrane heme binding proteins (Hbps). The structural genes of these highly homologous proteins are expressed differently depending on oxygen, temperature and heme concentrations. These proteins were hypothesized as being involved in various cellular processes according to their ability to bind heme and their regulation profile. In this report, we investigated the roles of the four Hbps of Bartonella henselae, responsible for cat scratch disease. We show that Hbps can bind heme in vitro. They are able to enhance the efficiency of heme uptake when co-expressed with a heme transporter in Escherichia coli. Using B. henselae Hbp knockdown mutants, we show that these proteins are involved in defense against the oxidative stress, colonization of human endothelial cell and survival in the flea.

Liu, M. F., X. P. Wu, et al. (2008). "The functions of deoxyribonuclease II in immunity and development." DNA and Cell Biology 27(5): 223-228.

Apoptosis, which is usually accompanied by DNA degradation, is important not only for the homeostasis of metazoans but also for mammalian development. If DNA is not properly degraded in these processes, it can cause diverse diseases, such as anemia, cataracts, and some autoimmune diseases. A large effort has been made to identify these nucleases that are responsible for these effects. In contrast to Deoxyribonuclease I (DNase I), Deoxyribonuclease II (DNase II) has been less well characterized in these processes. Additionally, enzymes of DNase II family in Trichinella spiralis,

which is an intracellular parasitic nematode, are also considered involved in the development of the nematode. We have compiled information from studies on DNase II from various organisms and found some nonclassic features in these enzymes of T. spiralis. Here we have reviewed the characterization and functions of DNase II in these processes and predicted the functions of these enzymes in T. spiralis during host invasion and development.

Liu, P., X. P. Wu, et al. (2013). "Screening of early antigen genes of adult-stage Trichinella spiralis using pig serum from different stages of early infection." Veterinary Parasitology 194(2-4): 222-225.

The goal of this work was to identify novel, early antigens present in Trichinella spiralis. To this end, a cDNA library generated from 3-day old adult worms (Ad3) was immunologically screened using serum from a pig infected with 20,000 muscle larvae. The serum was obtained from multiple, time course bleeds coinciding with early worm development: Seventeen positive clones were isolated using serum obtained at 20 days post infection (dpi). All clones corresponded to one gene that exhibited high sequence identity with the T. spiralis ATP-dependent RNA helicase DDX19B which is involved in parasite growth and development. In addition, nine additional positive clones representing 5 unique genes were identified when the library was screened with 30 dpi serum; four of these five genes displayed high similarity with members of a putative T. spiralis serine protease family known to be involved in host invasion and host-parasite interactions. The remaining gene aligned with the T. spiralis hypothetical ORF 11.30. The identification of these antigens provides potential candidates for the early diagnosis of trichinellosis and for the development of a vaccine against this parasite.

Lortholary, O., J. P. Gangneux, et al. (2011). "Epidemiological trends in invasive aspergillosis in France: the SAIF network (2005-2007)." Clinical Microbiology and Infection 17(12): 1882-1889.

A prospective (20052007) hospital-based multicentre surveillance of EORTC/MSG-proven or probable invasive aspergillosis (IA) cases whatever the underlying diseases was implemented in 12 French academic hospitals. Admissions per hospital and transplantation procedures were obtained. Cox regression models were used to determine risk factors associated with the 12-week overall mortality. With 424 case-patients included, the median incidence/hospital was 0.271/103 admissions (range 0.0720.910) without significant alteration of incidence and seasonality over time. Among the 393 adults (62% men, 56 years (1684 years)), 15% had proven IA, 78% haematological conditions, and 92.9% had lung involvement. Acute leukaemia (34.6%) and allogeneic stem cell transplantation (21.4%) were major host factors, together with chronic lymphoproliferative disorders (21.6%), which emerged as a new high-risk group. The other risk host factors consisted of solid organ transplantation (8.7%), solid tumours (4.3%), systemic inflammatory diseases (4.6%) and chronic respiratory diseases (2.3%). Serum galactomannan tests were more often positive (=69%) for acute leukaemia and allogeneic stem cell transplantation than for the others (<42%; p <10-3). When positive (n = 245), cultures mainly yielded Aspergillus fumigatus (79.7%). First-line antifungal therapy consisted of voriconazole, caspofungin, lipid formulations of amphotericin, or any combination therapy (52%, 14%, 8% and 19.9%, respectively). Twelve-week overall mortality was 44.8% (95% CI, 39.850.0); it was 41% when first-line therapy included voriconazole and 60% otherwise (p <0.001). Independent

factors for 12-week mortality were older age, positivity for both culture and galactomannan and central nervous system or pleural involvement, while any strategy containing voriconazole was protective.

Luo, H. J., W. Y. Huang, et al. (2011). "The absence of MyD88 has no effect on the induction of alternatively activated macrophage during Fasciola hepatica infection (Retracted article. See vol. 13, 3, 2011)." Bmc Immunology 12.

Background: Alternatively activated macrophages (AAM phi) play important roles in allergies and responses to parasitic infections. However, whether signaling through toll-like receptors (TLRs) plays any role in AAM phi induction when young Fasciola hepatica penetrates the liver capsule and migrates through the liver tissue is still unclear. Results: The data show that the lack of myeloid differentiation factor 88 (MyD88) has no effect on the AAM phi derived from the bone marrow (BMM phi) in vitro and does not impair the mRNA expression of arginase-1, resistin-like molecule (RELM alpha), and Ym1 in BMM phi s. The Th2 cytokine production bias in splenocytes was not significantly altered in F. hepatica-infected mice in the absence of MyD88 in vitro and in the pleural cavity lavage in vivo. In addition, MyD88-deficiency has no effect on the arginase production of the F. hepatica elicited macrophages (Fe M phi s), production of RELM alpha and Ym1 proteins and mRNA expression of Ym1 and RELM alpha of macrophages in the peritoneal cavity 6 weeks post F. hepatica infection. Conclusions: The absence of MyD88 has no effect on presence of AAM phi 6 weeks post F. hepatica infection.

Luo, H. L., W. Y. Huang, et al. (2012). "The absence of MyD88 has no effect on the induction of alternatively activated macrophage during Fasciola hepatica infection (Retraction of vol 12, 63, 2011)." Bmc Immunology 13.

Machado, M. L. S., L. Ferreiro, et al. (2011). "Malassezia dermatitis in dogs in Brazil: diagnosis, evaluation of clinical signs and molecular identification." Veterinary Dermatology 22(1): 46-52.

Skin carriage and quantification of Malassezia yeasts were evaluated in 180 healthy dogs (group 1) and 117 dogs with clinical signs (pruritus, erythema, lichenification/seborrhoea, excoriations and alopecia) that could be related to Malassezia dermatitis (group 2) in Brazil. The lesions in the group 2 dogs were evaluated using CADESI-03 scores. Samples were collected from five different anatomical areas. Direct examination was performed using the tape strip technique, and results were expressed as the mean number of yeasts per x1000 microscopic field per dog. For mycological culture, a single piece of sterilized carpet was applied to the same areas sampled for cytology, and transferred onto Dixon's modified medium. Yeast populations were expressed as mean colony forming units (CFU)/plate. Malassezia isolates were characterized by polymerase chain reaction-restriction endonuclease analysis of the large subunit (LSU) of ribosomal RNA gene. The probability of culturing Malassezia from dogs with skin lesions was significantly higher ($P < 0.001$) than from healthy dogs. There was a linear trend between CADESI-03 score and mean CFU/plate. Group 2 dogs with positive cultures had higher CADESI-03 scores than those with negative cultures (P

< 0.05). Almost all isolates were identified as Malassezia pachydermatis. Only one isolate (group 2) was identified as Malassezia furfur. These data suggest that dogs with skin disorders harbouring Malassezia yeasts in quantities higher than 120 mean CFU/plate should be considered as having Malassezia dermatitis. The presence of Malassezia appears to exacerbate clinical lesions in dogs.

Mahany, J. J., N. Lewis, et al. (2008). "A phase IB study evaluating BSI-201 in combination with chemotherapy in subjects with advanced solid tumors." Journal of Clinical Oncology 26(15).

Maillard, R., B. Grimard, et al. (2006). "Effects of cow age and pregnancy on Bartonella infection in a herd of dairy cattle." Journal of Clinical Microbiology 44(1): 42-46.

Bartonella spp. are small hemotropic bacteria infecting mammals. Four Bartonella species have been recently described in cattle and wild ruminants. To date, the biology and possible pathogenic role of Bartonella species isolated from ruminants are poorly understood. Therefore, a dairy herd of 448 cows and heifers was surveyed in order to establish the prevalence of Bartonella bovis and B. chomelii infections, the level of bacteremia, and the relationship between bacteremia and age or pregnancy status. The putative impact of Bartonella infection on production performance (individual milk cell count, milk yield) and reproductive status (success of artificial insemination [AI], placental retention, embryonic death, and abortion) was also assessed. The overall mean prevalence of B. bovis bacteremia was 59%, with the highest prevalence in heifers (92.5%). No B. chomelii was isolated, and 95% (114/120) of the B. bovis strains isolated and tested by PCR-restriction fragment length polymorphism belonged to type I. The level of bacteremia was higher in pregnant cows than in nonpregnant cows (P = 0.05), and the level of bacteremia rose during the last two-thirds of gestation (P < 0.001). There was no correlation between bacteremia and milk yield, individual milk cell count, success of first AI, interval between two calvings, or incidence of abortion and embryonic death. The interval from calving to first AI was shorter and the incidence of placental retention was lower in bacteremic animals than in nonbacteremic ones (P = 0.03 and P = 0.01, respectively).

Marignac, G., F. Barrat, et al. (2010). "Murine model for Bartonella birtlesii infection: New aspects." Comparative Immunology Microbiology and Infectious Diseases 33(2): 95-107.

As a model of persistent infection, various aspects of Bartonella birtlesii infection in laboratory mice, including some immunodeficient mice, are presented, particularly focusing on conditions mimicking natural infection. Bacteraemia was explored using different mice strains routes and inoculum doses (3.4-5 x 10(7) CFU/mouse). Mice became bacteraemic for 5 (C57B16/6) to 10 weeks (Balb/c, Swiss) with peaks ranging from 2 x 103 to 105 CFU/mL of blood. The ID route induced the most precocious bacteraemia (day 3) while the higher and longer bacteraemia in immunocompetent mice was obtained with SC when infecting Balb/c with approximately 10(3) CFU/mouse. As opposed to ID, SC and IV routes, bacteraemia was obtained with the oral and ocular routes only for high doses (10(7)) and in 33-66% mice. It was significantly higher and longer in CD4-/- mice compared to CD8-/- and double KO mice at most time points. CD8-/- mice and the control

group had near to superimposed kinetics. These results confirm the relevance of the present model.

Masi, S., S. Chauffour, et al. (2012). "Seasonal Effects on Great Ape Health: A Case Study of Wild Chimpanzees and Western Gorillas." Plos One 7(12).

Among factors affecting animal health, environmental influences may directly or indirectly impact host nutritional condition, fecundity, and their degree of parasitism. Our closest relatives, the great apes, are all endangered and particularly sensitive to infectious diseases. Both chimpanzees and western gorillas experience large seasonal variations in fruit availability but only western gorillas accordingly show large changes in their degree of frugivory. The aim of this study is to investigate and compare factors affecting health (through records of clinical signs, urine, and faecal samples) of habituated wild ape populations: a community (N = 46 individuals) of chimpanzees (Pan troglodytes) in Kanyawara, Kibale National Park (Uganda), and a western gorilla (G. gorilla) group (N = 13) in Bai Hokou in the Dzanga-Ndoki National Park (Central African Republic). Ape health monitoring was carried out in the wet and dry seasons (chimpanzees: July-December 2006; gorillas: April-July 2008 and December 2008-February 2009). Compared to chimpanzees, western gorillas were shown to have marginally greater parasite diversity, higher prevalence and intensity of both parasite and urine infections, and lower occurrence of diarrhea and wounds. Parasite infections (prevalence and load), but not abnormal urine parameters, were significantly higher during the dry season of the study period for western gorillas, who thus appeared more affected by the large temporal changes in the environment in comparison to chimpanzees. Infant gorillas were the most susceptible among all the age/sex classes (of both apes) having much more intense infections and urine blood concentrations, again during the dry season. Long term studies are needed to confirm the influence of seasonal factors on health and parasitism of these great apes. However, this study suggest climate change and forest fragmentation leading to potentially larger seasonal fluctuations of the environment may affect patterns of ape parasitism and further exacerbate health impacts on great ape populations that live in highly seasonal habitats.

Melisi, D., V. Ossovskaya, et al. (2009). "Oral Poly(ADP-Ribose) Polymerase-1 Inhibitor BSI-401 Has Antitumor Activity and Synergizes with Oxaliplatin against Pancreatic Cancer, Preventing Acute Neurotoxicity." Clinical Cancer Research 15(20): 6367-6377.

Purpose: Development of novel agents and drug combinations are urgently needed for treatment of pancreatic cancer. Oxaliplatin belongs to an important class of DNA-damaging organoplatinum agents, useful in pancreatic cancer therapy. However, increased ability of cancer cells to recognize and repair DNA damage enables resistance to these agents. Poly (ADP ribose) polymerase-1 is a sensor of DNA damage with key roles in DNA repair. Here, we report the therapeutic activity of the poly (ADP ribose) polymerase-1 inhibitor BSI-401, as a single agent and in combination with oxaliplatin in orthotopic nude mouse models of pancreatic cancer, and its effect on oxaliplatin-induced acute neurotoxicity. Experimental Design: We determined in vitro the effect of BSI-401 and its synergism with oxaliplatin on the growth of pancreatic cancer cells. Activity of different dosages of parenteral and oral BSI-401, alone and in combination with oxaliplatin, was

evaluated in orthotopic nude mouse models with luciferase-expressing pancreatic cancer cells. The effect of BSI-401 in preventing oxaliplatin-induced acute cold allodynia was measured in rats using a temperature-control led plate. Results: BSI-401 alone and in synergism with oxaliplatin significantly inhibited the growth of pancreatic cancer cells in vitro. In nude mice, i.p. [200 mg/kg once a week (QW) x 4] and oral [400 mg/kg days 1-5 of each week (QD5 + R2) x 4] administration of BSI-401 significantly reduced tumor burden and prolonged survival (46 versus 144 days, P = 0.0018; 73 versus 194 days, P = 0.0017) compared with no treatment. BSI-401 combined with oxaliplatin had potent synergistic antitumor activity (46 versus 132 days, P = 0.0063), and significantly (P = 0.0148) prevented acute oxaliplatin-induced neurotoxicity. Conclusions: BSI-401, alone or in combination with oxaliplatin, is a promising new therapeutic agent that warrants further evaluation for treatment of pancreatic cancer. (Clin Cancer Res 2009;15(20):6367-77)

Michelet, L., S. Bonnet, et al. (2013). "Discriminating Francisella tularensis and Francisella-like endosymbionts in Dermacentor reticulatus ticks: Evaluation of current molecular techniques." Veterinary Microbiology 163(3-4): 399-403.

Francisella tularensis, the causative agent of tularemia, is commonly transmitted by ticks. To ensure accurate F. tularensis reporting rates in epidemiological surveys, specific discrimination between F. tularensis and Francisella-like tick endosymbionts (FLEs) is absolutely critical. Four molecular available techniques capable of distinguishing Francisella spp. were compared here for the first time in French Dermacentor reticulatus ticks in order to estimate their specificity as well as their ease and speed of use. Results showed that tul4 and fopA real-time PCR assays can easily and effectively discriminate between F. tularensis and FLEs in D. reticulatus. In addition, a high prevalence of FLEs in D. reticulatus collected in France was reported by the use of fopA real-time PCR assay (79%). Finally, phylogenetic analysis showed that FLEs isolated from D. reticulatus correspond to a well-defined group compared to FLEs originating from various tick species.

Moutailler, S., B. Roche, et al. (2011). "Host Alternation Is Necessary to Maintain the Genome Stability of Rift Valley Fever Virus." Plos Neglected Tropical Diseases 5(5).

Background: Most arthropod-borne viruses (arboviruses) are RNA viruses, which are maintained in nature by replication cycles that alternate between arthropod and vertebrate hosts. Arboviruses appear to experience lower rates of evolution than RNA viruses that replicate in a single host. This genetic stability is assumed to result from a fitness trade-off imposed by host alternation, which constrains arbovirus genome evolution. To test this hypothesis, we used Rift Valley fever virus (RVFV), an arbovirus that can be transmitted either directly (between vertebrates during the manipulation of infected tissues, and between mosquitoes by vertical transmission) or indirectly (from one vertebrate to another by mosquito-borne transmission). Methodology/Principal Findings: RVFV was serially passaged in BHK21 (hamster) or Aag2 (Aedes aegypti) cells, or in alternation between the two cell types. After 30 passages, these single host-passaged viruses lost their virulence and induced protective effects against a challenge with a virulent virus. Large deletions in the NSs gene that encodes the virulence factor were detectable from the 15(th) serial passage onwards in

BHK21 cells and from the 10(th) passage in Aag2 cells. The phosphoprotein NSs is not essential to viral replication allowing clones carrying deletions in NSs to predominate as they replicate slightly more rapidly. No genetic changes were found in viruses that were passaged alternately between arthropod and vertebrate cells. Furthermore, alternating passaged viruses presenting complete NSs gene remained virulent after 30 passages. Conclusions/Significance: Our results strongly support the view that alternating replication is necessary to maintain the virulence factor carried by the NSs phosphoprotein.

Negre, A., E. Bensignor, et al. (2009). "Evidence-based veterinary dermatology: a systematic review of interventions for Malassezia dermatitis in dogs." Veterinary Dermatology 20(1): 1-12.

The aim of this systematic review was to evaluate the efficacy of antifungal treatments for Malassezia dermatitis in dogs and, when possible, to propose recommendation for or against their use. Electronic searches were carried out using PubMed MEDLINE (R), CABDirect and CONSULTANT database. The volumes of Advances in Veterinary Dermatology, the proceedings of ESVD/ECVD and AAVD/ACVD congresses were hand-searched for studies relevant to this review. All articles and book chapters discussing treatment of Malassezia dermatitis were scanned for additional citations. Lastly, a request was sent to the Vetderm Listserv to share recent clinical trials. The analysis evaluated study design, methodology quality, subject enrolment quality, type of interventions and outcome measures. The searches identified 35 articles, and 14 trials that fulfilled the following selection criteria: (i) in vivo clinical trials, (ii) dogs showing clinical lesions of Malassezia dermatitis and (iii) enrolment of at least five dogs. Among these, only eight studies fulfilled the following additional criterion: (iv) prospective in vivo clinical trials reporting clinical and mycological outcome measures. A total number of 14 different treatment protocols included four blinded, randomized and controlled trials (quality of evidence grade A), four controlled studies lacking blinding and/or randomization (grade B), five open uncontrolled trials (grade C) and one descriptive study (grade D). This systematic review allowed us to recommend, with good evidence, the use of only one topical treatment of Malassezia dermatitis (2% miconazole nitrate +2% chlorhexidine, twice a week for 3 weeks) and with fair evidence the use of two systemic treatments with azole derivatives (ketoconazole, 10 mg kg(-1) day(-1) and itraconazole, 5 mg kg(-1) day(-1) for 3 weeks).

Nieguitsila, A., P. Arne, et al. (2011). "Relative efficiencies of two air sampling methods and three culture conditions for the assessment of airborne culturable fungi in a poultry farmhouse in France." Environmental Research 111(2): 248-253.

Fungal elements represent a significant part of the biological contaminants that could be detected in the air of animal facilities. The aim of this study was to assess the relative efficiencies of two air sampling methods and three culture conditions for the quantification of airborne culturable fungi in a poultry farmhouse in France. Air samples were collected every week throughout a 15-week period. Two devices were simultaneously used a rotative cup air sampler (CIP 10-M, Arelco, France) and an air sampler based on filtration (Airport MD8, Sartorius, Germany). Culture of airborne viable fungi was performed on malt extract agar (ME) and dichloran glycerol-18 (DG 18) at 25 or 37 C. CIP 10-M and AirPort MD8 were shown to display comparable performances but significant differences

were observed between culture conditions for Aspergillus spp. ($p < 0.01$), Scopulariopsis spp. ($p=0.02$) and unidentified molds ($p < 0.01$).

Nieguitsila, A., O. Goldenberg, et al. (2010). "Molecular monitoring of fungal communities in air samples by denaturing high-performance liquid chromatography (D-HPLC)." Journal of Applied Microbiology 109(3): 910-917.

Aims: To describe a new molecular technique for the assessment of fungal diversity in the air. Methods and Results: Air samples were collected every week in a henhouse in France during a 15-week period. After air sampling, the collecting membrane was diluted, and the liquid was used for subsequent cultivation and molecular analysis: PCR-temperature temporal gradient electrophoresis (TTGE), which has already been used for the identification of fungal species in air samples and PCR-denaturing high-performance liquid chromatography (D-HPLC), a new technique for the analysis of complex microbial populations. D-HPLC profiles were reproducible from run-to-run, and several fungal organisms could be identified at the species level by sequencing. Conclusions: PCR-D-HPLC enabled the identification of fungal species (both Ascomycota and Basidiomycota) that may be encountered in air. The new technique allowed the detection of more fungal species than did the PCR-TTGE technique. However, some fungal species were detected only by PCR-TTGE, suggesting that PCR-D-HPLC and PCR-TTGE are complementary. Significance and Impact of the Study: PCR-D-HPLC represents a considerable saving in time over currently available procedures for detection and identification of fungal organisms in air. However, the fungal diversity detected by PCR-D-HPLC or by PCR-TTGE was lower than that revealed by culture.

Nockler, K., S. Reckinger, et al. (2009). "Comparison of three artificial digestion methods for detection of non-encapsulated Trichinella pseudospiralis larvae in pork." Veterinary Parasitology 159(3-4): 341-344.

In a ring trial involving five laboratories (A, B, C, D, and E), three different methods of artificial digestion were compared for the detection of non-encapsulated Trichinella pseudospiralis larvae in minced meat. Each sample panel consisted often 1 g minced pork samples. All samples in each panel were derived from a bulk meat preparation with a nominal value of either 7 or 17 larvae per g (Ipg). Samples were tested for the number of muscle larvae using the magnetic stirrer method (labs A, B, and E), stomacher method (lab B), and Trichomatic 35 (R) (labs C and D). T. pseudospiralis larvae were found in all 120 samples tested. For samples with 7 Ipg, larval recoveries were significantly higher using the stomacher method versus the magnetic stirrer method, but there were no significant differences for samples with 17 Ipg. In comparing laboratory results irrespective of the method used, lab B detected a significantly higher number of larvae than lab E for samples with 7 Ipg, and lab E detected significantly less larvae than labs A, B, and D in samples with 17 Ipg. The lowest overall variation for quantitative results (i.e. larval recoveries which were outside the tolerance range) was achieved by using the magnetic stirrer method (22%), followed by the stomacher method (25%), and Trichomatic 35 (R) (30%). Results revealed that T. pseudospiralis larvae in samples with a nominal value of 7 and 17 Ipg can be detected by all three methods of artificial digestion.

O'Shaughnessy, J. and A. Blackwood-Chirchir (2011). "Iniparib in Metastatic Triple-Negative Breast Cancer REPLY." New England Journal of Medicine 364(18): 1781-1781.

O'Shaughnessy, J., C. Osborne, et al. (2009). "Final Results of a Randomized Phase II Study Demonstrating Efficacy and Safety of BSI-201, a Poly (ADP-Ribose) Polymerase (PARP) Inhibitor, in Combination with Gemcitabine/Carboplatin (G/C) in Metastatic Triple Negative Breast Cancer (TNBC)." Cancer Research 69(24): 686S-687S.

O'Shaughnessy, J., C. Osborne, et al. (2009). "Efficacy of BSI-201, a poly (ADP-ribose) polymerase-1 (PARP1) inhibitor, in combination with gemcitabine/carboplatin (G/C) in patients with metastatic triple-negative breast cancer (TNBC): results of a randomized phase II trial." Ejc Supplements 7(3): 7-7.

O'Shaughnessy, J., C. Osborne, et al. (2010). "FINAL EFFICACY AND SAFETY RESULTS OF A RANDOMIZED PHASE II STUDY OF THE PARP INHIBITOR INIPARIB (BSI-201) IN COMBINATION WITH GEMCITABINE/CARBOPLATIN (G/C) IN METASTATIC TRIPLE NEGATIVE BREAST CANCER (TNBC)." Annals of Oncology 21: 5-5.

O'Shaughnessy, J., C. Osborne, et al. (2011). "Iniparib plus Chemotherapy in Metastatic Triple-Negative Breast Cancer." New England Journal of Medicine 364(3): 205-214.

Background: Triple-negative breast cancers have inherent defects in DNA repair, making this cancer a rational target for therapy based on poly(adenosine diphosphate-ribose) polymerase (PARP) inhibition. Methods: We conducted an open-label, phase 2 study to compare the efficacy and safety of gemcitabine and carboplatin with or without iniparib, a small molecule with PARP-inhibitory activity, in patients with metastatic triple-negative breast cancer. A total of 123 patients were randomly assigned to receive gemcitabine (1000 mg per square meter of body-surface area) and carboplatin (at a dose equivalent to an area under the concentration-time curve of 2) on days 1 and 8 -- with or without iniparib (at a dose of 5.6 mg per kilogram of body weight) on days 1, 4, 8, and 11 -- every 21 days. Primary end points were the rate of clinical benefit (i.e., the rate of objective response [complete or partial response] plus the rate of stable disease for greater/equal 6 months) and safety. Additional end points included the rate of objective response, progression-free survival, and overall survival. Results: The addition of iniparib to gemcitabine and carboplatin improved the rate of clinical benefit from 34% to 56% (P=0.01) and the rate of overall response from 32% to 52% (P=0.02). The addition of iniparib also prolonged the median progression-free survival from 3.6 months to 5.9 months (hazard ratio for progression, 0.59; P=0.01) and the median overall survival from 7.7 months to 12.3 months (hazard ratio for death, 0.57; P=0.01). The most frequent grade 3 or 4 adverse events in either treatment group included neutropenia, thrombocytopenia, anemia, fatigue or asthenia,

leukopenia, and increased alanine aminotransferase level. No significant difference was seen between the two groups in the rate of adverse events. Conclusions: The addition of iniparib to chemotherapy improved the clinical benefit and survival of patients with metastatic triple-negative breast cancer without significantly increased toxic effects. On the basis of these results, a phase 3 trial adequately powered to evaluate overall survival and progression-free survival is being conducted. (Funded by BiPar Sciences [now owned by Sanofi-Aventis]; ClinicalTrials.gov number, NCT00540358.) N Engl J Med 2011;364:205-14.

O'Shaughnessy, J., M. Telli, et al. (2011). "Phase 3 Study of Iniparib (I) Plus Gemcitabine (G) and Carboplatin (C) in Metastatic Triple-negative Breast Cancer (mTNBC) - Results of an Exploratory Analysis by Prior Therapy." European Journal of Cancer 47: S338-S338.

O'Shaughnessy, J., M. Yoffe, et al. (2009). "Triple negative breast cancer: a phase 2, multi-center, open-label, randomized trial of gemcitabine/carboplatin (G/C), with or without BSI-201, a PARP inhibitor." Cancer Research 69(2): 193S-193S.

Ossovskaya, V. S., G. Dolganov, et al. (2009). "Loss of function genetic screens reveal MTGR1 as an intracellular repressor of beta 1 integrin-dependent neurite outgrowth." Journal of Neuroscience Methods 177(2): 322-333.

Integrins are transmembrane receptors that promote neurite growth and guidance. To identify regulators of integrin-dependent neurite outgrowth. here we used two loss of function genetic screens in SH-SY5Y neuroblastoma cells. First, we screened a genome-wide retroviral library of genetic suppressor elements (GSEs). Among the many genes identified in the GSE screen, we isolated the hematopoetic transcriptional factor MTGR1 (myeloid translocation gene-related protein-1). Treatment of SH-SY5Y cells with MTGR1 siRNA enhanced neurite outgrowth and concurrently increased expression of GAP-43, a protein linked to neurite outgrowth. Second, we transduced SH-SY5Y with a genome-wide GFP-labeled lentiviral siRNA library, which expressed 40,000 independent siRNAs targeting 8500 human genes. From this screen we isolated GFI1 (growth factor independence-1), which, like MTGR1, is a member of the myeloid translocation gene on 8q22 (MTG8)/ETO protein complex of nuclear repressor proteins. These results reveal novel contributions of MTGR1 and GFI1 to the regulation of neurite outgrowth and identify novel repressors of integrin-dependent neurite outgrowth. Published by Elsevier B.V.

Pasquetti, M., Y. Graser, et al. (2012). "Use of microsatellite markers for typing of Microsporum canis isolates causing pseudomycetoma in cats." Mycoses 55: 152-153.

Pastiu, A. I., A. Gyorke, et al. (2013). "In Romania, exposure to Toxoplasma gondii occurs twice as often in swine raised for familial consumption as in hunted wild boar, but occurs rarely, if ever, among fattening pigs raised in confinement." Parasitology Research 112(6): 2403-2407.

A wide range of swine husbandry practices prevail in Romania: pork for human consumption is derived from hunting wild boar, from household rearing of small numbers of backyard pigs, and from indoor, industrial production of swine raised in confinement indoors. Romania thus represents an instructive place for evaluating the influence of animal management on the exposure risk of the zoonotic parasite, Toxoplasma gondii. The fact that many Romanians eat uncooked or undercooked pork, especially when raised for household consumption, elevates the public health imperative to understand these risks. The aim of the study, therefore, was to evaluate the seroprevalence of T. gondii in pigs and wild boars from Romania. During 2008-2010, we collected 3,595 serum samples from pigs (fattening pigs, sows, backyard pigs) and 150 serum samples from wild boars. The sera were assayed by immunofluorescence antibody test (cutoff, 1:32) for antibodies against T. gondii. The overall seroprevalence of T. gondii infection was 23.1 % (829/3,595) in pigs and 16 % (24/150) in wild boars. The seroprevalence was significantly higher ($p < 0.001$) in backyard pigs (30.5 %; 783/2,564) than in sows (12.4 %; 46/371) or fattening pigs (none of the sera was positive). The management system (indoor pigs versus backyard pigs) represented the most important factor in the epidemiology of T. gondii infection. The proximity of backyard pigs to the definitive host of this parasite (cats), as well as their access to contaminated meat products, elevated their exposure risk well above that of pigs raised in confinement, and even above that of wild boars inhabiting sylvatic environments.

Peano, A., M. Pasquetti, et al. (2012). "Antifungal resistance of Malassezia pachydermatis: fact or fiction? Personal contribution and a literature review." Mycoses 55: 155-155.

Pin, D., E. Videmont, et al. (2011). "FIRST DESCRIPTION OF ONYCHOMYCOSIS CAUSED BY CHRYSOSPORIUM KERATINOPHILUM IN CAPTIVE BENNETT'S WALLABIES (MACROPUS RUFOGRISEUS RUFOGRISEUS)." Journal of Zoo and Wildlife Medicine 42(1): 156-159.

Seven Bennett's wallabies (Macropus rufogriseus rufogriseus) presented within a period of several months with onychodystrophy, onychomadesis, and severe digital tumefaction. Histopathologic findings included a pseudocarcinomatous hyperplasia of the claw matrix surrounding a cavity filled with keratin and septate hyphae stained with periodic acid Schiff reagent. The fungal species Chrysosporium keratinophilum was identified on cultures. The wallabies were orally treated with ketoconazole (15 mg/kg s.i.d.) for 20 wk. Material and enclosures were cleaned and sprayed with 0.2% enilconazole solution once a month over a period of 4 mo. No improvement of advanced cases was observed, but no new case appeared for the next 6 mo. The positive Mycological culture and the invasion of tissues on histopathologic examination suggested that the fungal species C. keratinophilum was implicated in this claw disease. This is the first report of onychomycosis caused by C. keratinophilum in animals.

Podsiadly, E., N. Haddad, et al. (2012). "Characterization of Polish feline B. henselae isolates by multiple-locus tandem repeat analysis and pulse-field gel electrophoresis." Annals of Agricultural and Environmental Medicine 19(1): 39-43.

Knowledge about molecular epidemiology of B. henselae is important for recognizing the geographical distribution of strains and identification of isolates virulent for humans. Eleven Polish feline B. henselae isolates were typed, using 2 different techniques: pulse-field gel electrophoresis (PFGE) and multiple-locus variable-number tandem repeat analysis (MLVA). PFGE analysis distinguished 6 different PFGE types, with subtypes within 3 of them, whereas 10 MLVA types were assigned. Global diversity index (D.I.) for MLVA equaled 0.93. For 7 isolates, the results of MLVA confirmed cluster assignments based on PFGE. Both PFGE and MLVA results were in accordance with epidemiological data. Although PFGE has been previously demonstrated to be a suitable method for the differentiation of B. henselae isolates/strains, our results show the superiority of MLVA over PFGE with respect to higher discriminatory power, distinguishing genotypes I and II isolates, easier analysis of results, and possibility to compare the numerical data obtained by different laboratories. With MLVA, 7 new profiles were observed, compared to previous results from around the world; whereas 3 known profiles were previously described mainly in European B. henselae isolates. Our results confirm that some VNTR profiles can be used as specific geographical markers.

Poirel, L., P. Nordmann, et al. (2013). "Extended-Spectrum beta-Lactamase CTX-M-15-Producing Klebsiella pneumoniae of Sequence Type ST274 in Companion Animals." Antimicrobial Agents and Chemotherapy 57(5): 2372-2375.

Screening of extended-spectrum beta-lactamase (ESBL)-producing Gram-negative bacteria in companion animals living in the Paris area in France identified a high rate of CTX-M-15-producing Klebsiella pneumoniae. Those isolates were recovered during the 2010-2011 period from both infections and asymptomatic colonizations. Sequence typing revealed that most of these isolates belonged to sequence type ST274. Interestingly, the bla(CTX-M-15) gene was located on a specific and novel plasmid scaffold. These findings highlight that companion animals may be reservoirs for CTX-M-15-producing K. pneumoniae evolving separately from the human reservoir of CTX-M-15 producers.

Portier, J., D. Jouet, et al. (2011). "NEW DATA IN FRANCE ON THE TREMATODE ALARIA ALATA (GOEZE, 1792) OBTAINED DURING TRICHINELLA INSPECTIONS." Parasite-Journal De La Societe Francaise De Parasitologie 18(3): 271-275.

The trematode Alaria alata is a cosmopolite parasite found in red foxes (Vulpes vulpes), the main definitive host in Europe. In contrast only few data are reported in wild boars (Sus scrofa), a paratenic host. The aim of this paper is to describe the importance and distribution of Alaria alata mesocercariae in wild boars, information is given by findings of these larvae during Trichinella mandatory meat inspection on wild boars' carcasses aimed for human consumption. More than a hundred cases of mesocercariae positive animals are found every year in the East of France. First investigations on the parasite's resistance to deep-freezing in meat are presented in this work.

Portier, J., D. Jouet, et al. (2012). "Detection of Planorbis planorbis and Anisus vortex as first intermediate hosts of Alaria alata (Goeze, 1792) in natural conditions in France: Molecular evidence." Veterinary Parasitology 190(1-2): 151-158.

Alaria alata (Goeze, 1792), a trematode that parasitizes canids, usually needs two intermediate hosts to complete its life cycle: an aquatic freshwater snail and an amphibian. Although many studies have been undertaken on the wild boar's role as paratenic host, owing to the potential threat to human health, few have sought to identify the snails that act as first intermediate hosts in natural conditions. Adopting a molecular approach, with specific markers for a portion of the second internal transcribed spacer (ITS-2), we detected haplotypes of A. alata furcocercariae in two snail species (Planorbis planorbis and Anisus vortex), identified by molecular analysis (ribosomal 18S, mitochondrial 16S and COI). This study provides the first description of snails naturally emitting A. alata furcocercaria in Western Europe.

Richomme, C., E. Afonso, et al. (2010). "Seroprevalence and factors associated with Toxoplasma gondii infection in wild boar (Sus scrofa) in a Mediterranean island." Epidemiology and Infection 138(9): 1257-1266.

Knowledge of the factors affecting the presence of Toxoplasma gondii in wildlife is limited. Here we analyse which local landscape characteristics are associated with the presence of toxoplasmosis in wild boar, Sus scrota, on the island of Corsica, France. Meat juice samples from 1399 wild boars collected during two hunting seasons were tested for T. gondii antibodies using the modified agglutination test (titre 1:4). The overall seroprevalence was 0.55 (95% CI 0.50-0.59) for the first year and 0.33 (95% CI 0.29-0.35) for the second year. Seroprevalence varied according to age and county. At the county level, seropositivity in adults was related to farm density during year 1, and to habitat fragmentation, farm density and altitude during year 2. The exposure of wild boar to T. gondii is thus variable according to landscape characteristics and probably results in a variable risk of transmission of toxoplasmosis to humans.

Rolain, J. M., M. Vayssier-Taussat, et al. (2012). "Genome Sequence of Bartonella birtlesii, a Bacterium Isolated from Small Rodents of the Genus Apodemus." Journal of Bacteriology 194(17): 4779-4779.

Bartonella birtlesii is a facultative intracellular bacterium isolated from the blood of small mammals of the genus Apodemus. The present study reports the draft genome of Bartonella birtlesii strain IBS 135(T) (CIP 106691(T)).

Rolain, J. M., M. Vayssier-Taussat, et al. (2013). "Partial Disruption of Translational and Posttranslational Machinery Reshapes Growth Rates of Bartonella birtlesii." Mbio 4(2).

Specialization of bacteria in a new niche is associated with genome repertoire changes, and speciation in bacterial specialists is associated with genome reduction. Here, we tested a signature-tagged mutant library of 3,456 Bartonella birtlesii clones to detect mutants that could grow rapidly in vitro. Overall, we found 124 mutants that grew faster than the parental wild-type strain in vitro. We sequenced the genomes of the four mutants with the most rapid growth (formed visible colonies in only 1 to 2 days compared with 5 days for the wild type) and compared them to the parental isolate genome. We found that the number of disrupted genes associated with translation in the 124 rapid-growth clones was significantly higher than the number of genes involved in translation in the full genome ($P < 10(-6)$). Analysis of transposon integration in the genome of the four most rapidly growing clones revealed that one clone lacked one of the two wild-type RNA ribosomal operons. Finally, one of the four clones did not induce bacteremia in our mouse model, whereas infection with the other three resulted in a significantly lower bacterial count in blood than that with the wild-type strain. IMPORTANCE Here, we show that specialization in a specific niche could be caused by the disruption of critical genes. Most of these genes were involved in translation, and we show that evolution of obligate parasitism bacteria was specifically associated with disruption of translation system-encoding genes.

Roqueplo, C., L. Halos, et al. (2011). "TOXOPLASMA GONDII IN WILD AND DOMESTIC ANIMALS FROM NEW CALEDONIA." Parasite-Journal De La Societe Francaise De Parasitologie 18(4): 345-348.

Samples (serum or meat juice) collected from 205 animals in New Caledonia in April 2009 were tested for antibodies against Toxoplasma gondii by ELISA using the multi-species ID Screen Toxoplasmosis Indirect kit (IDVET, Montpellier). Antibodies to T. gondii were detected in 2 % (1/49) of the pigs, in 3.3 % (1/30) of the cattle, in 13.8 % (4/29) of Rusa deers, in 16 % (4/25) of the horses, in 32.8 % (21/64) of the dogs, and in 50 % (4/8) of cats. Statistically, no significant difference was observed between T gondii seroprevalence and age or sex. No survey on the prevalence of T gondii in animals has ever been conducted in New Caledonia and this is the first serological evidence of T gondii in Rusa deer (Cervus timorensis russa). These results indicate an important circulation of T gondii exists in the animal populations of New Caledonia. In view of humans being exposed, it is advisable to insist on sanitary education and on respect for good hygienic and food practice.

Roussel, S., G. Reboux, et al. (2012). "Microbiological evaluation of ten French archives and link to occupational symptoms." Indoor Air 22(6): 514-522.

Fungi that damage documents in archives may harm workers health, depending on which mold species are inhaled, the concentrations of fungal species inhaled, and individual factors. Our aim was to identify and quantify fungi in archives and to investigate possible links with the symptoms experienced by workers. Ten French archives were sampled using an air impactor and electrostatic dust collectors. Allergies and general symptoms felt by 144 workers were reported using a self-report questionnaire. Utilizing culture-based analysis methods along with qPCR, Penicillium chrysogenum, Cladosporium sphaerospermum, and Aspergillus versicolor were the three main fungi in air and dust in terms of quantity and frequency. Median fungal concentrations in storage areas, ranged from 30 to 465 CFU/m3. People working in the most contaminated archives did not report more symptoms of

allergy than others. However, workers in contact with moldy documents reported more headaches (odds ratio, 2.4; 95% confidence interval, 1.15.3), fatigue (OR, 2.9; 95% CI, 1.26.7), eye irritation (OR, 5.4; 95% CI, 1.914.9), throat irritation (OR, 2.4; 95% CI, 1.05.7), coughing (OR, 3.2; 95% CI, 1.28.4), and rhinorrhea (OR, 2.6; 95% CI, 1.06.4) than others. Other parameters such as dust levels and concentrations of metabolites and chemical substances should be considered as confounding factors in further investigations to isolate the role of molds. Practical Implications Most studies about fungi and archives deal with the conservation of manuscripts and documents, and few discuss workers health problems. Our study shows that archives do not represent a highly contaminated environment. Symptoms felt by workers were more often linked to direct contact with moldy documents than to high concentrations of mold in the air of archive storage areas. This study provides data on concentration levels in archives that could be used to interpret microbiological investigations in this type of environment in the future.

Sanches, E. M. C., L. Ferreiro, et al. (2011). "Phylogenetic analysis of Pneumocystis from pig lungs obtained from slaughterhouses in southern and midwestern regions of Brazil." Arquivo Brasileiro De Medicina Veterinaria E Zootecnia 63(5): 1154-1159.

The Pneumocystis genus is comprised of pathogens dwelling in the lungs of terrestrial, aerial, and aquatic mammals. Occasionally they induce severe pneumonitis, particularly in hosts with severe impairment of the immune system and progressively may fill pulmonary alveolar cavities causing respiratory failure. Molecular genetic studies revealed that Pneumocystis gene sequences present a marked divergence with the host species concerned. In the present study, the genetic diversity of Pneumocystis obtained from lungs of swines was examined by analyzing mitochondrial large subunit (mtLSU) and small subunit (mtSSU) rRNA sequences. The samples were obtained from two slaughterhouses located in two Brazilian states. Phylogenetic analysis demonstrated that genetic groupings within Pneumocystis organisms were in accordance with those of the corresponding hosts and that two clusters were formed. In conclusion, these data show that there are genetically distinct porcine Pneumocystis genotypes with at least two separate clusters in Brazil.

Seyedmousavi, S., J. Guillot, et al. (2013). "Phaeohyphomycoses, Emerging Opportunistic Diseases in Animals." Clinical Microbiology Reviews 26(1): 19-35.

Emerging fungal diseases due to black yeasts and relatives in domestic or wild animals and in invertebrates or cold- and warm-blooded vertebrates are continually being reported, either as novel pathogens or as familiar pathogens affecting new species of hosts. Different epidemiological situations can be distinguished, i.e., occurrence as single infections or as zoonoses, and infection may occur sporadically in otherwise healthy hosts. Such infections are found mostly in mammals but also in cold-blooded animals, are frequently subcutaneous or cerebral, and bear much similarity to human primary disorders. Infections of the nervous system are mostly fatal, and the source and route of infection are currently unknown. A third epidemiological situation corresponds to pseudoepidemics, i.e., infection of a large host population due to a common source. It is often observed and generally hypothesized that the susceptible animals are under stress, e.g., due to poor housing conditions of mammals or to a change of basins in the case of fishes. The descriptions in this

article represent an overview of the more commonly reported and recurring black fungi and the corresponding diseases in different types of animals.

Svirshchevskaya, E. V., M. A. Shevchenko, et al. (2009). "Susceptibility of mice to invasive aspergillosis correlates with delayed cell influx into the lungs." International Journal of Immunogenetics 36(5): 289-299.

P>Ubiquitous fungus Aspergillus fumigatus (A. fumigatus) is involved in invasive pulmonary aspergillosis (IPA), a frequent infection in immunocompromized patients. Genetic differences are likely to play a role predisposing to IPA. This study was aimed to compare six genetically different mouse strains in their susceptibility to IPA and to determine possible mechanisms involved in the pathogenesis of this infection. Immunosuppressed BALB/c and C57BL/6 mice infected with A. fumigatus conidia were more resistant to IPA than DBA/1, DBA/2, CBA, and A/Sn strains. Phagocytosis of A. fumigatus conidia by blood polymorphonuclear neutrophils (PMN) or bone marrow derived dendritic cells showed no difference between strains. All IPA susceptible strains demonstrated decreased PMN influx into the lungs during infection compared with resistant strains. Flow cytometry analysis of the composition of lung infiltrating cells showed that IPA susceptible mice had a decreased number of phagocytes before the infection. After infection the numbers of Gr-1(+)CD11b(+) PMN cells in the lungs of immunosuppressed mice increased from 10-20% to 50-60% while the percentage of CD11(+)F4/80(+) resident macrophages was unchanged. Among susceptible strains DBA/2 and A/Sn have a defect in C5 component of complement. Injection of normal serum into complement deficient but not into complement sufficient CBA or DBA/1 mice significantly improved their survival. We showed that complement replacement significantly increased PMN homing to the lungs of complement deficient mice. Thus, defect in complement system can predispose to IPA. Our results demonstrated that early influx of PMN into the lungs of mice is important for the resistance to IPA.

Takumi, K., P. Teunis, et al. (2009). "Transmission risk of human trichinellosis." Veterinary Parasitology 159(3-4): 324-327.

Trichinella is a food-borne parasitic zoonoses and human cases are still reported in Europe mainly due to the consumption of pig meat originating from small backyard farms. Infections originating from industrialized pig farming have not been reported for decades in Europe, due to control measures to prevent the transmission of Trichinella from wildlife by indoor housing and good management practices. Therefore, risk-based monitoring programs might replace individual carcass control in industrialized pig farming as described in EU legislation SANCO 2075/2005. Transmission of Trichinella species between wildlife and the risk that may pose to humans via consumption of contaminated pork meat has not been studied quantitatively. One pathway by which human trichinellosis can occur is the rat-pig-human route. To evaluate the transmission risk though this pathway the dose responses of rat, pig, and human were studied. Experimental T spiralis infection was performed in rats with doses of as few as 10 parasites and the data set was analysed using a newly developed dose response model that describes larvae per gram (LPG). Experimental T. spiralis infection in pig was analysed in a similar way. Furthermore nine published outbreaks of human

trichinellosis were analysed to determine the dose response in humans. The risk of human trichinellosis via the rat-pig-human transmission was simulated by the Monte Carlo method. A pair of female and male parasites representing the lowest infection pressure from the environment, led to the probability of human trichinellosis by consumption of 100 g of raw pork meat equal to 5% via the studied rat-pig-human pathway. In the absence of rodent control near the farm, a low infection pressure from wildlife presents a relatively high risk of human trichinellosis via consumption of uncooked pork meat. (C) 2008 Published by Elsevier B.V.

Thierry, S., B. Durand, et al. (2012). "Assessment of Aspergillus fumigatus pathogenicity in aerosol-challenged chickens (Gallus gallus) belonging to two lineages." Mycoses 55: 154-154.

Thierry, S., B. Durand, et al. (2013). "Assessment of Aspergillus fumigatus pathogenicity in aerosol-challenged chickens (Gallus gallus) belonging to two lineages." Comparative Immunology Microbiology and Infectious Diseases 36(4): 379-385.

Infection due to the mold Aspergillus fumigatus remains a common and life-threatening infection in many animals, especially birds. Animal models are still required to better understand the physiopathology of infection and evaluate diagnostic tools and treatment Procedures. The aim of the present study was to assess the pathogenicity of A. fumigatus in two lineages of chicken (Gallus gallus): SPF White Leghorn PA12 layers and conventional JA657 broilers. Four-day-old birds were experimentally infected in an inhalation chamber in order to reproduce a "natural" contamination and to obtain a large repartition of conidia into the respiratory tract. Half of the chicks were injected subcutaneously with dexamethasone for 4 days before the infective challenge. At days 0 and 7, the effects of chicken lineage and immunosuppressive treatment on pulmonary fungal burden were analyzed using two linear mixed models. The pathogenicity of A. fumigatus varied according to the lineage: no clinical signs and no mortality were observed in layer chickens whereas more than 50% of mortality occurred in broilers. The effect of immunosuppressive treatment was also demonstrated, notably on animals weight but also on mortality.

Thierry, S., D. Y. Wang, et al. (2010). "Multiple-locus variable-number tandem repeat analysis for molecular typing of Aspergillus fumigatus." Bmc Microbiology 10.

Background: Multiple-locus variable-number tandem repeat (VNTR) analysis (MLVA) is a prominent subtyping method to resolve closely related microbial isolates to provide information for establishing genetic patterns among isolates and to investigate disease outbreaks. The usefulness of MLVA was recently demonstrated for the avian major pathogen Chlamydophila psittaci. In the present study, we developed a similar method for another pathogen of birds: the filamentous fungus Aspergillus fumigatus. Results: We selected 10 VNTR markers located on 4 different chromosomes (1, 5, 6 and 8) of A. fumigatus. These markers were tested with 57 unrelated isolates from different hosts or their environment (53 isolates from avian species in France, China or Morocco, 3 isolates from humans collected at CHU Henri Mondor hospital in France and the reference strain CBS 144.89). The Simpson index for individual markers ranged from 0.5771 to 0.8530. A combined loci index

calculated with all the markers yielded an index of 0.9994. In a second step, the panel of 10 markers was used in different epidemiological situations and tested on 277 isolates, including 62 isolates from birds in Guangxi province in China, 95 isolates collected in two duck farms in France and 120 environmental isolates from a turkey hatchery in France. A database was created with the results of the present study http://minisatellites.u-psud.fr/MLVAnet/. Three major clusters of isolates were defined by using the graphing algorithm termed Minimum Spanning Tree (MST). The first cluster comprised most of the avian isolates collected in the two duck farms in France, the second cluster comprised most of the avian isolates collected in poultry farms in China and the third one comprised most of the isolates collected in the turkey hatchery in France. Conclusions: MLVA displayed excellent discriminatory power. The method showed a good reproducibility. MST analysis revealed an interesting clustering with a clear separation between isolates according to their geographic origin rather than their respective hosts.

Thierry, S., D. Y. Wang, et al. (2012). "Simple and highly discriminatory VNTR-based methods for the typing of Aspergillus fumigatus and A. flavus isolates from different geographic origins and different hosts." Mycoses 55: 71-72.

Toussain, G., F. Botterel, et al. (2012). "Sinus fungal balls: characteristics and management in patients with host factors for invasive infection." Rhinology 50(3): 269-276.

Background: The characteristics of sinus fungal ball (SFB), classically considered being a non-invasive form of fungal infection, in patients with host factors for invasive fungal infection (IFI) are unknown. Objective: To characterize SFB and their management in patients with host factors for IFI. Methodology: Retrospective single-centre study of the clinical, radiology, histology and mycology records of patients treated for SFB between 1997 and 2007. Patients with and without host factors for IFI were compared. Results: One hundred eighty one patients were classified into two groups: 19 (group 1) with and 162 (group 2) without host factors for IFI. In group 1, SFB were asymptomatic in 26.3% of the cases, ethnnoido-sphenoidal sinuses were more frequently involved than in group 2 and fungal culture was positive in 37.5% of the cases. The main species was Aspergillus sp. in both groups. Four cases of complicated SFB were observed, only in patients of group 1. Cure without recurrence was obtained in both groups by endonasal surgery, combined with triazole therapy in complicated forms with osteolysis. Conclusion: In patients with host factors for IFI, SFB more frequently involves deep sinuses and can be complicated by clinical signs suggestive of invasion and radiological signs of osteolysis, with no histological evidence of fungal invasion.

Trap, C., B. Q. Fu, et al. (2006). "Cloning and analysis of a cDNA encoding a putative serine protease comprising two trypsin-like domains of Trichinella spiralis." Parasitology Research 98(4): 288-294.

The cDNA encoding a putative serine protease, TsSerP, was cloned by degenerative polymerase chain reaction and screening of the cDNA library from Trichinella spiralis adult-newborn larvae stage. Sequence analysis revealed the presence of two trypsin-like serine protease domains flanking a hydrophilic domain, with the catalytic triad residue histidine in the alpha domain

substituted by an arginine residue. Southern blots indicated that this was a single copy gene in the parasite genome. Northern blots demonstrated a single 2.3-kb transcript during the muscle larvae and adult stages of T. spiralis. The recombinant protein from the TsSerP beta domain (beta SerP) was produced but not recognised by T. spiralis-infected swine serum. An anti-beta SerP polyclonal serum detected a 69-kDa polypeptide in the soluble antigens of T. spiralis muscle larvae. Immunolocalisation analysis located TsSerP on the inner layer of the cuticle and oesophagus of the parasite, suggesting a potential role in its moulting and/or digestive functions.

Vayssier-Taussat, M., D. Le Rhun, et al. (2009). Insights in Bartonella Host Specificity. Rickettsiology and Rickettsial Diseases. K. E. Hechemy, P. Brouqui, J. E. Samuel and D. A. Raoult. 1166: 127-132.

The genus Bartonella comprises a unique group of emerging gram-negative, intracellular bacteria that can cause a long-lasting intraerythrocytic bacteremia in their reservoir hosts. In recent years, the widespread occurrence and diversity of these bacteria has been increasingly recognized. This has resulted in a dramatic expansion of the genus Bartonella to 24 currently described species or subspecies, among which at least half have been associated with human disease. Bartonella infections have been observed in virtually all species examined, extending from humans to carnivores, ungulates, rodents, lagomorphs, insectivores, and bats. Adaptation by Bartonellae to such a diverse range of mammals has resulted in host specificity, and all validated Bartonella species described to date are capable of parasitizing only a limited number of animal species. In this review, the possible mechanisms explaining the specificity of each Bartonella species for its reservoir host are discussed.

Vayssier-Taussat, M., D. Le Rhun, et al. (2010). "The Trw Type IV Secretion System of Bartonella Mediates Host-Specific Adhesion to Erythrocytes." Plos Pathogens 6(6).

Bacterial pathogens typically infect only a limited range of hosts; however, the genetic mechanisms governing host-specificity are poorly understood. The alpha-proteobacterial genus Bartonella comprises 21 species that cause host-specific intraerythrocytic bacteremia as hallmark of infection in their respective mammalian reservoirs, including the human-specific pathogens Bartonella quintana and Bartonella bacilliformis that cause trench fever and Oroya fever, respectively. Here, we have identified bacterial factors that mediate host-specific erythrocyte colonization in the mammalian reservoirs. Using mouse-specific Bartonella birtlesii, human-specific Bartonella quintana, cat-specific Bartonella henselae and rat-specific Bartonella tribocorum, we established in vitro adhesion and invasion assays with isolated erythrocytes that fully reproduce the host-specificity of erythrocyte infection as observed in vivo. By signature-tagged mutagenesis of B. birtlesii and mutant selection in a mouse infection model we identified mutants impaired in establishing intraerythrocytic bacteremia. Among 45 abacteremic mutants, five failed to adhere to and invade mouse erythrocytes in vitro. The corresponding genes encode components of the type IV secretion system (T4SS) Trw, demonstrating that this virulence factor laterally acquired by the Bartonella lineage is directly involved in adherence to erythrocytes. Strikingly, ectopic expression of Trw of rat-specific B. tribocorum in cat-specific B. henselae or human-specific B. quintana expanded their host range for erythrocyte infection to rat, demonstrating that Trw mediates host-specific

erythrocyte infection. A molecular evolutionary analysis of the trw locus further indicated that the variable, surface-located TrwL and TrwJ might represent the T4SS components that determine host-specificity of erythrocyte parasitism. In conclusion, we show that the laterally acquired Trw T4SS diversified in the Bartonella lineage to facilitate host-restricted adhesion to erythrocytes in a wide range of mammals.

Villena, I., B. Durand, et al. (2012). "New strategy for the survey of Toxoplasma gondii in meat for human consumption." Veterinary Parasitology 183(3-4): 203-208.

Monitoring of Toxoplasma infection in animals destined for human consumption is a great challenge for human toxoplasmosis prevention. This study aimed to compare results obtained from a naturally infected population of sheep using different tests and targeting an original matrix: meat samples and muscle fluids collected at the slaughterhouse. A commercial ELISA test was performed on diaphragm fluids from 419 ovine carcasses collected at the slaughterhouse. A MAT (modified agglutination test) was performed on heart fluids obtained from the same animals. In addition, all hearts were bioassayed in mice. Serological test agreement, the relative sensitivity of ELISA MAT and mouse bioassay as well as a correlation between titres and parasite isolation probability were statistically evaluated. The overall agreement (kappa coefficient = 0.64) of ELISA on diaphragm fluids and MAT on heart fluids is substantial and subsequently both tests can be used for epidemiological studies. Relative sensitivity was higher for MAT performed on cardiac fluids (90%) than ELISA on diaphragm fluid (61%). For both serological tests, relative sensitivity is lower in lambs younger than 12 months. Relative sensitivity of mouse inoculation was 42%. A significant correlation was obtained between increasing MAT titres and probability to isolate live parasite from the heart. When the fluid titre was higher than 1:16, parasites were isolated in 65% of cases. When it was lower, isolation failed in 95% of the cases. According to our results, cardiac fluids appear to be a relevant matrix for toxoplasmosis survey in meat.

Vourc'h, G., L. Halos, et al. (2009). "Animals, arbovirus and man." Virologie 13(2): 67-72.

Wang, D. Y., M. Gricourt, et al. (2012). "Azole-resistance in Aspergillus fumigatus: A side effect of fungal drugs use in avian farms?" Mycoses 55: 88-88.

Wang, D. Y., L. Hadj-Henni, et al. (2012). "Simple and Highly Discriminatory VNTR-Based Multiplex PCR for Tracing Sources of Aspergillus flavus Isolates." Plos One 7(9).

Aspergillus flavus is second only to A. fumigatus in causing invasive aspergillosis and it is the major agent responsible for fungal sinusitis, keratitis and endophthalmitis in many countries in the Middle East, Africa and Southeast Asia. Despite the growing challenge due to A. flavus, data on the molecular epidemiology of this fungus remain scarce. The objective of the present study was to develop a new typing method based on the detection of VNTR (Variable number tandem repeat)

markers. Eight VNTR markers located on 6 different chromosomes (1, 2, 3, 5, 7 and 8) of A. flavus were selected, combined by pairs for multiplex amplifications and tested on 30 unrelated isolates and six reference strains. The Simpson index for individual markers ranged from 0.398 to 0.818. A combined loci index calculated with all the markers yielded an index of 0.998. The MLVA (Multiple Locus VNTR Analysis) technique proved to be specific and reproducible. In a second time, a total of 55 isolates from Chinese avian farms and from a Tunisian hospital have been evaluated. One major cluster of genotypes could be defined by using the graphing algorithm termed Minimum Spanning Tree. This cluster comprised most of the isolates collected in an avian farm in southern China. The MLVA technique should be considered as an excellent and cost-effective typing method that could be used in many laboratories without the need for sophisticated equipment.

Wang, S. H., X. P. Zhu, et al. (2009). "Molecular cloning and characterization of heat shock protein 70 from Trichinella spiralis." Acta Tropica 110(1): 46-51.

A cDNA encoding heat shock protein 70 of Trichinella spiralis (Ts-Hsp70) was identified by immunoscreening the adult T. spiralis cDNA library with rabbit antisera against T. spiralis adult extracts. The open reading frame of Ts-Hsp70 (DNA encoded a 623-amino acid peptide with a predicted molecular weight of 68.7 kDa, which shares a high degree of sequence conservation with HSP70s from other parasites. Recombinant Ts-Hsp70 was expressed in Escherichia coli and purified with nickel column chromatography. Western blot analysis showed that recombinant Ts-Hsp70 could be recognized not only by trichinellosis patient sera, but also by T. spiralis-infected sera from rabbits, swine, and mice. Mice vaccinated with recombinant Ts-Hsp70 formulated with Freund's adjuvant exhibited strong humoral immune responses indicated by high titer of IgG antibody and significant muscle larval reduction (37%) after being challenged with T. spiralis larvae. The present results indicate that Ts-Hsp70 is a possible candidate vaccine against T. spiralis infection.

Watier-Grillot, S., I. Vallee, et al. (2011). "STRAYED DOGS SENTINELS OF TRICHINELLA BRITOVI INFECTION IN KOSOVO." Parasite-Journal De La Societe Francaise De Parasitologie 18(3): 281-283.

Wu, X. P., B. Q. Fu, et al. (2009). "Identification of antigenic genes in Trichinella spiralis by immunoscreening of cDNA libraries." Veterinary Parasitology 159(3-4): 272-275.

Genes encoding antigens of adult worm, newborn larvae and muscle larvae of Trichinella spiralis were identified by immunoscreening their corresponding cDNA libraries. The cDNA libraries of T. spiralis adult (3 day old, Ad3) and newborn larvae (NBL) were screened using the serum of a pig infected with 20,000 muscle larvae (ML) at 26 days post-infection (dpi). Fifty-two positive clones representing 18 unique genes were obtained from the Ad3 cDNA library. The deduced amino acid sequences of 8 cDNAs were sequence homologues of the serine protease-like protein family. In the screening of NBL cDNA library, 81 positive clones representing 8 unique genes were isolated and of these, 70 clones corresponded to an NBL stage-specific serine protease gene. The ML cDNA library was screened using pig anti-Trichinella serum obtained at 60 dpi and 18 positive clones representing

8 unique genes were identified. Ten clones encoded a protein that is identical to a T. spiralis serine protease inhibitor. In general, our results revealed that antigenic serine protease-like proteins were found during the two invasive stages, Ad and NBL when these libraries were screened using 26 dpi antiserum, whereas a serine protease inhibitor was found in abundance in the ML library when it is screened using 60 dpi antiserum. These data are consistent with serine proteases playing an important role during the invasive stages of Trichinella infections, but become inhibited or internally controlled when the parasite enters a more stable, non-developing environment.

Yepez-Mulia, L., C. Montano-Escalona, et al. (2009). "Differential activation of mast cells by antigens from Trichinella spiralis muscle larvae, adults, and newborn larvae." Veterinary Parasitology 159(3-4): 253-257.

Mast cell (MC) hyperplasia and activation are prominent features in Trichinella spiralis infection. Indeed a temporal correlation has been shown between the kinetics of intestinal mastocytosis, release of inflammatory mediators from MC, and adult worm loss, which constitutes a major component of the defense against T. spiralis infection. It is well known that during the intestinal phase of trichinellosis, muscle larvae (ML) and adult worms (AD) enter into contact with the host; however, interaction with MC may also occur during migration of newborn larvae (NBL). Therefore, it is plausible that antigens from these developmental stages could activate MC. We have previously demonstrated by in vitro assays that T. spiralis muscle larval (TSL-1) antigens activate MC through an Ig-independent mechanism leading to the release of histamine, MC protease 5, IL-4 and TNF alpha. In this work we evaluated whether total antigens from AD or NBL could activate unsensitized MC and we compared this activation with the activation seen when MC are stimulated with TSL-1 antigens. MC activation was also tested with affinity chromatography purified antigens from NBL using the monoclonal antibody CE-4 that recognizes NBL surface components. The results obtained in this study showed that AD total extracts and TSL-1 antigens induced the release of histamine but not beta-hexosaminidase from unsensitized MC, suggesting a selective secretion of MC mediators. In contrast, NBL total extracts or purified NBL antigens did not induce the release of either histamine or beta-hexosaminidase from MC. Interestingly, AD and ML are the stages that interact with the host during the intestinal phase of infection. The mechanisms involved in TSL-1 and AD activation of unsensitized MC may function together with other mechanisms of MC activation in host protection against T. spiralis. m 2008 Published by Elsevier B.V.

Zocevic, A., P. Mace, et al. (2011). "Identification of Trichinella spiralis early antigens at the pre-adult and adult stages." Parasitology 138(4): 463-471.

Three expression cDNA libraries from Trichinella spiralis worms 14 h, 20 h and 48 h post-infection (p.i.) were screened with serum from pigs experimentally infected with 20000 T. spiralis muscle larvae. Twenty-nine positive clones were isolated from the 14 h p.i. cDNA library, corresponding to 8 different genes. A putative excretory-secretory protein similar to that of T. pseudospiralis was identified. Three clones corresponded to a T. spiralis serine proteinase inhibitor known to be involved in diverse functions such as blood coagulation and modulation of

inflammation. Screening of the 20 h p.i. cDNA library selected 167 positive clones representing 12 different sequences. The clone with the highest redundancy encoded a small polypeptide having no sequence identity with any known proteins from Trichinella or other organisms. Fourteen clones displayed sequence identity with the heat shock protein (HSP) 70. HSPs are produced as an adaptive response of the parasite to the hostile environment encountered in the host intestine but their mechanism of action is not yet well defined. From the 48 h p.i. T. spiralis cDNA library, 91 positive clones were identified representing 7 distinct sequences. Most of the positive clones showed high similarity with a member of a putative T. spiralis serine protease family. This result is consistent with a possible major role for serine proteases during invasive stages of Trichinella infection and host-parasite interactions.

2014

Arias-Goeta, C., S. Moutailler, et al. (2014). "Chikungunya virus adaptation to a mosquito vector correlates with only few point mutations in the viral envelope glycoprotein." Infect Genet Evol 24: 116-126.

Like most arthropod-borne viruses (arboviruses), chikungunya virus (CHIKV) is a RNA virus maintained in nature in an alternating cycle of replication between invertebrate and vertebrate hosts. It has been assumed that host alternation restricts arbovirus genome evolution and imposes fitness trade-offs. Despite their slower rates of evolution, arboviruses still have the capacity to produce variants capable to exploit new environments. To test whether the evolution of the newly emerged epidemic variant of CHIKV (E1-226V) is constrained by host alternation, the virus was alternately-passaged in hamster-derived BHK-21 cells and Aedes aegypti-derived Aag-2 cells. It was also serially-passaged in BHK-21 or Aag-2 cells to promote adaptation to one cell type and presumably, fitness cost in the bypassed cell type. After 30 passages, obtained CHIKV strains were genetically and phenotypically characterized using in vitro and in vivo systems. Serially- and alternately-passaged strains can be distinguished by amino-acid substitutions in the E2 glycoprotein, responsible for receptor binding. Two substitutions at positions E2-64 and E2-208 only lower the dissemination of the variant E1-226V in Ae. aegypti. These amino-acid changes in the E2 glycoprotein might affect viral infectivity by altering the interaction between CHIKV E1-226V and the cellular receptor on the midgut epithelial cells in Ae. aegypti but not in Aedesalbopictus.

Bonnet, S., L. Michelet, et al. (2014). "Identification of parasitic communities within European ticks using next-generation sequencing." PLoS Negl Trop Dis 8(3): e2753.

BACKGROUND: Risk assessment of tick-borne and zoonotic disease emergence necessitates sound knowledge of the particular microorganisms circulating within the communities of these major vectors. Assessment of pathogens carried by wild ticks must be performed without a priori, to allow for the detection of new or unexpected agents. METHODOLOGY/PRINCIPAL FINDINGS: We evaluated the potential of Next-Generation Sequencing techniques (NGS) to produce an inventory of parasites carried by questing ticks. Sequences corresponding to parasites from two distinct genera were

recovered in Ixodes ricinus ticks collected in Eastern France: Babesia spp. and Theileria spp. Four Babesia species were identified, three of which were zoonotic: B. divergens, Babesia sp. EU1 and B. microti; and one which infects cattle, B. major. This is the first time that these last two species have been identified in France. This approach also identified new sequences corresponding to as-yet unknown organisms similar to tropical Theileria species. CONCLUSIONS/SIGNIFICANCE: Our findings demonstrate the capability of NGS to produce an inventory of live tick-borne parasites, which could potentially be transmitted by the ticks, and uncovers unexpected parasites in Western Europe.

Clement, M., G. Fornasa, et al. (2014). "Upholding the T cell immune-regulatory function of CD31 inhibits the formation of T/B immunological synapses in vitro and attenuates the development of experimental autoimmune arthritis in vivo." J Autoimmun.

CD31, a trans-homophilic inhibitory receptor expressed on both T- and B-lymphocytes, drives the mutual detachment of interacting leukocytes. Intriguingly, T cell CD31 molecules relocate to the immunological synapse (IS), where the T and B cells establish a stable interaction. Here, we show that intact CD31 molecules, which are able to drive an inhibitory signal, are concentrated at the periphery of the IS but are excluded from the center of the IS. At this site, were the cells establish the closest contact, the CD31 molecules are cleaved, and most of the extracellular portion of the protein, including the trans-homophilic binding sites, is shed from the cell surface. T cells lacking CD31 trans-homophilic binding sites easily establish stable interactions with B cells; at the opposite, CD31 signaling agonists inhibit T/B IS formation as well as the ensuing helper T cell activation and function. Confocal microscopy and flow cytometry analysis of experimental T/B IS shows that the T cell inhibitory effects of CD31 agonists depend on SHP-2 signaling, which reduces the phosphorylation of ZAP70. The analysis of synovial tissue biopsies from patients affected by rheumatoid arthritis showed that T cell CD31 molecules are excluded from the center of the T/B cell synapses in vivo. Interestingly, the administration of CD31 agonists in vivo significantly attenuated the development of the clinical signs of collagen-induced arthritis in DBA1/J mice. Altogether, our data indicate that the T cell co-inhibitory receptor CD31 prevents the formation of functional T/B immunological synapses and that therapeutic strategies aimed at sustaining CD31 signaling will attenuate the development of autoimmune responses in vivo.

Cosson, J. F., L. Michelet, et al. (2014). "Genetic characterization of the human relapsing fever spirochete Borrelia miyamotoi in vectors and animal reservoirs of Lyme disease spirochetes in France." Parasit Vectors 7: 233.

BACKGROUND: In France as elsewhere in Europe the most prevalent TBD in humans is Lyme borreliosis, caused by different bacterial species belonging to Borrelia burgdorferi sensu lato complex and transmitted by the most important tick species in France, Ixodes ricinus. However, the diagnosis of Lyme disease is not always confirmed and unexplained syndromes occurring after tick bites have become an important issue. Recently, B. miyamotoi belonging to the relapsing fever group and transmitted by the same Ixodes species has been involved in human disease in Russia, the USA and the Netherlands. In the present study, we investigate the presence of B. miyamotoi along with other Lyme Borreliosis spirochetes, in ticks and possible animal reservoirs collected in France. METHODS:

We analyzed 268 ticks (Ixodes ricinus) and 72 bank voles (Myodes glareolus) collected and trapped in France for the presence of DNA from B. miyamotoi as well as from Lyme spirochetes using q-PCR and specific primers and probes. We then compared the French genotypes with those found in other European countries. RESULTS: We found that 3% of ticks and 5.55% of bank voles were found infected by the same B. miyamotoi genotype, while co-infection with other Lyme spirochetes (B. garinii) was identified in 12% of B. miyamotoi infected ticks. Sequencing showed that ticks and rodents carried the same genotype as those recently characterized in a sick person in the Netherlands. CONCLUSIONS: The genotype of B. miyamotoi circulating in ticks and bank voles in France is identical to those already described in ticks from Western Europe and to the genotype isolated from a sick person in The Netherlands. This results suggests that even though no human cases have been reported in France, surveillance has to be improved. Moreover, we showed that ticks could simultaneously carry B. miyamotoi and Lyme disease spirochetes, increasing the problem of co-infection in humans.

Davoust, B., O. Mediannikov, et al. (2014). "[Serological survey of animal toxoplasmosis in Senegal.]." Bull Soc Pathol Exot.

Toxoplasma gondii is an obligate, intracellular, parasitic protozoan within the phylum Apicomplexa that causes toxoplasmosis in mammalian hosts (including humans) and birds. We used modified direct agglutination test for the screening of the animals' sera collected in Senegal. In total, 419 animals' sera have been studied: 103 bovines, 43 sheep, 52 goats, 63 horses, 13 donkeys and 145 dogs. The collection of sera was performed in four different regions of Senegal: Dakar, Sine Saloum, Kedougou and Basse Casamance from 2011 to 2013. We have revealed antibodies in 13% of bovines, 16% of sheep, 15% of goats, 30% of horses, 23% of donkeys and 67% of dogs. Private dogs from villages were more often to have the anti-Toxoplasma antibodies compared to security society-owned dogs from Dakar. It may be explained by different meal consumed by dogs (factory-produced meal for dogs from Dakar vs. irregular sources for village dogs). Intense circulation of T. gondii in the studied zone may explain the unusually high seroprevalence among horses and donkeys. Tropical climate with high temperature and humidity is favorable for the conservation of oocysts of T. gondii. Results presented here may contribute to the evaluation of the risks of toxoplasmosis in humans in Senegal.

Djokic, V., R. Blaga, et al. (2014). "Mini-FLOTAC for counting Toxoplasma gondii oocysts from cat feces - Comparison with cell counting plates." Exp Parasitol 147C: 67-71.

Oocysts of Toxoplasma gondii represent one of the most common environmental contaminants causing the zoonotic infection toxoplasmosis. The aim of the present study was to compare the Mini-FLOTAC device with traditional cell counting plates (Kova Slide) for the detection of T. gondii oocysts from feline feces. Two types of experiments were performed: (i) purified oocysts were counted in different dilutions and (ii) specific pathogen free T. gondii-negative cat feces was inoculated with numbers of purified oocysts and counting was performed directly from feces. Our analysis showed a thousand times higher sensitivity of Mini-FLOTAC (5 x 102 oocysts) compared to Kova Slide (5 x 105 oocysts). Also, when compared by McNemar's test, counting of the purified

oocysts showed a higher sensitivity of Mini-FLOTAC compared to Kova Slide, for a dilution of 103 oocysts/ml (chi2 = 6.1; P <0.05). A better sensitivity was also found with Mini-FLOTAC in dilutions of 105 and 104 oocysts/ml, when counted from feces (chi2 = 4.2 and 8.1, respectively, P <0.05). Our results show that Mini-FLOTAC is more sensitive than traditional methods of T. gondii oocysts detection and quantification is more accurate. Furthermore, Mini-FLOTAC simplicity and cost effectiveness allow it to be used with light microscopes in any laboratory or field conditions. We therefore recommend its use for regular screening. Further studies are needed to validate Mini-FLOTAC for the detection of oocysts in soil and water samples in field conditions.

Drut, A., I. Bublot, et al. (2014). "Comparative microbiological features of Bartonella henselae infection in a dog with fever of unknown origin and granulomatous lymphadenitis." Med Microbiol Immunol 203(2): 85-91.

We report the first documented case of Bartonella henselae infection in a dog from France and the first isolation of B. henselae from a dog with fever of unknown origin. This observation contributes to the "One Health" concept focusing on zoonotic pathogens emerging from companion animals. A 1-year-old female German shepherd dog was referred for evaluation of fever of unknown origin of 1 month duration. Diagnostic investigations confirmed diffuse pyogranulomatous lymphadenitis. The dog became afebrile, and lymph node size normalized in response to a 6-week course of doxycycline. Retrospectively, Bartonella DNA was amplified from an EDTA-anticoagulated blood sample obtained before antimicrobial therapy, with the gtlA fragment sharing 99 % identity with the 350-bp gtlA fragment of the B. henselae Houston-1 strain. The same strain was isolated in the blood of three healthy cats from the household. Two months after discontinuation of doxycycline, the dog experienced a febrile relapse. Bartonella DNA was again amplified from blood prior to and immediately after administration of a 6-week course azithromycin therapy. However, without administration of additional medications, PCR was negative 9 months after azithromycin therapy and the dog remains clinically healthy 12 months following the second course of antibiotics. The medical management of this case raises several clinically relevant comparative infectious disease issues, including the extent to which Bartonella spp. contribute to fever of unknown origin and pyogranulomatous inflammatory diseases in dogs and humans, and the potential of doxycycline and azithromycin treatment failures. The possibility that dogs could constitute an underestimated reservoir for B. henselae transmission to people is also discussed.

Dugat, T., A. Chastagner, et al. (2014). "A new multiple-locus variable-number tandem repeat analysis reveals different clusters for Anaplasma phagocytophilum circulating in domestic and wild ruminants." Parasit Vectors 7: 439.

BACKGROUND: Anaplasma phagocytophilum is a tick-borne intragranulocytic alpha-proteobacterium. It is the causative agent of tick-borne fever in ruminants, and of human granulocytic anaplasmosis in humans, two diseases which are becoming increasingly recognized in Europe and the USA. However, while several molecular typing tools have been developed over the last years, few of them are appropriate for in-depth exploration of the epidemiological cycle of this bacterium. Therefore we have developed a Multiple-Locus Variable number tandem repeat (VNTR)

Analysis typing technique for A. phagocytophilum. METHODS: Five VNTRs were selected based on the HZ human-derived strain genome, and were tested on the Webster human-derived strain and on 123 DNA samples: 67 from cattle, 7 from sheep, 15 from roe deer, 4 from red deer, 1 from a reindeer, 2 from horses, 1 from a dog, and 26 from ticks. RESULTS: From these samples, we obtained 84 different profiles, with a diversity index of 0.96 (0.99 for vertebrate samples, i.e. without tick samples). Our technique confirmed that A. phagocytophilum from roe deer or domestic ruminants belong to two different clusters, while A. phagocytophilum from red deer and domestic ruminants locate within the same cluster, questioning the respective roles of roe vs red deer as reservoir hosts for domestic ruminant strains in Europe. As expected, greater diversity was obtained between rather than within cattle herds. CONCLUSIONS: Our technique has great potential to provide detailed information on A. phagocytophilum isolates, improving both epidemiological and phylogenic investigations, thereby helping in the development of relevant prevention and control measures.

Dugat, T., V. Loux, et al. (2014). "Comparative genomics of first available bovine Anaplasma phagocytophilum genome obtained with targeted sequence capture." BMC Genomics 15(1): 973.

BACKGROUND: Anaplasma phagocytophilum is a zoonotic and obligate intracellular bacterium transmitted by ticks. In domestic ruminants, it is the causative agent of tick-borne fever, which causes significant economic losses in Europe. As A. phagocytophilum is difficult to isolate and cultivate, only nine genome sequences have been published to date, none of which originate from a bovine strain.Our goals were to; 1/ develop a sequencing methodology which efficiently circumvents the difficulties associated with A. phagocytophilum isolation and culture; 2/ describe the first genome of a bovine strain; and 3/ compare it with available genomes, in order to both explore key genomic features at the species level, and to identify candidate genes that could be specific to bovine strains. RESULTS: DNA was extracted from a bovine blood sample infected by A. phagocytophilum. Following a whole genome capture approach, A. phagocytophilum DNA was enriched 197-fold in the sample and then sequenced using Illumina technology. In total, 58.9% of obtained reads corresponded to the A. phagocytophilum genome, covering 85.3% of the HZ genome. Then by performing comparisons with nine previously-sequenced A. phagocytophilum genomes, we determined the core genome of these ten strains. Following analysis, 1281 coding DNA sequences, including 1001 complete sequences, were detected in the A. phagocytophilum bovine genome, of which four appeared to be unique to the bovine isolate. These four coding DNA sequences coded for "hypothetical proteins of unknown function" and require further analysis. We also identified nine proteins common to both European domestic ruminants tested. CONCLUSION: Using a whole genome capture approach, we have sequenced the first A. phagocytophilum genome isolated from a cow. To the best of our knowledge, this is the first time that this method has been used to selectively enrich pathogenic bacterial DNA from samples also containing host DNA. The four proteins unique to the A. phagocytophilum bovine genome could be involved in host tropism, therefore their functions need to be explored.

Grellet, A., S. Chastant-Maillard, et al. (2014). "Risk factors of weaning diarrhea in puppies housed in breeding kennels." Prev Vet Med 117(1): 260-265.

Diarrhea represents one of the most frequent disorders in dogs. In puppies, degradation of feces quality is associated with a reduced daily weight gain and an increased risk of death. Prevention of diarrhea in puppies requires a global approach encompassing enteropathogens, environment and management practices especially when housed in groups. The purpose of this study was to determine prevalence of enteropathogens in puppies in breeding kennels and to identify risk factors of diarrhea. Two hundred and sixty six puppies (between 5 and 14weeks of age) from 29 French breeding kennels were included. For each kennel, data about environment, management of the kennel and puppies' characteristics (age, sex and breed) were collected. For each puppy, fecal consistency and fecal excretion of enteropathogens (viruses and parasites) was evaluated. At least one enteropathogen was identified in 77.1% of puppies and 24.8% of puppies presented abnormal feces. The main risk factor of weaning diarrhea was fecal excretion of canine parvovirus type 2 (odds ratio=5; confidence interval 95%: 1.7-14.7). A targeted sanitary and medical prophylaxis against canine parvovirus type 2 should be implemented to decrease risk of weaning diarrhea.

Kroemer, S., F. El Garch, et al. (2014). "Antibiotic susceptibility of bacteria isolated from infections in cats and dogs throughout Europe (2002-2009)." Comp Immunol Microbiol Infect Dis 37(2): 97-108.

A monitoring program of the pre-treatment susceptibility of clinical isolates of bacteria from diseased dogs and cats was active between the years 2002 and 2009. Susceptibility of each isolated strain to a panel of nine antibiotics (amoxicillin/clavulanic acid, ampicillin, penicillin, clindamycin, doxycycline, enrofloxacin, marbofloxacin, trimethoprim and trimethoprim/sulfamethoxazole) was assessed. The Minimum Inhibitory Concentration (MIC) of marbofloxacin was also determined by a standardized microdilution technique following CLSI recommendations. In total, 1857 bacterial strains were collected throughout Europe from cases of otitis, respiratory, urinary and dermatological infections. Although bacterial susceptibility varied for each of the antibiotics within the panel, patterns of susceptibility were similar to those described in the literature for comparable time periods and geographical areas. With a clinical resistance varying from 0 to 14.48% against the isolated strains, marbofloxacin susceptibility was very high and remains an effective antibiotic for the treatment of otitis, urinary, respiratory and dermatological infections in companion animals.

Liao, C., M. Liu, et al. (2014). "Characterisation of a Plancitoxin-1-Like DNase II Gene in Trichinella spiralis." PLoS Negl Trop Dis 8(8): e3097.

BACKGROUND: Deoxyribonuclease II (DNase II) is a well-known acidic endonuclease that catalyses the degradation of DNA into oligonucleotides. Only one or a few genes encoding DNase II have been observed in the genomes of many species. 125 DNase II-like protein family genes were predicted in the Trichinella spiralis (T. spiralis) genome; however, none have been confirmed. DNase II is a monomeric nuclease that contains two copies of a variant HKD motif in the N- and C-termini. Of these 125 genes, only plancitoxin-1 (1095 bp, GenBank accession no. XM_003370715.1) contains the HKD motif in its C-terminus domain. METHODOLOGY/PRINCIPAL FINDINGS: In this study, we cloned and characterised the plancitoxin-1 gene. However, the sequences of plancitoxin-1 cloned from T. spiralis were shorter than the predicted sequences in GenBank. Intriguingly, there were two HKD motifs in the N- and C-termini in the cloned sequences. Therefore, the gene with shorter sequences

was named after plancitoxin-1-like (Ts-Pt, 885 bp) and has been deposited in GenBank under accession number KF984291. The recombinant protein (rTs-Pt) was expressed in a prokaryotic expression system and purified by nickel affinity chromatography. Western blot analysis showed that rTs-Pt was recognised by serum from T. spiralis-infected mice; the anti-rTs-Pt serum recognised crude antigens but not ES antigens. The Ts-Pt gene was examined at all T. spiralis developmental stages by real-time quantitative PCR. Immunolocalisation analysis showed that Ts-Pt was distributed throughout newborn larvae (NBL), the tegument of adults (Ad) and muscle larvae (ML). As demonstrated by DNase zymography, the expressed proteins displayed cation-independent DNase activity. rTs-Pt had a narrow optimum pH range in slightly acidic conditions (pH 4 and pH 5), and its optimum temperature was 25 degrees C, 30 degrees C, and 37 degrees C. CONCLUSIONS: This study indicated that Ts-Pt was classified as a somatic protein in different T. spiralis developmental stages, and demonstrated for the first time that an expressed DNase II protein from T. spiralis had nuclease activity.

Liu, X. Y. and S. I. Bonnet (2014). "Hard tick factors implicated in pathogen transmission." PLoS Negl Trop Dis 8(1): e2566.

Ticks are the most common arthropod vector, after mosquitoes, and are capable of transmitting the greatest variety of pathogens. For both humans and animals, the worldwide emergence or re-emergence of tick-borne disease is becoming increasingly problematic. Despite being such an important issue, our knowledge of pathogen transmission by ticks is incomplete. Several recent studies, reviewed here, have reported that the expression of some tick factors can be modulated in response to pathogen infection, and that some of these factors can impact on the pathogenic life cycle. Delineating the specific tick factors required for tick-borne pathogen transmission should lead to new strategies in the disruption of pathogen life cycles to combat emerging tick-borne disease.

Liu, X. Y., M. Cote, et al. (2014). "Impact of feeding system and infection status of the blood meal on Ixodes ricinus feeding." Ticks Tick Borne Dis 5(3): 323-328.

Artificial membrane feeding systems are effective tools for both tick rearing and studying tick-borne pathogen transmission. In order to compare the effects of the type of feeding system on tick engorgement, Ixodes ricinus ticks were either fed on an artificial membrane feeding system or on live mice. Sheep and chicken blood were used with the membrane system to assess the effects of blood origin on tick engorgement. To investigate the effects of blood meal infection on tick engorgement, ticks were either fed with Bartonella-infected or uninfected blood, both via membrane feeding and on mice. The proportion of engorged ticks, the duration of tick feeding, and the weight of engorged ticks were assessed. Feeding on the artificial system led to a longer duration of tick feeding and a lower proportion of engorged ticks than when fed on mice, however, the weight of engorged ticks was unaffected. The proportion and weight of engorged ticks, as well as the duration of feeding were not affected by blood origin. Feeding on an infected blood meal or on infected mice decreased the proportion and the weight of engorged ticks, but did not affect tick feeding duration.

Liu, X. Y., J. de la Fuente, et al. (2014). "IrSPI, a tick serine protease inhibitor involved in tick feeding and Bartonella henselae infection." PLoS Negl Trop Dis 8(7): e2993.

Ixodes ricinus is the most widespread and abundant tick in Europe, frequently bites humans, and is the vector of several pathogens including those responsible for Lyme disease, Tick-Borne Encephalitis, anaplasmosis, babesiosis and bartonellosis. These tick-borne pathogens are transmitted to vertebrate hosts via tick saliva during blood feeding, and tick salivary gland (SG) factors are likely implicated in transmission. In order to identify such tick factors, we characterized the transcriptome of female I. ricinus SGs using next generation sequencing techniques, and compared transcriptomes between Bartonella henselae-infected and non-infected ticks. High-throughput sequencing of I. ricinus SG transcriptomes led to the generation of 24,539 isotigs. Among them, 829 and 517 transcripts were either significantly up- or down-regulated respectively, in response to bacterial infection. Searches based on sequence identity showed that among the differentially expressed transcripts, 161 transcripts corresponded to nine groups of previously annotated tick SG gene families, while the others corresponded to genes of unknown function. Expression patterns of five selected genes belonging to the BPTI/Kunitz family of serine protease inhibitors, the tick salivary peptide group 1 protein, the salp15 super-family, and the arthropod defensin family, were validated by qRT-PCR. IrSPI, a member of the BPTI/Kunitz family of serine protease inhibitors, showed the highest up-regulation in SGs in response to Bartonella infection. IrSPI silencing impaired tick feeding, as well as resulted in reduced bacterial load in tick SGs. This study provides a comprehensive analysis of I. ricinus SG transcriptome and contributes significant genomic information about this important disease vector. This in-depth knowledge will enable a better understanding of the molecular interactions between ticks and tick-borne pathogens, and identifies IrSPI, a candidate to study now in detail to estimate its potentialities as vaccine against the ticks and the pathogens they transmit.

Michelet, L., S. Delannoy, et al. (2014). "High-throughput screening of tick-borne pathogens in Europe." Front Cell Infect Microbiol 4: 103.

Due to increased travel, climatic, and environmental changes, the incidence of tick-borne disease in both humans and animals is increasing throughout Europe. Therefore, extended surveillance tools are desirable. To accurately screen tick-borne pathogens (TBPs), a large scale epidemiological study was conducted on 7050 Ixodes ricinus nymphs collected from France, Denmark, and the Netherlands using a powerful new high-throughput approach. This advanced methodology permitted the simultaneous detection of 25 bacterial, and 12 parasitic species (including; Borrelia, Anaplasma, Ehrlichia, Rickettsia, Bartonella, Candidatus Neoehrlichia, Coxiella, Francisella, Babesia, and Theileria genus) across 94 samples. We successfully determined the prevalence of expected (Borrelia burgdorferi sensu lato, Anaplasma phagocytophilum, Rickettsia helvetica, Candidatus Neoehrlichia mikurensis, Babesia divergens, Babesia venatorum), unexpected (Borrelia miyamotoi), and rare (Bartonella henselae) pathogens in the three European countries. Moreover we detected Borrelia spielmanii, Borrelia miyamotoi, Babesia divergens, and Babesia venatorum for the first time in Danish ticks. This surveillance method represents a major improvement in epidemiological studies, able to facilitate comprehensive testing of TBPs, and which can also be customized to monitor emerging diseases.

Okujava, R., P. Guye, et al. (2014). "A translocated effector required for bartonella dissemination from derma to blood safeguards migratory host cells from damage by co-translocated effectors." PLoS Pathog 10(6): e1004187.

Numerous bacterial pathogens secrete multiple effectors to modulate host cellular functions. These effectors may interfere with each other to efficiently control the infection process. Bartonellae are Gram-negative, facultative intracellular bacteria using a VirB type IV secretion system to translocate a cocktail of Bartonella effector proteins (Beps) into host cells. Based on in vitro infection models we demonstrate here that BepE protects infected migratory cells from injurious effects triggered by BepC and is required for in vivo dissemination of bacteria from the dermal site of inoculation to blood. Human endothelial cells (HUVECs) infected with a DeltabepE mutant of B. henselae (Bhe) displayed a cell fragmentation phenotype resulting from Bep-dependent disturbance of rear edge detachment during migration. A DeltabepCE mutant did not show cell fragmentation, indicating that BepC is critical for triggering this deleterious phenotype. Complementation of DeltabepE with BepEBhe or its homologues from other Bartonella species abolished cell fragmentation. This cyto-protective activity is confined to the C-terminal Bartonella intracellular delivery (BID) domain of BepEBhe (BID2.EBhe). Ectopic expression of BID2.EBhe impeded the disruption of actin stress fibers by Rho Inhibitor 1, indicating that BepE restores normal cell migration via the RhoA signaling pathway, a major regulator of rear edge retraction. An intradermal (i.d.) model for B. tribocorum (Btr) infection in the rat reservoir host mimicking the natural route of infection by blood sucking arthropods allowed demonstrating a vital role for BepE in bacterial dissemination from derma to blood. While the Btr mutant DeltabepDE was abacteremic following i.d. inoculation, complementation with BepEBtr, BepEBhe or BIDs.EBhe restored bacteremia. Given that we observed a similar protective effect of BepEBhe on infected bone marrow-derived dendritic cells migrating through a monolayer of lymphatic endothelial cells we propose that infected dermal dendritic cells may be involved in disseminating Bartonella towards the blood stream in a BepE-dependent manner.

Oltean, M., Z. Kalmar, et al. (2014). "European Mustelids Occupying Pristine Wetlands in the Danube Delta are Infected with Trichinella Likely Derived from Domesticated Swine." J Wildl Dis.

Abstract We analyzed 32 specimens from nine species of Mustelidae for Trichinella; six infections from two Trichinella species were observed from three host species. This provides documentation of Trichinella in Mustela erminea and Martes foina in Romania and Trichinella spiralis in a mustelid host from Europe. Trichinella spiralis continues to be a public challenge characterized by a wide host range and geographical distribution (Pozio 2007). During the past 20 yr, Romania has had the most reported human cases of trichinellosis in the world (Blaga et al. 2007). Transmission occurs among domesticated swine, rats, and wild mammals that feed by scavenging or predation (Pozio 2000). Trichinella transmission to humans may occur by consumption of meat of livestock infected after exposure to wildlife (Pozio et al. 2009).

Ouchene, N., N. A. Ouchene-Khelifi, et al. (2014). "Study of Giardia spp., Cryptosporidium spp. and Eimeria spp. infections in dairy cattle in Algeria." Journal of parasitology and vector biology 6(4): 61-65.

Portier, J., I. Vallee, et al. (2014). "Increasing circulation of Alaria alata mesocercaria in wild boar populations of the Rhine valley, France, 2007-2011." Vet Parasitol 199(3-4): 153-159.

The presence of the mesocercarial stage of Alaria alata (Goeze, 1792) in wild boar meat represents a potential risk for human, but little is known about the circulation of mesocercaria in wild boar populations. Routine Trichinella inspection, mandatorily performed in wild boar in France, also allowed detecting mesocercaria. We analyzed the results of this detection in the carcasses of 27,582 wild boars hunted in 2007-2011, in 502 hunting areas of the Rhine valley. Prevalence was globally low (0.6%), but 12% of the hunting areas were affected. These were clustered in lowlands of the Rhine valley, and prevalence strongly decreased with increasing elevation. In the lowlands, prevalence doubled between 2007 and 2011. This time trend and the geographic aggregation of positive wild boars suggest risk management measures based on targeted surveillance, control and prevention.

Rizzoli, A., C. Silaghi, et al. (2014). "Ixodes ricinus and its transmitted pathogens in urban and peri-urban areas in Europe: new hazards and relevance for public health. ." Frontiers in Public Health 2.

Slezak, K., Z. Krupova, et al. (2014). "Association of germ-free mice with a simplified human intestinal microbiota results in a shortened intestine." Gut Microbes 5(2): 176-182.

Genetic, nutritional, and gut microbiota-derived factors have been proposed to play a role in the development of the whole intestine that is around 40% longer in PRM/Alf mice compared with other mouse strains. The PRM/Alf genotype explains 60% of this length difference. The remaining 40% are due to a maternal effect that could depend on the gut microbiota transmitted by the mother to their pups. Germ-free PRM/Alf mice and C3H/He mice were associated with a simplified human microbiota (SIHUMI) to study its impact on gut length. The small intestines of the SIHUMI-associated mice were 16.4% (PRM/Alf) and 9.7% (C3H/He) shorter than those of the corresponding germ-free counterparts. Temporal temperature gradient gel electrophoresis and quantitative real-time PCR revealed differences in microbiota composition between both SIHUMI-associated mouse strains. Anaerostipes caccae was one log lower in PRM/Alf mice than in C3H/He mice. Since polyamines and short-chain fatty acids (SCFAs) are important intestinal growth factors, their concentrations were explored. Cecal concentrations of putrescine, spermine, spermidine, and N-acetylspermine were 1.5-fold, 3.7-fold, 2.2-fold, and 1.4-fold higher, respectively, in the SIHUMI-C3H/He mice compared with the SIHUMI-PRM/Alf mice. In addition, cecal acetate, propionate, and butyrate concentrations in SIHUMI-C3H/He mice were 1.4-fold, 1.1-fold, and 2.1-fold higher, respectively, than in SIHUMI-PRM/Alf mice. These results indicate that polyamines and SCFAs did not promote gut lengthening in any of the two mouse strains. This suggests that as yet unknown factors provided by the SIHUMI prevented gut lengthening in the SIHUMI-associated mice compared with the germfree mice.

Vaumourin, E., G. Vourc'h, et al. (2014). "To be or not to be associated: power study of four statistical modeling approaches to identify parasite associations in cross-sectional studies." Front Cell Infect Microbiol 4: 62.

A growing number of studies are reporting simultaneous infections by parasites in many different hosts. The detection of whether these parasites are significantly associated is important in medicine and epidemiology. Numerous approaches to detect associations are available, but only a few provide statistical tests. Furthermore, they generally test for an overall detection of association and do not identify which parasite is associated with which other one. Here, we developed a new approach, the association screening approach, to detect the overall and the detail of multi-parasite associations. We studied the power of this new approach and of three other known ones (i.e., the generalized chi-square, the network and the multinomial GLM approaches) to identify parasite associations either due to parasite interactions or to confounding factors. We applied these four approaches to detect associations within two populations of multi-infected hosts: (1) rodents infected with Bartonella sp., Babesia microti and Anaplasma phagocytophilum and (2) bovine population infected with Theileria sp. and Babesia sp. We found that the best power is obtained with the screening model and the generalized chi-square test. The differentiation between associations, which are due to confounding factors and parasite interactions was not possible. The screening approach significantly identified associations between Bartonella doshiae and B. microti, and between T. parva, T. mutans, and T. velifera. Thus, the screening approach was relevant to test the overall presence of parasite associations and identify the parasite combinations that are significantly over- or under-represented. Unraveling whether the associations are due to real biological interactions or confounding factors should be further investigated. Nevertheless, in the age of genomics and the advent of new technologies, it is a considerable asset to speed up researches focusing on the mechanisms driving interactions between parasites.

Vayssier-Taussat, M., E. Albina, et al. (2014). "Shifting the paradigm from pathogens to pathobiome: new concepts in the light of meta-omics." Front Cell Infect Microbiol 4: 29.

The concept of pathogenesis has evolved considerably over recent years, and the scenario "a microbe + virulence factors = disease" is probably far from reality in a number of cases. Actual pathogens have extremely broad biological diversity and are found in all major groups of microorganisms (viruses, bacteria, fungi, protozoa...). Their pathogenicity results from strong and often highly specific interactions they have with either their microbial environment, hosts and/or arthropod vectors. In this review, we explore the contribution of metagenomic approaches toward understanding pathogens within the context of microbial communities. With this broader view, we discussed the concept of "pathobiome" and the research questions that this raises.

Zocevic, A., S. A. Lacour, et al. (2014). "Primary characterization and assessment of a T. spiralis antigen for the detection of Trichinella infection in pigs." Vet Parasitol 205(3-4): 558-567.

A clone, designated L20h-Ts3, was selected by immunoscreening of cDNA libraries of Trichinella spiralis worms collected 14h, 20h and 48h post-infection (p.i.) from mice intestines. L20h-Ts3 encodes the full-length of a conserved hypothetical protein of 13.1kDa involving putative interaction with the immune system. PCR analysis showed that L20h-Ts3 mRNA is constitutively expressed throughout T. spiralis life cycle and not restricted to intestinal stages. The L20h-Ts3 fusion protein was obtained in an Escherichia coli expression system and purified by Ni-affinity chromatography before inoculation into mice in order to produce polyclonal antibodies. Then, immunohistochemical study and Western blot analysis revealed its presence within the stichosome of T. spiralis and in excretory/secretory products strengthening a putative fundamental role for the parasite's survival such as host tissue invasion or modification of the host muscular cell phenotype. L20h-Ts3 fusion protein was recognized in Western blot as soon as 15-20 days p.i. by sera from pigs experimentally infected with 20,000 muscle larvae (ML) of T. spiralis. Thus, an indirect L20h-Ts3 ELISA was designed and evaluated using sera from experimentally infected pigs by comparison with the only ELISA currently available for trichinellosis purposes. A gain of precocity from 7 up to 14 days and detection up to 25 weeks p.i. was possible with the L20h-Ts3 ELISA offering a large window for trichinellosis detection. The L20h-Ts3 ELISA was less effective in the case of low infections in pigs. Nevertheless, these results show that the L20h-Ts3 ELISA has a real interest due to its precocity and stability of detection in time. The association of the L20h-Ts3 fusion protein with other antigenic proteins identified previously could appreciably improve the serological test and facilitate its standardization.

2015

Ait Lbacha, H., S. Alali, et al. (2015). "High Prevalence of Anaplasma spp. in Small Ruminants in Morocco." Transbound Emerg Dis.

The prevalence of infection by Anaplasma spp. (including Anaplasma phagocytophilum) was determined using blood smear microscopy and PCR through screening of small ruminant blood samples collected from seven regions of Morocco. Co-infections of Anaplasma spp., Babesia spp, Theileria spp. and Mycoplasma spp. were investigated and risk factors for Anaplasma spp. infection assessed. A total of 422 small ruminant blood samples were randomly collected from 70 flocks. Individual animal (breed, age, tick burden and previous treatment) and flock data (GPS coordinate of farm, size of flock and livestock production system) were collected. Upon examination of blood smears, 375 blood samples (88.9%) were found to contain Anaplasma-like erythrocytic inclusion bodies. Upon screening with a large spectrum PCR targeting the Anaplasma 16S rRNA region, 303 (71%) samples were found to be positive. All 303 samples screened with the A. phagocytophilum-specific PCR, which targets the msp2 region, were found to be negative. Differences in prevalence were found to be statistically significant with regard to region, altitude, flock size, livestock production system, grazing system, presence of clinical cases and application of tick and tick-borne diseases prophylactic measures. Kappa analysis revealed a poor concordance between microscopy and PCR (k = 0.14). Agreement with PCR is improved by considering microscopy and packed cell volume (PCV) in parallel. The prevalence of double infections was found to be 1.7, 2.5 and 24% for Anaplasma-Babesia, Anaplasma-Mycoplasma and Anaplasma-Theileria, respectively. Co-infection

with three or more haemoparasites was found in 1.6% of animals examined. In conclusion, we demonstrate the high burden of anaplasmosis in small ruminants in Morocco and the high prevalence of co-infections of tick-borne diseases. There is an urgent need to improve the control of this neglected group of diseases.

Azzag, N., E. Petit, et al. (2015). "Prevalence of select vector-borne pathogens in stray and client-owned dogs from Algiers." Comp Immunol Microbiol Infect Dis 38: 1-7.

Data on the prevalence of vector-borne diseases agents infecting canines in Algeria is currently lacking. The purpose of this study is to assess by serological and molecular methods the prevalence of select arthropod borne-bacterial infections in client-owned and stray dogs. Antibodies to Anaplasma phagocytophilum were the most prevalent at 47.7%, followed by Borrelia burgdorferi s.l. at 37.6%, Ehrlichia canis at 30.0%, Bartonella henselae at 32.4% and Bartonella vinsonii subsp. berkhoffii at 27%. Seroprevalence was statistically significantly higher in stray dogs than those owned by clients. Seropositivity was not associated with health status, except for E. canis. Molecular evaluation indicates that 17.8% of the 213 analyzed dogs were positive for Ehrlichia and Anaplasma with a prevalence of 4.2% for E. canis, 14.1% for Anaplama platys and 0% for A. phagocytophilum. Seven (7.1%) of the tested dogs were positive for Bartonella spp. with two characterized as Bartonella rochalimae, four as B. henselae and one as B.v. subsp. berkhoffii.

Baneth, G., S. M. Thamsborg, et al. (2015). "Major Parasitic Zoonoses Associated with Dogs and Cats in Europe." J Comp Pathol.

Some of the most important zoonotic infectious diseases are associated with parasites transmitted from companion animals to man. This review describes the main parasitic zoonoses in Europe related to dogs and cats, with particular emphasis on their current epidemiology. Toxoplasmosis, leishmaniosis, giardiosis, echinococcosis, dirofilariosis and toxocariosis are described from the animal, as well as from the human host perspectives, with an emphasis on parasite life cycle, transmission, pathogenicity, prevention and identification of knowledge gaps. In addition, priorities for research and intervention in order to decrease the risks and burden of these diseases are presented. Preventing zoonotic parasitic infections requires an integrated multidisciplinary 'One Health' approach involving collaboration between veterinary and medical scientists, policy makers and public health officials.

Bermudez-Humaran Luis, G., T. Allain, et al. (2015). COMPOSITIONS FOR THE INHIBITION OF GIARDIA LAMBLIA. INRA. EP14306265.1.

Bouhsira, E., M. Franc, et al. (2015). "The efficacy of a selamectin (Stronghold (R)) spot on treatment in the prevention of Bartonella henselae transmission by Ctenocephalides felis in cats, using a new high-challenge model." Parasitol Res 114(3): 1045-1050.

Bartonella henselae is the causative agent of cat scratch disease in humans, which is recognized as an emerging zoonotic disease. Ctenocephalides felis is the main vector, and transmission of B. henselae infection between cats and humans occurs mainly through infected flea feces. Control of feline infestation with this arthropod vector therefore provides an important strategy for the prevention of infection of both humans and cats. In the present study, a new challenge model is used to evaluate the efficacy of selamectin (Stronghold((R)) spot on) in the prevention of B. henselae transmission by C. felis. In this new challenge model, domestic cats were infected by direct application of B. henselae-positive fleas. The fleas used for infestation were infected by feeding on blood that contained in vitro-cultured B. henselae. The direct application of the fleas to the animals and the use of different B. henselae strains ensured a high and consistent challenge. Two groups of six cats were randomly allocated on pre-treatment flea counts to either control (untreated cats) or the selamectin-treated group with one pipette per cat according to the label instruction. Stronghold (selamectin 6 % spot on solution) was administered on days 0 and 32. On days 3, 10, 19, 25, and 31, each cat was infested by direct application of 20 fleas that fed on blood inoculated with B. henselae. Polymerase chain reaction (PCR) on pooled fleas confirmed that the fleas were infected. Blood samples were collected from each cat on days -3 (prior to flea infestation and treatment), 9, 17, 24, 30, 37, and 44 and assayed for B. henselae antibodies using an indirect immunofluorescence (IFA), for the presence of bacteria by bacterial culture and for B. henselae DNA presence by PCR. Cats were also assessed on a daily basis for general health. There were no abnormal health observations during the study and none of the animals required concomitant treatment. None of the cats displayed any clinical signs of bartonellosis during the study. In the untreated group, all cats became bacteremic within 17 to 44 days. None of the selamectin-treated cats became positive during the study. It was concluded that Stronghold((R)) spot on administered to cats was efficacious in the prevention of the transmission of B. henselae by fleas to cats in a high-challenge model.

Boulouis HJ, A.-C. L., Th. Dugat et Haddad N. Les animaux vertébrés et les maladies dues à des bactéries vectorisées par les tiques. Revue Francophone des Laboratoires. Mai 2015 ; 472, 35-45.

Cavana, P., E. Bensignor, et al. (2015). "Nematode dermatitis due to Angiostrongylus vasorum infection in a dog." Vet Dermatol 26(4): 293-e265.

BACKGROUND: Angiostrongylus vasorum is a nematode that primarily infects Canidae. The adult parasites are found in the pulmonary arterial circulation and the right side of the heart. The most common clinical sign is respiratory dysfunction. Bleeding, neurological, ocular, cardiovascular and gastrointestinal disorders are also reported. Skin lesions are very unusual. HYPOTHESIS/OBJECTIVES: This report describes a nematode dermatitis due to A. vasorum infection. To the best of the authors' knowledge, this is the first case of a dog infected with this parasite that initially presented with skin lesions only. ANIMAL: A 3-year-old female Weimaraner dog presented with a crusted papular dermatitis on the bridge of the nose and on the pinnae, and an erythematous pododermatitis with erosions and perionyxis of one digit of 1 week's duration. Two weeks later the dog developed respiratory distress. METHODS AND RESULTS: Skin scrapings and fungal culture were negative for parasites and dermatophytes. Histopathological examination showed dermal

granulomas and pyogranulomas with eosinophils centred around parasitic elements compatible with nematode larvae. Angiostrongylus vasorum DNA was demonstrated in skin biopsies. Chest radiographs were compatible with verminous pneumonia and a Baermann test revealed A. vasorum larvae. The dog was treated orally with fenbendazole, with rapid improvement and complete cure after 3 months. CONCLUSIONS AND CLINICAL IMPORTANCE: Angiostrongylus vasorum should be considered in dogs presented with skin lesions and respiratory signs. Skin biopsy, chest radiographs and Baermann test should be included in the diagnostic investigation.

Chastant-Maillard, S., H. J. Boulouis, et al. (2015). "Lack of transplacental transmission of Bartonella bovis." Comp Immunol Microbiol Infect Dis 38: 41-46.

Transplacental transmission of Bartonella spp. has been reported for rodents, but not for cats and has never been investigated in cattle. The objective of this study was to assess vertical transmission of Bartonella in cattle. Fifty-six cow-calf pairs were tested before (cows) and after (calves) caesarean section for Bartonella bacteremia and/or serology, and the cotyledons were checked for gross lesions and presence of the bacteria. None of the 29 (52%) bacteremic cows gave birth to bacteremic calves, and all calves were seronegative at birth. Neither placentitis nor vasculitis were observed in all collected cotyledons. Bartonella bovis was not detected in placental cotyledons. Therefore, transplacental transmission of B. bovis and multiplication of the bacteria in the placenta do not seem likely. The lack of transplacental transmission may be associated with the particular structure of the placenta in ruminants or to a poor affinity/agressiveness of B. bovis for this tissue.

Clement, M., G. Fornasa, et al. (2015). "Upholding the T cell immune-regulatory function of CD31 inhibits the formation of T/B immunological synapses in vitro and attenuates the development of experimental autoimmune arthritis in vivo." J Autoimmun 56: 23-33.

CD31, a trans-homophilic inhibitory receptor expressed on both T- and B-lymphocytes, drives the mutual detachment of interacting leukocytes. Intriguingly, T cell CD31 molecules relocate to the immunological synapse (IS), where the T and B cells establish a stable interaction. Here, we show that intact CD31 molecules, which are able to drive an inhibitory signal, are concentrated at the periphery of the IS but are excluded from the center of the IS. At this site, were the cells establish the closest contact, the CD31 molecules are cleaved, and most of the extracellular portion of the protein, including the trans-homophilic binding sites, is shed from the cell surface. T cells lacking CD31 trans-homophilic binding sites easily establish stable interactions with B cells; at the opposite, CD31 signaling agonists inhibit T/B IS formation as well as the ensuing helper T cell activation and function. Confocal microscopy and flow cytometry analysis of experimental T/B IS shows that the T cell inhibitory effects of CD31 agonists depend on SHP-2 signaling, which reduces the phosphorylation of ZAP70. The analysis of synovial tissue biopsies from patients affected by rheumatoid arthritis showed that T cell CD31 molecules are excluded from the center of the T/B cell synapses in vivo. Interestingly, the administration of CD31 agonists in vivo significantly attenuated the development of the clinical signs of collagen-induced arthritis in DBA1/J mice. Altogether, our data indicate that the T cell co-inhibitory receptor CD31 prevents the formation of functional T/B immunological synapses

and that therapeutic strategies aimed at sustaining CD31 signaling will attenuate the development of autoimmune responses in vivo.

Cong, W., Q. F. Meng, et al. (2015). "Toxoplasma gondii, Dirofilaria immitis, feline immunodeficiency virus (FIV), and feline leukemia virus (FeLV) infections in stray and pet cats (Felis catus) in northwest China: co-infections and risk factors." Parasitol Res.

This study was conducted to estimate the prevalence of Toxoplasma gondii, Dirofilaria immitis, feline immunodeficiency virus (FIV), and feline leukemia virus (FeLV) infections among stray and pet cats in Lanzhou, northwest China, and to identify the influence of age, gender, and regions on seropositivity. T. gondii antibodies were examined in cat sera by the modified agglutination test (MAT). The circulating antigens of D. immitis and FeLV and specific antibodies to FIV were examined using kits commercially available. The overall prevalence of T. gondii, FIV, FeLV, and D. immitis was 19.34, 9.12, 11.33, and 3.04 %, respectively. For the genetic characterization of T. gondii genotypes in cats, genomic DNA was extracted from the seropositive cats and the T. gondii B1 gene was amplified using a semi-nested PCR. DNA samples giving positive B1 amplification were then genotyped using multilocus PCR-RFLP. Two T. gondii genotypes (ToxoDB#9 and ToxoDB#1) were identified. Results of the multivariate logistic regression analysis showed that older cats are more likely to be seropositive than juveniles for T. gondii, FIV, FeLV, and D. immitis. This is the first report of T. gondii genotypes in cats in northwest China. Moreover, the present study is the first study of retrovirus and D. immitis seroprevalence in cats in China. The results revealed that T. gondii, FIV, and FeLV infections are common in stray and pet cats in northwest China.

Dugat, T., A. C. Lagree, et al. (2015). "Opening the black box of Anaplasma phagocytophilum diversity: current situation and future perspectives." Front Cell Infect Microbiol 5: 61.

Anaplasma phagocytophilum is a zoonotic obligate intracellular bacterium known to be transmitted by ticks belonging to the Ixodes persulcatus complex. This bacterium can infect several mammalian species, and is known to cause diseases with variable symptoms in many domestic animals. Specifically, it is the causative agent of tick-borne fever (TBF), a disease of important economic impact in European domestic ruminants, and human granulocytic anaplasmosis (HGA), an emerging zoonotic disease in Asia, USA and Europe. A. phagocytophilum epidemiological cycles are complex and involve different ecotypes, vectors, and mammalian host species. Moreover, the epidemiology of A. phagocytophilum infection differs greatly between Europe and the USA. These different epidemiological contexts are associated with considerable variations in bacterial strains. Until recently, few A. phagocytophilum molecular typing tools were available, generating difficulties in completely elucidating the epidemiological cycles of this bacterium. Over the last few years, many A. phagocytophilum typing techniques have been developed, permitting in-depth epidemiological exploration. Here, we review the current knowledge and future perspectives regarding A. phagocytophilum epidemiology and phylogeny, and then focus on the molecular typing tools available for studying A. phagocytophilum genetic diversity.

Fleischman, D. A., B. B. Chomel, et al. (2015). "Bartonella Infection among Cats Adopted from a San Francisco Shelter, Revisited." Appl Environ Microbiol 81(18): 6446-6450.

Bartonella infection among cats from shelters can pose a health risk to adopters. Bartonella henselae is the most common species, with B. clarridgeiae and B. koehlerae being less common. The lower rates of infection by the latter species may reflect their rarity or an inefficiency of culture techniques. To assess the incidence of infection, blood cultures, serology, and PCR testing were performed on 193 kittens (6 to 17 weeks old) and 158 young adult cats (5 to 12 months old) from a modern regional shelter. Classical B. henselae culture medium was compared to a medium supplemented with insect cell growth factors. Bartonella colonies were isolated from 115 (32.8%) animals, including 50 (25.9%) kittens and 65 (41.1%) young adults. Therefore, young adults were twice as likely to be culture positive as kittens. Enhanced culture methods did not improve either the isolation rate or species profile. B. henselae was isolated from 40 kittens and 55 young adults, while B. clarridgeiae was cultured from 10 animals in each group. B. koehlerae was detected in one young adult by PCR only. B. henselae genotype II was more commonly isolated from young adults, and genotype I was more frequently isolated from kittens. Kittens were 4.7 times more likely to have a very high bacterial load than young adults. A significantly higher incidence of bacteremia in the fall and winter than in the spring and summer was observed. Bartonella antibodies were detected in 10% (19/193) of kittens and 46.2% (73/158) of young adults, with culture-positive kittens being 9.4 times more likely to be seronegative than young adults.

Grellet, A., S. E. Makhlouf, et al. (2015). "Efficacy of guar gum-based ronidazole capsules as a treatment for Tritrichomonas foetus infection in cats." J Feline Med Surg.

OBJECTIVES: The aims of the study were to determine the in vitro drug release of guar gum-coated capsules of ronidazole, and to evaluate the pharmacokinetics and efficacy of this formulation for the treatment of cats naturally infected with Tritrichomonas foetus. METHODS: The pharmacokinetics of ronidazole were evaluated in five healthy cats and five cats infected with T foetus. In a second step, the clinical efficacy of these capsules was evaluated by a controlled, randomised, double-blind clinical trial performed in 47 infected cats from French catteries. In this study, cats were randomly allocated to either the ronidazole treatment group (n = 25) or a placebo group (n = 22). Ronidazole (30 mg/kg) q24h for 14 days was administered to the treated cats. After 14 days of treatment, the presence of T foetus was tested by conventional PCR assay. RESULTS: In the pharmacokinetic study, a delayed peak plasma concentration was observed in healthy and infected cats, with no significant difference between these two groups (mean geometric mean of 9 h for time to maximum plasma concentration [Tmax], 21.6 microg/ml for time to maximum plasma concentration [Cmax] and 467.4 mug/h/ml for the area under the curve [AUC] in healthy cats; and 9.4 h for Tmax, 17.1 microg/ml for Cmax and 481 mug/h/ml for AUC in infected cats). In the clinical trial, T foetus was detected in 16% of cats from the treated group and 82% of cats from the placebo group at the end of the study ($P < 0.001$). No clinical signs of adverse drug reactions were observed. CONCLUSIONS AND RELEVANCE: Oral administration of guar gum-coated capsules of ronidazole at a dose of 30 mg/kg once daily for 14 days delays the peak plasma concentration and eradicates infection in most cases.

2016

Bai, X., X. L. Wang, et al. (2016). "The roles of supernatant of macrophage treated by excretory-secretory products from muscle larvae of Trichinella spiralis on the differentiation of C2C12 myoblasts." Vet Parasitol.

The excretory-secretory products (ESPs) released by the muscle-larvae (ML) stage of Trichinella spiralis have been suggested to be involved in nurse cell formation. However, the molecular mechanisms by which ML-ESPs modulate nurse cell formation remain unclear. Macrophages exert either beneficial or deleterious effects on tissue repair, depending on their activation/polarization state. They are crucial for skeletal muscle repair, notably, via their actions on myogenic precursor cells. However, these interactions during T. spiralis infection have not been characterized. In the present study, the ability of conditioned medium (CM) from J774A.1 macrophages treated with ML-ESPs to influence the differentiation of murine myoblasts, and the mechanisms of this influence, were investigated in vitro. The results showed that the expression of Myogenic Regulatory Factors (MRFs) MyoD and myogenin, myosin heavy chain (MyHC), and the p21 cyclin-dependent kinase inhibitor were reduced in CM treated cells compared to their expression in the control group. These findings indicated that CM inhibited myoblast differentiation. Conversely, CM promoted myoblast proliferation and increased cyclin D1 levels. Taken together, results of our study suggested that CM can indirectly influence myoblast differentiation and proliferation, which provides a new method for the elucidation of the complex mechanisms involved in cell-parasite and cell-cell interactions during T. spiralis infection.

Baneth, G., S. M. Thamsborg, et al. (2016). "Major Parasitic Zoonoses Associated with Dogs and Cats in Europe." J Comp Pathol 155(1 Suppl 1): S54-74.

Some of the most important zoonotic infectious diseases are associated with parasites transmitted from companion animals to man. This review describes the main parasitic zoonoses in Europe related to dogs and cats, with particular emphasis on their current epidemiology. Toxoplasmosis, leishmaniosis, giardiosis, echinococcosis, dirofilariosis and toxocariosis are described from the animal, as well as from the human host perspectives, with an emphasis on parasite life cycle, transmission, pathogenicity, prevention and identification of knowledge gaps. In addition, priorities for research and intervention in order to decrease the risks and burden of these diseases are presented. Preventing zoonotic parasitic infections requires an integrated multidisciplinary 'One Health' approach involving collaboration between veterinary and medical scientists, policy makers and public health officials.

BERMUDEZ-HUMARAN, L., T. ALLAIN, et al. (2016). Compositions for the Inhibition of Giardia Lamblia.
http://worldwide.espacenet.com/publicationDetails/biblio?FT=D&date=20160211&DB=&locale=fr_EP&CC=WO&NR=2016020544A1&KC=A1&ND=4. France.

Berthoin, L., B. Toussaint, et al. (2016). "Targeted release of transcription factors for cell reprogramming by a natural micro-syringe." Int J Pharm 513(1-2): 678-687.

Ectopic expression of defined transcription factors (TFs) for cell fate handling has proven high potential interest in reprogramming differentiated cells, in particular for regenerative medicine, ontogenesis study and cell based modelling. Pluripotency or transdifferentiation induction as TF mediated differentiation is commonly produced by transfer of genetic information with safety concerns. The direct delivery of proteins could represent a safer alternative but still needs significant advances to be efficient. We have successfully developed the direct delivery of proteins by an attenuated bacterium with a type 3 secretion system that does not require challenging and laborious steps for production and purification of recombinant molecules. Here we show that this natural micro-syringe is able to inject TFs to primary human fibroblasts and cord blood CD34+ hematopoietic stem cells. The signal sequence for vectorization of the TF Oct4 has no effect on DNA binding to its nucleic target. As soon as one hour after injection, vectorized TFs are detectable in the nucleus. The injection process is not associated with toxicity and the bacteria can be completely removed from cell cultures. A three days targeted release of Oct4 or Sox2 embryonic TFs results in the induction of the core pluripotency genes expression in fibroblasts and CD34+ hematopoietic stem cells. This micro-syringe vectorization represents a new strategy for TF delivery and has potential applications for cell fate reprogramming.

Bonnet, S. (2016). "Mise en place d'une méthode alternative au modèle animal pour l'infection et le gorgement des tiques." Bulletin des Anciens Elèves de l'Institut Pasteur 58(227): 48-52.

Chomel, B. B., S. Molia, et al. (2016). "Isolation of Bartonella henselae and Two New Bartonella Subspecies, Bartonellakoehlerae Subspecies boulouisii subsp. nov. and Bartonella koehlerae Subspecies bothieri subsp. nov. from Free-Ranging Californian Mountain Lions and Bobcats." PLoS One 11(3): e0148299.

Domestic cats are the natural reservoir of Bartonella henselae, B. clarridgeiae and B. koehlerae. To determine the role of wild felids in the epidemiology of Bartonella infections, blood was collected from 14 free-ranging California mountain lions (Puma concolor) and 19 bobcats (Lynx rufus). Bartonella spp. were isolated from four (29%) mountain lions and seven (37%) bobcats. These isolates were characterized using growth characteristics, biochemical reactions, molecular techniques, including PCR-RFLP of selected genes or interspacer region, pulsed-field gel electrophoresis (PFGE), partial sequencing of several genes, and DNA-DNA hybridization. Two isolates were identical to B. henselae genotype II. All other isolates were distinguished from B. henselae and B. koehlerae by PCR-RFLP of the gltA gene using endonucleases HhaI, TaqI and AciI, with the latter two discriminating between the mountain lion and the bobcat isolates. These two novel isolates displayed specific PFGE profiles distinct from B. henselae, B. koehlerae and B. clarridgeiae. Sequences of amplified gene fragments from the three mountain lion and six bobcat isolates were closely related to, but distinct from, B. henselae and B. koehlerae. Finally, DNA-DNA hybridization studies

demonstrated that the mountain lion and bobcat strains are most closely related to B. koehlerae. We propose naming the mountain lion isolates B. koehlerae subsp. boulouisii subsp. nov. (type strain: L-42-94), and the bobcat isolates B. koehlerae subsp. bothieri subsp. nov. (type strain: L-17-96), and to emend B. koehlerae as B. koehlerae subsp. koehlerae. The mode of transmission and the zoonotic potential of these new Bartonella subspecies remain to be determined.

Cong, W., Q. F. Meng, et al. (2016). "Toxoplasma gondii, Dirofilaria immitis, feline immunodeficiency virus (FIV), and feline leukemia virus (FeLV) infections in stray and pet cats (Felis catus) in northwest China: co-infections and risk factors." Parasitol Res 115(1): 217-223.

This study was conducted to estimate the prevalence of Toxoplasma gondii, Dirofilaria immitis, feline immunodeficiency virus (FIV), and feline leukemia virus (FeLV) infections among stray and pet cats in Lanzhou, northwest China, and to identify the influence of age, gender, and regions on seropositivity. T. gondii antibodies were examined in cat sera by the modified agglutination test (MAT). The circulating antigens of D. immitis and FeLV and specific antibodies to FIV were examined using kits commercially available. The overall prevalence of T. gondii, FIV, FeLV, and D. immitis was 19.34, 9.12, 11.33, and 3.04 %, respectively. For the genetic characterization of T. gondii genotypes in cats, genomic DNA was extracted from the seropositive cats and the T. gondii B1 gene was amplified using a semi-nested PCR. DNA samples giving positive B1 amplification were then genotyped using multilocus PCR-RFLP. Two T. gondii genotypes (ToxoDB#9 and ToxoDB#1) were identified. Results of the multivariate logistic regression analysis showed that older cats are more likely to be seropositive than juveniles for T. gondii, FIV, FeLV, and D. immitis. This is the first report of T. gondii genotypes in cats in northwest China. Moreover, the present study is the first study of retrovirus and D. immitis seroprevalence in cats in China. The results revealed that T. gondii, FIV, and FeLV infections are common in stray and pet cats in northwest China.

Della Rossa, P., K. Tantrakarnapa, et al. (2016). "Environmental factors and public health policy associated with human and rodent infection by leptospirosis: a land cover-based study in Nan province, Thailand." Epidemiol Infect 144(7): 1550-1562.

Leptospirosis incidence has increased markedly since 1995 in Thailand, with the eastern and northern parts being the most affected regions, particularly during flooding events. Here, we attempt to overview the evolution of human prevalence during the past decade and identify the environmental factors that correlate with the incidence of leptospirosis and the clinical incidence in humans. We used an extensive survey of Leptospira infection in rodents conducted in 2008 and 2009 and the human incidence of the disease from 2003 to 2012 in 168 villages of two districts of Nan province in Northern Thailand. Using an ad-hoc developed land-use cover implemented in a geographical information system we showed that humans and rodents were not infected in the same environment/habitat in the land-use cover. High village prevalence was observed in open habitat near rivers for the whole decade, or in 2008-2009 mostly in rice fields prone to flooding, whereas infected rodents (2008-2009) were observed in patchy habitat with high forest cover, mostly situated on sloping ground areas. We also investigated the potential effects of public health campaigns conducted after the dramatic flood event of 2006. We showed that, before 2006, human incidence in

villages was explained by the population size of the village according to the environmental source of infection of this disease, while as a result of the campaigns, human incidence in villages after 2006 appeared independent of their population size. This study confirms the role of the environment and particularly land use, in the transmission of bacteria, emphasized by the effects of the provincial public health campaigns on the epidemiological pattern of incidence, and questions the role of rodents as reservoirs.

Deng, H., Q. Pang, et al. (2016). "Identification and functional analysis of invasion associated locus B (IalB) in Bartonella species." Microb Pathog 98: 171-177.

Bartonellosis is caused by the genus Bartonella. Bartonella is widely distributed in the ruminants, cats, dogs, rodents and other mammals including humans. At least 13 species or subspecies of Bartonella are zoonotic, and each species appears to be highly adapted to one or a limited number of reservoir animals in which it is asymptomatic, while it can be transmitted to humans in which a variety of clinical manifestations can be caused. It was reported that Bartonella henselae infection rate among domestic cats was high in nature, making it one of the leading, important, and easily neglected zoonotic diseases. The aims of this study were to identify the expression, localization, immunogenicity and functional mechanism of Bartonella virulence factor IalB. We found that recombinant IalB protein could react with the serum from infected reservoir hosts and anti-IalB polyclonal antibodies could react with different Bartonella species by western blot analysis. According to these results, we proposed that IalB protein and anti-IalB antibodies would be good candidates for diagnosis of Bartonella infection by antigen-based anti-IalB antibodies or antibody-based IalB antigen capture immunoassay, respectively. We also found that IalB had a putative 22-amino-acid signal sequence and little IalB was localized to the outer membrane of Bartonella birtlesii by electron microscopy assay. Incubation with anti-IalB polyclonal antibodies resulted in inhibition of the invasion of mouse erythrocytes by B. birtlesii. According to these results, we propose that IalB could be a secreted protein that facilitates Bartonella entry into erythrocytes. In conclusion, these results improve our understanding of IalB as a candidate for immunodiagnosis and how IalB affects Bartonella-erythrocyte entry.

Ding, J., X. Bai, et al. (2016). "Developmental profile of select immune cells in mice infected with Trichinella spiralis during the intestinal phase." Vet Parasitol.

Trichinella spiralis can cause immunosuppression during the intestinal phase of early infection. However, changes in the peripheral blood during T. spiralis early infection remain unclear. Here, select immune cells in mice infected with 500 muscle larvae (ML) of T. spiralis during the intestinal phase of infection were studied. First, the recovery rates of the intestinal worms and female fecundity were determined, and the results showed that the intestinal worms were completely eliminated at 17 days post-infection (dpi) and that large numbers of new-born larvae (NBL) were generated from 5 to 9dpi. Using flow cytometry, it was shown that the number of CD4+ T cells and CD8+ T cells increased over the entire intestinal phase, except on 7dpi when CD4+ T cells decreased significantly compared to the control groups. Although both CD4+ and CD8+ T cells increased, CD8+ T cells increased more than CD4+ T cells, leading to a lower CD4+/CD8+ ratio

compared to the control group. Subsequently, a depression of the proliferative response of T cells to concanavalin A (Con A) was noticed at 7 and 11dpi. Although the proliferative response of B cells to LPS was enhanced, the number of B cells from mouse peripheral blood stimulated by T. spiralis antigens showed no differences with the control group prior to 11dpi. The expression of CD14 on monocyte-macrophages decreased during the same period, which meant that the antigen-presenting response was reduced in the immune system of the infected mice. Moreover, the alternatively activated macrophages were induced in T. spiralis early infection. These data provide a better understanding of the development of the intestinal immune response in mice infected with T. spiralis.

Djokic, V., R. Blaga, et al. (2016). "Toxoplasma gondii infection in pork produced in France." Parasitology 143(5): 557-567.

The aim of this study was to assess the seroprevalence of the Toxoplasma gondii parasite in pork produced in France, and to determine infection risk factors. An innovative survey was designed based on annual numbers of slaughtered pigs from intensive and outdoor farms in France. A total of 1549 samples of cardiac fluids were collected from pig hearts to determine seroprevalence using a Modified Agglutination Test. Of those, 160 hearts were bio-assayed in mice to isolate live parasites. The overall seroprevalence among fattening pigs was 2.9%. The adjusted seroprevalence in pigs from intensive farms was 3.0%; the highest in sows (13.4%); 2.9% in fattening pigs and 2.6% in piglets. Adjusted seroprevalence in fattening animals from outdoor farms was 6.3%. Strains were isolated from 41 animals and all were genotyped by Restriction Fragment Length Polymorphism as type II. Risk-factor analysis showed that the risk of infection was more than three times higher for outdoor pigs, and that sows' risk was almost five times higher than that of fattening animals. This study provides further evidence of extensive pork infection with T. gondii regardless of breeding systems, indicating that farm conditions are still insufficient to guarantee 'Toxoplasma-free pork'.

Djokic, V., C. Fablet, et al. (2016). "Factors associated with Toxoplasma gondii infection in confined farrow-to-finish pig herds in western France: an exploratory study in 60 herds." Parasit Vectors 9: 466.

BACKGROUND: Infection by Toxoplasma gondii postnatally can occur after ingestion of contaminated meat or water (tissue cysts/oocysts). In Europe, percentage of meat borne infections is estimated between 30 and 63 %, out of which pork makes the most important source. The aim of this study was to (i) investigate the seroprevalence of T. gondii in intensive pig farms from western France; and (ii) identify the risk factors associated with seropositivity. METHODS: Data were collected between November 2006 and February 2008 in 60 intensive farrow-to-finish farms, where sera were taken from 3595 fattening pigs, weaned and suckling piglets. Information about three classes of potential seropositivity risk factors were obtained through a questionnaire concerning: (i) breeding characteristics; (ii) farm management; and (iii) husbandry and hygiene. The modified agglutination test (MAT) was used for detection of specific anti T. gondii antibodies in pig sera, starting from 1/6 dilution. RESULTS: The overall proportion of seropositive animals was 6.9 %, but the proportion of herds with at least one positive pig was 100 %. Multivariate logistic mixed model showed an

increased seropositivity risk in weaned compared to suckling piglets, and a decreasing risk for mid-sized and large farms. The presence of a Danish entry facility, that clearly separates clean and dirty areas, had a protective effect on T. gondii seropositivity as well. CONCLUSIONS: The observed proportion of herds with at least one T. gondii seropositive animal provides further evidence that even in confined conditions of pig breeding, infection occurs, and is common. The highest risk for acquiring T. gondii is at the end of weaning period. Smaller confined pig farms demonstrate higher T. gondii seropositivity levels. This study also showed that Danish entry on farm buildings provides effective protection against T. gondii.

Dubois, A., M. Galan, et al. (2016). "Microevolution of bank voles (Myodes glareolus) at neutral and immune-related genes during multiannual dynamic cycles: Consequences for Puumala hantavirus epidemiology." Infect Genet Evol.

Understanding how host dynamics, including variations of population size and dispersal, may affect the epidemiology of infectious diseases through ecological and evolutionary processes is an active research area. Here we focus on a bank vole (Myodes glareolus) metapopulation surveyed in Finland between 2005 and 2009. Bank vole is the reservoir of Puumala hantavirus (PUUV), the agent of nephropathia epidemica (NE, a mild form of hemorrhagic fever with renal symptom) in humans. M.glareolus populations experience multiannual density fluctuations that may influence the level of genetic diversity maintained in bank voles, PUUV prevalence and NE occurrence. We examine bank vole metapopulation genetics at presumably neutral markers and immune-related genes involved in susceptibility to PUUV (Tnf-promoter, Tlr4, Tlr7 and Mx2 gene) to investigate the links between population dynamics, microevolutionary processes and PUUV epidemiology. We show that genetic drift slightly and transiently affects neutral and adaptive genetic variability within the metapopulation. Gene flow seems to counterbalance its effects during the multiannual density fluctuations. The low abundance phase may therefore be too short to impact genetic variation in the host, and consequently viral genetic diversity. Environmental heterogeneity does not seem to affect vole gene flow, which might explain the absence of spatial structure previously detected in PUUV in this area. Besides, our results suggest the role of vole dispersal on PUUV circulation through sex-specific and density-dependent movements. We find little evidence of selection acting on immune-related genes within this metapopulation. Footprint of positive selection is detected at Tlr-4 gene in 2008 only. We observe marginally significant associations between Mx2 genotype and PUUV genogroups. These results show that neutral processes seem to be the main factors affecting the evolution of these immune-related genes at a contemporary scale, although the relative effects of neutral and adaptive forces could vary temporally with density fluctuations. Immune related gene polymorphism may in turn partly influence PUUV epidemiology in this metapopulation.

Dugat, T., D. Haciane, et al. (2016). "Short Report: Identification of a Potential Marker of Anaplasma Phagocytophilum Associated with Cattle Abortion." Transbound Emerg Dis.

Anaplasma phagocytophilum is a tick-borne pathogen that causes tick-borne fever in domestic ruminants. Tick-borne fever is characterized by diverse symptoms and occasionally causes abortions in domestic ruminants, resulting in significant economic impact. However, in France, the

potential frequency of A. phagocytophilum-related abortions is unknown, and thus, it remains difficult to estimate the full extent of its economic impact. This gap in our knowledge is likely explained, at least in part, by the absence of suitable and specific tools capable of detecting A. phagocytophilum associated with abortion. Our objective was to identify a genetic marker able to differentiate A. phagocytophilum strains isolated from domestic ruminants that had aborted compared to those that had not. Thus, we typed a total of 123 A. phagocytophilum obtained from cattle, of which 25 originated from cows that had aborted, via multiple-locus variable-number tandem repeat (VNTR) analysis. These included 56 new A. phagocytophilum samples and 67 previously published A. phagocytophilum samples. A multivariate logistic model demonstrated that the triple-repeat allele of the APV-A VNTR was statistically more frequent in A. phagocytophilum from cattle that had aborted, compared to A. phagocytophilum from cattle that had not aborted ($P = 0.03$), while controlling for any regional effects ($P < 0.0001$). For four other VNTR, there were no statistical associations between specific alleles and abortion. The APV-A triple-repeat VNTR allele could thus act as a marker of A. phagocytophilum involved in abortions. If this hypothesis is confirmed in additional samples from other regions, this marker could then be utilized in the development of A. phagocytophilum abortive strain surveillance measures.

Dugat, T., M. N. Rossignol, et al. (2016). "Draft Anaplasma phagocytophilum Genome Sequences from Five Cows, Two Horses, and One Roe Deer Collected in Europe." Genome Announc 4(6).

Anaplasma phagocytophilum is a zoonotic tick-borne intracellular bacterium responsible for granulocytic anaplasmosis. As it is difficult to isolate and cultivate, only 20 A. phagocytophilum genomes have been sequenced to date. Here, we present eight A. phagocytophilum genome sequences obtained using alternative approaches based on sequence capture technology.

Dugat, T., G. Zanella, et al. (2016). "Multiple-locus variable-number tandem repeat analysis potentially reveals the existence of two groups of Anaplasma phagocytophilum circulating in cattle in France with different wild reservoirs." Parasit Vectors 9(1): 596.

BACKGROUND: Anaplasma phagocytophilum is the causative agent of tick-borne fever, a disease with high economic impact for domestic ruminants in Europe. Epidemiological cycles of this species are complex, and involve different ecotypes circulating in various host species. To date, these epidemiological cycles are poorly understood, especially in Europe, as European reservoir hosts (i.e. vertebrate hosts enabling long-term maintenance of the bacterium in the ecosystem), of the bacterium have not yet been clearly identified. In this study, our objective was to explore the presence, the prevalence, and the genetic diversity of A. phagocytophilum in wild animals, in order to better understand their implications as reservoir hosts of this pathogen. METHODS: The spleens of 101 wild animals were collected from central France and tested for the presence of A. phagocytophilum DNA by msp2 qPCR. Positive samples were then typed by multi-locus variable-number tandem repeat (VNTR) analysis (MLVA), and compared to 179 previously typed A. phagocytophilum samples. RESULTS: Anaplasma phagocytophilum DNA was detected in 82/101 (81.2%) animals including 48/49 red deer (98%), 20/21 roe deer (95.2%), 13/29 wild boars (44.8%), and 1/1 red fox. MLVA enabled the discrimination of two A. phagocytophilum groups: group A

contained the majority of A. phagocytophilum from red deer and two thirds of those from cattle, while group B included a human strain and variants from diverse animal species, i.e. sheep, dogs, a horse, the majority of variants from roe deer, and the remaining variants from cattle and red deer. CONCLUSIONS: Our results suggest that red deer and roe deer are promising A. phagocytophilum reservoir host candidates. Moreover, we also showed that A. phagocytophilum potentially circulates in at least two epidemiological cycles in French cattle. The first cycle may involve red deer as reservoir hosts and cattle as accidental hosts for Group A strains, whereas the second cycle could involve roe deer as reservoir hosts and at least domestic ruminants, dogs, horses, and humans as accidental hosts for Group B strains.

Ereqat, S., A. Nasereddin, et al. (2016). "Molecular Evidence of Bartonella Species in Ixodid Ticks and Domestic Animals in Palestine." Front Microbiol 7: 1217.

Ticks play an important role in disease transmission as vectors for human and animal pathogens, including the Gram-negative pathogen Bartonella. Here, we evaluated the presence of Bartonella in ixodid ticks and domestic animals from Palestine. We tested 633 partly engorged ticks and 139 blood samples from domestic animals (dogs, sheep and camels) for Bartonella using ITS-PCR. Bartonella DNA was detected in 3.9% of the tested ticks. None of the ticks collected from sheep and goats were positive for Bartonella. Seventeen R. sanguineus ticks (17/391; 4.3%) collected from dogs were infected with B. rochalimae (n = 10), B. chomelii (n = 6), and B. koehlerae (n = 1). Four H. dromedarri ticks (4/63; 6.3%) obtained from camels were infected with B. bovis (n = 2) and B. rochalimae (n = 2). Among canine blood samples (n = 110), we found one asymptomatic female dog to be infected with B. rochalimae (0.9%). The detection of zoonotic Bartonella species in this study should raise awareness of these vector-borne diseases among physicians, veterinarians and public health workers and highlight the importance of surveillance and preventive measures in the region.

Galan, M., M. Razzauti, et al. (2016). "16S rRNA Amplicon Sequencing for Epidemiological Surveys of Bacteria in Wildlife." mSystems 1(4).

The human impact on natural habitats is increasing the complexity of human-wildlife interactions and leading to the emergence of infectious diseases worldwide. Highly successful synanthropic wildlife species, such as rodents, will undoubtedly play an increasingly important role in transmitting zoonotic diseases. We investigated the potential for recent developments in 16S rRNA amplicon sequencing to facilitate the multiplexing of the large numbers of samples needed to improve our understanding of the risk of zoonotic disease transmission posed by urban rodents in West Africa. In addition to listing pathogenic bacteria in wild populations, as in other high-throughput sequencing (HTS) studies, our approach can estimate essential parameters for studies of zoonotic risk, such as prevalence and patterns of coinfection within individual hosts. However, the estimation of these parameters requires cleaning of the raw data to mitigate the biases generated by HTS methods. We present here an extensive review of these biases and of their consequences, and we propose a comprehensive trimming strategy for managing these biases. We demonstrated the application of this strategy using 711 commensal rodents, including 208 Mus musculus domesticus, 189 Rattus rattus, 93 Mastomys natalensis, and 221 Mastomys erythroleucus, collected from 24

villages in Senegal. Seven major genera of pathogenic bacteria were detected in their spleens: Borrelia, Bartonella, Mycoplasma, Ehrlichia, Rickettsia, Streptobacillus, and Orientia. Mycoplasma, Ehrlichia, Rickettsia, Streptobacillus, and Orientia have never before been detected in West African rodents. Bacterial prevalence ranged from 0% to 90% of individuals per site, depending on the bacterial taxon, rodent species, and site considered, and 26% of rodents displayed coinfection. The 16S rRNA amplicon sequencing strategy presented here has the advantage over other molecular surveillance tools of dealing with a large spectrum of bacterial pathogens without requiring assumptions about their presence in the samples. This approach is therefore particularly suitable to continuous pathogen surveillance in the context of disease-monitoring programs. IMPORTANCE Several recent public health crises have shown that the surveillance of zoonotic agents in wildlife is important to prevent pandemic risks. High-throughput sequencing (HTS) technologies are potentially useful for this surveillance, but rigorous experimental processes are required for the use of these effective tools in such epidemiological contexts. In particular, HTS introduces biases into the raw data set that might lead to incorrect interpretations. We describe here a procedure for cleaning data before estimating reliable biological parameters, such as positivity, prevalence, and coinfection, using 16S rRNA amplicon sequencing on an Illumina MiSeq platform. This procedure, applied to 711 rodents collected in West Africa, detected several zoonotic bacterial species, including some at high prevalence, despite their never before having been reported for West Africa. In the future, this approach could be adapted for the monitoring of other microbes such as protists, fungi, and even viruses.

Grellet, A., R. M. Heilmann, et al. (2016). "Influence of Breed Size, Age, Fecal Quality, and Enteropathogen Shedding on Fecal Calprotectin and Immunoglobulin A Concentrations in Puppies During the Weaning Period." J Vet Intern Med 30(4): 1056-1064.

BACKGROUND: Fecal calprotectin and immunoglobulin A (IgA) are markers of intestinal inflammation and immunity in adult dogs. HYPOTHESIS: Fecal calprotectin and IgA concentrations in puppies are not influenced by fecal moisture in puppies but by enteropathogen shedding. ANIMALS: Three hundred and twenty-four puppies. METHODS: Fecal consistency was assessed by gross examination. Fecal moisture was evaluated before and after lyophilization. Canine parvovirus and coronavirus were detected in feces by qPCR and qRT-PCR respectively. Giardia intestinalis antigen was quantified by ELISA. The standard McMaster flotation technique was used to detect eggs and oocysts in feces. Fecal calprotectin and IgA concentrations were quantified by in-house radioimmunoassays. RESULTS: For each marker (IgA and calprotectin), a strong positive correlation was observed between concentration in fresh feces and concentration in fecal dry matter. 75.6% of the puppies were found to be infected by at >/=1 of the enteropathogens evaluated. Fecal calprotectin concentration was significantly influenced by age (P = .001), with higher concentrations in younger puppies, but not by viral (P = .863) or parasitic infection (P = .791). Fecal IgA concentration was significantly influenced by enteropathogen shedding (P = .01), with a lower fecal IgA concentration in puppies shedding at >/=1 enteropathogen compared to puppies without any enteropathogen shedding, but not by age. CONCLUSIONS: Fecal calprotectin and IgA are of no diagnostic value to detect presence of enteropathogens in clinically healthy puppies or puppies with abnormal feces, but could help to better understand the maturation of digestive tract.

Gulia-Nuss, M., A. B. Nuss, et al. (2016). "Genomic insights into the Ixodes scapularis tick vector of Lyme disease." Nat Commun 7: 10507.

Ticks transmit more pathogens to humans and animals than any other arthropod. We describe the 2.1 Gbp nuclear genome of the tick, Ixodes scapularis (Say), which vectors pathogens that cause Lyme disease, human granulocytic anaplasmosis, babesiosis and other diseases. The large genome reflects accumulation of repetitive DNA, new lineages of retro-transposons, and gene architecture patterns resembling ancient metazoans rather than pancrustaceans. Annotation of scaffolds representing approximately 57% of the genome, reveals 20,486 protein-coding genes and expansions of gene families associated with tick-host interactions. We report insights from genome analyses into parasitic processes unique to ticks, including host 'questing', prolonged feeding, cuticle synthesis, blood meal concentration, novel methods of haemoglobin digestion, haem detoxification, vitellogenesis and prolonged off-host survival. We identify proteins associated with the agent of human granulocytic anaplasmosis, an emerging disease, and the encephalitis-causing Langat virus, and a population structure correlated to life-history traits and transmission of the Lyme disease agent.

Karadjian, G., A. Hassanin, et al. (2016). "Highly rearranged mitochondrial genome in Nycteria parasites (Haemosporidia) from bats." Proc Natl Acad Sci U S A 113(35): 9834-9839.

Haemosporidia parasites have mostly and abundantly been described using mitochondrial genes, and in particular cytochrome b (cytb). Failure to amplify the mitochondrial cytb gene of Nycteria parasites isolated from Nycteridae bats has been recently reported. Bats are hosts to a diverse and profuse array of Haemosporidia parasites that remain largely unstudied. There is a need to obtain more molecular data from chiropteran parasites. Such data would help to better understand the evolutionary history of Haemosporidia, which notably include the Plasmodium parasites, malaria's agents. We use next-generation sequencing to obtain the complete mitochondrial genome of Nycteria parasites from African Nycteris grandis (Nycteridae) and Rhinolophus alcyone (Rhinolophidae) and Asian Megaderma spasma (Megadermatidae). We report four complete mitochondrial genomes, including two rearranged mitochondrial genomes within Haemosporidia. Our results open outlooks into potentially undiscovered Haemosporidian diversity.

Khatat, S., D. Rosenberg, et al. (2016). " Lungworm Eucoleus aerophilus (Capillaria aerophila) infection in a feline immunodeficiency virus-positive cat in France." Journal of Feline Medicine and Surgery Open Reports 2(1):2055116916651649.

Khlyap, L. A., M. Kosoy, et al. (2016). "[Rats of the Genus Rattus as Hosts for Natural Focal Infectious Agents]." Med Parazitol (Mosk)(1): 47-52.

The paper reviews the significance of rats of the genus Rattus as hosts for zoogenous infections in a genus formation area (Southeast Asia) as compared to the invasion part of the genus area. The rats of the genus Rattus and their related disease agents are shown to be a uniqe model for the formation and development of a host-pathogen system. In the modern period of urbanization growth, the rats are among few species of warm-blooded vectors that can maintain the anthropurgic foci of feral nidal infections in the cities and towns and transmit their pathogens to the urban population. There are all prerequisites for the high activity of these foci in the native area of rats. By having settled, the rats have carried infectious agents outside this area along all continents in historical times. During invasions, the rats have become carriers of many other infections.

Michelet, L., G. Joncour, et al. (2016). "Tick species, tick-borne pathogens and symbionts in an insular environment off the coast of Western France." Ticks Tick Borne Dis 7(6): 1109-1115.

Insular environments provide ideal natural conditions to study disease ecology, especially emerging diseases, due to clear differentiation between local and long-distance transmission. Such environments are of particular interest regarding tick-borne pathogens (TBP), since animal exchange with the mainland (along with any ticks they carry) is limited, and because such locations could lie on migratory routes for birds carrying ticks. Therefore both tick species and TBP may display different prevalence than those observed on the continent. As such, an epidemiological survey was performed on Belle-Ile-en-Mer, an island off the coast of Western France, in order to estimate the prevalence of tick species and the microorganisms they carried. Three tick species, Dermacentor marginatus, D. reticulatus, and Haemaphysalis punctata were collected at five different sites in 2010 and 2011. All ticks were tested for pathogen's and symbiont's DNA by (i) PCR for Anaplasma spp., Borrelia spp., Rickettsia spp.; (ii) real-time PCR for Francisella tularensis, Francisella-like endosymbionts (FLE) and Coxiella spp. and (iii) PCR-RLB for Babesia-Theileria spp. Pathogen DNA detected in D. marginatus including Borrelia spp. (18%), Rickettsia spp. (13%) which was identified as R. slovaca, Babesia spp. (8%), and Theileria spp. (1%). Pathogens detected in D. reticulatus including Rickettsia spp. (31%) identified as R. raoulti, Francisella-like endosymbiont (86%), and Babesia spp (21%). Pathogens detected in H. punctata including Rickettsia spp. (1%) identified as R. aeschlimannii, FLE (0.4%), Babesia spp. (18%), and Theileria spp. (7%). Anaplasma spp., F. tularensis, or Coxiella spp. were not detected in any of the collected ticks. This study represents the first epidemiological survey of the insular Belle-Ile-en-Mer environment. It demonstrated the presence of expected pathogens, consistent with reports from island veterinarians or physicians, as well as unexpected pathogens, raising questions about their potential introduction through infected animals and/or their dispersion by migratory birds.

Molia, S., R. W. Kasten, et al. (2016). "Isolation of Bartonella henselae, Bartonella koehlerae subsp. koehlerae, Bartonella koehlerae subsp. bothieri and a new subspecies of B. koehlerae from free-ranging lions (Panthera leo) from South Africa, cheetahs (Acinonyx jubatus) from Namibia and captive cheetahs from California." Epidemiol Infect 144(15): 3237-3243.

Bartonellae are blood- and vector-borne Gram-negative bacteria, recognized as emerging pathogens. Whole-blood samples were collected from 58 free-ranging lions (Panthera leo) in South

Africa and 17 cheetahs (Acinonyx jubatus) from Namibia. Blood samples were also collected from 11 cheetahs (more than once for some of them) at the San Diego Wildlife Safari Park. Bacteria were isolated from the blood of three (5%) lions, one (6%) Namibian cheetah and eight (73%) cheetahs from California. The lion Bartonella isolates were identified as B. henselae (two isolates) and B. koehlerae subsp. koehlerae. The Namibian cheetah strain was close but distinct from isolates from North American wild felids and clustered between B. henselae and B. koehlerae. It should be considered as a new subspecies of B. koehlerae. All the Californian semi-captive cheetah isolates were different from B. henselae or B. koehlerae subsp. koehlerae and from the Namibian cheetah isolate. They were also distinct from the strains isolated from Californian mountain lions (Felis concolor) and clustered with strains of B. koehlerae subsp. bothieri isolated from free-ranging bobcats (Lynx rufus) in California. Therefore, it is likely that these captive cheetahs became infected by an indigenous strain for which bobcats are the natural reservoir.

Moutailler, S., I. Popovici, et al. (2016). "Diversity of viruses in Ixodes ricinus, and characterization of a neurotropic strain of Eyach virus." New Microbes New Infect 11: 71-81.

Ticks transmit more pathogens-including bacteria, parasites and viruses-than any other arthropod vector. Although the epidemiological status of many tick-borne bacteria is very well characterized, tick-borne viruses are still relatively under-studied. Recently, several novel tick-borne viruses have been isolated from human febrile illnesses following tick bites, indicating the existence of other potential new and unknown tick-borne viruses. We used high-throughput sequencing to analyse the virome of Ixodes ricinus, the main vector of tick-borne pathogens in Europe. The majority of collected viral sequences were assigned to two potentially novel Nairovirus and Phlebovirus viruses, with prevalence rates ranging from 3.95% to 23.88% in adults and estimated to be between 0.14% and 72.16% in nymphs. These viruses could not be isolated from the brains of inoculated immunocompromised mice, perhaps indicating that they are unable to infect vertebrates. Within the I. ricinus virome, we also identified contigs with >90% identity to the known Eyach virus. Initially isolated in the 1980s, this virus was indirectly associated with human disease, but had never been extensively studied. Eyach virus prevalence varied between 0.07% and 5.26% in ticks from the French Ardennes and Alsace regions. Eyach virus was successfully isolated following intracerebral inoculation of immunocompromised mice with Eyach virus-positive tick extracts. This virus was also able to multiply and persist in the blood of immunocompetent mice inoculated by intraperitoneal injection, and caused brain infections in three of nine juveniles, without any obvious deleterious effects.

Moutailler, S., C. Valiente Moro, et al. (2016). "Co-infection of Ticks: The Rule Rather Than the Exception." PLoS Negl Trop Dis 10(3): e0004539.

INTRODUCTION: Ticks are the most common arthropod vectors of both human and animal diseases in Europe, and the Ixodes ricinus tick species is able to transmit a large number of bacteria, viruses and parasites. Ticks may also be co-infected with several pathogens, with a subsequent high likelihood of co-transmission to humans or animals. However few data exist regarding co-infection prevalences, and these studies only focus on certain well-known pathogens. In addition to pathogens, ticks also carry symbionts that may play important roles in tick biology, and could

interfere with pathogen maintenance and transmission. In this study we evaluated the prevalence of 38 pathogens and four symbionts and their co-infection levels as well as possible interactions between pathogens, or between pathogens and symbionts. METHODOLOGY/PRINCIPAL FINDINGS: A total of 267 Ixodes ricinus female specimens were collected in the French Ardennes and analyzed by high-throughput real-time PCR for the presence of 37 pathogens (bacteria and parasites), by rRT-PCR to detect the presence of Tick-Borne encephalitis virus (TBEV) and by nested PCR to detect four symbionts. Possible multipartite interactions between pathogens, or between pathogens and symbionts were statistically evaluated. Among the infected ticks, 45% were co-infected, and carried up to five different pathogens. When adding symbiont prevalences, all ticks were infected by at least one microorganism, and up to eight microorganisms were identified in the same tick. When considering possible interactions between pathogens, the results suggested a strong association between Borrelia garinii and B. afzelii, whereas there were no significant interactions between symbionts and pathogens. CONCLUSION/SIGNIFICANCE: Our study reveals high pathogen co-infection rates in ticks, raising questions about possible co-transmission of these agents to humans or animals, and their consequences to human and animal health. We also demonstrated high prevalence rates of symbionts co-existing with pathogens, opening new avenues of enquiry regarding their effects on pathogen transmission and vector competence.

Note, O. P., S. A. Azouaou, et al. (2016). "Phenotype-specific apoptosis induced by three new triterpenoid saponins from Albizia glaberrima (Schumach. & Thonn.) Benth." Fitoterapia 109: 80-86.

As part of our search of new bioactive saponins from Cameroonian medicinal plants, phytochemical investigation of the roots of Albizia glaberrima led to the isolation of three new oleanane-type saponins, named glaberrimosides A-C (1-3). Their structures were established by direct interpretation of their spectral data, mainly HRESIMS, 1D NMR (1H, 13C NMR, and DEPT) and 2D NMR (COSY, ROESY, HSQC and HMBC) as 3-O-[alpha-L-arabinopyranosyl-(1 --> 6)-[beta-D-glucopyranosyl-(1 --> 2)]-beta-D-glucopyranosyl]-28-O-[beta-D-glucopyranosyl-(1 --> 6)-[beta-d-glucopyranosyl-(1 --> 2)]-beta-D-glucopyranosyl]-oleanolic acid (1), 3-O-[alpha-L-arabinopyranosyl-(1 --> 6)-[beta-D-glucopyranosyl-(1 --> 2)]-beta-D-glucopyranosyl]-28-O-[beta-D-glucopyranosyl-(1 --> 6)-beta-D-glucopyranosyl]-oleanolic acid (2), and 3-O-[beta-D-glucopyranosyl-(1-->2)-beta-D-glucopyranosyl]-28-O-[beta-D-glucopyran osyl-(1 --> 6)-[beta-D-fucopyranosyl-(1 --> 2)]-beta-D-glucopyranosyl]-oleanolic acid (3). The pro-apoptotic effect of the three saponins was evaluated on three human cell lines (pancreatic carcinoma AsPC-1, hematopoietic monocytic THP-1, and human fibroblast cell line BJ). Saponins 1-3 specifically induced apoptosis of pancreatic carcinoma cell (AsPC-1) in a dose-dependent manner. More interestingly, there were inactive on monocytic (THP-1) and normal human fibroblast (BJ) cell lines.

Paul, R. E., M. Cote, et al. (2016). "Environmental factors influencing tick densities over seven years in a French suburban forest." Parasit Vectors 9(1): 309.

BACKGROUND: Worldwide changes in socio-economic and environmental factors and the global climate are recognised causes of variation in tick distribution and density. Thus it is of great importance that new studies address the changing risk of infection for exposed populations. In

Europe, Ixodes ricinus ticks are the most common vectors of several pathogens impacting veterinary and public health that have colonised suburban habitats. METHODS: This study aimed to evaluate longitudinal I. ricinus questing densities and infection rates over 7 years in a French suburban forested area with high human population density. Ticks were collected in spring yearly between 2008 and 2014 and, out of a total of 8594 collected I. ricinus, a representative subset of adult females (n = 259) were individually examined for the presence of several pathogens via PCR. RESULTS: Nymph densities peaked in 2009-2011, and then declined in 2012-2014. Changes in monthly temperature only had a modest impact on this variation. In contrast, analysis revealed a complex intra-annual relationship between mean nymph density and both concurrent and lagged mean monthly temperatures. The following pathogens were detected in the studied area: Anaplasma phagocytophilum, Rickettsia helvetica, Babesia venatorum and B. divergens, Francisella tularensis, Borrelia miyamotoi, B. afzelii/valaisiana, B. garinii/lusitaniae and Bartonella spp. CONCLUSION: Our findings reinforce the conclusion that ticks are important vectors of pathogenic microorganisms in suburban forests and suggest that despite complex intra-annual relationships between tick densities and temperature, there is no evidence for a climate-associated increase in infection risk over the 7-year period. Rather, tick densities are likely to be strongly influenced by population density fluctuations in vertebrate host species and wildlife management. Further detailed studies on the impact of climate change on tick population densities are required.

Pionnier, N., E. Brotin, et al. (2016). "Neutropenic Mice Provide Insight into the Role of Skin-Infiltrating Neutrophils in the Host Protective Immunity against Filarial Infective Larvae." PLoS Negl Trop Dis 10(4): e0004605.

Our knowledge and control of the pathogenesis induced by the filariae remain limited due to experimental obstacles presented by parasitic nematode biology and the lack of selective prophylactic or curative drugs. Here we thought to investigate the role of neutrophils in the host innate immune response to the infection caused by the Litomosoides sigmodontis murine model of human filariasis using mice harboring a gain-of-function mutation of the chemokine receptor CXCR4 and characterized by a profound blood neutropenia (Cxcr4(+/1013)). We provided manifold evidence emphasizing the major role of neutrophils in the control of the early stages of infection occurring in the skin. Firstly, we uncovered that the filarial parasitic success was dramatically decreased in Cxcr4(+/1013) mice upon subcutaneous delivery of the infective stages of filariae (infective larvae, L3). This protection was linked to a larger number of neutrophils constitutively present in the skin of the mutant mice herein characterized as compared to wild type (wt) mice. Indeed, the parasitic success in Cxcr4(+/1013) mice was normalized either upon depleting neutrophils, including the pool in the skin, or bypassing the skin via the intravenous infection of L3. Second, extending these observations to wt mice we found that subcutaneous delivery of L3 elicited an increase of neutrophils in the skin. Finally, living L3 larvae were able to promote in both wt and mutant mice, an oxidative burst response and the release of neutrophil extracellular traps (NET). This response of neutrophils, which is adapted to the large size of the L3 infective stages, likely directly contributes to the anti-parasitic strategies implemented by the host. Collectively, our results are demonstrating the contribution of neutrophils in early anti-filarial host responses through their capacity to undertake different anti-filarial strategies such as oxidative burst, degranulation and NETosis.

Ribadeau Dumas, F., N. Haddad, et al. (2016). "Post-exposure prophylaxis against rabies is still needed after a bite from a vaccinated animal." BMJ 352: i730.

Ruetsch, C., P. Delaunay, et al. (2016). "Inadequate labeling of pork sausages prepared in Corsica causing a trichinellosis outbreak in France." Parasite 23: 27.

Three cases of human trichinellosis due to Trichinella britovi were reported in 2015 in the Southeast of France resulting from consumption of raw pork sausages (figatelli) prepared in Corsica. Fourteen other people ate figatelli from the same batch but were not infected due to the figatelli being well cooked. This is the first reported human trichinellosis outbreak due to consumption of Corsican sausages prepared from uncontrolled pork. Consumption of raw figatelli is a common tradition in Corsica. As a result, the health recommendation to cook the product well is not always applied. In the present case, the figatelli product label was not sufficiently visible to advise consumers of the risks associated with uncooked pork.

Shen, Z., G. Coupier, et al. (2016). "Inversion of hematocrit partition at microfluidic bifurcations." Microvasc Res 105: 40-46.

Partitioning of red blood cells (RBCs) at the level of bifurcations in the microcirculatory system affects many physiological functions yet it remains poorly understood. We address this problem by using T-shaped microfluidic bifurcations as a model. Our computer simulations and in vitro experiments reveal that the hematocrit (varphi0) partition depends strongly on RBC deformability, as long as varphi0<20% (within the normal range in microcirculation), and can even lead to complete deprivation of RBCs in a child branch. Furthermore, we discover a deviation from the Zweifach-Fung effect which states that the child branch with lower flow rate recruits less RBCs than the higher flow rate child branch. At small enough varphi0, we get the inverse scenario, and the hematocrit in the lower flow rate child branch is even higher than in the parent vessel. We explain this result by an intricate up-stream RBC organization and we highlight the extreme dependence of RBC transport on geometrical and cell mechanical properties. These parameters can lead to unexpected behaviors with consequences on the microcirculatory function and oxygen delivery in healthy and pathological conditions.

Svitalkova, Z. H., D. Harustiakova, et al. (2016). "Candidatus Neoehrlichia mikurensis in ticks and rodents from urban and natural habitats of South-Western Slovakia." Parasit Vectors 9: 2.

BACKGROUND: Candidatus Neoehrlichia mikurensis (CNM) is an emerging tick-borne pathogen causing severe disease in immunocompromised patients. In Europe, Ixodes ricinus is the primary vector and rodents act as reservoir hosts. New data on the prevalence of CNM in ticks and rodents contribute to the knowledge on the distribution of endemic areas and circulation of the bacterium in natural foci. METHODS: Questing ticks were collected and rodents were trapped in

urban/suburban and natural habitats in South-Western Slovakia from 2011 to 2014. DNA from questing and rodent-attached ticks and rodent tissues were screened for CNM by real-time PCR. Rodent spleen samples positive for CNM were characterised at the groEL gene locus. Spatial and temporal differences in CNM prevalence in ticks and rodents and co-infections of ticks with CNM and Anaplasma phagocytophilum were analysed. RESULTS: The presence of CNM was confirmed in questing and rodent-attached I. ricinus ticks and in rodents. Total prevalence in both ticks and rodents was significantly higher in the natural habitat (2.3% and 10.1%, respectively) than in the urban/suburban habitat (1.0% and 3.3%, respectively). No seasonal pattern in CNM prevalence in ticks was observed, but prevalence in rodents was higher in autumn than in spring. CNM was detected in Apodemus flavicollis, Myodes glareolus, Microtus arvalis and Micromys minutus, with the highest prevalence in M. arvalis (30%). By screening CNM dissemination in rodent tissues, infection was detected in lungs of all specimens with positive spleens and in blood, kidney, liver and skin of part of those individuals. Infection with CNM was detected in 1.3% of rodent attached I. ricinus ticks. Sequences of a fragment of the groEL gene from CNM-positive rodents showed a high degree of identity with sequences of the gene amplified from ticks and infected human blood from Europe. Only 0.1% of CNM-positive questing ticks carried A. phagocytophilum. Ticks infected with CNM prevailed in the natural habitat (67.2%), whereas ticks infected with A. phagocytophilum prevailed in the urban/suburban habitat (75.0%). CONCLUSION: The study confirmed the circulation of CNM between I. ricinus ticks and rodents in South-Western Slovakia, and indicates a potential risk of contracting human infections.

Vanpé, C., L. Debeffe, et al. (2016). "Immune gene variability influences roe deer natal dispersal. . ." Oikos doi: 10.1111/oik.02904.

Vayssier-Taussat, M., S. Moutailler, et al. (2016). "Identification of Novel Zoonotic Activity of Bartonella spp., France." Emerg Infect Dis 22(3): 457-462.

Certain Bartonella species are known to cause afebrile bacteremia in humans and other mammals, including B. quintana, the agent of trench fever, and B. henselae, the agent of cat scratch disease. Reports have indicated that animal-associated Bartonella species may cause paucisymptomatic bacteremia and endocarditis in humans. We identified potentially zoonotic strains from 6 Bartonella species in samples from patients who had chronic, subjective symptoms and who reported tick bites. Three strains were B. henselae and 3 were from other animal-associated Bartonella spp. (B. doshiae, B. schoenbuchensis, and B. tribocorum). Genomic analysis of the isolated strains revealed differences from previously sequenced Bartonella strains. Our investigation identifed 3 novel Bartonella spp. strains with human pathogenic potential and showed that Bartonella spp. may be the cause of undifferentiated chronic illness in humans who have been bitten by ticks.

Yang, Y., I. Vallee, et al. (2016). "Identification and characterization of immunodominant linear epitopes on the antigenic region of a serine protease in newborn Trichinella larvae." J Helminthol 90(2): 232-237.

An immunodominant serine protease of Trichinella spiralis named NBL1 showed encouraging potential in early diagnosis of trichinellosis in pigs and elicited protective immune responses during infection of animals. To further define serological reagents for diagnostic use, the specific epitopes on NBL protein recognized by the antibody responses of different susceptible hosts need to be defined. The present study described comprehensive mapping of immunodominant linear epitopes in the antigenic region (NBL-C, the C-terminal part of the protein) using various serum samples obtained from three kinds of hosts - pig, wild boar and mice. We identified six peptides which were commonly recognized by sera from pigs experimentally infected with Trichinella and pigs immunized with rNBL1-C; five and four peptides were recognized by sera from wild boars and mice infected with Trichinella, respectively. Three peptides (NBL1-6, -7 and -9) were commonly recognized by antisera in all three hosts, which share the sequence PSSGSRPTYP. We also found that one peptide (NBL1-12) was only recognized by antibodies from pigs immunized with rNBL1-C. The identification of specific epitopes targeted by the host antibody response is important both for understanding the natural response to infection and for the development of subunit vaccines and diagnostic tools for trichinellosis.

2017

Ait Lbacha, H., S. Alali, et al. (2017). "High Prevalence of Anaplasma spp. in Small Ruminants in Morocco." Transbound Emerg Dis 64(1): 250-263.

The prevalence of infection by Anaplasma spp. (including Anaplasma phagocytophilum) was determined using blood smear microscopy and PCR through screening of small ruminant blood samples collected from seven regions of Morocco. Co-infections of Anaplasma spp., Babesia spp, Theileria spp. and Mycoplasma spp. were investigated and risk factors for Anaplasma spp. infection assessed. A total of 422 small ruminant blood samples were randomly collected from 70 flocks. Individual animal (breed, age, tick burden and previous treatment) and flock data (GPS coordinate of farm, size of flock and livestock production system) were collected. Upon examination of blood smears, 375 blood samples (88.9%) were found to contain Anaplasma-like erythrocytic inclusion bodies. Upon screening with a large spectrum PCR targeting the Anaplasma 16S rRNA region, 303 (71%) samples were found to be positive. All 303 samples screened with the A. phagocytophilum-specific PCR, which targets the msp2 region, were found to be negative. Differences in prevalence were found to be statistically significant with regard to region, altitude, flock size, livestock production system, grazing system, presence of clinical cases and application of tick and tick-borne diseases prophylactic measures. Kappa analysis revealed a poor concordance between microscopy and PCR (k = 0.14). Agreement with PCR is improved by considering microscopy and packed cell volume (PCV) in parallel. The prevalence of double infections was found to be 1.7, 2.5 and 24% for Anaplasma-Babesia, Anaplasma-Mycoplasma and Anaplasma-Theileria, respectively. Co-infection with three or more haemoparasites was found in 1.6% of animals examined. In conclusion, we demonstrate the high burden of anaplasmosis in small ruminants in Morocco and the high prevalence of co-infections of tick-borne diseases. There is an urgent need to improve the control of this neglected group of diseases.

Ait Lbacha, H., Z. Zouagui, et al. (2017). ""Candidatus anaplasma camelii" in one-humped camels (Camelus dromedarius) in Morocco: a novel and emerging anaplasma species?" Infect Dis Poverty 6(1): 1.

BACKGROUND: There has been a growing interest in camel anaplasmosis due to its recent emergence in this reservoir species and concerns for its zoonotic potential. The epidemiology of anaplasmosis in camels therefore remains poorly understood mostly because camels belong to marginalised poor and often transhumant populations whose interests are largely neglected. Most studies of anaplasmosis in camels have relied on microscopy and serology for diagnosis and only three studies, undertaken in Tunisia, Saudia Arabia and China, have used molecular diagnostics. The present work characterises Anaplasmataceae strains circulating in the Camelus dromedarius reservoir in Morocco using PCR. METHODS: Camels (n = 106) were randomly sampled from 6 regions representing different agro-ecological areas in southern Morocco. Whole blood was collected and screened using PCR methods targeting the gene groEL. Anaplasmataceae strains were characterised by sequence analysis of the gene groEL. RESULTS: A total of 39.62% (42/106) camels screened were positive for Anaplasmataceae spp. GenBank BLAST analysis of five positive sequenced samples revealed that all strains were 100% identical to "Candidatus Anaplasma camelii". Phylogenetic investigation and genetic characterisation of the aligned segment (650 bp) of the gene groEL confirmed high similarity with A. platys. CONCLUSION: This study demonstrates the circulation of a previously unidentified species of the genus Anaplasma in Morocco which is genetically close to the agent causing canine anaplasmosis but whose main reservoir is thought to be Camelus dromedarius. TRIAL REGISTRATION NUMBER: This study is not a clinical trial and therefore a trial registration number does not apply.

Ayhan, N., A. Baklouti, et al. (2017). "Practical Guidelines for Studies on Sandfly-Borne Phleboviruses: Part I: Important Points to Consider Ante Field Work." Vector Borne Zoonotic Dis 17(1): 73-80.

The purpose of this review is to provide practical information to help researchers intending to perform "from field to laboratory" studies on phleboviruses transmitted by sandflies. This guideline addresses the different steps to be considered starting from the field collection of sandflies to the laboratory techniques aiming at the detection, isolation, and characterization of sandfly-borne phleboviruses. In this guideline article, we address the impact of various types of data for an optimal organization of the field work intending to collect wildlife sandflies for subsequent virology studies. Analysis of different data sets should result in the geographic positioning of the trapping stations. The overall planning, the equipment and tools needed, the manpower to be deployed, and the logistics to be anticipated and set up should be organized according to the objectives of the field study for optimal efficiency.

Basso, W., F. Grimm, et al. (2017). "Experimental Toxoplasma gondii infections in pigs: Humoral immune response, estimation of specific IgG avidity and the challenges of reproducing vertical transmission in sows." Vet Parasitol 236: 76-85.

Ten pregnant sows were experimentally inoculated per os with T. gondii in order to investigate vertical and galactogenic transmission of the parasite and the evolution and maturation of the specific IgG humoral response in the sows and piglets. Five seronegative sows received 104T. gondii (CZ isolate clone H3) sporulated oocysts during late-pregnancy (Exp. 1), three sows received 104 oocysts during mid-pregnancy (Exp. 2) and three sows from Exp. 1 (and two seronegative sows) were re-inoculated with 105 oocysts during a further pregnancy (late-pregnancy) (Exp. 3). Besides, six 4.5 week-old piglets inoculated per os with 5x103 oocysts were also included in the serological investigations. All animals seroconverted (PrioCHECK Toxoplasma Ab porcine ELISA, Prionics, Switzerland) by 2-3 weeks post inoculation (wpi) and remained seropositive for at least 38 weeks or until euthanasia. Four chronically infected sows from Exp. 1 and 2 were serologically monitored during a further pregnancy and no reactivation, but a decrease of the antibody levels was observed at farrowing (Exp. 4). In all experiments, the specific IgG-avidity was initially low, increased during the course of infection and after re-inoculations. An avidity index (AI) >/=40% could be used to rule out recent infections (<8 weeks) in most (15 of 16) animals. In some piglets (18.6% of 70) delivered by inoculated sows (Exp. 1 and 2), maternal antibodies were still detectable at 2 months (but not by 3 months) of age, with constant high avidity values, comparable to those of the dams at farrowing. In all experiments, the sows remained asymptomatic and delivered non-infected offspring at term. A total of 208 normal and 5 stillborn piglets delivered by the inoculated sows (Exp. 1-4) tested serologically negative before colostrum uptake. Placentas (n=88) from all sows and tissues (brain, liver, lung, heart, and masseter muscle) from 56 delivered piglets were analysed histopathologically and by real-time PCR for T. gondii with negative results. Colostrum and milk samples from all sows were negative by real-time PCR for T. gondii DNA. In addition, no seroconversion was observed in 16 piglets from seronegative dams that were transferred to infected dams one day after birth to detect a possible infection through colostrum or milk during the suckling period. Although vertical transmission of T. gondii was demonstrated in naturally infected pigs, many factors involved in the outcome of vertical transmission and congenital toxoplasmosis in pigs are still unknown.

Belkhiria, J., B. B. Chomel, et al. (2017). "Prevalence and Potential Risk Factors for Bartonella Infection in Tunisian Stray Dogs." Vector Borne Zoonotic Dis 17(6): 388-397.

Bartonellae are blood-borne and vector-transmitted pathogens, some are zoonotic, which have been reported in several Mediterranean countries. Transmission from dogs to humans is suspected, but has not been clearly demonstrated. Our objectives were to determine the seroprevalence of Bartonella henselae, Bartonella vinsonii subsp. berkhoffii, Bartonella clarridgeiae, and Bartonella bovis (as a proxy for Candidatus Bartonella merieuxii) in stray dogs from Tunisia, identify the Bartonella species infecting the dogs and evaluate potential risk factors for canine infection. Blood samples were collected between January and November 2013 from 149 dogs in 10 Tunisian governorates covering several climatic zones. Dog-specific and geographic variables were analyzed as potential risk factors for Bartonella spp. seropositivity and PCR-positivity. DNA was extracted from the blood of all dogs and tested by PCR for Bartonella, targeting the ftsZ and rpoB genes. Partial sequencing was performed on PCR-positive dogs. Twenty-nine dogs (19.5%, 95% confidence interval: 14-27.4) were seropositive for one or more Bartonella species, including 17 (11.4%) for B. vinsonii subsp. berkhoffii, 14 (9.4%) for B. henselae, 13 (8.4%) for B. clarridgeiae, and 7 (4.7%) for B. bovis. Statistical analysis revealed a few potential risk factors, mainly dog's age and

breed, latitude and average winter temperature. Twenty-two (14.8%) dogs, including 8 of the 29 seropositive dogs, were PCR-positive for Bartonella based on the ftsZ gene, with 18 (81.8%) of these 22 dogs also positive for the rpoB gene. Partial sequencing showed that all PCR-positive dogs were infected with Candidatus B. merieuxii. Dogs from arid regions and regions with cold average winter temperatures were less likely to be PCR-positive than dogs from other climatic zones. The widespread presence of Bartonella spp. infection in Tunisian dogs suggests a role for stray dogs as potential reservoirs of Bartonella species in Tunisia.

Bonnet, S. I., R. E. Paul, et al. (2017). "First identification of Rickettsia helvetica in questing ticks from a French Northern Brittany Forest." PLoS Negl Trop Dis 11(3): e0005416.

Tick-borne rickettsiae are considered to be emerging, but data about their presence in western Europe are scarce. Ixodes ricinus ticks, the most abundant and widespread tick species in western Europe, were collected and tested for the presence of several tick-borne pathogens in western France, a region never previously explored in this context. There was a high tick abundance with a mean of 4 females, 4.5 males, and 23.3 nymphs collected per hour per collector. Out of 622 tested ticks, specific PCR amplification showed the presence of tick symbionts as well as low prevalence of Borrelia burgdorferi (0.8%), Bartonella spp. (0.17%), and Anaplasma phagocytophilum (0.09%). The most prevalent pathogen was Rickettsia helvetica (4.17%). This is the first time that this bacteria has been detected in ticks in this region, and this result raises the possibility that bacteria other than those classically implicated may be involved in rickettsial diseases in western France.

Charrel, R. N., L. Lempereur, et al. (2017). "European Network for Neglected Vectors and Vector-Borne Infections COST Action Guidelines: What Is This About and What Is This For?" Vector Borne Zoonotic Dis 17(1): 1.

de la Fuente, J., S. Antunes, et al. (2017). "Tick-Pathogen Interactions and Vector Competence: Identification of Molecular Drivers for Tick-Borne Diseases." Front Cell Infect Microbiol 7: 114.

Ticks and the pathogens they transmit constitute a growing burden for human and animal health worldwide. Vector competence is a component of vectorial capacity and depends on genetic determinants affecting the ability of a vector to transmit a pathogen. These determinants affect traits such as tick-host-pathogen and susceptibility to pathogen infection. Therefore, the elucidation of the mechanisms involved in tick-pathogen interactions that affect vector competence is essential for the identification of molecular drivers for tick-borne diseases. In this review, we provide a comprehensive overview of tick-pathogen molecular interactions for bacteria, viruses, and protozoa affecting human and animal health. Additionally, the impact of tick microbiome on these interactions was considered. Results show that different pathogens evolved similar strategies such as manipulation of the immune response to infect vectors and facilitate multiplication and transmission. Furthermore, some of these strategies may be used by pathogens to infect both tick and mammalian hosts. Identification of interactions that promote tick survival, spread, and pathogen transmission provides the opportunity to disrupt these interactions and lead to a reduction in tick burden and the

prevalence of tick-borne diseases. Targeting some of the similar mechanisms used by the pathogens for infection and transmission by ticks may assist in development of preventative strategies against multiple tick-borne diseases.

Dubois, A., M. Galan, et al. (2017). "Microevolution of bank voles (Myodes glareolus) at neutral and immune-related genes during multiannual dynamic cycles: Consequences for Puumala hantavirus epidemiology." Infect Genet Evol 49: 318-329.

Understanding how host dynamics, including variations of population size and dispersal, may affect the epidemiology of infectious diseases through ecological and evolutionary processes is an active research area. Here we focus on a bank vole (Myodes glareolus) metapopulation surveyed in Finland between 2005 and 2009. Bank vole is the reservoir of Puumala hantavirus (PUUV), the agent of nephropathia epidemica (NE, a mild form of hemorrhagic fever with renal symptom) in humans. M. glareolus populations experience multiannual density fluctuations that may influence the level of genetic diversity maintained in bank voles, PUUV prevalence and NE occurrence. We examine bank vole metapopulation genetics at presumably neutral markers and immune-related genes involved in susceptibility to PUUV (Tnf-promoter, Tlr4, Tlr7 and Mx2 gene) to investigate the links between population dynamics, microevolutionary processes and PUUV epidemiology. We show that genetic drift slightly and transiently affects neutral and adaptive genetic variability within the metapopulation. Gene flow seems to counterbalance its effects during the multiannual density fluctuations. The low abundance phase may therefore be too short to impact genetic variation in the host, and consequently viral genetic diversity. Environmental heterogeneity does not seem to affect vole gene flow, which might explain the absence of spatial structure previously detected in PUUV in this area. Besides, our results suggest the role of vole dispersal on PUUV circulation through sex-specific and density-dependent movements. We find little evidence of selection acting on immune-related genes within this metapopulation. Footprint of positive selection is detected at Tlr-4 gene in 2008 only. We observe marginally significant associations between Mx2 genotype and PUUV genogroups. These results show that neutral processes seem to be the main factors affecting the evolution of these immune-related genes at a contemporary scale, although the relative effects of neutral and adaptive forces could vary temporally with density fluctuations. Immune related gene polymorphism may in turn partly influence PUUV epidemiology in this metapopulation.

Grellet, A., S. E. Makhlouf, et al. (2017). "Efficacy of guar gum-based ronidazole capsules as a treatment for Tritrichomonas foetus infection in cats." J Feline Med Surg 19(2): 177-184.

Objectives The aims of the study were to determine the in vitro drug release of guar gum-coated capsules of ronidazole, and to evaluate the pharmacokinetics and efficacy of this formulation for the treatment of cats naturally infected with Tritrichomonas foetus. Methods The pharmacokinetics of ronidazole were evaluated in five healthy cats and five cats infected with T foetus. In a second step, the clinical efficacy of these capsules was evaluated by a controlled, randomised, double-blind clinical trial performed in 47 infected cats from French catteries. In this study, cats were randomly allocated to either the ronidazole treatment group (n = 25) or a placebo group (n = 22). Ronidazole (30 mg/kg) q24h for 14 days was administered to the treated cats. After

14 days of treatment, the presence of T foetus was tested by conventional PCR assay. Results In the pharmacokinetic study, a delayed peak plasma concentration was observed in healthy and infected cats, with no significant difference between these two groups (mean geometric mean of 9 h for time to maximum plasma concentration [Tmax], 21.6 microg/ml for time to maximum plasma concentration [Cmax] and 467.4 mug/h/ml for the area under the curve [AUC] in healthy cats; and 9.4 h for Tmax, 17.1 microg/ml for Cmax and 481 mug/h/ml for AUC in infected cats). In the clinical trial, T foetus was detected in 16% of cats from the treated group and 82% of cats from the placebo group at the end of the study (P <0.001). No clinical signs of adverse drug reactions were observed. Conclusions and relevance Oral administration of guar gum-coated capsules of ronidazole at a dose of 30 mg/kg once daily for 14 days delays the peak plasma concentration and eradicates infection in most cases.

Gutierrez, R., M. Vayssier-Taussat, et al. (2017). "Guidelines for the Isolation, Molecular Detection, and Characterization of Bartonella Species." Vector Borne Zoonotic Dis 17(1): 42-50.

Bartonellae are fastidious, facultative, intracellular vector-borne bacteria distributed among mammalian reservoirs worldwide. The pathogenic potential of many Bartonella spp. has increased the interest in these bacteria and advanced their research. Isolation of Bartonella spp. is laborious using classical bacteriological methods and requires specific conditions and prolonged incubation periods. In contrast, molecular methods for detection of Bartonella DNA are considered as more practical and sensitive than the former. Among the molecular methods, the use of real-time PCR assays for primary screening of Bartonella spp., followed by several molecular confirmatory assays, using either conventional or real-time PCR, is recommended. Although primary isolation of Bartonella is a laborious task, we encourage its application to all PCR-positive samples as this is the most reliable proof for the presence of live bacteria. Moreover, a successful trial will enable a broader molecular characterization and speciation of isolated colonies. The present guideline gathers and summarizes recommendations, including advantages and limitations of isolation and molecular detection of Bartonella from mammalian and arthropod samples.

Huemer, H., J. Prudhomme, et al. (2017). "Practical Guidelines for Studies on Sandfly-Borne Phleboviruses: Part II: Important Points to Consider for Fieldwork and Subsequent Virological Screening." Vector Borne Zoonotic Dis 17(1): 81-90.

In this series of review articles entitled "Practical guidelines for studies on sandfly-borne phleboviruses," the important points to be considered at the prefieldwork stage were addressed in part I, including parameters to be taken into account to define the geographic area for sand fly trapping and how to organize field collections. Here in part II, the following points have been addressed: (1) factors influencing the efficacy of trapping and the different types of traps with their respective advantages and drawbacks, (2) how to process the trapped sand flies in the field, and (3) how to process the sand flies in the virology laboratory. These chapters provide the necessary information for adopting the most appropriate procedures depending on the requirements of the study. In addition, practical information gathered through years of experience of translational projects is included to help newcomers to fieldwork studies.

Jensen, P. M., C. S. Christoffersen, et al. (2017). "Transmission differentials for multiple pathogens as inferred from their prevalence in larva, nymph and adult of Ixodes ricinus (Acari: Ixodidae)." Exp Appl Acarol 71(2): 171-182.

Ixodes ricinus serves as vector for a range of microorganisms capable of causing clinical illness in humans. The microorganisms occur in the same vector populations and are generally affected by the same tick-host interactions. Still, the instars have different host preferences which should manifest in different transmission patterns for various microorganisms in the tick populations, i.e., most microorganisms increase in prevalence rate from larvae to nymphs because their reservoirs are among small mammals and birds that serve as blood hosts for larvae. Other microorganisms, like Anaplasma phagocytophilum, mainly increase in prevalence rates from nymphs to adults, because their reservoirs are larger ungulates that serve as primary blood hosts for nymphs and adults. We sampled a representative sample of ticks from 12 locations on Zealand and Funen, Denmark, and investigated the differences in prevalence rate of infection in larvae, nymphs and adults for multiple pathogens. Prevalence of infection for larvae, nymphs and adults, respectively, was: 0, 1.5 and 4.5% for Borrelia burgdorferi; 0, 4.2 and 3.9% for Borrelia garinii; 0, 6.6 and 6.1% for Borrelia afzelii; 0, 0 and 0.6% for Borrelia valaisiana; 0, 3.7 and 0.6% for Borrelia spielmanii; 0, 0.7 and 1.2% for Babesia divergens; 0, 0, 0.6% for Babesia venatorum; 0, 1.5 and 6.1% for A. phagocytophilum. The results were in general compatible with the hypothesis i.e., that differences in blood host for larvae and nymphs define differences in transmission of infectious agents, but other factors than differences in blood hosts between larvae and nymphs may also be important to consider.

Klun, I., A. Uzelac, et al. (2017). "The first isolation and molecular characterization of Toxoplasma gondii from horses in Serbia." Parasit Vectors 10(1): 167.

BACKGROUND: Consumption of undercooked or insufficiently cured meat is a major risk factor for human infection with Toxoplasma gondii. Although horsemeat is typically consumed rare or undercooked, information on the risk of T. gondii from infected horse meat to humans is scarce. Here, we present the results of a study to determine the presence of T. gondii infection in slaughter horses in Serbia, and to attempt to isolate viable parasites. METHODS: The study included horses from all regions of Serbia slaughtered at two abattoirs between June 2013 and June 2015. Blood sera were tested for the presence of specific IgG T. gondii antibodies by the modified agglutination test (MAT), and samples of trypsin-digested heart tissue were bioassayed in mice. Cyst-positive mouse brain homogenates were subjected to DNA extraction and T. gondii strains were genotyped using 15 microsatellite markers (MS). RESULTS: A total of 105 slaughter horses were sampled. At the 1:6 cut-off 48.6% of the examined horses were seropositive, with the highest titre being 1:400. Viable parasites were isolated from two grade type mares; both parasite isolates (RS-Eq39 and RS-Eq40) were T. gondii type III, and both displayed an increased lethality for mice with successive passages. These are the first cases of isolation of T. gondii from horses in Serbia. When compared with a worldwide collection of 61 type III and type III-like strains, isolate RS-Eq39 showed a combination of MS lengths similar to a strain isolated from a duck in Iran, and isolate RS-Eq40 was identical in all markers to three strains isolated from a goat from Gabon, a sheep from France and a pig from Portugal. Interestingly, the source horses were one seronegative and one weakly seropositive.

CONCLUSIONS: The isolation of viable T. gondii parasites from slaughter horses points to horsemeat as a potential source of human infection, but the fact that viable parasites were isolated from horses with only a serological trace of T. gondii infection presents further evidence that serology may not be adequate to assess the risk of toxoplasmosis from horsemeat consumption. Presence of T. gondii type III in Serbia sheds more light into the potential origin of this archetypal lineage in Europe.

Limon, G., W. Beauvais, et al. (2017). "Cross-Sectional Study of Toxoplasma gondii Infection in Pig Farms in England." Foodborne Pathog Dis 14(5): 269-281.

Ingestion of undercooked meat has been proposed as an important source of human Toxoplasma gondii infection. To ascertain the contribution of meat consumption to the risk of human infection, estimates of the prevalence of infection in meat-producing animals are required. A cross-sectional study was conducted to assess T. gondii infection in pigs raised in England, to identify risk factors for infection, and to compare performance of two serological tests: modified agglutination test (MAT) and enzyme-linked immunosorbent assay (ELISA). Blood samples from 2071 slaughter pigs originating from 131 farms were collected and 75 (3.6%) were found to be positive by MAT. Positive pigs originated from 24 farms. A subset of samples (n = 492) were tested using ELISA, and a significant disagreement ($p < 0.001$) was found between the two tests. An empirical Bayes approach was used to estimate the farm-level prevalence and the probability of each individual farm having at least one positive animal, considering the uncertainty arising from the sampling strategy and the imperfect test performance. The adjusted farm-level prevalence was 11.5% (95% credible interval of positive farms 8.4-16.0%). Two different criteria were used for classifying farms as infected: (1) >/=50% probability of having at least one infected pig (n = 5, 6.8%) and (2) >/=10% probability (n = 15, 20.5%). Data on putative risk factors were obtained for 73 farms. Using a 10% cutoff, the relative risk (RR) of infection was higher in farms where cats have direct access to pigs' food (RR = 2.6; p = 0.04), pigs have outdoor access (RR = 3.0; p = 0.04), and farms keeping </=200 pigs (RR = 3.9; p = 0.02), with strong collinearity between the three variables. The findings suggest a low level of T. gondii infection in the farms studied, most of which are likely to send to slaughter batches comprising 100% uninfected pigs. These results provide key inputs to quantitatively assess the T. gondii risk posed by pork to consumers.

Lupo, A., P. Chatre, et al. (2017). "Clonal Spread of Acinetobacter baumannii Sequence Type 25 Carrying blaOXA-23 in Companion Animals in France." Antimicrob Agents Chemother 61(1).

Melo, L. C., M. N. Boisson, et al. (2017). "OXA-48-producing ST372 Escherichia coli in a French dog." J Antimicrob Chemother 72(4): 1256-1258.

Raileanu, C., S. Moutailler, et al. (2017). "Borrelia Diversity and Co-infection with Other Tick Borne Pathogens in Ticks." Front Cell Infect Microbiol 7: 36.

Identifying Borrelia burgdorferi as the causative agent of Lyme disease in 1981 was a watershed moment in understanding the major impact that tick-borne zoonoses can have on public health worldwide, particularly in Europe and the USA. The medical importance of tick-borne diseases has long since been acknowledged, yet little is known regarding the occurrence of emerging tick-borne pathogens such as Borrelia spp., Anaplasma phagocytophilum, Rickettsia spp., Bartonella spp., "Candidatus Neoehrlichia mikurensis", and tick-borne encephalitis virus in questing ticks in Romania, a gateway into Europe. The objective of our study was to identify the infection and co-infection rates of different Borrelia genospecies along with other tick-borne pathogens in questing ticks collected from three geographically distinct areas in eastern Romania. We collected 557 questing adult and nymph ticks of three different species (534 Ixodes ricinus, 19 Haemaphysalis punctata, and 4 Dermacentor reticulatus) from three areas in Romania. We analyzed ticks individually for the presence of eight different Borrelia genospecies with high-throughput real-time PCR. Ticks with Borrelia were then tested for possible co-infections with A. phagocytophilum, Rickettsia spp., Bartonella spp., "Candidatus Neoehrlichia mikurensis", and tick-borne encephalitis virus. Borrelia spp. was detected in I. ricinus ticks from all sampling areas, with global prevalence rates of 25.8%. All eight Borrelia genospecies were detected in I. ricinus ticks: Borrelia garinii (14.8%), B. afzelii (8.8%), B. valaisiana (5.1%), B. lusitaniae (4.9%), B. miyamotoi (0.9%), B. burgdorferi s.s (0.4%), and B. bissettii (0.2%). Regarding pathogen co-infection 64.5% of infected I. ricinus were positive for more than one pathogen. Associations between different Borrelia genospecies were detected in 9.7% of ticks, and 6.9% of I. ricinus ticks tested positive for co-infection of Borrelia spp. with other tick-borne pathogens. The most common association was between B. garinii and B. afzelii (4.3%), followed by B. garinii and B. lusitaniae (3.0%). The most frequent dual co-infections were between Borrelia spp. and Rickettsia spp., (1.3%), and between Borrelia spp. and "Candidatus Neoehrlichia mikurensis" (1.3%). The diversity of tick-borne pathogens detected in this study and the frequency of co-infections should influence all infection risk evaluations following a tick bite.

Roqueplo, C., R. Blaga, et al. (2017). "Seroprevalence of Toxoplasma gondii in hunted wild boars (Sus scrofa) from southeastern France." Folia Parasitol (Praha) 64.

Toxoplasma gondii (Nicolle et Manceaux, 1908) is an obligate intracellular, parasitic protozoan within the phylum Apicomplexa that causes toxoplasmosis in mammalian hosts (including humans) and birds. Since meat of wild boar, Sus scrofa (Linnaeus), has been demonstrated to be a potential source of human infection, a careful evaluation of the prevalence of infection with T. gondii in hunted animals is needed to protect public health. In the Var area in southeastern France, we performed a spatio-temporal survey in order to investigate the prevalence of IgG antibodies in wild boars shot by hunters in the Canjuers military camp during two subsequent hunting seasons. Of 841 wild boars screened, antibodies (IgG) to T. gondii (modified agglutination test, cut-off 1 : 6) were found in 141 (16.8%) muscle extract samples. A significant association ($p < 0.001$) was found between positivity and age, but not gender, and hunting districts. The results obtained indicate that consumption of raw or undercooked meat from wild boars carries an important risk of infection with T. gondii. Wild boars may be considered as a bioindicator of parasite circulation in this ecosystem.

Stuckey, M. J., H. J. Boulouis, et al. (2017). "Potentially Zoonotic Bartonella in Bats from France and Spain." Emerg Infect Dis 23(3): 539-541.

We detected Bartonella in 11 of 109 insectivorous bats from France and 1 of 26 bats from Spain. These genetic variants are closely related to bat-associated Bartonella described in Finland and the United Kingdom and to B. mayotimonensis, the agent of a human endocarditis case in the United States.

Woudstra, C., P. Fach, et al. (2017). "Draft Genome Sequences of 12 Feline Bartonella henselae Isolates." Genome Announc 5(13).

Bartonella henselae is the main causative agent of cat scratch disease. In this report, we present the draft genome sequences of 12 strains of Bartonella henselae originating from the United States, Denmark, and France. These strains were isolated from cats and belonged to either 16S rRNA genotype I or 16S rRNA genotype II.

Zintl, A., S. Moutailler, et al. (2017). "Ticks and Tick-borne diseases in Ireland." Ir Vet J 70: 4.

Throughout Europe interest in tick-borne agents is increasing, particularly with regard to those that can cause human disease. The reason for this is the apparent rise in the incidence of many tick-borne diseases (TBD's). While there has never been a national survey of ticks or TBD's in Ireland, the trend here appears to be the reverse with a decline in the incidence of some agents seemingly associated with decreasing tick numbers particularly on agricultural land. In the absence of robust baseline data, however, this development cannot be confirmed. This review collates the limited information available from several dated published records on tick species and a small number of studies focused on certain TBD's. Some pilot data on tick density and TBD agents collected in 2016 are also presented. The aim is to explore the particular situation in Ireland with regard to ticks and TBD's and to provide a reference for future workers in the field.