Subjek : Avian Diseases
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Archie C.A. Clements, Dirk U. Pfeiffer, Emerging viral zoonoses: Frameworks for spatial and spatiotemporal risk assessment and resource planning, The Veterinary Journal, Volume 182, Issue 1, October 2009, Pages 21-30, ISSN 1090-0233, DOI: 10.1016/j.tvjl.2008.05.010.
(http://www.sciencedirect.com/science/article/B6WXN-4T8337S-1/2/8dd2cb0abd00b5467a4f5c7daf643215)
Abstract:
Spatial epidemiological tools are increasingly being applied to emerging viral zoonoses (EVZ), partly because of improving analytical methods and technologies for data capture and management, and partly because the demand is growing for more objective ways of allocating limited resources in the face of the emerging threat posed by these diseases. This review documents applications of geographical information systems (GIS), remote sensing (RS) and spatially-explicit statistical and mathematical models to epidemiological studies of EVZ.
Landscape epidemiology uses statistical associations between environmental variables and diseases to study and predict their spatial distributions. Phylogeography augments epidemiological knowledge by studying the evolution of viral genetics through space and time. Cluster detection and early warning systems assist surveillance and can permit timely interventions. Advanced statistical models can accommodate spatial dependence present in epidemiological datasets and can permit assessment of uncertainties in disease data and predictions. Mathematical models are particularly useful for testing and comparing alternative control strategies, whereas spatial decision-support systems integrate a variety of spatial epidemiological tools to facilitate widespread dissemination and interpretation of disease data. Improved spatial data collection systems and greater practical application of spatial epidemiological tools should be applied in real-world scenarios.
Keywords: Spatial analysis; Geographical information systems; Rift Valley fever; West Nile virus; Highly pathogenic avian influenza; Rabies; Risk analysis

Eunok Jung, Shingo Iwami, Yasuhiro Takeuchi, Tae-Chang Jo, Optimal control strategy for prevention of avian influenza pandemic, Journal of Theoretical Biology, Volume 260, Issue 2, 21 September 2009, Pages 220-229, ISSN 0022-5193, DOI: 10.1016/j.jtbi.2009.05.031.
(http://www.sciencedirect.com/science/article/B6WMD-4WGK4R5-4/2/935fdd5d08951b12c180457d609a088e)
Abstract:
The spread of H5N1 virus to Europe and continued human infection in Southeast Asia have heightened pandemic concern. Although, fortunately, sustained human-to-human transmissions have not been reported yet, it is said that a pandemic virus which can be easily transmitted among humans certainly emerges in the future. In this study, we extended the previous studies for the prevention of the pandemic influenza to evaluate the time-dependent optimal prevention policies, which are associated with elimination policy and quarantine policy, considering its execution cost. Actually, the execution cost affects the optimal strategy of prevention policies and the prevention of the disease spread. We found that the quarantine policy is very important rather than the elimination policy during the disease spread, even if the unit execution cost of the quarantine policy is more expensive than that of the elimination policy. And also, the change of the unit execution cost does affect the total cumulative cost of the optimal prevention policies but does not affect the relative frequency of each cumulative execution cost. Furthermore, interestingly, we revealed that an optimal strategy to reduce the number of total infected humans might increase a chance of invadability of the mutant influenza.

Keywords: Epidemic model; Avian influenza; Optimal control theory; Elimination policy; Quarantine policy; Invadability

Benjamin Roche, Camille Lebarbenchon, Michel Gauthier-Clerc, Chung-Ming Chang, Frederic Thomas, Francois Renaud, Sylvie van der Werf, Jean-Francois Guegan, Water-borne transmission drives avian influenza dynamics in wild birds: The case of the 2005-2006 epidemics in the Camargue area, Infection, Genetics and Evolution, Volume 9, Issue 5, September 2009, Pages 800-805, ISSN 1567-1348, DOI: 10.1016/j.meegid.2009.04.009.
(http://www.sciencedirect.com/science/article/B6W8B-4W3HX83-1/2/ea1ce6181466a3c2fe748de536c5d7a4)
Abstract:
Transmission and persistence of avian influenza viruses (AIV) among wildlife remains an unresolved issue because it depends both on the ecology of the host (e.g. population density, migration) and on the environment (e.g. AIV persistence in water). We have developed a mathematical model that accounts for both AIV epidemics and bird community dynamics. The model is parameterized using bird counts and AIV prevalence data. Results suggest that the transmission patterns driving the dynamics of infection at our study site (Camargue, South of France) involved both a density-dependent and a water-borne transmission processes. Water-borne transmission is, however, the main determinant of the disease dynamics and observed prevalence level. This pattern of transmission highlights the importance of the persistence of viral particles in water in AIV dynamics in wild birds.
Keywords: Influenza A; Water-borne transmission; Mathematical modeling

C.P. Jewell, T. Kypraios, R.M. Christley, G.O. Roberts, A novel approach to real-time risk prediction for emerging infectious diseases: A case study in Avian Influenza H5N1, Preventive Veterinary Medicine, Volume 91, Issue 1, Special Issue: GisVet 2007, 1 September 2009, Pages 19-28, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2009.05.019.
(http://www.sciencedirect.com/science/article/B6TBK-4WJ2CBB-1/2/66e9bce866a210bea2478c960f9f7e13)
Abstract:
Mathematical simulation modelling of epidemic processes has recently become a popular tool in guiding policy decisions for potential disease outbreaks. Such models all rely on various parameters in order to specify quantities such as transmission and detection rates. However, the values of these parameters are peculiar to an individual outbreak, and estimating them in advance of an epidemic has been the major difficulty in the predictive credibility of such approaches.
The obstruction to classical approaches in estimating model parameters has been that of missing data: (i) an infected individual is only detected after the onset of clinical signs, we never observe the time of infection directly; (ii) if we wish to make inference on an epidemic while it is in progress (in order to predict how it might unfold in the future), we must take into account the fact that there may be individuals who are infected but not yet detected.
In this paper we apply a reversible-jump Markov chain Monte Carlo algorithm to a combined spatial and contact network model constructed in a Bayesian context to provide a real-time risk prediction during an epidemic. Using the example of a potential Avian H5N1 epidemic in the UK poultry industry, we demonstrate how such a technique can be used to give real-time predictions of quantities such as the probability of individual poultry holdings becoming infected, the risk that individual holdings pose to the population if they become infected, and the number and whereabouts of infected, but not yet detected, holdings. Since the methodology generalises easily to many epidemic situations, we anticipate its use as a real-time decision-support tool for targetting disease control to critical transmission processes, and for monitoring the efficacy of current control policy.
Keywords: Epidemic; Inference; Prediction; Bayesian; Reversible jump MCMC; Risk

Shingo Iwami, Yasuhiro Takeuchi, Xianning Liu, Shinji Nakaoka, A geographical spread of vaccine-resistance in avian influenza epidemics, Journal of Theoretical Biology, Volume 259, Issue 2, 21 July 2009, Pages 219-228, ISSN 0022-5193, DOI: 10.1016/j.jtbi.2009.03.040.
(http://www.sciencedirect.com/science/article/B6WMD-4W1BVDP-3/2/571cc59966fdfeb43256289f0896bede)
Abstract:
Vaccination can be a useful tool for control of avian influenza outbreaks in poultry, but its use is reconsidered in most of the countries worldwide because of its negative effects on the disease control. One of the most important negative effects is the potential for emergence of vaccine-resistant viruses. Actually, in the vaccination program in China and Mexico, several vaccine-resistant strains were confirmed. Vaccine-resistant strains usually cause a loss of the protection effectiveness of vaccination. Therefore, a vaccination program that engenders the emergence of the resistant strain might promote the spread of the resistant strain and undermine the control of the infectious disease, even if the vaccination protects against the transmission of a vaccine-sensitive strain. We designed and analyzed a deterministic patch-structured model in heterogeneous areas (with or without vaccination) illustrating transmission of vaccine-sensitive and vaccine-resistant strains during a vaccination program. We found that the vaccination program can eradicate the vaccine-sensitive strain but lead to a prevalence of vaccine-resistant strain. Further, interestingly, the replacement of viral strain could occur in another area without vaccination through a migration of non-infectious individuals due to an illegal trade of poultry. It is also a novel result that only a complete eradication of both strains in vaccination area can achieve the complete eradication in another areas. Thus we can obtain deeper understanding of an effect of vaccination for better development of vaccination strategies to control avian influenza spread.
Keywords: Epidemic model; Patch-structured model; Avian influenza; Vaccination program; Geographical spread; Illegal poultry trade

Iris I. Levin, Diana C. Outlaw, F. Hernan Vargas, Patricia G. Parker, Plasmodium blood parasite found in endangered Galapagos penguins (Spheniscus mendiculus), Biological Conservation, In Press, Corrected Proof, Available online 19 July 2009, ISSN 0006-3207, DOI: 10.1016/j.biocon.2009.06.017.
(http://www.sciencedirect.com/science/article/B6V5X-4WT39TN-1/2/d2291d01fc761094e87d9f2287d9ad6c)
Abstract:
This is the first report of a Plasmodium blood parasite found in the Galapagos Archipelago. Phylogenetic analyses place this parasite, recovered from endangered Galapagos penguins (Spheniscus mendiculus), within the genus Plasmodium, and suggest a close relationship to some of the most dangerous lineages of Plasmodium that have been known to cause severe mortality and morbidity in captive penguin populations. Infectious disease is an increasingly important cause of global species extinctions, and extinctions due to avian pox and avian malaria (Plasmodium relictum) have been well documented in Hawaiian avifauna. Plasmodium blood parasites had not been detected in Galapagos birds until now, despite previous microscopic and molecular screening of many of the species, including the Galapagos penguin. While penguin populations now appear healthy, it is unclear whether this parasite will have an obvious impact on their survival and reproduction, particularly during El Nino events, which cause stress due to reduced food availability. It is possible that this parasite arrived with or shortly after the recent arrival of an introduced mosquito, Culex quinquefasciatus, known elsewhere as a competent vector of Plasmodium blood parasites.
Keywords: Malaria; Vector; Mosquito; Extinction; Wildlife diseases

S.H. Lee, H.S. Lillehoj, D.W. Park, S.I. Jang, A. Morales, D. Garcia, E. Lucio, R. Larios, G. Victoria, D. Marrufo, Erik P. Lillehoj, Protective effect of hyperimmune egg yolk IgY antibodies against Eimeria tenella and Eimeria maxima infections, Veterinary Parasitology, Volume 163, Issues 1-2, 7 July 2009, Pages 123-126, ISSN 0304-4017, DOI: 10.1016/j.vetpar.2009.04.020.
(http://www.sciencedirect.com/science/article/B6TD7-4W38RMW-1/2/efb21ec5772036bb65e0bdaab4c8a0f2)
Abstract:
Avian coccidiosis is caused by several distinct species of Eimeria protozoa and is the major parasitic disease of poultry of economic importance. As an alternative strategy to control avian coccidiosis without using prophylactic medications, we have investigated the efficacy of inducing passive immunity against coccidiosis by orally feeding hyperimmune IgY antibodies. In this study, a commercially available egg yolk powder, Supracox(R) (SC), a purified IgY fraction of egg yolk prepared from hens hyperimmunized with three major species of Eimeria oocysts, were continuously fed to young chicks from hatch. Upon orally infecting these broiler chicks with Eimeria tenella and Eimeria maxima oocysts at 1 week of age, they showed significantly higher body weight gains ($P < 0.05$) compared to the untreated controls. Furthermore, SC-fed chicks showed significantly less intestinal lesions and reduced fecal oocyst output compared to the untreated controls following oral infections with E. tenella and E. maxima. These results provide clear evidence that passive immunization of chicks with hyperimmune egg yolk IgY antibodies provide significant protection against E. tenella or E. maxima infections.
Keywords: Egg yolk IgY; Coccidiosis; Eimeria; Chickens; Passive immunization

Carol J. Cardona, Zheng Xing, Christian E. Sandrock, Cristina E. Davis, Avian influenza in birds and mammals, Comparative Immunology, Microbiology and Infectious Diseases, Volume 32, Issue 4, Avian Influenza, July 2009, Pages 255-273, ISSN 0147-9571, DOI: 10.1016/j.cimid.2008.01.001.
(http://www.sciencedirect.com/science/article/B6T5H-4SHFSM3-1/2/c8b96214bd2d8c39a9e941cb8a727721)
Abstract:
The disease syndromes caused by avian influenza viruses are highly variable depending on the host species infected, its susceptibility and response to infection and the virulence of the infecting viral strain. Although avian influenza viruses have a broad host range in general, it is rare for an individual strain or subtype to infect more than one species. The H5N1 highly pathogenic avian influenza virus (HPAIV) lineages of viruses that descended from A/goose/Guandong/96 (H5N1 HPAIV) are unusual in the diversity of species they have infected worldwide. Although the species affected by H5N1 HPAI in the field and those that have been experimentally studied are diverse, their associated disease syndromes are remarkably similar across species. In some species, multi-organ failure and death are rapid and no signs of the disease are observed. Most prominently in this category are chickens and other avian species of the order Galliformes. In other species, neurologic signs develop resulting in the death of the host. This is what has been reported in domestic cats (Carnivora), geese (Anseriformes), ratites (Struthioniformes), pigeons inoculated with high doses (Columbiformes) and ducks infected with H5N1 HPAIV isolated since 2002 (Anseriformes). In some other species, the disease is more prolonged and although multi-organ failure and death are the eventual outcomes, the signs of disease are more extensive. Predominantly, these species include humans (Primates) and the laboratory models of human disease, the ferret (Carnivora), mouse (Rodentia) and cynamologous macaques (Primates). Finally, some species are more resistant to infection with H5N1 HPAIV and show few or no signs of disease. These species include pigeons in some studies (Columbiformes), ducks inoculated with pre-2002 isolates (Anseriformes), and pigs (Artiodactyla).

Keywords: Avian influenza; H5N1 highly pathogenic avian influenza; Disease; Lesions; Birds; Mammals; Grippe aviaire; Grippe aviaire H5N1 hautement pathogene; Maladie; Lesions; Oiseaux; Mammiferes

Blanca Lupiani, Sanjay M. Reddy, The history of avian influenza, Comparative Immunology, Microbiology and Infectious Diseases, Volume 32, Issue 4, Avian Influenza, July 2009, Pages 311-323, ISSN 0147-9571, DOI: 10.1016/j.cimid.2008.01.004.
(http://www.sciencedirect.com/science/article/B6T5H-4SNGRKV-1/2/bd67bb37c3c1cb5a8c6c85f3bef9de39)
Abstract:
The first description of avian influenza (AI) dates back to 1878 in northern Italy, when Perroncito [Perroncito E. Epizoozia tifoide nei gallinacei. Annali Accad Agri Torino 1878;21:87-126] described a contagious disease of poultry associated with high mortality. The disease, termed 'fowl plague', was initially confused with the acute septicemic form of fowl cholera. However, in 1880, soon after its first description, Rivolta and Delprato [as reported by Stubs EL. Fowl pest, In: Biester HE, Devries L, editors. Diseases of poultry. 1st ed. Ames, IO: Iowa State College Press; 1943. p. 493-502] showed it to be different from fowl cholera, based on clinical and pathological properties, and called it Typhus exudatious gallinarum. In 1901, Centanni and Savunzzi [Centanni E, Savonuzzi E, La peste aviaria I & II, Communicazione fatta all'accademia delle scienze mediche e naturali de Ferrara, 1901] determined that fowl plague was caused by a filterable virus; however, it was not until 1955 that the classical fowl plague virus was shown to be a type A influenza virus based on the presence of type A influenza virus type-specific ribonucleoprotein [Schafer W. Vergleichender sero-immunologische Untersuchungen uber die Viren der Influenza und klassischen Geflugelpest. Z Naturf 1955;10b:81-91]. The term fowl plague was substituted by the more appropriate term highly pathogenic avian influenza (HPAI) at the First International Symposium on Avian Influenza [Proceedings of the First International Symposium on Avian Influenza. Beltsville, MD. 1981, Avian Dis 47 (Special Issue) 2003.] and will be used throughout this review when referring to any previously described fowl plague virus.
Keywords: Virus de la grippe aviaire; Peste aviaire; Hautement pathogene; Faiblement pathogene; Pandemie de grippe; Fowl plague; Avian influenza; History; Highly pathogenic; Low pathogenic; Waterfowl

Karen S. Yee, Tim E. Carpenter, Carol J. Cardona, Epidemiology of H5N1 avian influenza, Comparative Immunology, Microbiology and Infectious Diseases, Volume 32, Issue 4, Avian Influenza, July 2009, Pages 325-340, ISSN 0147-9571, DOI: 10.1016/j.cimid.2008.01.005.
(http://www.sciencedirect.com/science/article/B6T5H-4SD1KNP-1/2/ed4758258e9993f95311f101c157867e)
Abstract:
High pathogenic (HP) H5N1 avian influenza (AI) infection has been reported in domestic poultry, wildlife, and human populations since 1996. Risk of infection is associated with direct contact with infected birds. The mode of H5N1 spread from Asia to Europe, Africa and the Far East is unclear; risk factors such as legal and illegal domestic poultry and exotic bird trade, and migratory bird movements have been documented. Measures used to control disease such as culling, stamping out, cleaning and disinfection, and vaccination have not been successful in eradicating H5N1 in Asia, but have been effective in Europe.
Keywords: Orthomyxoviridae; Highly Pathogenic Avian Influenza; Poultry diseases; Pandemic surveillance; Wild aquatic birds; Distribution; Spread; Volaille; Maladies aviaires; Gibier migratoire; Grippe aviaire hautement pathogene; Orthomyxoviridae; Surveillance de la pandemie; Epidemiologie

David E. Swayne, Avian influenza vaccines and therapies for poultry, Comparative Immunology, Microbiology and Infectious Diseases, Volume 32, Issue 4, Avian Influenza, July 2009, Pages 351-363, ISSN 0147-9571, DOI: 10.1016/j.cimid.2008.01.006.
(http://www.sciencedirect.com/science/article/B6T5H-4SCTSPD-1/2/020ef2ca93aa7527081fa5e4643e5853)
Abstract:
Vaccines have been used in avian influenza (AI) control programs to prevent, manage or eradicate AI from poultry and other birds. The best protection is produced from the humoral response against the hemagglutinin (HA) protein. A variety of vaccines have been developed and tested under experimental conditions with a few receiving licensure and field use following demonstration of purity, safety, efficacy and potency. Current licensed vaccines are predominately inactivated whole AI vaccines, typically produced from low pathogenicity (LP) AI virus strains, or occasionally from high pathogenicity AI virus strains. Recently, reverse genetic procedures have been developed that allow construction of vaccine strains using a genetically altered HA gene (changing HP HA proteolytic cleavage site to LP) and a backbone of internal gene segments for safe, high growth production. Other licensed AI vaccines include recombinant fowl poxvirus vector with an AI H5 insert and a recombinant Newcastle disease virus vector with an AI H5 gene insert. The latter vaccine can be mass administered via aerosol application.
Keywords: Avian influenza; Vaccine; Protection; Efficacy; Potency; grippe aviaire; vaccin; protection; efficacite; puissance

Etienne Thiry, Diane Addie, Sandor Belak, Corine Boucraut-Baralon, Herman Egberink, Tadeusz Frymus, Tim Gruffydd-Jones, Katrin Hartmann, Margaret J. Hosie, Albert Lloret, Hans Lutz, Fulvio Marsilio, Maria Grazia Pennisi, Alan D. Radford, Uwe Truyen, Marian C. Horzinek, H5N1 avian influenza in cats. ABCD guidelines on prevention and management, Journal of Feline Medicine & Surgery, Volume 11, Issue 7, July 2009, Pages 615-618, ISSN 1098-612X, DOI: 10.1016/j.jfms.2009.05.011.
(http://www.sciencedirect.com/science/article/B6WJC-4WCWP0G-G/2/23d1a0053bdfed62d45152409117676d)
Abstract: Overview
Avian influenza is a disease of birds, caused by a type A influenza virus. The subtype H5N1 avian influenza occurs primarily in birds and infection varies from mild disease with little or no mortality to a highly fatal, rapidly spreading epidemic (highly pathogenic avian influenza). It is extremely rare for cats to be infected and there are only very few confirmed reports of the disease in cats in Europe.Infection
Cats can be infected via the respiratory and oral routes (eg, by eating infected birds). The key precondition for infection is that the cat lives in an area where H5N1 virus infection has been confirmed in birds. Additionally, the cat should have had outdoor access to an environment where waterfowl is present, or contact with poultry or uncooked poultry meat, or close contact with an H5N1-infected, sick cat during the first week of infection.Clinical suspicion
Clinical signs in cats may include fever, lethargy, dyspnoea, conjunctivitis and rapid death. Neurological signs (circling, ataxia) have also been recorded.Diagnosis
The veterinary authorities should be notified. Oropharyngeal, nasal and/or rectal swabs or faecal samples of suspected cases should be submitted for PCR and/or virus isolation. Post-mortem samples of lung and mediastinal lymph nodes should be obtained. Particular care should be taken when handling the cat and/or samples.Disease management
The virus is sensitive to all standard medical disinfectants. Cats with suspected H5N1 infection should be kept in strict isolation. Owners should be advised to confine the cat to a separate room prior to bringing it to the veterinary clinic.Vaccination and disease prevention

No H5N1 vaccines are commercially available for cats. In the event of confirmed cases of H5N1 avian influenza in birds in the area, owners should keep their cats indoors until further information is available, and follow official regulations.

A. Gioffre, G. Echeverria-Valencia, A. Arese, C. Morsella, S. Garbaccio, F. Delgado, M. Zumarraga, F. Paolicchi, A. Cataldi, M.I. Romano, Characterization of the Apa antigen from M. avium subsp. paratuberculosis: A conserved Mycobacterium antigen that elicits a strong humoral response in cattle, Veterinary Immunology and Immunopathology, In Press, Corrected Proof, Available online 24 June 2009, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2009.06.008.
(http://www.sciencedirect.com/science/article/B6TD5-4WKTWT0-1/2/7bb4336c980f925b52cf53e7f442bb3c)
Abstract:
Johne's disease or paratuberculosis is widespread in almost all countries and remains difficult to eradicate. Nowadays, diagnosis of Mycobacterium avium subsp. paratuberculosis (MPTB) infection is one of the main concerns. In this work, we evaluated the expression, biochemical properties and antigenicity of the Apa antigen, encoded by the gene annotated as MAP1569, in the MPTB genome. We confirmed its expression in MPTB and its glycosylation by the ConA binding assay. Although the MPTB-Apa is not an immunodominant antigen, MPTB-infected cattle showed a strong humoral response to recombinant Apa by Western blot and ELISA. Milk was also a suitable sample to be tested by ELISA. We comparatively analysed the humoral cross-reactivity to the Apa from MPTB (MPTB-Apa) and the orthologue from Mycobacterium tuberculosis (MT-Apa, identical to that from Mycobacterium bovis) in both infected and control cows. Response of M. bovis- and MPTB-infected animals against MT-Apa was similar ($P = 0.6985$) but the response of the M. bovis-infected ones to MPTB-Apa was differential, being significantly diminished ($P < 0.0001$). Although 6 out 45 animals from MPTB-infected herds responded to MPTB-Apa stimulation in the IFN[gamma] release assay, we found no significant differences when compared infected herds with non-infected ones ($P = 0.34$). This antigen, in contrast to bovine Purified Protein Derivative (PPDb), was strongly represented in avian PPD (PPDa), as shown by the recognition of BALB/c mice hyperimmune sera against MPTB-Apa by Dot-blot immunoassay. We therefore demonstrated the antigenicity of Apa in MPTB-infected animals and a differential response to the recombinant antigen when compared to M. bovis-infected animals. These traits herein described, added to the usefulness of milk samples to detect IgG anti-Apa, could be important for routine screening in dairy cattle, considering a multiantigenic approach to overcome the lack of immunodominance.
Keywords: Antigen; M. avium subsp. paratuberculosis; Paratuberculosis; Johne's disease

Ronan G. Shaughnessy, Kieran G. Meade, Sarah Cahalane, Brenda Allan, Carla Reiman, John J. Callanan, Cliona O'Farrelly, Innate immune gene expression differentiates the early avian intestinal response between Salmonella and Campylobacter, Veterinary Immunology and Immunopathology, In Press, Corrected Proof, Available online 21 June 2009, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2009.06.007.
(http://www.sciencedirect.com/science/article/B6TD5-4WK43N8-1/2/100156438f509dd63f4c310800ac91ef)
Abstract:
Salmonella enterica serovar Typhimurium and Campylobacter jejuni are major human pathogens, yet colonise chickens without causing pathology. The aim of this study was to compare intestinal innate immune responses to both bacterial species, in a 4-week-old broiler chicken model. Challenged and control birds were sacrificed and tissue samples taken for histopathology and RNA extraction. No significant clinical or pathological changes were observed in response to infection with either bacterial species. Expression of selected genes involved in pathogen detection and the innate immune response were profiled in caecal tissues by quantitative real-time

PCR. TLR4 and TLR21 gene expression was transiently increased in response to both bacterial species ($P < 0.05$). Significant increases in TLR5 and TLR15 gene expression were detected in response to S. Typhimurium but not to C. jejuni. Transient increases of proinflammatory cytokine (IL6 and IFNG) and chemokine (IL8 and K60) genes increased as early as 6 h in response to S. Typhimurium. Minimal cytokine gene expression was detected in response to C. jejuni after 20 h. IL8 gene expression however, was significantly increased by 24-fold ($P < 0.01$).
The differential expression profiles of innate immune genes in both infection models shed light on the tailored responses of the host immune system to specific microbes. It is further evidence that innate regulation of these responses is an important prerequisite to preventing development of disease.
Keywords: Chicken; Commensal; Campylobacter; Salmonella; Innate immune gene expression

Chulseung Lee, Daesub Song, Bokyu Kang, Dongsuk Kang, Jungeun Yoo, Kwonil Jung, Gunsuk Na, Kichang Lee, Bongkyun Park, Jinsik Oh, A serological survey of avian origin canine H3N2 influenza virus in dogs in Korea, Veterinary Microbiology, Volume 137, Issues 3-4, 12 June 2009, Pages 359-362, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2009.01.019.
(http://www.sciencedirect.com/science/article/B6TD6-4VDS8DH-2/2/1edcfdc4a80fa580688a98323afde8df)
Abstract:
Canine H3N2 influenza viruses of avian origin were recently isolated and found to induce disease in dogs. Results of serologic analysis indicate that avian origin canine influenza virus can spread rapidly through local dog populations, which indicates its potential for becoming established in dogs throughout Korea.
Keywords: Canine influenza virus; H3N2; Serologic analysis; Dog; Avian

Norberto Anibal Maidana, Hyun Mo Yang, Spatial spreading of West Nile Virus described by traveling waves, Journal of Theoretical Biology, Volume 258, Issue 3, Special Issue: Mathematics in Biointeractions - Based on the Talks at the Second Conference on Computational and Mathematical Population Dynamics, 7 June 2009, Pages 403-417, ISSN 0022-5193, DOI: 10.1016/j.jtbi.2008.12.032.
(http://www.sciencedirect.com/science/article/B6WMD-4V9S493-1/2/df61fda809a3de7f90951ccaa6481742)
Abstract:
In this work, we propose a spatial model to analyze the West Nile Virus propagation across the USA, from east to west. West Nile Virus is an arthropod-borne flavivirus that appeared for the first time in New York City in the summer of 1999 and then spread prolifically among birds. Mammals, such as humans and horses, do not develop sufficiently high bloodstream titers to play a significant role in the transmission, which is the reason to consider the mosquito-bird cycle. The model aims to study this propagation based on a system of partial differential reaction-diffusion equations taking the mosquito and the avian populations into account. Diffusion and advection movements are allowed for both populations, being greater in the avian than in the mosquito population. The traveling wave solutions of the model are studied to determine the speed of disease dissemination. This wave speed is obtained as a function of the model's parameters, in order to assess the control strategies. The propagation of West Nile Virus from New York City to California state is established as a consequence of the diffusion and advection movements of birds. Mosquito movements do not play an important role in the disease dissemination, while bird advection becomes an important factor for lower mosquito biting rates.
Keywords: West Nile Virus; Reaction-diffusion equation; Traveling waves; Wave speed; Sensitivity analysis

Qingping Luo, Hongliang Huang, Wei Zou, Hanbing Dan, Xuebo Guo, Anding Zhang, Zhengjun Yu, Huanchun Chen, Meilin Jin, An indirect sandwich ELISA for the detection of avian influenza H5 subtype viruses using anti-hemagglutinin protein monoclonal antibody, Veterinary Microbiology, Volume 137, Issues 1-2, 28 May 2009, Pages 24-30, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.12.009.
(http://www.sciencedirect.com/science/article/B6TD6-4V4KPTB-2/2/9d87cdf80646cfe38c9c04b8e67494ac)
Abstract:
A sandwich ELISA test using AIV H5 subtype specific monoclonal antibody (clone 2H4) to an epitope of hemagglutinin protein has been developed. The monoclonal antibody was used to capture the antigen from clinical samples (swabs and tissues). Captured antigens from clinical samples were detected using polyclonal sera, purified AIV H5N1 particles were titrated in the sandwich ELISA and the limit of detection was determined to be approximately 1.0 ng of influenza viral protein in virus preparations. Fifteen AIV strains of H1-H15 subtypes and some other pathogens were tested by this system, and the test is specific to H5 subtype viruses as it failed to detect other AIV subtype viruses and other pathogens. Varieties of clinical samples originating from laboratory experiments (n = 382) and from fields (n = 288) were employed to test the efficacy of DAS-ELISA test. The test compared very well with the traditional method for detection of influenza virus: virus isolation (VI) in embryonated chicken eggs. In comparison to virus isolation the sensitivity and specificity of sandwich ELISA were found to be 98.6% and 97.6% respectively. In addition, the DAS-ELISA was used to test samples of experimentally infected birds and clinical samples obtained from central China in 2005. The assay proved to be sensitive and specific for the rapid detection of AIV H5 subtype virus form the tissues and swabs in infected animals.
Keywords: Avian infectious H5 subtype viruses; AIV; DAS-ELISA; Monoclonal antibody

N. Sedlmaier, K. Hoppenheidt, H. Krist, S. Lehmann, H. Lang, M. Buttner, Generation of avian influenza virus (AIV) contaminated fecal fine particulate matter (PM2.5): Genome and infectivity detection and calculation of immission, Veterinary Microbiology, In Press, Corrected Proof, Available online 20 May 2009, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2009.05.005.
(http://www.sciencedirect.com/science/article/B6TD6-4WBC1R3-1/2/d3683be347b1aa9b25d28b53d7fbcf50)
Abstract:
As a model for aerosol transmission, chicken feces was spiked with avian influenza virus (AIV) subtype H10N7 and used to generate a fine particulate matter aerosol. For this an innovative aerosol chamber was developed, that collected PM2.5 on quartz microfiber filters. With AIV contaminated PM2.5 dust-coated filters different incubation times ranging from 0 to 4 days and storage mainly at +4 and +20 [degree sign]C and at different relative humidity (RH) were performed. Embryonic death in inoculated hen's eggs with filter elute was the AIV infectivity read out. To determine viral genome presence quantitative real time RT-PCR was applied.
The filter elutes contained AIV genome as well as viable virus whereby +20 [degree sign]C indicated a borderline temperature for infectious virus stability. In addition, high relative humidity was critical for AIV viability in PM2.5. The results allowed a dispersion calculation of infectious AIV in aerosols assuming a worst case scenario for an AIV outbreak in poultry farms. Thus exposure to AIV associated with PM2.5 is possible near to infected farms and may be a serious risk for fatal influenza disease in both man and animals. Airborne transmission should be effectively preventable by dispersion of water combined with disinfection into the inside air as well as the exhaust air stream of AIV infected farms.
Keywords: Avian influenza virus; Chicken feces; Fine particulate matter (PM2.5); Airborne transmission; Quartz microfiber filters

Emilio Del Cacho, Margarita Gallego, Hyun S. Lillehoj, Fernando Lopez-Bernard, Caridad Sanchez-Acedo, Avian follicular and interdigitating dendritic cells: Isolation and morphologic, phenotypic, and functional analyses, Veterinary Immunology and Immunopathology, Volume 129, Issues 1-2, 15 May 2009, Pages 66-75, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2008.12.015.
(http://www.sciencedirect.com/science/article/B6TD5-4V47C8S-4/2/30376d521d240caa92f091e58d8bebd5)
Abstract:
An antiserum against Eimeria tenella sporozoites was used to localize and isolate Ag-binding cells in intestinal cecal tonsils of parasite-infected chickens. Based on their tissue localization, ultrastructural features, and expression of surface markers, two subpopulations of cells were isolated, CD45+ interdigitating dendritic cells (IDCs) and CD45- follicular dendritic cells (FDCs). IDCs expressed MHC class I, MHC class II, and selectin, induced the proliferation of allogeneic naive CD4+ T cells, and increased the secretion of IFN-[gamma] by autologous T cells. FDCs expressed surface IgG, IgM, ICAM-1, and VCAM-1, stimulated the proliferation of LPS-treated allogeneic B cells, and augmented the secretion of IgG by LPS-treated autologous B cells. Final cell yields were 6 x 105 to 8 x 105 cells per chicken with >95% purity. In summary, this combination of methods using Abs against E. tenella and CD45 made it possible for the first time to obtain a highly enriched IDCs and FDCs which are functionally active in chickens. This novel method will enable the detailed biochemical and immunological characterizations of avian dendritic cells and facilitate the investigation of their role in initiating immune response in normal and disease states.
Keywords: Dendritic cells; Parasitic protozoan infections; Chickens; Coccidiosis; Antigen presentation/processing; Mucosa

Bernd Hoffmann, Martin Beer, Scott M. Reid, Peter Mertens, Chris A.L. Oura, Piet A. van Rijn, Marek J. Slomka, Jill Banks, Ian H. Brown, Dennis J. Alexander, Donald P. King, A review of RT-PCR technologies used in veterinary virology and disease control: Sensitive and specific diagnosis of five livestock diseases notifiable to the World Organisation for Animal Health, Veterinary Microbiology, In Press, Corrected Proof, Available online 6 May 2009, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2009.04.034.
(http://www.sciencedirect.com/science/article/B6TD6-4W7B0DY-1/2/b6967a20cb4ec01c7696a72e96ee6979)
Abstract:
Real-time, reverse transcription polymerase chain reaction (rRT-PCR) has become one of the most widely used methods in the field of molecular diagnostics and research. The potential of this format to provide sensitive, specific and swift detection and quantification of viral RNAs has made it an indispensable tool for state-of-the-art diagnostics of important human and animal viral pathogens. Integration of these assays into automated liquid handling platforms for nucleic acid extraction increases the rate and standardisation of sample throughput and decreases the potential for cross-contamination. The reliability of these assays can be further enhanced by using internal controls to validate test results. Based on these advantageous characteristics, numerous robust rRT-PCRs systems have been developed and validated for important epizootic diseases of livestock. Here, we review the rRT-PCR assays that have been developed for the detection of five RNA viruses that cause diseases that are notifiable to the World Organisation for Animal Health (OIE), namely: foot-and-mouth disease, classical swine fever, bluetongue disease, avian influenza and Newcastle disease. The performance of these tests for viral diagnostics and disease control and prospects for improved strategies in the future are discussed.
Keywords: Polymerase chain reaction; Real-time PCR; FMDV; AIV; NDV; CSFV; BTV

H.M. Yassine, M. Khatri, Y.J. Zhang, C.W. Lee, B.A. Byrum, J. O'Quin, K.A. Smith, Y.M. Saif, Characterization of triple reassortant H1N1 influenza A viruses from swine in Ohio, Veterinary

Microbiology, In Press, Corrected Proof, Available online 4 May 2009, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2009.04.028.
(http://www.sciencedirect.com/science/article/B6TD6-4W6YJ7P-1/2/e0ce57dda2fbdd81bd172efbdeba37e4)
Abstract:
An H1N1 influenza A virus, A/swine/Ohio/24366/07, was isolated from pigs in an Ohio county fair. Twenty-six people who came in contact with the infected pigs developed respiratory disease and two of these people were laboratory confirmed as H1N1 by the Centers for Disease Control and Prevention (CDC). The A/swine/Ohio/24366/07 virus we isolated from swine was shown at the CDC to have 100% identical genome sequence to the human virus associated with the county fair. This prompted us to characterize three swine and two human origin H1N1 influenza A viruses isolated at different time points in the State of Ohio. The three swine viruses were shown to be triple reassortant viruses harboring genes of human (PB1), swine (HA, NA, NP, M, and NS), and avian (PB2 and PA) lineage viruses. Although viruses evaluated in this study were isolated during a short time interval (3 years), genetic drift was observed within the HA and NA genes, including changes at the receptor binding and antigenic sites of HA1 protein. Nevertheless, all viruses exhibited antigenic similarity as evaluated with hemagglutination inhibition and virus neutralizing tests. Internal genes were similar to other reassortant viruses of various subtypes currently circulating in the United States. Interestingly, two of the swine viruses including the 2007 isolate replicated well in human airway epithelial cells, however, another virus isolated in 2006 showed very little replication.
Keywords: Influenza A viruses; H1N1; Triple reassortants

Virginie Rolland, Christophe Barbraud, Henri Weimerskirch, Assessing the impact of fisheries, climate and disease on the dynamics of the Indian yellow-nosed Albatross, Biological Conservation, Volume 142, Issue 5, May 2009, Pages 1084-1095, ISSN 0006-3207, DOI: 10.1016/j.biocon.2008.12.030.
(http://www.sciencedirect.com/science/article/B6V5X-4VPCVMM-3/2/ecbc6f9ddae7d709eeb1b3f128915fad)
Abstract:
Many seabird populations are currently decreasing, especially albatrosses for which the primary threat is recognised to be mortality in fisheries. Introduced predators, climate change and other factors such as diseases can also have large impacts on seabirds. Here, we assessed the relative effect of three potential threats: climate, fisheries and diseases on the demography of an endangered marine predator and modelled its population dynamics to project its size under different scenarios. We based our study on a long-term monitoring of a colony of individually marked Indian yellow-nosed albatrosses at Amsterdam Island, subtropical Indian Ocean, that has declined during the past twenty years. We found no evidence for an impact of legal tuna longlining on demographic parameters. Hatching success was lower during El Nino years but survival (0.902 +/- 0.011) was not affected by climatic factors. Avian cholera caused high chick mortality (0.808 +/- 0.181) which in turn probably triggered the high emigration rate (0.038 +/- 0.011) through dispersal of failed breeders. This colony has a high risk of extinction. However, the rest of the population at Amsterdam Island seemingly not affected to the same extent, declined but stabilised since 1998. Matrix models indicated that lowered adult survival and the very low breeding success, resulting in low recruitment, have both contributed to the decline of the yellow-nosed albatross colony until the mid-1990s, but that more recent decline was primarily caused by low fledging success. Our results highlight that potential threats such as fisheries, diseases or climate have to be considered simultaneously to disentangle their roles when assessing the conservation status of a marine predator species.
Keywords: Climate; Disease; Immigration; Longlining; Population modelling; Yellow-nosed albatross

Phan Q. Minh, Roger S. Morris, Birgit Schauer, Mark Stevenson, Jackie Benschop, Hoang V. Nam, Ron Jackson, Spatio-temporal epidemiology of highly pathogenic avian influenza outbreaks in the two deltas of Vietnam during 2003-2007, Preventive Veterinary Medicine, Volume 89, Issues 1-2, 1 May 2009, Pages 16-24, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2009.01.004.
(http://www.sciencedirect.com/science/article/B6TBK-4VNCBVK-1/2/8fab1a4f50d25bd017d7d9c311b59667)
Abstract:
Outbreaks of highly pathogenic avian influenza A subtype H5N1 have occurred in Vietnam as a series of epidemic waves since December 2003. We describe the spatial and temporal patterns of the HPAI H5N1 epidemics in the Red River Delta in the north (785 outbreaks in 606 communes) and the Mekong River Delta in the south of Vietnam (1313 outbreaks in 837 communes), where the epidemics were concentrated. Throughout the study period the percentage of outbreaks affecting ducks increased steadily to a peak of 78% during the 2006/2007 epidemic in both deltas. Five of the seven epidemic waves occurred in the period of active poultry population buildup immediately prior to the Vietnamese New Year (Tết festival). Recorded outbreaks were clustered in space and time within both deltas, consistent with infection transmission occurring via a combination of local and long-distance spread. Our analyses demonstrate that the epidemiology of HPAI in Vietnam has changed over the 4-year study period, with outbreaks now occurring in the warmer months of the year and ducks featuring more prominently as affected species. To determine the relative importance of local and long-distance spread on infection transmission, precise details of outbreak location, date of onset of clinical signs, and size and composition of the poultry population at risk need to be recorded during future outbreak responses.
Keywords: Avian influenza; Spatio-temporal analysis; Poultry; Disease control; Vietnam

X.J. Meng, Hepatitis E virus: Animal reservoirs and zoonotic risk, Veterinary Microbiology, In Press, Corrected Proof, Available online 20 March 2009, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2009.03.017.
(http://www.sciencedirect.com/science/article/B6TD6-4VWB17W-2/2/0db412f51f384d67ab52a6c8307fc957)
Abstract:
Hepatitis E virus (HEV) is a small, non-enveloped, single-strand, positive-sense RNA virus of approximately 7.2 kb in size. HEV is classified in the family Hepeviridae consisting of four recognized major genotypes that infect humans and other animals. Genotypes 1 and 2 HEV are restricted to humans and often associated with large outbreaks and epidemics in developing countries with poor sanitation conditions, whereas genotypes 3 and 4 HEV infect humans, pigs and other animal species and are responsible for sporadic cases of hepatitis E in both developing and industrialized countries. The avian HEV associated with Hepatitis-Splenomegaly syndrome in chickens is genetically and antigenically related to mammalian HEV, and likely represents a new genus in the family. There exist three open reading frames in HEV genome: ORF1 encodes non-structural proteins, ORF2 encodes the capsid protein, and the ORF3 encodes a small phosphoprotein. ORF2 and ORF3 are translated from a single bicistronic mRNA, and overlap each other but neither overlaps ORF1. Due to the lack of an efficient cell culture system and a practical animal model for HEV, the mechanisms of HEV replication and pathogenesis are poorly understood. The recent identification and characterization of animal strains of HEV from pigs and chickens and the demonstrated ability of cross-species infection by these animal strains raise potential public health concerns for zoonotic HEV transmission. It has been shown that the genotypes 3 and 4 HEV strains from pigs can infect humans, and vice versa. Accumulating evidence indicated that hepatitis E is a zoonotic disease, and swine and perhaps other animal species are reservoirs for HEV. A vaccine against HEV is not yet available.

Keywords: Hepatitis E virus (HEV); Swine HEV; Avian HEV; Zoonosis; Cross-species infection; Food safety; Pigs; Chickens

Taher Harkinezhad, Tom Geens, Daisy Vanrompay, Chlamydophila psittaci infections in birds: A review with emphasis on zoonotic consequences, Veterinary Microbiology, Volume 135, Issues 1-2, Special Issue: Chlamydioses, 16 March 2009, Pages 68-77, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.09.046.
(http://www.sciencedirect.com/science/article/B6TD6-4TFW997-9/2/547b61056fdac8627050fc773bbd7085)
Abstract:
The first part of the present review gives an overview on the history of infectious agents of the order Chlamydiales and the general infection biology of Chlamydophila (C.) psittaci, the causative agent of psittacosis. In the second part, the classification of C. psittaci strains, as well as issues of epidemiology of avian chlamydiosis., disease transmission routes, clinical disease, public health significance, present legislation and recommendations for prevention and control are reviewed.
Keywords: Chlamydophila psittaci; Review; Infection biology; Epidemiology; Diagnosis; Zoonosis; Prevention

Caroline Van Droogenbroeck, Delphine S.A. Beeckman, Kristel Verminnen, Maja Marien, Hans Nauwynck, Leopold de Thibault de Boesinghe, Daisy Vanrompay, Simultaneous zoonotic transmission of Chlamydophila psittaci genotypes D, F and E/B to a veterinary scientist, Veterinary Microbiology, Volume 135, Issues 1-2, Special Issue: Chlamydioses, 16 March 2009, Pages 78-81, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.09.047.
(http://www.sciencedirect.com/science/article/B6TD6-4TFW997-6/2/ff542013eb4313fc91b6a5b8a468c0c3)
Abstract:
Two groups of five 1-day-old conventional turkeys were housed in negative pressure stables to become experimentally infected with Avian Metapneumovirus (aMPV) and Ornithobacterium rhinotracheale (ORT) at the age of 3 weeks. However, during the first 2 weeks, turkeys started to show respiratory disease characterized by rhinitis and dyspnoea. Routine bacterial and viral diagnoses remained negative. Therefore, pharyngeal swabs from the turkeys and from the veterinary scientist handling the animals were examined for the presence of Chlamydophila (C.) psittaci by using a combination of cell culture, nested PCR and ompA genotype-specific quantitative real-time PCR, as well as by serology. Results revealed simultaneous transmission of C. psittaci outer membrane protein A (ompA) genotypes D, F and E/B from infected turkeys to the veterinary scientist.
Keywords: Chlamydophila psittaci; Respiratory disease; Zoonosis; Turkeys; Genotyping; Diagnostic methods

Lucy Chappell, Peter Kaiser, Paul Barrow, Michael A. Jones, Claire Johnston, Paul Wigley, The immunobiology of avian systemic salmonellosis, Veterinary Immunology and Immunopathology, Volume 128, Issues 1-3, Special Issue: The 8th International Veterinary Immunology Symposium (8th IVIS), 15 March 2009, Pages 53-59, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2008.10.295.
(http://www.sciencedirect.com/science/article/B6TD5-4TPF49G-T/2/f4f6ccb1149e88214b21ca63220f7fd5)
Abstract: Summary
Avian systemic salmonellosis is primarily caused by Salmonella enterica serovar Gallinarum and serovar Pullorum causing the diseases Fowl Typhoid and Pullorum Disease respectively. During infection interaction with the immune system occurs in three main phases. First is invasion via the gastrointestinal tract. Infection with S. Pullorum or S. Gallinarum does not cause substantial inflammation, unlike S. Typhimurium or S. Enteritidis. Through in vitro models it was found that S.

Gallinarum does not induce expression of CXC chemokines or pro-inflammatory cytokines such as IL-1[beta] or IL-6, whilst in an in vivo model S. Pullorum infection leads to down-regulation of CXCLi1 and CXCLi2 in the ileum. The absence of flagella in S. Gallinarum and S. Pullorum means they are not recognised by TLR5, which is believed to play a key role in the initiation of inflammatory responses, though other pathogen-factors are likely to be involved. The second phase is establishing systemic infection.Salmonella invade macrophages and probably dendritic cells and are translocated to the spleen and liver, where replication occurs. Salmonella survival is dependent on the Salmonella pathogenicity island 2 type III secretion system, which inhibits antimicrobial activity by preventing fusion of lysosymes with the phagocytic vacuole and by modulation of MHC and cytokine expression. Studies in resistant and susceptible chicken lines have shown that the interaction with macrophages is central to the progression of infection or immunological clearance. Primary macrophages from resistant animals are more efficient in killing Salmonella through respiratory burst and by induction of cytokine expression including the initiation of protective Th1 responses that leads to the third phase. Where replication of Salmonella is not controlled the death of the animal usually results. If the innate immune system is not able to control replication then cellular and humoral responses, primarily mediated through Th1-associated cytokines, are able to clear infection. In S. Pullorum a significant number of animals develop persistent infection of splenic macrophages. Here we show preliminary evidence of modulation of adaptive immunity away from a Th1 response to facilitate the development of the carrier state. In carrier animals persistence may lead to reproductive tract and egg infection associated with a decline in CD4+ T cell numbers and function associated with the onset of sexual maturity in hens.
Keywords: Salmonella; Macrophage; Cytokine; Carrier state; Chicken; Fowl typhoid; Pullorum Disease

Maswati M. Amin, Nyree D. Phillips, Tom La, David J. Hampson, Vaccination with an autogenous bacterin fails to prevent colonization by Brachyspira intermedia in experimentally infected laying chickens, Veterinary Microbiology, Volume 133, Issue 4, 2 February 2009, Pages 372-376, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.07.007.
(http://www.sciencedirect.com/science/article/B6TD6-4T2M5X3-3/2/ba470af547b91fcce0b6d4aabd3a3c95)
Abstract:
Avian intestinal spirochaetosis (AIS) is a disease complex affecting adult laying and breeding chickens associated with infection by anaerobic intestinal spirochaetes of the genus Brachyspira. Options for control of AIS are limited, as few effective antimicrobial agents are registered for use in laying chickens. One of the two most commonly encountered pathogenic species in AIS is B. intermedia, and the aim of the current study was to determine whether a B. intermedia bacterin vaccine would help control AIS caused by this species. An autogenous bacterin was prepared from B. intermedia strain HB60 and given twice intramuscularly at a 3-week interval to 12 laying chickens housed in individual cages. Twelve non-vaccinated control chickens were placed in adjacent cages in the same room. Two weeks after the second vaccination all the chickens were experimentally challenged with B. intermedia HB60 by crop tube. Subsequently faeces were cultured for spirochaetes every 2-3 days, faecal water content and chicken weight were measured weekly, and egg numbers and weights were recorded daily. Serum was taken prior to both vaccinations, at the time of challenge and at euthanasia. The chickens were killed 6 weeks post-challenge. The vaccinated chickens showed seroconversion to the vaccine, but antibody levels declined significantly post-infection. In comparison, the non-vaccinated chickens showed seroconversion post-infection. The reason for the reduction in the antibody levels in the vaccinated chickens after infection was not explained. At some point all the chickens excreted spirochaetes in their faeces, and the duration of excretion was not different between vaccinated and non-vaccinated chickens. There were no differences in faecal water content, chicken weights, egg

production, or gross and microscopic caecal lesions between vaccinated and non-vaccinated chickens. In conclusion, an autogenous bacterin vaccine did not prevent infection with B. intermedia in laying chickens.
Keywords: Brachyspira intermedia; Vaccine; Chickens; Avian intestinal spirochaetosis

Mieke G.R. Matthijs, Mark P. Ariaans, R. Marius Dwars, Jo H.H. van Eck, Annemarie Bouma, Arjan Stegeman, Lonneke Vervelde, Course of infection and immune responses in the respiratory tract of IBV infected broilers after superinfection with E. coli, Veterinary Immunology and Immunopathology, Volume 127, Issues 1-2, 15 January 2009, Pages 77-84, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2008.09.016.
(http://www.sciencedirect.com/science/article/B6TD5-4THJGGM-1/2/67efb0c1d5a0b6fd1b442fddb0452ccd)
Abstract:
Colibacillosis results from infection with avian pathogenic Escherichia coli bacteria. Healthy broilers are resistant to inhaled E. coli, but previous infection with vaccine or virulent strains of Infectious Bronchitis Virus (IBV) predisposes birds for severe colibacillosis. The aim of this study was to investigate how IBV affects the course of events upon infection with E. coli. Broilers were inoculated with IBV H120 vaccine virus or virulent M41 and challenged 5 days later with E. coli 506. A PBS and E. coli group without previous virus inoculation were included. Sections of trachea, lung and airsacs were stained for CD4, CD8, [gamma][delta]-TCR, [alpha][beta]1-TCR, and for macrophages (KUL-01) and both pathogens. Changes in the mucociliary barrier of trachea, lung and airsacs did not predispose for bacterial superinfection. The disease in the lungs of the E. coli group and both IBV/E. coli groups was similar. Lesions in the airsacs were more pronounced and of longer duration in the IBV/E. coli groups. The immunocytological changes differed substantially between the E. coli group and both IBV/E. coli groups. In trachea, lungs and airsacs the CD4+ and CD8+ populations were significantly larger than in the E. coli and PBS groups. In the lungs and the airsacs the macrophages were more numerous in the IBV/E. coli and the E. coli groups than in the PBS group. The presence of high numbers of T cells and macrophages in IBV infected birds most likely induced an altered immune response, which is responsible for the enhanced clinical signs of colibacillosis.
Keywords: Chicken; Infection; Immunology; IBV; Vaccine

P.K. Biswas, H. Barua, G.M.N. Uddin, D. Biswas, A. Ahad, N.C. Debnath, Serosurvey of five viruses in chickens on smallholdings in Bangladesh, Preventive Veterinary Medicine, Volume 88, Issue 1, 1 January 2009, Pages 67-71, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2008.06.018.
(http://www.sciencedirect.com/science/article/B6TBK-4T8R1M5-1/2/b0d1327cf20f07fa1cdbcb9d909ef207)
Abstract:
A serologic survey was undertaken in chickens in smallholdings in Bangladesh for avian influenza A virus (AIV), egg drop syndrome '76 virus (EDS'76V), infectious bronchitis virus (IBV), Newcastle disease virus (NDV) and reovirus (RV) in three phases: January 2002-May 2003, September 2003-August 2004, and August 2005-March 2006. Four hundred thirty-six sera collected in the 2nd phase, 295 in the first phase, 755 in the 1st plus 2nd phases and 295 in the 1st phase were investigated for AIV, EDS'76V, IBV and RV, respectively, using enzyme linked immunosorbent assays. All 854 sera collected in the three phases were screened for NDV using hemagglutination inhibition test. In chickens 20% were seropositive to AIV, 3% to EDS'76V, 74% to IBV, 88% to NDV, and 47% to RV. The seroprevalence in flocks was 23% to AIV, 6% to EDS'76V, 79% to IBV, 89% to NDV and 56% to RV. Twenty-five percent chickens had >=10 log2 HI titers to NDV.
Keywords: Seroprevalences; Avian influenza virus; Newcastle disease virus; Village chickens

Shengwang Liu, Xiaonan Zhang, Yu Wang, Chengren Li, Qiaoran Liu, Zongxi Han, Qinxia Zhang, Xiangang Kong, Guangzhi Tong, Evaluation of the protection conferred by commercial vaccines and attenuated heterologous isolates in China against the CK/CH/LDL/97I strain of infectious bronchitis coronavirus, The Veterinary Journal, Volume 179, Issue 1, January 2009, Pages 130-136, ISSN 1090-0233, DOI: 10.1016/j.tvjl.2007.08.018.
(http://www.sciencedirect.com/science/article/B6WXN-4R1NNNK-3/2/2712cdef361e2b7fa9b0e63bfc73feb9)
Abstract:
Avian infectious bronchitis virus (IBV) causes tremendous economic losses to the poultry industry worldwide. Different serotypes of this virus show little cross-protection. The present study investigated the genotypic relationship between CK/CH/LDL/97I-type strains and reference IBVs based on S1 gene comparisons and the protection provided by vaccination with commercial vaccines and attenuated homologous and heterologous strains. Phylogenetic analysis and the comparison of S1 showed that CK/CH/LDL/97I-type virus might be a new serotype compared to vaccine strains and other types of IBV isolates in China. Protection efficacy was evaluated by morbidity, mortality, and virus re-isolation from the challenged chicks. Complete protection by IBV vaccination was provided by the homologous strain but sufficient respiratory protection was not provided by the commercial vaccines. Heterologous strains against CK/CH/LDL/97I challenge and the development of a vaccine against CK/CH/LDL/97I-type IBV will be necessary to control infectious bronchitis disease in poultry. Further development of the attenuated CK/CH/LDL/97I strain may provide a valuable contribution towards this goal.
Keywords: Infection bronchitis coronavirus; Spike protein; Cross-protection; Homologous; Heterologous

James F.X. Wellehan Jr., April L. Childress, Rachel E. Marschang, April J. Johnson, Elaine W. Lamirande, John F. Roberts, Mary L. Vickers, Jack M. Gaskin, Elliott R. Jacobson, Consensus nested PCR amplification and sequencing of diverse reptilian, avian, and mammalian orthoreoviruses, Veterinary Microbiology, Volume 133, Issues 1-2, 1 January 2009, Pages 34-42, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.06.011.
(http://www.sciencedirect.com/science/article/B6TD6-4STB0F4-1/2/cb8ceaed53dea9f7d922e2ebab96f13f)
Abstract:
The orthoreoviruses are segmented RNA viruses that infect diverse vertebrate host species. While the most common human orthoreovirus, Mammalian Reovirus, is not typically associated with significant disease, the majority of Orthoreovirus species have been shown to cause significant and often fatal disease in reptiles, birds, and primates. There is significant potential for jumping species. A consensus nested-PCR method was designed for investigation of the RNA-dependent RNA polymerase gene of Orthoreovirus and Aquareovirus. This protocol was used to obtain sequencing template from reoviruses of three different vertebrate classes. Bayesian and maximum likelihood phylogenetic analysis found that all viruses analyzed clustered in the genus Orthoreovirus, that reptile reoviruses formed three distinct clusters, and that an African grey parrot reovirus clustered with Nelson Bay virus from bats. This PCR method may be useful for obtaining templates for initial sequencing of novel orthoreoviruses from diverse vertebrate hosts.
Keywords: Reovirus; Orthoreovirus; Reptiles; Birds; Reptilian orthoreovirus; Nelson Bay virus; Consensus PCR; Polymerase

M. Moravkova, P. Hlozek, V. Beran, I. Pavlik, S. Preziuso, V. Cuteri, M. Bartos, Strategy for the detection and differentiation of Mycobacterium avium species in isolates and heavily infected tissues, Research in Veterinary Science, Volume 85, Issue 2, October 2008, Pages 257-264, ISSN 0034-5288, DOI: 10.1016/j.rvsc.2007.10.006.

(http://www.sciencedirect.com/science/article/B6WWR-4R71KKG-3/2/0c07581baa4381bdfad22dcc9c79e05f)
Abstract:
The members of Mycobacterium avium species, comprising M. avium subsp. paratuberculosis, M. a. hominissuis, M. a. avium, M. a. silvaticum, are currently the most prevalent opportunistic pathogenic mycobacteria causing mycobacterial infection in animals and humans. The ability to distinguish between these subspecies is of relevance for proper diagnosis and control programmes of the diseases. The aim of this study was to design a fast and specific PCR strategy for the detection and differentiation of M. avium subspecies from the solid plate cultures for use in routine veterinary diagnosis. We have developed a multiplex PCR based on IS900, IS901, IS1245 and the dnaJ gene. This method allows the detection of M. a. paratuberculosis, M. a. hominissuis and M. a. avium/M. a. silvaticum in one PCR reaction and theoretically enables mixed infections of M. a. paratuberculosis and M. a. avium or M. a. paratuberculosis and M. a. hominissuis to be revealed. The sensitivity of this multiplex PCR is 103 CFU for each bacterial strain in one PCR reaction, which also enabled the use of this test directly for DNA isolated from the tissue of the heavily infected sheep.
Keywords: Avian tuberculosis; Insertion sequences; Mycobacteriosis; Paratuberculosis; Johne's disease

Cristiana Portz, Nilzane Beltrao, Thales Quedi Furian, Alfredo Bianco Junior, Marisa Macagnan, Josiane Griebeler, Carlos Andre Veiga Lima Rosa, Edson Moleta Colodel, David Driemeier, Alberto Back, Ortrud Monika Barth Schatzmayr, Claudio Wageck Canal, Natural infection of turkeys by infectious laryngotracheitis virus, Veterinary Microbiology, Volume 131, Issues 1-2, 18 September 2008, Pages 57-64, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.02.029.
(http://www.sciencedirect.com/science/article/B6TD6-4S33N5P-1/2/891afe164dc216bfef1695ebf5c1be32)
Abstract:
The infectious laryngotracheitis virus (ILTV) is an important respiratory pathogen of chickens that also infects pheasants and peafowl. Epidemiologically non-related commercial turkey flocks with clinical signs such as tracheitis, swollen sinuses, conjunctivitis and expectoration of bloody mucus were examined for the presence of the virus. Laboratory ILTV detection was performed by virus isolation in embryonated eggs and cell cultures, PCR and sequencing of amplification products, histopathology, indirect immunofluorescence and electron microscopy. One ILTV turkey isolate was also experimentally inoculated into susceptible chickens and turkeys, reproducing a mild respiratory disease. This is the first description of natural infections with ILTV in turkeys.
Keywords: Infectious laryngotracheitis virus; Turkey; Avian pathology; Diagnosis

Hai Yu, Rong-Hong Hua, Tian-Chao Wei, Yan-Jun Zhou, Zhi-Jun Tian, Guo-Xin Li, Tian-Qiang Liu, Guang-Zhi Tong, Isolation and genetic characterization of avian origin H9N2 influenza viruses from pigs in China, Veterinary Microbiology, Volume 131, Issues 1-2, 18 September 2008, Pages 82-92, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.02.024.
(http://www.sciencedirect.com/science/article/B6TD6-4S0JN0D-2/2/cc3f76a94103d194e7c6e2d655138181)
Abstract:
As pigs are susceptible to infection with both avian and human influenza A viruses, they have been proposed to be an intermediate host for the adaptation of avian influenza viruses to humans. In April 2006, a disease caused by highly pathogenic porcine reproductive and respiratory syndrome virus (PRRSV) occurred in several pig farms and subsequently overwhelmed almost half of China with more than 2,000,000 cases of pig infection. Here we report a case in which four swine H9N2 influenza viruses were isolated from pigs infected by highly pathogenic PRRSVs in Guangxi province in China. All the eight gene segments of the four swine H9N2 viruses are highly

homologous to A/Pigeon/Nanchang/2-0461/00 (H9N2) or A/Wild Duck/Nanchang/2-0480/00 (H9N2). Phylogenetic analyses of eight genes show that the swine H9N2 influenza viruses are of avian origin and may be the descendants of A/Duck/Hong Kong/Y280/97-like viruses. Molecular analysis of the HA gene indicates that our H9N2 isolates might have high-affinity binding to the [alpha]2,6-NeuAcGal receptor found in human cells. In conclusion, our finding provides further evidence about the interspecies transmission of avian influenza viruses to pigs and emphasizes the importance of reinforcing swine influenza virus (SIV) surveillance, especially after the emergence of highly pathogenic PRRSVs in pigs in China.
Keywords: Swine influenza; Avian H9N2 influenza virus; Porcine reproductive and respiratory syndrome virus; Genetic analysis; Molecular analysis

George W. Beran, Disease and destiny-mystery and mastery, Preventive Veterinary Medicine, Volume 86, Issues 3-4, Special Issue:Schwabe Symposia 2004-2006. Perspectives on Veterinary Epidemiology in Public Health, Animal Production and Preventive Medicine, 15 September 2008, Pages 198-207, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2008.05.001.
(http://www.sciencedirect.com/science/article/B6TBK-4T0X2HR-1/2/57d01a06fe70bd0be5e944eb3a08f62a)
Abstract:
When early people made their appearance, zoonotic infectious diseases were already waiting, but epidemic diseases did not appear in human history until people began to live in large numbers under conditions of close contact, mainly during the last 10,000 years. Disease has decimated urban populations, conquered armies, and disrupted society. The focus here is on (1) the plague of Athens and the Black Death; (2) smallpox, influenza, and rabies; (3) avian influenza prion diseases, and foot & mouth disease; and (4) emerging and re-emerging diseases. All have veterinary public health associations.
In Athens, Greece, in 430 BC, when the Spartans ravaged the countryside, hordes crowded into Athens so that orderly movements, space in which to live, and adequate supplies of food became impossible. Crowding of any population fosters disease transmission; chaos and disorder enhance it all the more. Out of northern Egypt came a terrible plague from across the Mediterranean Sea. The identity of the plague of Athens remains unsure, but the well-considered conclusion is Rift Valley Fever, a mosquito borne, viral zoonosis. The Black Death, also called the Plague, raged in Asia for centuries. In 1347, the Black Death was brought by a ship out of Asia to Sicily. The scenes of devastation were repeated throughout Europe, with 90% or more of the people dying in city after city.
Influenza, too, has been a cause of periodic human epidemics, but the great pandemic of influenza occurred in the last months of World War I. In the years of highest occurrence, more than half the world's population became clinically infected. If veterinary public health had been born earlier, it could have led to elucidating the epidemiology of influenza and the plagues of Athens, Europe, and Asia. In turn, smallpox had also caused continual tragedy. In 1796, Edward Jenner began to harvest pustules of cowpox from children or infected cows and inject them into susceptible children. In 1980, the World Health Organization declared that smallpox had been eliminated from the world. Rabies, though, still strikes terror.
A number of animal diseases, broadly termed emerging and re-emerging diseases, need surveillance because they have the potential to impact human health. From late in 2003 to 2007, the highly pathogenic H5N1 influenza virus in poultry infected at least 121 people and caused 62 deaths in four countries. The prion diseases, too, all have very high numbers in concentrated contacts. To control these diseases, veterinary public health is essential, with diagnosis, epidemiological surveillance, clinical manifestations, and prevention as primary measures.
Keywords: Zoonoses; Pandemics; Historic diseases

Frederick A. Murphy, Emerging zoonoses: The challenge for public health and biodefense, Preventive Veterinary Medicine, Volume 86, Issues 3-4, Special Issue:Schwabe Symposia 2004-2006. Perspectives on Veterinary Epidemiology in Public Health, Animal Production and Preventive Medicine, 15 September 2008, Pages 216-223, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2008.02.009.
(http://www.sciencedirect.com/science/article/B6TBK-4S9R1TD-2/2/74bf428a8db13ce7f83cb0e6b36021c3)
Abstract:
The concept of new and emerging diseases has captured the public interest and has revitalized the public health infectious disease research community. This interest has also resulted in competition for funding and turf wars between animal health and public health scientists and public officials and, in some cases, has delayed and hindered progress toward effective prevention, control and biodefense. There is a dynamic list of outbreaks causing substantial morbidity and mortality in humans and often in the reservoir animal species. Some agents have the potential to grow into major epidemics. There are many determinants that influence the emergence of diseases of concern that require the use of current understanding of the nature of agent persistence and spread. Additional factors that are global must be added to plans for prevention and control. To this complex mix has been added the potential for accidental or malicious release of agents. The nature of emerging infectious agents and their impact is largely unpredictable. Models that strive to predict the dynamics of agents may be useful but can also blind us to increasing disease risks if it does not match a specific model. Field investigations of early events will be critical and should drive prevention and control actions. Many disease agents have developed strategies to overcome extremes of reservoir qualities like population size and density. Every infectious agent spreads easier when its hosts are closer together. Zoonoses must be dealt with at the interface of human and animal health by all available information. Lessons learned from the emergence of and response to agents like West Nile virus, H5N1 avian influenza, SARS and bovine spongiform encephalopathy, the cause of new-variant Creutzfeldt-Jakob disease in humans, must be used to create better plans for response and meet the challenge for public health and biodefense.
Keywords: Emerging zoonoses; Control and prevention; Preparedness and biodefense

Marcos R. Buim, Melissa Buzinhani, Mauricio Yamaguti, Rosangela C. Oliveira, Elena Mettifogo, Jorge Timenetsky, Antonio J. Piantino Ferreira, Intraspecific variation in 16S rRNA gene of Mycoplasma synoviae determined by DNA sequencing, Comparative Immunology, Microbiology and Infectious Diseases, In Press, Corrected Proof, Available online 4 September 2008, ISSN 0147-9571, DOI: 10.1016/j.cimid.2008.07.005.
(http://www.sciencedirect.com/science/article/B6T5H-4TC8J3J-1/2/ae4320e8b149ff1faa602ad107a47fb0)
Abstract:
Mycoplasma synoviae (MS) is an important avian pathogen may cause both respiratory disease and joint inflammation synovitis in poultry, causing economic losses to the Brazilian poultry industry. The genotypic variation in 16S rRNA gene is unknown. Partial sequences of 16S rRNA gene of 19 strains of M. synoviae were sequenced and analyzed in order to obtain molecular characterization and evaluation of the genetic variability of strains from distinct Brazilian areas of poultry production. Different polymorphic patterns were observed. The number of polymorphic alterations in the studied strains ranged from 0 to 6. The nucleotide variations, including deletion, insertion and substitutions, ranged from 3 to 5. The genotypic diversity observed in this study may be explained by spontaneous mutations that may occur when a lineage remains in the same flock for long periods. The culling and reposition in poultry flocks may be responsible for the entry of new strains in different areas.

Keywords: Mycoplasma synoviae; Genotypic variation; Poultry; 16S rRNA gene; Mycoplasma synoviae; variation genotypique; volaille; gene rRNA 16S

Sung-Hyen Lee, Hyun S. Lillehoj, Erik P. Lillehoj, Soo-Muk Cho, Dong-Woon Park, Yeong-Ho Hong, Hye-Kyung Chun, Hong-Ju Park, Immunomodulatory properties of dietary plum on coccidiosis, Comparative Immunology, Microbiology and Infectious Diseases, Volume 31, Issue 5, September 2008, Pages 389-402, ISSN 0147-9571, DOI: 10.1016/j.cimid.2007.06.005.
(http://www.sciencedirect.com/science/article/B6T5H-4PC90JT-1/2/d19be8a2c1c338f75878e5cd946fa82e)
Abstract:
The current study was conducted to evaluate the effect of dietary supplementation with a lyophilized powder made from plums (P) on host protective immune responses against avian coccidiosis, the most economically important parasitic disease of poultry. One-day-old White Leghorn chickens were fed from the time of hatch with a standard diet either without P (control and P 0 groups) or supplemented with P at 0.5% (P 0.5) or 1.0% (P 1.0) of the diet. Animals in the P 0, P 0.5, and P 1.0 groups were orally challenged with 5000 sporulated oocysts of Eimeria acervulina at day 12 post-hatch, while control animals were uninfected. Dietary supplementation of P increased body weight gain, reduced fecal oocyst shedding, and increased the levels of mRNAs for interferon-[gamma] and interleukin-15 in the P 1.0 group at 10 days post-infection compared with the P 0 group. Furthermore, chickens fed either the P 0.5 or P 1.0 diets exhibited significantly greater spleen cell proliferation compared with the non-plum P 0 group. These results indicate that plum possesses immune enhancing properties, and that feeding chickens a plum-supplemented diet augments protective immunity against coccidiosis.
Keywords: Plum; Immunomodulation; Chicken; Coccidiosis; Eimeria; Lymphocytes; Cytokines; Prune; Immunomodulation; Poulet; Coccidiose; Eimeria; Lymphocytes; Cytokines

Rebeka Lucijana Bercic, Brigita Slavec, Miha Lavric, Mojca Narat, Olga Zorman-Rojs, Peter Dovc, Dusan Bencina, A survey of avian Mycoplasma species for neuraminidase enzymatic activity, Veterinary Microbiology, Volume 130, Issues 3-4, 25 August 2008, Pages 391-397, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2008.02.004.
(http://www.sciencedirect.com/science/article/B6TD6-4RV7YD2-4/2/cc7364d365760f62d564c839dfe6499a)
Abstract:
Among 23 currently recognized avian Mycoplasma (AM) species only Mycoplasma gallisepticum, Mycoplasma synoviae, Mycoplasma meleagridis and Mycoplasma iowae cause disease and loss of production in chickens and/or turkeys. Because neuraminidases are considered virulence factors in many pathogenic microorganisms the aim of our study was to determine which AM species possess neuraminidase enzymatic activity (NEAC). Small samples of AM cells were assayed for NEAC using the chromogenic substrate 5-bromo-4-chloro-3-indolyl-[alpha]-d-N-acetylneuraminic acid. In the case of positive NEAC reaction the substrate gave the insoluble indigoblue product what enabled simple test and easy estimation of NEAC. M. gallisepticum and M. synoviae which share sequences of the gene encoding neuraminidase (sialidase NanH) exhibited considerable levels of NEAC. However, NEAC levels differed among their strains, as well as among cultures of different strains. Only certain cultures of the type strain of M. meleagridis showed NEAC, whereas among six serovars of M. iowae only serovar I (type strain 695) showed NEAC. Weak NEAC was detectable in M. anseris, M. cloacale and M. pullorum, whereas the type strain of M. corogypsi (BV1) showed strong NEAC. Our study provides novel informations about NEAC in AM species and suggests that higher invasiveness and possibly, the pathological processes might be associated with their NEAC.
Keywords: Avian Mycoplasma species; Neuraminidase activity

Julia Marschall, Bianka Schulz, Timm C. Harder Priv-Doz, Thomas W. Vahlenkamp Priv-Doz, Janine Huebner, Elke Huisinga, Katrin Hartmann, Prevalence of influenza A H5N1 virus in cats from areas with occurrence of highly pathogenic avian influenza in birds, Journal of Feline Medicine & Surgery, Volume 10, Issue 4, August 2008, Pages 355-358, ISSN 1098-612X, DOI: 10.1016/j.jfms.2008.03.007.
(http://www.sciencedirect.com/science/article/B6WJC-4T1SKJH-1/2/91bca948cb049afd87c8ce2688cc387b)
Abstract:
Natural and experimental infections have shown that cats are susceptible to highly pathogenic avian influenza A virus subtype H5N1 (HPAIV H5N1). Cats can be severely affected and die from the disease, but subclinical infections have also been reported. To learn more about the role of cats in the spread of the virus and about the risk posed to cats, the prevalence of H5N1 virus was examined in 171 cats from areas in Germany and Austria in which birds infected with HPAIV H5N1 had been found. Pharyngeal swabs were examined for H5N1 virus using real-time polymerase chain reaction, and serum samples were tested for antibodies to influenza virus. None of the cats showed evidence of infection with H5N1 virus. Prevalence of H5N1 virus was determined to be <1.8% (95% confidence interval (CI): 0.000000-0.017366); prevalence of antibodies was <2.6% (95% CI: 0.000000-0.025068).

Julia Marschall, Katrin Hartmann, Avian influenza A H5N1 infections in cats, Journal of Feline Medicine & Surgery, Volume 10, Issue 4, August 2008, Pages 359-365, ISSN 1098-612X, DOI: 10.1016/j.jfms.2008.03.005.
(http://www.sciencedirect.com/science/article/B6WJC-4SYDB1R-2/2/09c16ad8d8f88eb36448d7de8817d8a4)
Abstract:
Although cats had been considered resistant to disease from influenza virus infection, domestic cats and large felids are now known to be naturally und experimentally susceptible to infection with highly pathogenic avian influenza virus H5N1 (HPAIV H5N1). The virus causes systemic infection, lung and liver being the mainly affected organs. Infected cats show fever, depression, dyspnoea, and neurological signs, but subclinical infections have also occurred. Mostly, cats have been infected by direct contact with affected birds, especially by eating raw poultry; transmission from cat to cat may also occur. Little is known about the role of cats in the epidemiology of the virus. So far, no reassortment between avian and mammalian influenza viruses has occurred in cats, but experts fear that cats might give the virus an opportunity to adapt to mammals. This publication gives a review on avian influenza in cats with a focus on practical aspects for veterinarians.

Chi-Young Wang, Chia-Jen Hsu, Heng-Ju Chen, Julius L.C. Chulu, Hung-Jen Liu, Development of a reliable assay protocol for identification of diseases (RAPID)-bioactive amplification with probing (BAP) for detection of Newcastle disease virus, Veterinary Microbiology, Volume 130, Issues 1-2, 27 July 2008, Pages 28-36, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2007.12.015.
(http://www.sciencedirect.com/science/article/B6TD6-4RH37WJ-1/2/d86c5c6b61324082d458671c0272b764)
Abstract:
Due to appearance of new genotypes of Newcastle disease virus (NDV) with no cross-protection and with vaccine strains, some outbreaks have been reported in Taiwan that caused significant damage to the poultry industry. A reliable assay protocol, (RAPID)-bioactive amplification with probing (BAP), for detection of NDV that uses a nested PCR and magnetic bead-based probe to increase sensitivity and specificity, was developed. Primers and probes were designed based on the conserved region of the F protein-encoding gene sequences of all NDV Taiwan isolates. The optimal annealing temperature for nested reverse transcription-polymerase chain reaction (RT-PCR) to amplify the gene was 61 [degree sign]C and optimal hybridization occurred when buffer

1x SSC and 0.5% SDS were used at 50 [degree sign]C. The sensitivity of RAPID-BAP was 1 copy/[mu]l for standard plasmids and 10 copy/[mu]l for transcribed F protein-encoding gene of NDV with comparable linearity (R2 = 0.984 versus R2 = 0.99). This sensitivity was superior to that of other techniques currently used. The assay was also highly specific because the negative controls, including classical swine fever virus, avian influenza virus, avian reovirus, and infectious bursa disease virus could not be detected. Thirty-four field samples were tested using conventional RT-PCR, nested RT-PCR, real-time quantitative RT-PCR, and RAPID-BAP assay and the positive rates were 24%, 30%, 41%, and 53%, respectively. The developed assay allows for rapid, correct, and sensitive detection of NDV and fulfils all of the key requirements for clinical applicability. It could reliably rule out false negative results from antibody-based assays and also facilitate a rapid diagnosis in the early phase of the disease for emergency quarantine that may help prevent large-scale outbreaks.
Keywords: Newcastle disease virus; RAPID-BAP assay; Real-time quantitative RT-PCR

Franz Rubel, Katharina Brugger, Michael Hantel, Sonja Chvala-Mannsberger, Tamas Bakonyi, Herbert Weissenbock, Norbert Nowotny, Explaining Usutu virus dynamics in Austria: Model development and calibration, Preventive Veterinary Medicine, Volume 85, Issues 3-4, 15 July 2008, Pages 166-186, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2008.01.006.
(http://www.sciencedirect.com/science/article/B6TBK-4S0R6JP-2/2/03068fc53bab9df8b23b8a84a60e4424)
Abstract:
Usutu virus (USUV), a flavivirus of the Japanese encephalitis virus complex, was for the first time detected outside Africa in the region around Vienna (Austria) in 2001 by Weissenbock et al. [Weissenbock, H., Kolodziejek, J., Url, A., Lussy, H., Rebel-Bauder, B., Nowotny, N., 2002. Emergence of Usutu virus, an African mosquito-borne flavivirus of the Japanese encephalitis virus group, central Europe. Emerg. Infect. Dis. 8, 652-656]. USUV is an arthropod-borne virus (arbovirus) circulating between arthropod vectors (mainly mosquitoes of the Culex pipiens complex) and avian amplification hosts. Infections of mammalian hosts or humans, as observed for the related West Nile virus (WNV), are rare. However, USUV infection leads to a high mortality in birds, especially blackbirds (Turdus merula), and has similar dynamics with the WNV in North America, which, amongst others, caused mortality in American robins (Turdus migratorius). We hypothesized that the transmission of USUV is determined by an interaction of developing proportion of the avian hosts immune and climatic factors affecting the mosquito population. This mechanism is implemented into the present model that simulates the seasonal cycles of mosquito and bird populations as well as USUV cross-infections. Observed monthly climate data are specified for the temperature-dependent development rates of the mosquitoes as well as the temperature-dependent extrinsic-incubation period. Our model reproduced the observed number of dead birds in Austria between 2001 and 2005, including the peaks in the relevant years. The high number of USUV cases in 2003 seems to be a response to the early beginning of the extraordinary hot summer in that year. The predictions indicate that >70% of the bird population acquired immunity, but also that the percentage would drop rapidly within only a couple of years. We estimated annually averaged basic reproduction numbers between (2004) and 1.35 (2003). Finally, extrapolation from our model suggests that only 0.2% of the blackbirds killed by USUV were detected by the Austrian USUV monitoring program [Chvala, S., Bakonyi, T., Bukovsky, C., Meister, T., Brugger, K., Rubel, F., Nowotny, N., Weissenbock, H., 2007. Monitoring of Usutu virus activity and spread by using dead bird surveillance in Austria, 2003-2005. Vet. Microbiol. 122, 237-245]. These results suggest that the model presented is able to quantitatively describe the process of USUV dynamics.
Keywords: Infectious disease; Usutu virus; West Nile virus; SIR model; Epidemic model; Basic reproduction number; Culex pipiens; Climate forcing; Seasons

Albert van Dijk, Edwin J.A. Veldhuizen, Henk P. Haagsman, Avian defensins, Veterinary Immunology and Immunopathology, Volume 124, Issues 1-2, 15 July 2008, Pages 1-18, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2007.12.006.
(http://www.sciencedirect.com/science/article/B6TD5-4RR8YMF-1/2/1c737676a3000c2655ad91fe53eed854)
Abstract:
Modulation of defensin expression may be one way to improve animal health and to reduce zoonotic diseases. Defensins are small, cationic, and amphipathic cysteine-rich antibiotic peptides found in plants, insects, mammals and birds. Whereas [alpha]- and [theta]-defensins appear to be absent in birds, several [beta]-defensins have been isolated from avian heterophils. In addition, [beta]-defensins were found to be constitutively or inducibly expressed at mucosal surfaces of the respiratory, intestinal and urogenital tracts. In this review the current knowledge of the defensin repertoire of birds, their tissue-specific expression, regulation and corresponding biological functions are described.
Keywords: Defensins; Antimicrobial Peptides; Innate immunity; Birds

Elizabeth B. Mitchell, Michelle G. Hawkins, Joao S. Orvalho, William P. Thomas, Congenital mitral stenosis, subvalvular aortic stenosis, and congestive heart failure in a duck, Journal of Veterinary Cardiology, Volume 10, Issue 1, June 2008, Pages 67-73, ISSN 1760-2734, DOI: 10.1016/j.jvc.2008.01.002.
(http://www.sciencedirect.com/science/article/B7RN0-4SHFSW6-1/2/0a25219db9e59670425e1d90eecdf3e5)
Abstract:
A 2.6-year-old duck was evaluated for respiratory difficulty. On the basis of physical, radiographic and echocardiographic findings, a diagnosis of congestive heart failure secondary to congenital mitral stenosis and subvalvular aortic stenosis was made. The duck did not respond well to medical therapy and was euthanized. The diagnosis was confirmed at necropsy.
Keywords: Congenital heart disease; Avian; Mitral stenosis; Subvalvular aortic stenosis; Congestive heart failure

S.P.S. Pillai, D.L. Suarez, M. Pantin-Jackwood, C.-W. Lee, Pathogenicity and transmission studies of H5N2 parrot avian influenza virus of Mexican lineage in different poultry species, Veterinary Microbiology, Volume 129, Issues 1-2, 25 May 2008, Pages 48-57, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2007.11.003.
(http://www.sciencedirect.com/science/article/B6TD6-4R40SM1-1/2/4a596915ce95176401a907f5acf8ed9c)
Abstract:
In 2004, a low pathogenic H5N2 influenza virus (A/parrot/CA/6032/04) was identified in a psittacine bird for the first time in the United States. Sequence and phylogenetic analysis of the hemagglutinin gene grouped the parrot isolate under the Mexican lineage H5N2 viruses (subgroup B) with highest similarity to recent chicken-origin isolates from Guatemala. Antigenic analysis further confirmed the close relatedness of the parrot isolate to Mexican lineage viruses, the highest cross-reactivity being demonstrated to Guatemala isolates. In vivo studies of the parrot isolate in chickens, ducks and turkeys showed that the virus, though did not cause any clinical signs, could replicate to high titers in these birds and efficiently transmit to contact control cage mates. The possibility that the parrot harboring the virus was introduced into the United States as a result of illegal trade across the border provides additional concern for the movement of foreign animal diseases from neighboring countries. Considering the potential threat of the virus to domestic poultry, efforts should be continued to prevent the entry and spread of influenza viruses by imposing effective surveillance and monitoring measures.
Keywords: H5N2; Influenza; Parrot; Pathogenicity; Transmission

Ingrid Halle, G.C. Perry, Editor, Avian Gut Function in Health and Disease, Carfax Publishing Company, Abingdon, Oxfordshire, UK (2006) 417 pp., Hardback, Price: [pound sign]70. 00, US$ 140.00, ISBN-10: 1-84593-1807, ISBN-13: 978-1-84593-1803., Animal Feed Science and Technology, Volume 142, Issues 1-2, 15 April 2008, Pages 192-193, ISSN 0377-8401, DOI: 10.1016/j.anifeedsci.2007.07.010.
(http://www.sciencedirect.com/science/article/B6T42-4PJ6BN4-5/2/8c9b654e9ef5c78f950340785f6dc4eb)

Lih-Chiann Wang, Chu-Hsiang Pan, Lucia Liu Severinghaus, Lu-Yuan Liu, Chi-Tsong Chen, Chang-En Pu, Dean Huang, Jihn-Tsair Lir, Shih-Chien Chin, Ming-Chu Cheng, Shu-Hwae Lee, Ching-Ho Wang, Simultaneous detection and differentiation of Newcastle disease and avian influenza viruses using oligonucleotide microarrays, Veterinary Microbiology, Volume 127, Issues 3-4, 18 March 2008, Pages 217-226, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2007.08.019.
(http://www.sciencedirect.com/science/article/B6TD6-4PFW697-2/2/535d9a6336dcd4c50bb1398d88f0c52f)
Abstract:
Newcastle disease (ND) and avian influenza (AI) are two of the most important zoonotic viral diseases of birds throughout the world. These two viruses often have a great impact upon the poultry industry. Both viruses are associated with transmission from wild to domestic birds, and often display similar signs that need to be differentiated. A rapid surveillance among wild and domestic birds is important for early disease detection and intervention, and is the basis for what measures should be taken. The surveillance, thus, should be able to differentiate the diseases and provide a detailed analysis of the virus strains. Here, we described a fast, simultaneous and inexpensive approach to the detection of Newcastle disease virus (NDV) and avian influenza virus (AIV) using oligonucleotide microarrays. The NDV pathotypes and the AIV haemagglutinin subtypes H5 and H7 were determined at the same time. Different probes on a microarray targeting the same gene were implemented in order to encompass the diversified virus strains or provide multiple confirmations of the genotype. This ensures good sensitivity and specificity among divergent viruses. Twenty-four virus isolates and twenty-four various combinations of the viruses were tested in this study. All viruses were successfully detected and typed. The hybridization results on microarrays were clearly identified with the naked eyes, with no further imaging equipment needed. The results demonstrate that the detection and typing of multiple viruses can be performed simultaneously and easily using oligonucleotide microarrays. The proposed method may provide potential for rapid surveillance and differential diagnosis of these two important zoonoses in both wild and domestic birds.
Keywords: Avian influenza; Newcastle disease; Oligonucleotide microarrays

Thierry van den Berg, Benedicte Lambrecht, Sylvie Marche, Mieke Steensels, Steven Van Borm, Michel Bublot, Influenza vaccines and vaccination strategies in birds, Comparative Immunology, Microbiology and Infectious Diseases, Volume 31, Issues 2-3, Aspects of vaccine development, March 2008, Pages 121-165, ISSN 0147-9571, DOI: 10.1016/j.cimid.2007.07.004.
(http://www.sciencedirect.com/science/article/B6T5H-4PRHKXN-1/2/c276a27406c4f7b2e666ec051a001c72)
Abstract:
Although it is well accepted that the present Asian H5N1 panzootic is predominantly an animal health problem, the human health implications and the risk of human pandemic have highlighted the need for more information and collaboration in the field of veterinary and human health. H5 and H7 avian influenza (AI) viruses have the unique property of becoming highly pathogenic (HPAI) during circulation in poultry. Therefore, the final objective of poultry vaccination against AI must be eradication of the virus and the disease. Actually, important differences exist in the control

of avian and human influenza viruses. Firstly, unlike human vaccines that must be adapted to the circulating strain to provide adequate protection, avian influenza vaccination provides broader protection against HPAI viruses. Secondly, although clinical protection is the primary goal of human vaccines, poultry vaccination must also stop transmission to achieve efficient control of the disease. This paper addresses these differences by reviewing the current and future influenza vaccines and vaccination strategies in birds.
Keywords: Influenza aviaire; Grippe; Vaccin; Vecteur; Sous-unite; Immunite; Surveillance; DIVA; Eradication; H5N1; Avian influenza; Flu; Vaccine; Vector; Subunit; Immunity; Surveillance; DIVA; Eradication; H5N1

Esther Schonewille, Amarjit Singh, Thomas W. Gobel, Wilhelm Gerner, Armin Saalmuller, Michael Hess, Fowl adenovirus (FAdV) serotype 4 causes depletion of B and T cells in lymphoid organs in specific pathogen-free chickens following experimental infection, Veterinary Immunology and Immunopathology, Volume 121, Issues 1-2, 15 January 2008, Pages 130-139, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2007.09.017.
(http://www.sciencedirect.com/science/article/B6TD5-4PT7WW0-6/2/7e5837a8ed2ea7ecae1abbc3b66549f4)
Abstract:
In the present investigation flow cytometric analysis and immunohistochemistry were applied together for the first time to gain new insights into the interaction between virulent fowl adenoviruses (FAdV) and the immune system of chickens. As a model for virulent FAdV infections a FAdV-4 strain was used, known as the aetiological agent of Hepatitis-Hydropericardium syndrome (HHS) in broilers sometimes also named Angara Disease. Specified pathogen-free chickens (SPF) were divided into three different groups. Group I was infected at first day of life with an attenuated form of the virus obtained through continuous cell culture passage with the virulent virus and then re-infected 3 weeks later with the virulent progenitor virus. Group II was solely infected with the virulent virus at 3 weeks and group III served as a negative control. Following infection with the virulent virus a decrease of CD3+, CD4+ and CD8+ cells was noticed in the spleen. This was accompanied by a decrease of CD4+ and CD8+ T-lymphocytes in the thymus. Those birds infected with the attenuated virus in first instance and challenged with the virulent virus did not show these pathological effects in the thymus. In the bursa of Fabricius a severe depletion of lymphocytes was observed by immunohistochemistry in birds, infected with the virulent virus. Taken together it can be concluded that an infection with FAdV-4 has profound effects on cells, of the humoral and cell-mediated immune responses. The effects are much more severe in the birds infected with the virulent virus only indicating that the preceding infection with the attenuated virus reduces significantly the adverse effects induced by the virulent virus.
Keywords: Fowl adenovirus serotype 4; Immunosuppression; Flow cytometric analysis; Immunohistochemistry; Cellular and humoral immune response; Avian immune system

N. Bunbury, C.G. Jones, A.G. Greenwood, D.J. Bell, Epidemiology and conservation implications of Trichomonas gallinae infection in the endangered Mauritian pink pigeon, Biological Conservation, Volume 141, Issue 1, January 2008, Pages 153-161, ISSN 0006-3207, DOI: 10.1016/j.biocon.2007.09.008.
(http://www.sciencedirect.com/science/article/B6V5X-4R0CR1X-2/2/db5d9fb5df302bf6cd10d224b00c6597)
Abstract:
Despite increasing recognition of the role of exotic pathogens in species decline, comprehensive studies of wildlife disease epidemiology in threatened species are rare. We investigated the epidemiology of the protozoan parasite Trichomonas gallinae, which causes the avian disease trichomonosis, in the five wild subpopulations of the endangered pink pigeon Columba mayeri in Mauritius. An average of 89% of the entire population was screened for T. gallinae infection every

2 months between September 2002 and April 2004. A total of 426 individual pink pigeons (all >3 months of age) was screened, and 359 (84.3%) of these tested positive for T. gallinae at least once. Average prevalence of T. gallinae infection across all subpopulations and sampling periods was 50.3% but ranged from 19.6% to 82.4%. Trichomonas gallinae infection was significantly different among subpopulations and prevalence gradually decreased over the entire screening period. Infection prevalence also increased with host age. Observed pathogenicity of T. gallinae was low; active trichomonosis signs were recorded in ca. 1.9% of birds which tested positive. However, birds which persistently tested positive for T. gallinae (33.5% of birds screened) were at least 10% less likely to survive 2 yrs post-screening than birds which tested negative at least once in three consecutive periods; a finding which should be considered by wildlife disease investigators if no pathogenic effects are apparent from the results of studies based on a single screening episode. We conclude that T. gallinae is an additional population limiting factor for pink pigeons and our study highlights the importance of screening other endangered columbids for this pathogen.
Keywords: Avian pathogen; Columbids; Conservation management; Mascarenes; Oceanic island; Wildlife disease

John N. Sofos, Challenges to meat safety in the 21st century, Meat Science, Volume 78, Issues 1-2, Symposium on Meat safety: From Abattoir to Consumer, January-February 2008, Pages 3-13, ISSN 0309-1740, DOI: 10.1016/j.meatsci.2007.07.027.
(http://www.sciencedirect.com/science/article/B6T9G-4P96265-1/2/35ca99c35796b19ef8f45ea5d3ceb832)
Abstract:
The safety of meat has been at the forefront of societal concerns in recent years, and indications exist that challenges to meat safety will continue in the future. Major meat safety issues and related challenges include the need to control traditional as well as 'new,' 'emerging,' or 'evolving' pathogenic microorganisms, which may be of increased virulence and low infectious doses, or of resistance to antibiotics or food related stresses. Other microbial pathogen related concerns include cross-contamination of other foods and water with enteric pathogens of animal origin, meat animal manure treatment and disposal issues, foodborne illness surveillance and food attribution activities, and potential use of food safety programs at the farm. Other issues and challenges include food additives and chemical residues, animal identification and traceability issues, the safety and quality of organic and natural products, the need for and development of improved and rapid testing and pathogen detection methodologies for laboratory and field use, regulatory and inspection harmonization issues at the national and international level, determination of responsibilities for zoonotic diseases between animal health and regulatory public health agencies, establishment of risk assessment based food safety objectives, and complete and routine implementation of HACCP at the production and processing level on the basis of food handler training and consumer education. Viral pathogens will continue to be of concern at food service, bacterial pathogens such as Escherichia coli O157:H7, Salmonella and Campylobacter will continue affecting the safety of raw meat and poultry, while Listeria monocytogenes will be of concern in ready-to-eat processed products. These challenges become more important due to changes in animal production, product processing and distribution; increased international trade; changing consumer needs and increased preference for minimally processed products; increased worldwide meat consumption; higher numbers of consumers at-risk for infection; and, increased interest, awareness and scrutiny by consumers, news media, and consumer activist groups. Issues such as bovine sponginform encephalopathy will continue to be of interest mostly as a target for eradication, while viral agents affecting food animals, such as avian influenza, will always need attention for prevention or containment.
Keywords: Meat; Safety; Pathogens; Hazards; Bacteria

Gert Jan Boender, Ronald Meester, Edo Gies, Mart C.M. De Jong, The local threshold for geographical spread of infectious diseases between farms, Preventive Veterinary Medicine, Volume 82, Issues 1-2, 15 November 2007, Pages 90-101, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2007.05.016.
(http://www.sciencedirect.com/science/article/B6TBK-4P2S21X-3/2/4cb5a84120cdd5555a6e9a83b87a4a4f)
Abstract:
We investigated the influence of the spatial pattern of farms on the geographical spread of infectious livestock diseases, such as classical swine fever, foot-and-mouth disease and avian influenza in a combined analytical-numerical approach. Our purpose of this paper is to develop a method to identify the areas in which an infection has the potential to spread in an outbreak. In our model, each infected farm can infect neighbouring farms and the probability of transmission is a function of the inter-farm distance (spatial kernel). Therefore, the density of farms in an area is a good indicator for the probability of a major outbreak. In the epidemiological nomenclature, such density corresponds to a local reproduction ratio and we studied the critical behaviour of both the local density and the local reproduction ratio. We found that a threshold can be defined above which major outbreaks can occur, and the threshold value depends on the spatial kernel. Our expression for the threshold value is derived based on scaling arguments and contains two parameters in the exponents of the equation. We estimated these parameters from numerical results for the spatial spread using one particular mathematical function for the form of the spatial kernel. Subsequently, we show that our expression for the threshold using these estimated parameters agrees very well with numerical results for a number of different other functional forms of the spatial kernel (thus suggesting that we are dealing with universal parameters). As an illustration of the practical relevance of the presented method, we calculated the threshold value for avian influenza in the Netherlands and use it to produce a risk map for this disease.
Keywords: Veterinary epidemiology; Spatial spread; Spatial kernel; High-risk areas

Zvonimir Poljak, Catherine E. Dewey, S. Wayne Martin, Jette Christensen, Susy Carman, Robert M. Friendship, Spatial clustering of swine influenza in Ontario on the basis of herd-level disease status with different misclassification errors, Preventive Veterinary Medicine, Volume 81, Issue 4, 16 October 2007, Pages 236-249, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2007.04.018.
(http://www.sciencedirect.com/science/article/B6TBK-4NT93NR-2/2/a1f6a4788760bd33ba130d6c926018f4)
Abstract:
This approach maximizes sensitivity of serology-based monitoring systems by considering spatial clustering of herds classified as false positive by herd testing, allowing outbreaks to be detected in an early phase. The primary objective of this study was to determine whether swine herds infected with influenza viruses cluster in space, and if so, where they cluster. The secondary objective was to investigate the combining of a multivariate spatial scan statistic with herd test results to maximize the sensitivity of the surveillance system for swine influenza. We tested for spatial clustering of swine influenza using the Cuzick-Edwards test as a global test. The location of the most likely spatial clusters of cases for each subtype and strain in a sample of 65 sow and 72 finisher herds in 2001 (Ontario, Canada), and 76 sow herds in 2003 (Ontario, Canada) was determined by a spatial scan statistic in a purely spatial Bernoulli model based on single and multiple datasets.
A case herd was defined by true herd-disease status for sow or finisher herds tested for H1N1, and by apparent herd-disease status for sow herds tested for two H3N2 strains (A/Swine/Colorado/1/77 (Sw/Col/77) and A/Swine/Texas/4199-2/98 (Sw/Tex/98)). In sow herds, there was no statistically significant clustering of H1N1 influenza after adjustment for pig-farm density. Similarly, spatial clustering was not found in finisher herds. In contrast, clustering of H3N2

Sw/Col/77 (prevalence ratio = 12.5) and H3N2 Sw/Tex/98 (prevalence ratio = 15) was identified in an area close to a region with documented isolation of avian influenza isolates from pigs.
For the H1N1 subtype tested by ELISA, we used an approach that minimized overall misclassification at the herd level. This could be more applicable for detecting clusters of positive farms when herd prevalence is moderate to high than when herd prevalence is low. For the H3N2 strains we used an approach that maximized herd-level sensitivity by minimizing the herd cut-off. This is useful in situations where prevalence of the pathogen is low. The results of applying a multivariate spatial scan statistic approach, led us to generate the hypothesis that an unknown variant of influenza of avian origin was circulating in swine herds close to an area where avian strains had previously been isolated from swine. Maximizing herd sensitivity and linking it with the spatial information can be of use for monitoring of pathogens that exhibit the potential for rapid antigenic change, which, consequently, might then lead to diminished cross-reactivity of routinely used assays and lower test sensitivity for the newly emerged variants. Veterinary authorities might incorporate this approach into animal disease surveillance programs that either substantiate freedom from disease, or are aimed at detecting early incursion of a pathogen, such as influenza virus, or both.
Keywords: Influenza; Swine; Scan statistic; Sentinel surveillance; Herd test; Spatial

M.S. Lee, M.C. Deng, Y.J. Lin, C.Y. Chang, Happy K. Shieh, J.Z. Shiau, C.C. Huang, Characterization of an H5N1 avian influenza virus from Taiwan, Veterinary Microbiology, Volume 124, Issues 3-4, 6 October 2007, Pages 193-201, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2007.04.021.
(http://www.sciencedirect.com/science/article/B6TD6-4NFH0BB-M/2/9f9566b0b26d1d05261b322feabea1c4)
Abstract:
In 2003, an avian influenza (AI) virus of H5N1 subtype (A/Duck/China/E319-2/03; Dk/CHN/E319-2/03) was isolated from a smuggled duck in Kinmen Island of Taiwan. Phylogenetic analysis and pairwise comparison of nucleotide and amino acid sequences revealed that the virus displayed high similarity to the H5N1 viruses circulating in Asia during 2004 and 2005. The hemagglutinin (HA) protein of the virus contained multiple basic amino acid residues (-RERRRKR-) adjacent to the cleavage site between the HA1 and HA2 domains, showing the highly pathogenic (HP) characteristics. The HP phenotype was confirmed by experimental infection of chickens, which led up to 100% mortality within 24-72 h postinfection. The virus replicated equally well in the majority of organs of the infected chickens with titers ranging from 107.5 to 104.7 50% embryo lethal dose (ELD50) per gram of tissue. In a mouse model the virus exhibits low pathogenic characteristics with a lethal infection observed only after applying high inoculating dose (>=107.6 ELD50) of the virus. The infectious virus particles were recovered only from the pulmonary system including trachea and lungs. Our study suggests that ducks infected with H5N1 AIV of HPAI pathotype showing no disease signs can carry the virus silently and that bird smuggling represent a serious risk for H5N1 HPAI transmission.
Keywords: Highly pathogenic avian influenza; H5N1; Surveillance; Interspecies transmission

An-ping WANG, Huai-chang SUN, Jian-ye WANG, Yong-juan WANG, Wei-feng YUAN, The Helper Activities of Different Avian Viruses for Propagation of Recombinant Avian Adeno-Associated Virus, Agricultural Sciences in China, Volume 6, Issue 10, October 2007, Pages 1269-1274, ISSN 1671-2927, DOI: 10.1016/S1671-2927(07)60172-2.
(http://www.sciencedirect.com/science/article/B82XG-4R8H6TS-G/2/9d0ad27a6917d185bd66a3e2f20b785b)
Abstract:
To compare the helper activities of different avian viruses for propagation of recombinant avian adeno-associated virus (rAAAV), AAV-293 cells were cotransfected with the AAAV vector pAITR-

GFP containing green fluorescent protein (GFP) gene, the AAAV helper vector pcDNA-ARC expressing the rep and cap genes, and the adenovirus helper vector pHelper expressing Ad5 E2A,E4, and VA-RNA genes. Chicken embryonic fibroblast (CEF) or chicken embryonic liver (CEL) cells were cotransfected with the AAAV vector and the AAAV helper vector, followed by infection with Marek's disease virus (MDV), avian adenovirus, chicken embryo lethal orphan (CELO) virus or infectious bursal disease virus (IBDV). Infectious rAAAV particles generated by the two strategies were harvested and titrated on CEF and CEL cells. A significantly higher viral titer was obtained with the helper activity provided by the pHelper vector than by MDV or CELO virus. Further experiments showed that rAAAV-mediated green fluorescent protein (gfp) expression was overtly enhanced by MDV or CELO virus super infection or treatment with sodium butyric acid, but not by IBDV super infection. These data demonstrated that MDV and CELO viruses could provide weak helper activity for propagation of rAAAV, and rAAAV-mediated transgene expression could be enhanced by super infection with the helper viruses.
Keywords: recombinant avian adeno-associated virus (rAAAV), helper viruses

Chongmas Antarasena, Rungtiva Sirimujalin, Porntip Prommuang, Naruepol Promkuntod, Praison Prommuang, Stuart D. Blacksell, The indirect immunofluorescence assay using cardiac tissue from chickens, quails and ducks for identification of influenza A virus during an outbreak of highly pathogenic avian influenza virus (H5N1): A rapid and simple screening tool for limited resource settings, Research in Veterinary Science, Volume 83, Issue 2, October 2007, Pages 279-281, ISSN 0034-5288, DOI: 10.1016/j.rvsc.2006.12.007.
(http://www.sciencedirect.com/science/article/B6WWR-4N0GDWY-1/2/d009dd5635cc6e926c707e5ec4cf47e5)
Abstract:
Here we describe the diagnostic utility of the indirect immunofluorescence assay (IFA) during a recent outbreak of highly pathogenic avian influenza (HPAI) subtype H5N1 virus in southern Thailand and demonstrate the usefulness of the cardiac tissue from infected chickens, quail, and ducks for diagnosis. The most reliable sample for IFA diagnosis of influenza A virus was cardiac tissue (83.0%; 44/53) which when divided by species (chicken, quail and duck cardiac tissues) gave respective positivity rates of 88% (22/25), 88.9% (16/18) and 60.0% (6/10). Cardiac tissue also gave the highest IFA intensity for the three species. We believe that the IFA method has wide applicability in developing countries or remote settings where clinically similar avian diseases with high morbidity and mortality such as Newcastle disease and fowl cholera are common and could be rapidly excluded thereby conserving valuable reference laboratory capacity for true HPAI outbreaks.
Keywords: Avian influenza; HPAI; H5N1; Immunofluorescence; Cardiac tissue

J.P. Dubey, D.M. Webb, N. Sundar, G.V. Velmurugan, L.A. Bandini, O.C.H. Kwok, C. Su, Endemic avian toxoplasmosis on a farm in Illinois: Clinical disease, diagnosis, biologic and genetic characteristics of Toxoplasma gondii isolates from chickens (Gallus domesticus), and a goose (Anser anser), Veterinary Parasitology, Volume 148, Issues 3-4, 30 September 2007, Pages 207-212, ISSN 0304-4017, DOI: 10.1016/j.vetpar.2007.06.033.
(http://www.sciencedirect.com/science/article/B6TD7-4P8H8J7-5/2/262b9d3076228a42a2dce8c2d56f9feb)
Abstract:
Clinical toxoplasmosis in chickens (Gallus domesticus) has been rarely reported in literature. Here we report that three chickens on a farm in Illinois developed neurological signs. One of these chickens was examined postmortem and it had non-suppurative encephalitis with numerous Toxoplasma gondii tachyzoites and tissue cysts. The identity of the protozoa was confirmed immunohistochemically by staining with T. gondii specific antibodies, and by transmission electron microscopy. The owner of the 3 chickens donated all 11 remaining chickens and a goose on his

property for the present study. All 11 chickens and a goose were euthanized, and blood, heart, brain, and 1 leg were obtained for T. gondii examination. Antibodies to T. gondii were found in sera of all chickens with titers of 1:40 in one, 1:320 in three, and 1:640 or higher in seven chickens tested by the modified agglutination test (MAT). The goose had a MAT titer of 1:320. For isolation of T. gondii, whole heart and brain and 50 g of leg muscles were digested in an acid-pepsin solution and bioassayed in four mice for each tissue. Viable T. gondii was isolated from tissues of all 11 chickens and the goose. Genotyping of these 12 T. gondii isolates using polymorphism at the genetic loci SAG1, SAG2, SAG3, BTUB, GRA6, c22-8, c29-2, L358, PK1, a new SAG2 and Apico revealed that all isolates had Type II alleles at all loci, indicating these T. gondii isolates belong to the predominant clonal Type II lineages. This is the first report of isolation of viable T. gondii from a domestic goose (Anser anser).
Keywords: Toxoplasma gondii; Chickens; Gallus domesticus; USA; Genotype; Goose; Anser anser

I. Tarpey, M.B. Huggins, Onset of immunity following in ovo delivery of avian metapneumovirus vaccines, Veterinary Microbiology, Volume 124, Issues 1-2, 20 September 2007, Pages 134-139, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2007.03.018.
(http://www.sciencedirect.com/science/article/B6TD6-4NC38TS-9/2/ade4daa5498568edd8e2b0b3f92b17e0)
Abstract:
Avian metapneumovirus (aMPV) is an important cause of disease in chickens and turkeys. As infection can occur early in life and spread of the virus throughout a flock is rapid, an early onset of immunity post-vaccination would be advantageous. We have studied the serological immune response and the onset of protective immunity of an aMPV vaccine delivered to chickens via the in ovo route compared to oculonasal delivery at day old. A 1000-fold lower dose delivered in ovo to chicken specific pathogen free (SPF) embryos, than vaccination at day old, provided a significantly higher antibody response. In the presence of maternally derived antibody (MDA), there was no significant difference in antibody response between the vaccination routes. However, the onset of immunity (OOI) for the vaccine delivered to MDA positive chicken embryos was 5 days post-hatch in comparison to 8 days post-hatch for the same dose of vaccine given at day old indicating that chicks would be protected against disease earlier in the field if vaccinated by the in ovo route. In further experiments the OOI for a turkey vaccine delivered to MDA positive turkey embryos was shown to be 8 days post-hatch.
Keywords: Avian metapneumovirus; Vaccines; In ovo; Seroconversion; Onset; Immunity; Chickens; Turkeys

Matthew A. Etterson, Julie R. Etterson, Francesca J. Cuthbert, A robust new method for analyzing community change and an example using 83 years of avian response to forest succession, Biological Conservation, Volume 138, Issues 3-4, September 2007, Pages 381-389, ISSN 0006-3207, DOI: 10.1016/j.biocon.2007.05.003.
(http://www.sciencedirect.com/science/article/B6V5X-4P2S2BW-3/2/8befcd300e778986bed4ae2a7ce309e2)
Abstract:
The composition of animal communities changes over time in response to natural processes (disease dynamics, plant community succession) and anthropogenic disturbances (habitat fragmentation, climate change). Detection and analysis of community change is important for regional and site-specific management and for conservation planning. However, formal time series of animal community composition are rare. We describe a distribution-free method for compiling time series from separate studies to test for changes in community composition. The method, based on rank-permutation, is robust to many problems associated with data from separate studies, including unequal sampling effort, variable-length intervals between sampling, and

different sampling protocols. We apply the technique to a time series constructed from five surveys of land bird community composition spanning 83 years of forest succession in northern lower Michigan, USA. We found increases in neotropical migrants, area-sensitive birds, and woodland birds. Despite high species turnover, the overall taxonomic composition of the land bird community did not show significant changes. Although more powerful tests can be applied when data are collected under consistent protocols, our approach is a useful alternative when such data are lacking. In the example provided, our method produced coherent results that are consistent with other published studies from the region.
Keywords: Bird communities; Rank-permutation; Forest succession; Eastern deciduous forest

Camille Lebarbenchon, Sylvie van der Werf, Frederic Thomas, Jean-Thierry Aubin, Saliha Azebi, Frederique Cuvelier, Patricia Jeannin, Vanessa Roca, Chung-Ming Chang, Yves Kayser, Benjamin Roche, Jean-Francois Guegan, Francois Renaud, Michel Gauthier-Clerc, Absence of detection of highly pathogenic H5N1 in migratory waterfowl in southern France in 2005-2006, Infection, Genetics and Evolution, Volume 7, Issue 5, September 2007, Pages 604-608, ISSN 1567-1348, DOI: 10.1016/j.meegid.2007.05.009.
(http://www.sciencedirect.com/science/article/B6W8B-4NSMMTS-3/2/67d509cea089c1db6b9c922ede48188d)
Abstract:
During fall 2005, the rapid and wide spread of highly pathogenic (HP) H5N1 avian influenza viruses (AIV) outside Asia alerted European health authorities. Because of abnormal and recurrent field mortality, wild migratory birds were considered to be the main dispersing agent of the virus at an intercontinental scale. European wintering wetlands, such as the Camargue (Rhone delta, France), are identified as potential hot spots for the risk of introduction and transmission of bird-borne diseases. In this study, we investigated the role of migratory waterbirds (mainly ducks) in the spread of HP H5N1 viruses. We combined molecular analysis of living and freshly killed birds with population surveillance (aerial censuses and death surveillance). We sampled 1345 birds belonging to 17 waterbird species (3 orders) in the Camargue between September 2005 and March 2006. The prevalence of AIV was 1.8%. We did not detect HP H5N1 virus. Population censuses did not reveal any population decreases nor abnormal mortalities. We discuss, in the light of these results, the implication of wild migratory ducks in the arrival of HP H5N1 AIV in Europe.
Keywords: Avian influenza; Anseriforms; Camargue

Dirk U. Pfeiffer, Phan Q. Minh, Vincent Martin, Michael Epprecht, Martin J. Otte, An analysis of the spatial and temporal patterns of highly pathogenic avian influenza occurrence in Vietnam using national surveillance data, The Veterinary Journal, Volume 174, Issue 2, September 2007, Pages 302-309, ISSN 1090-0233, DOI: 10.1016/j.tvjl.2007.05.010.
(http://www.sciencedirect.com/science/article/B6WXN-4P3M2CR-2/2/a7cf4e5234a636ef9407eef23ac9c8a1)
Abstract:
The objectives of this study were to describe the spatio-temporal pattern of an epidemic of highly pathogenic avian influenza (HPAI) in Vietnam and to identify potential risk factors for the introduction and maintenance of infection within the poultry population. The results indicate that during the time period 2004-early 2006 a sequence of three epidemic waves occurred in Vietnam as distinct spatial and temporal clusters. The risk of outbreak occurrence increased with a greater percentage of rice paddy fields, increasing domestic water bird and chicken density. It increased with reducing distance to higher population density aggregations, and in the third epidemic wave with increasing percentage of aquaculture. The findings indicate that agri-livestock farming systems involving domestic water birds and rice production in river delta areas are important for the maintenance and spread of infection. While the government's control measures appear to

have been effective in the South and Central parts of Vietnam, it is likely that in the North of Vietnam the vaccination campaign led to transmission of infection which was subsequently brought under control.
Keywords: Avian influenza; Epidemiology; Vietnam; Poultry; Vaccination; Disease control

R. Klopfleisch, P.U. Wolf, C. Wolf, T. Harder, E. Starick, M. Niebuhr, T.C. Mettenleiter, J.P. Teifke, Encephalitis in a Stone Marten (Martes foina) after Natural Infection with Highly Pathogenic Avian Influenza Virus Subtype H5N1, Journal of Comparative Pathology, Volume 137, Issues 2-3, August-October 2007, Pages 155-159, ISSN 0021-9975, DOI: 10.1016/j.jcpa.2007.06.001.
(http://www.sciencedirect.com/science/article/B6WHW-4PCH4NB-1/2/1f5c14807a847a82f0dcf45645e252c7)
Abstract: Summary
Recent outbreaks of disease in different avian species, caused by the highly pathogenic avian influenza virus (HPAIV), have involved infection by subtype H5N1 of the virus. This virus has also crossed species barriers and infected felines and humans. Here, we report the natural infection of a stone marten (Martes foina) from an area with numerous confirmed cases of H5N1 HPAIV infection in wild birds. Histopathological examination of tissues from this animal revealed a diffuse nonsuppurative panencephalitis with perivascular cuffing, multifocal gliosis and neuronal necrosis. Additionally, focal necrosis of pancreatic acinar cells was observed. Immunohistochemically, lesions in these organs were associated with avian influenza virus antigen in neurons, glial cells and pancreatic acinar cells. Thus, the microscopical lesions and viral antigen distribution in this stone marten differs from that recently described for cats naturally and experimentally infected with the same virus subtype. This is the first report of natural infection of a mustelid with HPAIV H5N1.
Keywords: brain; highly pathogenic avian influenza virus (HPAIV); Martes foina; stone marten

Daniela Gaspar da Silva, Emma Barton, Nancy Bunbury, Patricia Lunness, Diana J. Bell, Kevin M. Tyler, Molecular identity and heterogeneity of trichomonad parasites in a closed avian population, Infection, Genetics and Evolution, Volume 7, Issue 4, July 2007, Pages 433-440, ISSN 1567-1348, DOI: 10.1016/j.meegid.2007.01.002.
(http://www.sciencedirect.com/science/article/B6W8B-4MV0MB9-2/2/23cf7b2d8760fce0b132ccc8998fced1)
Abstract:
Columbids (pigeons and doves) are the primary host of Trichomonas gallinae, the flagellate protozoon which causes avian trichomoniasis, a widespread, often lethal disease. Although predominantly apathogenic, the organism is paradigmatic for the study of strain-specific virulence, with some strains causing greater than 75% mortality and epizootic die-offs in wildlife populations. In recent years, research on this important emerging pathogen has been neglected and genetic variation within the parasite has not hitherto been investigated. The pink pigeon (Columba mayeri), endemic to Mauritius and one of the world's rarest pigeons, suffers high levels of nestling/fledgling mortality from trichomoniasis. As a closed oceanic island population with recorded life-history parameters for all birds, this species represents a unique resource for the study of this host-parasite interaction. To investigate genetic variation within T. gallinae in Mauritian columbids, isolates were collected from pink pigeons and another widespread species, the Madagascar turtle-dove (Streptopelia picturata). Comparison of the 5.8S region of rDNA and surrounding internally transcribed spacer regions (ITS) showed no sequence variation between isolates or with an unrelated but previously sequenced T. gallinae isolate (Genbank). This confirmed all 24 isolates as T. gallinae, and defined this section of the genome as a good species marker. In contrast, Random Amplified Polymorphic DNA (RAPD) analysis of the isolates revealed considerable genotypic variation between isolates. RAPD genotypes appeared to correlate with geographic distribution and host species, suggesting inter-species transmission and rapid host adaptation by the parasite.

Keywords: Trichomonas gallinae; Endangered species; Molecular epidemiology; Molecular evolution; Pink pigeon

Shu-hong SUN, Zhi-zhong CUI, Li-xin QU, Maternal Antibody Protected Chicks from Growth Retardation and Immunosuppression Induced by Early Reticuloendotheliosis Virus Infection, Agricultural Sciences in China, Volume 6, Issue 6, June 2007, Pages 762-768, ISSN 1671-2927, DOI: 10.1016/S1671-2927(07)60110-2.
(http://www.sciencedirect.com/science/article/B82XG-4P48RF7-K/2/0e9a5e748982ddf14bb326ed4b14087d)
Abstract: Abstract
To determine if the maternal antibody from breeders vaccinated with cell culture-adapted reticuloendotheliosis virus (REV) could protect chicks from early REV infection, one-day-old chicks with or without anti-REV maternal antibodies were inoculated with REV, and then their growth rates and antibody titers to Newcastle disease virus (NDV) and avian influenza virus (AIV), after vaccination with inactivated vaccines, were compared. This study indicated that REV infection could cause growth retardation and severely inhibit immune reactions to inactivated vaccines against NDV and Avian influenza virus (AIV, H9 and H5) in one-day-old broilers without maternal antibodies specific to REV. Maternal antibody from breeders vaccinated with an attenuated REV vaccine effectively protected REV-challenged birds from growth retardation and immunosuppression on antibody reactions to NDV and AIV vaccines. Four weeks after vaccination, the HI titers to NDV, AIV-H9, and AIV-H5 in maternal antibody positive and negative groups were 3.36+/-2.04 versus 1.58+/-1.69 ($P<0.01$), 6.27+/-3.87 versus 0.71+/-1.60 ($P<0.01$), and 6.72+/-3.92 versus 0.54+/-1.44 ($P<0.01$). Maternal antibodies from breeders vaccinated with REV vaccine could successfully protect chicks from REV infection and effectively prevent REV-induced growth retardation and immunosuppression in antibody responses to NDV and AIV.
Keywords: reticuloendotheliosis virus; Newcastle disease virus; avian influenza virus; immunosuppression; maternal antibody

Kwonil Jung, Dae-Sub Song, Bo-Kyu Kang, Jin-Sik Oh, Bong-Kyun Park, Serologic surveillance of swine H1 and H3 and avian H5 and H9 influenza A virus infections in swine population in Korea, Preventive Veterinary Medicine, Volume 79, Issues 2-4, 16 May 2007, Pages 294-303, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2006.12.005.
(http://www.sciencedirect.com/science/article/B6TBK-4MT5513-2/2/8980864c5a8c1e22f5f8a14ea2d67aea)
Abstract:
Influenza A is a respiratory disease common in the swine industry. Three subtypes, H1N1, H1N2 and H3N2 influenza A viruses, are currently co-circulating in swine populations in Korea. An outbreak of the highly pathogenic avian influenza H5N1 virus occurred in domestic bird farms in Korea during the winter season of 2003. Pigs can serve as hosts for avian influenza viruses, enabling passage of the virus to other mammals and recombination of mammalian and avian influenza viruses, which are more readily transmissible to humans. This study reports the current seroprevalence of swine H1 and H3 influenza in swine populations in Korea by hemagglutination inhibition (HI) assay. We also investigated whether avian H5 and H9 influenza transmission occurred in pigs from Korea using both the HI and neutralization (NT) tests. 51.2% (380/742) of serum samples tested were positive against the swine H1 virus and 43.7% (324/742) were positive against the swine H3 virus by HI assay. The incidence of seropositivity against both the swine H1 virus and the swine H3 virus was 25.3% (188/742). On the other hand, none of the samples tested showed seropositivity against either the avian H5 virus or the avian H9 virus by the HI and NT tests. Therefore, we report the high current seroprevalence and co-infectivity of swine H1 and H3 influenza viruses in swine populations and the lack of seroepidemiological evidence of avian H5 and H9 influenza transmission to Korean pigs.

Keywords: Seroprevalence; Pigs; Swine influenza viruses; Avian influenza viruses; Korea

E. Thiry, A. Zicola, D. Addie, H. Egberink, K. Hartmann, H. Lutz, H. Poulet, M.C. Horzinek, Highly pathogenic avian influenza H5N1 virus in cats and other carnivores, Veterinary Microbiology, Volume 122, Issues 1-2, 16 May 2007, Pages 25-31, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2006.12.021.
(http://www.sciencedirect.com/science/article/B6TD6-4MRN9RJ-1/2/4efa39d8c104ce128548c0ba41a4719a)
Abstract:
The Asian lineage highly pathogenic avian influenza (HPAI) H5N1 virus is a known pathogen of birds. Only recently, the virus has been reported to cause sporadic fatal disease in carnivores, and its zoonotic potential has been dominating the popular media. Attention to felids was drawn by two outbreaks with high mortality in tigers, leopards and other exotic felids in Thailand. Subsequently, domestic cats were found naturally infected and experimentally susceptible to H5N1 virus. A high susceptibility of the dog to H3N8 equine influenza A virus had been reported earlier, and recently also HPAI H5N1 virus has been identified as a canine pathogen. The ferret, hamster and mouse are suitable as experimental animals; importantly, these species are also kept as pets. Experimental intratracheal and oral infection of cats with an HPAI H5N1 virus isolate from a human case resulted in lethal disease; furthermore, cats have been infected by the feeding of infected chickens. Spread of the infection from experimentally infected to in-contact cats has been reported. The epidemiological role of the cat and other pet animal species in transmitting HPAI H5N1 virus to humans needs continuous consideration and attention.
Keywords: Cat; Feline; Avian influenza; H5N1

DaPeng Peng, SiShun Hu, Yan Hua, YunCai Xiao, ZiLi Li, XiLiang Wang, DingRen Bi, Comparison of a new gold-immunochromatographic assay for the detection of antibodies against avian influenza virus with hemagglutination inhibition and agar gel immunodiffusion assays, Veterinary Immunology and Immunopathology, Volume 117, Issues 1-2, 15 May 2007, Pages 17-25, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2007.01.022.
(http://www.sciencedirect.com/science/article/B6TD5-4N1T1M3-1/2/3cce2cf13cb21aab6be6305948516e90)
Abstract:
A gold-immunochromatographic test-strip kit is used for the detection of IgG antibodies against the nucleocapsid protein of Avian Influenza Virus (AIV). Compared with the 'gold standard', i.e. hemagglutination inhibition (HI) and agar gel immunodiffusion (AGID) assays, the gold-immunochromatographic test strip has many advantages, such as high specificity, high sensitivity, convenience, is rapid and has low cost. The gold-immunochromatographic test strip provides a unique tool for the on-site surveillance and diagnosis of Avian Influenza.
Keywords: AIV; Antibody; Gold-immunochromatography test strip

Yu-Ching Lee, Sy-Jye C. Leu, Han-Chang Hung, Hsueh-Hsia Wu, I.-Jen Huang, Wen-Shyang Hsieh, Wen-Ta Chiu, Ming-Song Hsieh, Tsui-Fen Cheng, Yi-Yuan Yang, A dominant antigenic epitope on SARS-CoV spike protein identified by an avian single-chain variable fragment (scFv)-expressing phage, Veterinary Immunology and Immunopathology, Volume 117, Issues 1-2, 15 May 2007, Pages 75-85, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2007.02.001.
(http://www.sciencedirect.com/science/article/B6TD5-4N1T1M3-2/2/4a1fc83e4a31645480b4ecf7e501e606)
Abstract:
Severe acute respiratory syndrome (SARS) is a newly emergent human disease, which requires rapid diagnosis and effective therapy. Among antibody sources, immunoglobulin Y (IgY) is the major antibody found in chicken eggs and can be used as an alternative to mammalian antibodies

normally used in research and immunotherapy. In this study, phage-expressing chicken monoclonal scFv antibody was chosen and characterized with phage display antibody technology. Truncated fragments of SARS-CoV spike protein were cloned in pET-21 vector and expressed in BL-21 Escherichia coli (E. coli) cells. After purification, the purity of these recombinant spike proteins was examined on SDS-PAGE and their identity verified with Western blot analysis using anti-his antibodies and sera from convalescent stage SARS-CoV-infected patients. Using these bacteria-derived proteins to immunize chickens, it was found that polyclonal IgY antibodies in the egg yolk and sera were highly reactive to the immunogens, as shown by Western blot and immunocytochemical staining analysis. A phage displaying scFv library was also established from spleen B cells of immunized chicken with 5 x 107 clones. After four panning cycles, the eluted phage titer showed a 10-fold increase. In sequence analysis with chicken germline gene, five phage clones reacted, with large dissimilarities of between 31 and 62%, in the complementarity-determining regions, one dominant phage 4S1 had strong binding to fragment Se-e, located between amino acid residues 456-650 of the spike protein and this particular phage had significantly strong binding to SARS-CoV-infected Vero E6 cells. Based on the results, we conclude that generating specific scFv-expressing phage binders with the phage display system can be successfully achieved and that this knowledge can be applied in clinical or academic research.
Keywords: SARS-CoV; Spike protein; IgY; scFv-expressing phage binder

Mahesh Khatri, Jagdev M. Sharma, Replication of infectious bursal disease virus in macrophages and altered tropism of progeny virus, Veterinary Immunology and Immunopathology, Volume 117, Issues 1-2, 15 May 2007, Pages 106-115, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2007.02.002.
(http://www.sciencedirect.com/science/article/B6TD5-4N2KT82-2/2/29a7ea05b6517f172aeedebcecfcb92e)
Abstract:
We serially passaged classical infectious bursal disease virus (cIBDV) and antigenic variant IBDV (vIBDV) in an avian macrophage cell line, NCSU cells, referred as mcIBDV and mvIBDV respectively and examined the in vitro and in vivo characteristics of the macrophage-adapted viruses. NCSU adapted viruses caused earlier destruction of NCSU cells than the unadapted viruses. Nitric oxide (NO) was detected earlier in cultures infected with mcIBDV and mvIBDV than in cultures infected with cIBDV and vIBDV. cIBDV and vIBDV were able to infect DF-1 cells, a chicken embryo fibroblast cell line, only after one replication cycle in NCSU cells. The genetic basis of altered tropism of progeny virus from NCSU cells infected cultures was not identified. No aa substitutions were observed in hypervariable region of VP2 of cIBDV and vIBDV passaged 1 time in NCSU cells whereas both mcIBDV and mvIBDV had multiple aa substitutions. To assess protective efficacy of mcIBDV and mvIBDV, embryonated chicken eggs were inoculated with mcIBDV and mvIBDV at embryonation day 18 (ED 18) and challenged with a virulent cIBDV at 3 weeks of age. mcIBDV and mvIBDV were immunogenic and generated antibody responses and provided 100% protection against cIBDV.
Keywords: IBDV; Macrophages; Altered tropism

Sarah K. Williams, Jason Kempton, Susan B. Wilde, Alan Lewitus, A novel epiphytic cyanobacterium associated with reservoirs affected by avian vacuolar myelinopathy, Harmful Algae, Volume 6, Issue 3, April 2007, Pages 343-353, ISSN 1568-9883, DOI: 10.1016/j.hal.2006.07.005.
(http://www.sciencedirect.com/science/article/B73D7-4KNV2NW-1/2/67ed660b1559b153b035158c86616b24)
Abstract:
Avian vacuolar myelinopathy (AVM) is a newly discovered bird disease, which is killing bald eagles (Haliaeetus leucocephalus) and waterfowl in the southeastern United States. Surveys were

conducted to investigate exotic macrophytes (e.g. Hydrilla verticillata) as a substrate for attachment by toxic cyanobacteria that may be associated with the incidence of AVM. While the specific cause of the disease has not been confirmed, one hypothesis is that birds ingest a neurotoxin produced by cyanobacteria epiphytic on macrophytes. A strong relationship was found between the field abundance of a specific undescribed epiphytic cyanobacterium and the incidence of AVM. The undescribed species is a filamentous, heterocystous, true branching cyanobacterium. Morphological characteristics place the cyanobacterium in section V, order Stigonematales. The 16S rRNA sequence identity was determined from environmental isolates of this unknown Stigonematalan species using DGGE (denaturing gradient gel electrophoresis). The 16S rRNA sequence data were aligned with additional cyanobacteria sequences to determine designations for probe development, to lay groundwork for its formal description and to advance understanding of the species' phylogeny. Real-time PCR assays were developed for rapid, specific detection of the Stigonematales species from environmental samples. The genetic probe produced by this study will help test the hypothesized link between these cyanobacteria and AVM, and therefore help guide decisions on managing hydrilla and other invasive macrophytes in AVM-affected waters.
Keywords: Avian vacuolar myelinopathy (AVM); Cyanobacteria; Fulica americana; Haliaeetus leucocephalus; Hydrilla; Real-time PCR; Stigonematales; 16S

Maja Marien, Annemie Decostere, Luc Duchateau, Koen Chiers, Robrecht Froyman, Hans Nauwynck, Efficacy of enrofloxacin, florfenicol and amoxicillin against Ornithobacterium rhinotracheale and Escherichia coli O2:K1 dual infection in turkeys following APV priming, Veterinary Microbiology, Volume 121, Issues 1-2, 31 March 2007, Pages 94-104, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2006.11.012.
(http://www.sciencedirect.com/science/article/B6TD6-4MDWY2N-1/2/34b6390923e216bf75e22777134d830e)
Abstract:
Experimental groups of 15 susceptible 3-week-old turkeys were inoculated oculonasally with avian metapneumovirus (APV) subtype A and susceptible Escherichia coli O2:K1 and Ornithobacterium rhinotracheale (ORT) bacteria, with a 3 days interval between viral and bacterial inoculation and approximately 8 h between the two bacterial inoculations. The aims of the present study were to assess the efficacy of drinking-water administration of enrofloxacin for 3 and 5 days, amoxicillin for 5 days and florfenicol for 5 days for the treatment of the resulting respiratory disease, based on clinical and bacteriological examinations. Antimicrobial treatment started 1 day after dual bacterial inoculation. After infection, the birds were examined and scored for clinical signs daily, weighed at different times, and their tracheae swabbed daily. Five birds were euthanised and examined for macroscopic lesions at necropsy at 5 days post-bacterial inoculation (dpbi) and the remainder at 15 dpbi. Samples of the turbinates, trachea, lungs, sinuses, air sacs, heart, pericardium and liver were collected for bacteriological examination.
Recovery from respiratory disease caused by an APV/E. coli/ORT triple infection in 3-week-old turkey poults was overall most successful after enrofloxacin treatment, irrespective of treatment duration, followed by florfenicol treatment. Compared with the untreated group, clinical signs as well as ORT and E. coli multiplication in the respiratory tract were significantly reduced by both enrofloxacin treatments and the florfenicol treatment, with the enrofloxacin treatments showing significantly better reductions than the florfenicol treatment. Five-day treatment with amoxicillin, compared with the untreated group, did not cause a significant reduction in any of the aforementioned parameters.
Keywords: Antimicrobial treatment; Avian metapneumovirus; Escherichia coli O2:K1; Ornithobacterium rhinotracheale; Turkeys

Marius Gilbert, Xiangming Xiao, Prasit Chaitaweesub, Wantanee Kalpravidh, Sith Premashthira, Stephen Boles, Jan Slingenbergh, Avian influenza, domestic ducks and rice agriculture in Thailand, Agriculture, Ecosystems & Environment, Volume 119, Issues 3-4, March 2007, Pages 409-415, ISSN 0167-8809, DOI: 10.1016/j.agee.2006.09.001.
(http://www.sciencedirect.com/science/article/B6T3Y-4M2WNV0-1/2/10b44ef93c75316309184c1f369312ed)
Abstract:
Highly pathogenic avian influenza (HPAI) caused by H5N1 viruses has become a global scale problem which first emerged in southern China and from there spread to other countries in Southeast and East Asia, where it was first confirmed in end 2003. In previous work, geospatial analyses demonstrated that free grazing ducks played critical role in the epidemiology of the disease in Thailand in the winter 2004/2005, both in terms of HPAI emergence and spread. This study explored the geographic association between free grazing duck census counts and current statistics on the spatial distribution of rice crops in Thailand, in particular the crop calendar of rice production. The analysis was carried out using both district level rice statistics and rice distribution data predicted with the aid of remote sensing, using a rice-detection algorithm. The results indicated a strong association between the number of free grazing ducks and the number of months during which second-crop rice harvest takes place, as well as with the rice crop intensity as predicted by remote sensing. These results confirmed that free grazing duck husbandry was strongly driven by agricultural land use and rice crop intensity, and that this later variable can be readily predicted using remote sensing. Analysis of rice cropping patterns may provide an indication of the location of populations of free grazing ducks in other countries with similar mixed duck and rice production systems and less detailed duck census data. Apart from free ranging ducks and rice cropping, the role of hydrology and seasonality of wetlands and water bodies in the HPAI risk analysis is also discussed in relation to the presumed dry season aggregation of wild waterfowl and aquatic poultry offering much scope for virus transmission.
Keywords: Highly pathogenic avian influenza; Domestic ducks; Remote sensing; Agriculture intensification; Rice paddy production

Ying-Hen Hsieh, Chwan-Chuan King, Cathy W.S Chen, Mei-Shang Ho, Sze-Bi Hsu, Yi-Chun Wu, Impact of quarantine on the 2003 SARS outbreak: A retrospective modeling study, Journal of Theoretical Biology, Volume 244, Issue 4, 21 February 2007, Pages 729-736, ISSN 0022-5193, DOI: 10.1016/j.jtbi.2006.09.015.
(http://www.sciencedirect.com/science/article/B6WMD-4KX2DFG-6/2/6da8fa774fb6ead2ab6d219b600b3845)
Abstract:
During the 2003 Severe Acute Respiratory Syndrome (SARS) outbreak, traditional intervention measures such as quarantine and border control were found to be useful in containing the outbreak. We used laboratory verified SARS case data and the detailed quarantine data in Taiwan, where over 150,000 people were quarantined during the 2003 outbreak, to formulate a mathematical model which incorporates Level A quarantine (of potentially exposed contacts of suspected SARS patients) and Level B quarantine (of travelers arriving at borders from SARS affected areas) implemented in Taiwan during the outbreak. We obtain the average case fatality ratio and the daily quarantine rate for the Taiwan outbreak. Model simulations is utilized to show that Level A quarantine prevented approximately 461 additional SARS cases and 62 additional deaths, while the effect of Level B quarantine was comparatively minor, yielding only around 5% reduction of cases and deaths. The combined impact of the two levels of quarantine had reduced the case number and deaths by almost a half. The results demonstrate how modeling can be useful in qualitative evaluation of the impact of traditional intervention measures for newly emerging infectious diseases outbreak when there is inadequate information on the characteristics and clinical features of the new disease--measures which could become particularly important with

the looming threat of global flu pandemic possibly caused by a novel mutating flu strain, including that of avian variety.
Keywords: SARS; Emerging infectious diseases; Quarantine; Intervention; Discrete time compartmental model; Taiwan

M.L. Thom, J.C. Hope, M. McAulay, B. Villarreal-Ramos, T.J. Coffey, S. Stephens, H.M. Vordermeier, C.J. Howard, The effect of tuberculin testing on the development of cell-mediated immune responses during Mycobacterium bovis infection, Veterinary Immunology and Immunopathology, Volume 114, Issues 1-2, 15 November 2006, Pages 25-36, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2006.07.001.
(http://www.sciencedirect.com/science/article/B6TD5-4KMYFPD-1/2/c4f0205f0b98bed4ca50457bcb7fc3d4)
Abstract:
Protection against tuberculosis (TB) is associated with Th1-type cell-mediated immunity (CMI). Whilst the intradermal injection of partially purified derivatives of tuberculin (PPD) represents the classic test assessing the delayed type hypersensitivity (DTH) response used in both humans and cattle for diagnosing TB, it has been suggested that the test may modulate host CMI responses. To investigate the kinetics of the development of the DTH response and its subsequent effect on CMI responses, groups of 6-month old calves were inoculated intranasally with 8 x 104 cfu of Mycobacterium bovis, subjected to the comparative intradermal tuberculin test (TT) using bovine and avian PPD (PPD-B, PPD-A) at various time intervals post-infection, and immune responses compared. These included DTH, lymphocyte proliferation, IgG production, and synthesis of the cytokines: IFN[gamma], IL-10, IL-4, IL-6, and IL-13. All animals were subjected to post-mortem examination.
The kinetics of the development of the DTH response assessed in the TT was such that infected cattle could be identified as early as 3 weeks post-infection, which correlated with the detection of an antigen-specific IFN[gamma] response. Transient increases in plasma-derived IFN[gamma] as a result of TT during an established TB infection were more pronounced when blood was stimulated with PPD-A compared with PPD-B stimulation. This has the potential to mask diagnosis of infection as a result of the stronger avian-bias if the IFN[gamma] test is used the week following TT. Disease pathology was not affected by TT. A transient failure to a second TT was observed in 1 of 30 animals and the time (post-infection) at which the TT is administered may be of significance. In serum, IgG responses to PPD-B, which were undetectable prior to TT, were elevated after TT and were most pronounced in cattle that were TT at 6 weeks post-infection. Other cytokines were also affected by the TT; IL-4 mRNA levels increased and IL-6 mRNA levels decreased, whilst PPD-B specific IL-10 protein synthesis was enhanced. These observations may offer the potential for further diagnostic assays that could complement the TT and IFN[gamma] test.
Keywords: Tuberculosis; Mycobacterium bovis; Tuberculin test; Cytokines; Bovine

Peter Brown, Chiung Chu Chen, Shouyan Wang, Andrea A. Kuhn, Louise Doyle, Kielan Yarrow, Bart Nuttin, John Stein, Tipu Aziz, Involvement of Human Basal Ganglia In Offline Feedback Control of Voluntary Movement, Current Biology, Volume 16, Issue 21, 7 November 2006, Pages 2129-2134, ISSN 0960-9822, DOI: 10.1016/j.cub.2006.08.088.
(http://www.sciencedirect.com/science/article/B6VRT-4M8WTCF-S/2/705edbc83bbd2ef305c8485993d22e12)
Abstract: Summary
Practice makes perfect, but the neural substrates of trial-to-trial learning in motor tasks remain unclear. There is some evidence that the basal ganglia process feedback-related information to modify learning in essentially cognitive tasks [1], [2], [3] and [4], but the evidence that these key motor structures are involved in offline feedback-related improvement of performance in motor

tasks is paradoxically limited. Lesion studies in adult zebra finches suggest that the avian basal ganglia are involved in the transmission or production of an error signal during song [5], [6] and [7]. However, patients with Huntington's disease, in which there is prominent basal ganglia dysfunction, are not impaired in error-dependent modulation of future trial performance [8]. By directly recording from the subthalamic nucleus in patients with Parkinson's disease, we demonstrate that this nucleus processes error in trial performance at short latency. Local evoked activity is greatest in response to smallest errors and influences the programming of subsequent movements. Accordingly, motor parameters are least likely to change after the greatest evoked responses so that accurately performed trials tend to precede other accurate trials. This relationship is disrupted by electrical stimulation of the nucleus at high frequency. Thus, the human subthalamic nucleus is involved in feedback-based learning.
Keywords: SYSNEURO

S.E. Childs-Sanford, M.M. Garner, J.T. Raymond, E.S. Didier, G.V. Kollias, Disseminated Microsporidiosis due to Encephalitozoon hellem in an Egyptian Fruit Bat (Rousettus aegyptiacus), Journal of Comparative Pathology, Volume 134, Issue 4, May 2006, Pages 370-373, ISSN 0021-9975, DOI: 10.1016/j.jcpa.2006.01.004.
(http://www.sciencedirect.com/science/article/B6WHW-4K07N7F-3/2/f5d45e77e4478b1010b98966f787c8da)
Abstract: Summary
Disseminated microsporidiosis was diagnosed in an adult female Egyptian fruit bat that died unexpectedly in a zoo. Gross findings, which were minimal, included poor body condition, bilateral renomegaly, and mottling of the liver. Histopathological lesions, which were particularly pronounced in the urogenital tract and liver, consisted primarily of inflammation associated with intracytoplasmic microsporidian spores. Polymerase chain reaction -based methods were used to establish the identity of the microsporidian as Encephalitozoon hellem. E. hellem is an emerging cause of human and avian disease, manifested mainly as opportunistic infection in immunosuppressed patients. This report describes the first documented case of E. hellem in a non-human mammalian species.
Keywords: Encephalitozoon hellem; fruit bat; microsporidiosis; parasitic infection; Rousettus aegyptiacus

A. Marm Kilpatrick, Facilitating the evolution of resistance to avian malaria in Hawaiian birds, Biological Conservation, Volume 128, Issue 4, April 2006, Pages 475-485, ISSN 0006-3207, DOI: 10.1016/j.biocon.2005.10.014.
(http://www.sciencedirect.com/science/article/B6V5X-4HMNG63-2/2/7a4c5ff98309271042a5e9b44ca84578)
Abstract:
Research has shown that avian malaria plays an important role in limiting the distribution and population sizes of many Hawaiian birds, and that projected climate change is likely to eliminate most disease-free habitat in Hawai'i in the next century. I used a modeling approach, parameterized with demographic data from the literature and the field, to examine alternate management scenarios for the conservation of native Hawaiian birds. I examined the feasibility of using management in the form of rodent control to facilitate the evolution of resistance to malaria by increasing the survival and reproduction of native birds. Analysis of demographic data from seven native species, Akepa (Loxops coccineus), `Akohekohe (Palmeria dolei), Elepaio (Chasiempis sandwichensis), Hawai'i'amakihi (Hemignathus virens), Hawai'i creeper (Oreomystis mana), Omao (Myadestes obscurus), and Palila (Loxioides bailleui), suggest that differences in life history cause some species to be more susceptible to local extinctions from the transmission of malaria. Modeling results demonstrated that rodent control at middle, but not high, elevations can facilitate the evolution of resistance to malaria in several species of Hawaiian birds. Advocating a

management approach that encourages evolutionary change in endangered species contrasts with the traditional conservation paradigm but it may be the best strategy to reduce the impacts of one of the multiple stressors that have devastated the native bird community of Hawai'i.
Keywords: Management; Endangered species; Drepanidinae; Rodent control; Demography; Survival; Reproduction

M. Van Loock, K. Loots, S. Van de Zande, M. Van Heerden, H. Nauwynck, B.M. Goddeeris, D. Vanrompay, Pathogenic interactions between Chlamydophila psittaci and avian pneumovirus infections in turkeys, Veterinary Microbiology, Volume 112, Issue 1, 10 January 2006, Pages 53-63, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2005.10.013.
(http://www.sciencedirect.com/science/article/B6TD6-4HPD3R3-1/2/8f194aa32e7b5bbd7db89bbdbbe15f8a)
Abstract:
Both Chlamydophila psittaci and avian pneumovirus (APV) are highly prevalent in Belgian turkeys and might contribute to the respiratory disease complex observed in turkeys. Initial outbreaks of chlamydiosis occur mostly at the age of 4-8 weeks, often accompanied by an APV infection in APV non-vaccinated farms. Regardless APV vaccination, breakthroughs of APV infection from 8 weeks on do occur, a period when also a second C. psittaci infection appears. Therefore, this study examined the pathogenicity of an APV superinfection in C. psittaci predisposed turkeys. Turkeys were infected with C. psittaci, APV or with C. psittaci followed by APV. Simulating the impact of an APV infection during the acute phase or latent phase of a C. psittaci infection, turkeys have been infected with APV at 1 and 5 weeks post C. psittaci infection, respectively.
APV infection during the acute phase of a C. psittaci infection aggravates the severity of clinical signs, macroscopic lesions, pharyngeal APV excretion and histological tracheae lesions. In contrast, no clear interaction could be established after APV infection in latently C. psittaci infected specific pathogen-free (SPF) turkeys. This study clearly demonstrates the exacerbating role of APV during acute C. psittaci infection, which can play an important role in the respiratory disease complex of turkeys.
Keywords: Chlamydophila psittaci; Avian pneumovirus; Turkeys; Respiratory disease complex

William B. Monahan, Walter D. Koenig, Estimating the potential effects of sudden oak death on oak-dependent birds, Biological Conservation, Volume 127, Issue 2, January 2006, Pages 146-157, ISSN 0006-3207, DOI: 10.1016/j.biocon.2005.08.005.
(http://www.sciencedirect.com/science/article/B6V5X-4H3JJJ1-4/2/094a00f1ee734fa7a164305e1d8a8e7d)
Abstract:
Sudden oak death (SOD), a disease induced by the fungus-like pathogen Phytophthora ramorum, threatens to seriously reduce or eliminate several oak species endemic to the west coast of North America. We investigated how the disappearance of one of these species, coast live oak (Quercus agrifolia), may affect populations of five resident oak-affiliated California birds - acorn woodpecker (Melanerpes formicivorus), Nuttall's woodpecker (Picoides nuttallii), Hutton's vireo (Vireo huttoni), western scrub-jay (Aphelocoma californica), and oak titmouse (Baeolophus inornatus) - using geocoded data from Audubon Christmas Bird Counts, North American Breeding Bird Surveys, and the California Gap Analysis. Capitalizing on observed relationships between the focal bird species and both oak species diversity and areal extent, we modeled relative bird abundance while assuming complete loss of Q. agrifolia and complete, partial, or no loss of oak habitat following a disease sweep. Post-SOD projections of bird populations occurring within the range of coast live oak were on average 25-68% smaller and 13-49% more variable relative to pre-SOD estimates. SOD effects were greatest for habitats with low initial oak species diversity. Climatic SOD models predicted that the disease stands to negatively impact populations of all five focal bird species throughout 20% of California's coast live oak habitats. This study provides the first spatially explicit

insights into the potential effects of SOD on avian distribution and abundance. Results may be used to help prioritize conservation plans aimed at minimizing overall community level disturbances resulting from the disease.
Keywords: California birds; Sudden oak death; Quercus agrifolia; Oak woodlands

Jameson F. Chace, John J. Walsh, Urban effects on native avifauna: a review, Landscape and Urban Planning, Volume 74, Issue 1, 1 January 2006, Pages 46-69, ISSN 0169-2046, DOI: 10.1016/j.landurbplan.2004.08.007.
(http://www.sciencedirect.com/science/article/B6V91-4DW37D9-2/2/97cb0d7eb9639bfa290b17ea5068073f)
Abstract:
The effect of urbanization can be immense, yet our understanding is rudimentary. Here, we compile the most recent information on urban impacts on avian populations and communities. Compared to other vertebrates, birds are easily monitored by skilled observers and provide a mechanism to explore urban effects and responses to different urban designs. Taxonomically, bird communities in distinctly different habitats are most different in the least disturbed sites and the most similar in the most urbanized sites. Urbanization tends to select for omnivorous, granivorous, and cavity nesting species. Increased urbanization typically leads to an increase in avian biomass but a reduction in richness. Unlike most passerines, raptors may have home ranges that extend beyond the urban boundary and therefore do not need to meet all their ecological requirements within urban areas. Urban habitats are often of superior quality to raptors because there they are often free from persecution and have an adequate food supply. The processes that underlie the patterns of population and community level responses need more attention, but several areas of have been identified as being important. Birds respond to vegetation composition and structure, and urban areas that retain native vegetative characteristics retain more native species than those that do not. Avian fecundity in urban areas is a reflection of species-specific adaptability to urban resources, and to levels of nest predation and nest parasitism. Additionally, non-consumptive human activities that increase with urbanization are recognized as having negative impacts on avian populations and communities. Avian survivorship in urban areas is influenced by risk of collision with man-made objects, changes in the predator assemblage, food supply, and disease. Missing are thorough investigations in the regions of highest human population growth, e.g. Southeast Asia. Additionally, there is a paucity of information from regions of high avian diversity, e.g. tropical forests. Clearly, local knowledge and study is required before implementation of management policies to reduce urban impacts on bird communities. Hopefully, such policies will include long-term monitoring. Demographic parameters of fecundity and survivorship need to be examined in conjunction with measures of community diversity and density across the urban gradient to better understand the quality of different urban habitats, and the variation of quality among spatial patterns of urbanization within the native habitat matrix.
Keywords: Avian ecology; Birds; Landscape ecology; Urban planning; Urbanization

A. Kijlstra, I.A.J.M. Eijck, Animal health in organic livestock production systems: a review, NJAS - Wageningen Journal of Life Sciences, Volume 54, Issue 1, 2006, Pages 77-94, ISSN 1573-5214, DOI: 10.1016/S1573-5214(06)80005-9.
(http://www.sciencedirect.com/science/article/B94T2-4WFBS5K-5/2/cfb59ccbd82d6a8229a7d6c475f5431e)
Abstract:
Organic livestock production is a means of food production with a large number of rules directed towards a high status of animal welfare, care for the environment, restricted use of medical drugs and the production of a healthy product without residues (pesticides or medical drugs). The intentions of organic livestock production have been formulated by the International Federation of Organic Agriculture Movements (IFOAM) and were further implemented by EU regulation 2092/91

in the year 2000. The consequences of these rules for the health of the animals were not yet fully anticipated at the time these regulations were made and it has become clear that in some cases the rules are not clear enough, thereby even hampering the development of the production system. In this review we shall discuss the implications of these rules for animal health, whereby we shall focus on pig, poultry and dairy production systems. Disease prevention in organic farming is based on the principles that an animal that is allowed to exhibit natural behaviour is not subject to stress, is fed optimal (organic) feed, and will have a higher ability to cope with infections than animals reared in a conventional way. Fewer medical treatments would thus be necessary and if an animal would become diseased, alternative treatments instead of conventional drugs should be preferred. Although homeopathy or phytotherapy are recommended according to prevailing regulations, not many organic farmers use this treatment regimen because of lack of scientific evidence of effectiveness. Important health problems in organic livestock farming are often related to the outdoor access area, exposing the animals to various viral, bacterial and parasitic infections some of which may only influence the animals' own welfare whereas other ones may also endanger the health of conventional livestock (e.g. Avian Influenza) or pose a food safety (Campylobacter, Toxoplasma) problem to the consumer. Many preventive measures can be taken, such as using better animal breeds, optimized rearing conditions, pre- and probiotics, and addition of acids to the drinking water. In case of infectious disease, tight vaccination schedules may prevent serious outbreaks.
Keywords: organic production; homeopathy; infectious disease

G. Koch, A.R.W. Elbers, Outdoor ranging of poultry: a major risk factor for the introduction and development of High-Pathogenicity Avian Influenza, NJAS - Wageningen Journal of Life Sciences, Volume 54, Issue 2, 2006, Pages 179-194, ISSN 1573-5214, DOI: 10.1016/S1573-5214(06)80021-7.
(http://www.sciencedirect.com/science/article/B94T2-4WFBS65-6/2/def70d02ff1c7dbd022d4ce707f519d8)
Abstract:
High-Pathogenicity Avian Influenza (HPAI) is an extremely infectious viral disease of poultry. Public health concerns were raised when six persons died in Hong Kong in 1997 after exposure to HPAI-infected poultry. Its danger became imminent in the recent HPAI epidemic in South-East Asia when the virus expanded its geographical range via parts of central Asia to Europe, Africa and the Middle East. Wild birds are frequently carriers of influenza A viruses. Nearly all Avian Influenza (AI) viruses isolated from wild birds are low-pathogenic and cause no clinical problems in these birds. Only after low-pathogenicity viruses are introduced in poultry, in particular in chickens and turkeys, high-pathogenicity mutants emerge after a variable length of time. Biosecurity is the first line of defence against an introduction of AI into commercial poultry flocks. Any conceivable contact between possibly contaminated animals, areas around poultry houses contaminated with faecal material from wild birds and contaminated abiotic vectors on the one hand and domestic poultry on the other must be avoided. In this paper we shall discuss the worldwide occurrence of HPAI outbreaks, the existence of AI virus infections in wild birds, and possible strategies to reduce the risk of the introduction of AI viruses into domestic poultry flocks, with special reference to free ranging.
Keywords: wild birds; public health risk; Avian Influenza ecology

Matthew J. Wood, Catherine L. Cosgrove, The hitchhiker's guide to avian malaria, Trends in Ecology & Evolution, Volume 21, Issue 1, January 2006, Pages 5-7, ISSN 0169-5347, DOI: 10.1016/j.tree.2005.11.001.
(http://www.sciencedirect.com/science/article/B6VJ1-4HJS54S-3/2/b02c5c8d16f0984b67b2098e56140c02)
Abstract:

The ecological mechanisms underlying the dispersal of parasites are poorly understood, which is of particular concern in view of currently emerging infectious diseases. In a new study, Perez-Tris and Bensch examined the distribution and prevalence of avian malaria in a migratory bird across Western Europe. They concluded that repeated independent evolution of year-round transmission has enabled some avian malaria lineages to become more widespread, and more prevalent, than lineages that are transmitted only during the summer. This study blurs the boundaries of evolutionary ecology, epidemiology and macroecology with great potential for cross-disciplinary research.

Nicole L. Gottdenker, Timothy Walsh, Hernan Vargas, Jane Merkel, Gustavo U. Jimenez, R. Eric Miller, Murray Dailey, Patricia G. Parker, Assessing the risks of introduced chickens and their pathogens to native birds in the Galapagos Archipelago, Biological Conservation, Volume 126, Issue 3, December 2005, Pages 429-439, ISSN 0006-3207, DOI: 10.1016/j.biocon.2005.06.025.
(http://www.sciencedirect.com/science/article/B6V5X-4GX6J54-1/2/b011bc8aa4a5645671e80a61ef2d4be4)
Abstract:
Poultry production is an important economic activity on inhabited islands of the Galapagos archipelago. There has been a recent surge in both small-scale backyard chickens and larger scale broiler production associated with growth in the human population and the tourist industry. With increased poultry production, concerns have been expressed about the increasing risk of transfer of disease from chickens to native Galapagos bird species that may have little resistance to introduced pathogens [Wikelski, M., Foufopoulos, J., Vargas, H., Snell, H., 2004. Galapagos birds and diseases: invasive pathogens as threats for island species. Ecology and Society 9(5). Available from: URL:http://www.ecologyandsociety.org/vol9/iss1/art5]. This study evaluates risks posed by chicken disease to endemic and native Galapagos bird species, based on empirical evidence of pathogens present in chickens on the islands and a literature review of effects of these pathogens in wild species. Pathogens identified in domestic chicken populations of immediate avian conservation concern are Newcastle disease, Mycoplasma gallisepticum, and the proventricular parasite Dispharynx sp. Newcastle disease (avian paramyxovirus-1) poses an imminent threat to Galapagos penguins (Spheniscus mendiculus), flightless cormorants (Phalacrocorax harrisi), and lava gulls (Larus fuliginosus), species with very small population sizes (less than 1500 animals each). Additionally, litter from broiler farms could affect ecological processes in local ecosystems. Improved poultry biosecurity measures are urgently needed on the Galapagos Islands for avian disease management, yet developing these strategies presents political, social, and economic challenges.
Keywords: Galapagos islands; Native birds; Avian conservation; Pathogens; Chickens; Gallus gallus; Disease risk

Robert M. May, Infectious Disease: Can We Avert a Lethal Flu Pandemic?, Current Biology, Volume 15, Issue 22, 22 November 2005, Pages R922-R924, ISSN 0960-9822, DOI: 10.1016/j.cub.2005.10.063.
(http://www.sciencedirect.com/science/article/B6VRT-4HM7R39-D/2/0b05dd46e5554381594d841e255aab5f)
Abstract:
If avian flu becomes directly transmissible among humans, could we prevent a pandemic by using prophylactic antivirals? Possibly, if the virus is not too transmissible, and we react fast and efficiently.

Carita Schneitz, Competitive exclusion in poultry--30 years of research, Food Control, Volume 16, Issue 8, 7th Karlsruhe Nutrition Congress on Food Safety, October 2005, Pages 657-667, ISSN 0956-7135, DOI: 10.1016/j.foodcont.2004.06.002.

(http://www.sciencedirect.com/science/article/B6T6S-4D0Y3XG-1/2/f524fcddddf035e8333b125af42298d6)

Abstract:
The most effective and harmless method available to control intestinal disturbances in poultry is competitive exclusion or CE. The treatment is fully biological, it does not leave any residues and only one treatment on the day-of-hatch is normally enough. The concept was originally designed for Salmonella reduction in growing chickens but has with time been expanded to involve several other enteropathogens like chicken and human pathogenic Escherichia coli, Clostridium perfringens, Listeria and Campylobacter. The chicken intestinal flora has further been shown to be efficacious also in other avian species like turkey, quail and pheasant. Very little is known about the mechanism itself. Protection depends upon the administration of viable anaerobic bacteria and the two most often cited mechanisms are production of volatile fatty acids in the caeca, and occupation of sites on the mucosa. The CE treatment is applied either by spraying in the hatchery or on the farm or via the first drinking water on the farm. The treatment has also been given successfully to older birds after therapeutic doses of antibiotics to regenerate the intestinal microflora.
In addition to pathogen control, it has been shown in field studies that CE treatment enhances the growth and decreases the mortality of birds and improves the feed conversion. The nutritional effects of the treatment have been confirmed in well-controlled laboratory studies.
Research on CE has proceeded in many countries around the world already for 30 years since the first article in Nature in 1973 by Nurmi and Rantala and several commercial CE products have been developed.
Among factors that can affect the efficacy of the CE treatment are antimicrobials, stress and disease, moulting and feed withdrawal and infected breeders and contaminated hatchery area.
Keywords: Competitive exclusion; Poultry; Salmonella

Chun Xia, Tuanjun Hu, Tianyao Yang, Li Wang, Guangxian Xu, Changyou Lin, cDNA cloning, genomic structure and expression analysis of the goose (Anser cygnoides) MHC class I gene, Veterinary Immunology and Immunopathology, Volume 107, Issues 3-4, 15 September 2005, Pages 291-302, ISSN 0165-2427, DOI: 10.1016/j.vetimm.2005.05.005.
(http://www.sciencedirect.com/science/article/B6TD5-4GJV9YM-1/2/1ae599d1caa50cc52dc58686f8ce37fb)

Abstract:
To provide data for studies on avian disease resistance, goose MHC class I cDNA (Ancy-MHC I) was cloned from a goose cDNA library, it's genomic structure and expression analysis were investigated. The mature peptides of Ancy-MHC I cDNA encoded 333 amino acids. The genomic organization is composed of eight exons and seven introns. Based on the genetic distance, six Ancy-MHC I genes from six individuals can be classified into four lineages. A total of nineteen amino acid positions in peptide-binding domain showed high scores by Wu-kabat index analysis. The Ancy-MHC I amino acid sequence displayed seven critical HLA-A2 amino acids that bind with antigen polypeptides, and have an 85.4-98.9% amino acid homology with each genes, and a 59.8-66.0% amino acid homology with chicken MHC class I. Expression analyses using Q-RT-PCR to detect the tissue-specific expression of Ancy-MHC I mRNA in an adult goose. The result appeared that Ancy-MHC I cDNA was expressed in the liver, spleen, intestine, kidney, lung, pancreas, heart, brain, and skin. The phylogenetic tree appears to branch in an order consistent with accepted evolutionary pathways.
Keywords: Goose; MHC class I; Genome structure; Polypeptide binding domain; Expression analysis

Mohammad Q. Al-Natour, Mahmoud N. Abo-Shehada, Sero-prevalence of avian influenza among broiler-breeder flocks in Jordan, Preventive Veterinary Medicine, Volume 70, Issues 1-2, 12 August 2005, Pages 45-50, ISSN 0167-5877, DOI: 10.1016/j.prevetmed.2005.02.009.
(http://www.sciencedirect.com/science/article/B6TBK-4FS2378-2/2/9adbd55c202915e7dc255ae33ead0513)
Abstract:
Thirty blood samples were collected randomly from each of the 38 breeder-broiler farms in Jordan. Serum samples were examined using indirect ELISA for specific antibodies to avian influenza virus. The overall true flock-level sero-prevalence of avian influenza was 71% (95% CI: 55,83). Positive flocks had 2-30 sero-positive chickens and half of flocks had >20 sero-positive birds. The number of sero-positive flocks varied in the studied localities with more sero-positives in farms located within the migratory route of migratory wild fowl. The examined broiler-breeder flocks had no clinical signs, or noticeable decrease in egg production; mortalities were within the normal range (0.1-1%). The number of positive sera/flock correlated with flock size. There were a no significant (Pearsons r = 0.21, p = 0.21) correlation between positive flocks and age. A non-pathogenic AI virus infects broiler-breeder farms in Jordan. Wild local and migrating birds might promote the further spread of this virus in Jordan and other countries.
Keywords: Avian influenza; Poultry; Viral diseases; Broiler-breeder; ELISA; Age influence; Jordan

C.W. Canal, J.A. Leao, S.L.S. Rocha, M. Macagnan, C.A.V. Lima-Rosa, S.D. Oliveira, A. Back, Isolation and characterization of Ornithobacterium rhinotracheale from chickens in Brazil, Research in Veterinary Science, Volume 78, Issue 3, June 2005, Pages 225-230, ISSN 0034-5288, DOI: 10.1016/j.rvsc.2004.10.003.
(http://www.sciencedirect.com/science/article/B6WWR-4F1GYWB-4/2/defd309b8396895952f15167be6f77d1)
Abstract:
Ornithobacterium rhinotracheale (ORT) is a recently described species of bacterium associated with respiratory disease, growth retardation, mortality, and decreased egg production in chickens and turkeys. Pneumonia, pleuritis, and airsacculitis characterise the infection. ORT has been isolated in many countries but it is still considered exotic in Brazil. Up to date it is prohibited to import and produce reagents for diagnostic and vaccination control. The aim of this study was to isolate and identify the bacteria in chickens. Four isolates were obtained from tracheal swabs of broilers. They were isolated in blood agar with gentamicin and showed biochemical, morphological, antigenic and genetic characteristics of ORT. The results confirm that ORT is present in Brazil.
Keywords: Ornithobacterium rhinotracheale; Avian pathology; Isolation; Indentification; Respiratory disease; Chicken

M. Van Loock, T. Geens, L. De Smit, H. Nauwynck, P. Van Empel, C. Naylor, H.M. Hafez, B.M. Goddeeris, D. Vanrompay, Key role of Chlamydophila psittaci on Belgian turkey farms in association with other respiratory pathogens, Veterinary Microbiology, Volume 107, Issues 1-2, 25 April 2005, Pages 91-101, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2005.01.009.
(http://www.sciencedirect.com/science/article/B6TD6-4FJXN84-2/2/458f5bd52cfd5dac89f9d716aa28d9f7)
Abstract:
Two hundred turkey sera from eight Belgian and two French farms were tested for the presence of antibodies against avian pneumovirus (APV), Ornithobacterium rhinotracheale (ORT), Mycoplasma gallisepticum, Mycoplasma meleagridis and Chlamydophila psittaci. At slaughter, C. psittaci, APV and ORT antibodies were detected in 94, 34 and 6.5% of the turkeys, respectively. No antibodies against M. gallisepticum or M. meleagridis were present. Additionally, turkeys on three Belgian farms were examined from production onset until slaughter using both serology and

antigen or gene detection. All farms experienced two C. psittaci infection waves, at 3-6 and 8-12 weeks of age. Each first infection wave was closely followed by an ORT infection starting at the age of 6-8 weeks, which was still detectable when the second C. psittaci infection waves started. Animals on farm A were not vaccinated against APV leading to an APV subtype B outbreak accompanying the first C. psittaci infection wave. Despite subtype A APV vaccination on farms B and C, the second C. psittaci infection waves were accompanied (farm B) or followed (farm C) by a subtype B APV infection. On all farms respiratory signs always appeared together with a proven C. psittaci, APV and/or ORT infection. This study suggests an association between C. psittaci, APV and ORT, and indicates the multi-factorial aetiology of respiratory infections in commercial turkeys. All three pathogens should be considered when developing prevention strategies for respiratory disease.
Keywords: Chlamydophila psittaci; Seroprevalence; Avian pneumovirus; Ornithobacterium rhinotracheale

Tatiana Amabile de Campos, Eliana Guedes Stehling, Alessandra Ferreira, Antonio Fernando Pestana de Castro, Marcelo Brocchi, Wanderley Dias da Silveira, Adhesion properties, fimbrial expression and PCR detection of adhesin-related genes of avian Escherichia coli strains, Veterinary Microbiology, Volume 106, Issues 3-4, 10 April 2005, Pages 275-285, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2004.12.025.
(http://www.sciencedirect.com/science/article/B6TD6-4FK42JP-1/2/9fa4350b6e18391622f131fcceac679e)
Abstract:
Forty-nine avian pathogenic Escherichia coli (APEC) strains obtained from chickens suffering from septicemia (24), swollen head syndrome (14) and omphalitis (11), isolated from individuals in different regions of Brazil and from different outbreaks, were studied for their adhesion to trachea epithelial cells, fimbrial expression and hemagglutination capacity to different erythrocyte types. These results were compared with their content of fimbriae-related genes as detected by polymerase chain reaction (PCR) using specific pair of primers. The aim of these assays was to determine the importance of expression of adhesins in the pathogenic strains and to evaluate the presence of adhesin genes either previously described or not yet recognized for APEC strain. Thirty commensal strains isolated from poultry showing no signs of any of the above diseases were used to compare the results with the pathogenic isolates. The PCR assay demonstrated that septicaemic and swollen head syndrome strains had the highest number of adhesion-related genes of recognized importance in pathogenicity. Using different media for growth conditions, 40 different d-mannose resistant haemagglutination patterns were observed in this study, what indicates the expression of a great variability of surface agglutinins in these bacterial strains. Our results also showed that adhesion, whether d-mannose resistant (MRA) or d-mannose sensitive (MSA), is a characteristic observed in both pathogenic and commensal strains. Several strains with positive adherence had no genetic sequences related to the studied adhesin genes what indicates that our APEC strains probably possess a genome with adhesins genes besides those describe elsewhere and that have not yet been described.
Keywords: Avian; Escherichia coli; Adhesion; Fimbriae; Pathogencity

Bruce S. Seal, Mark G. Wise, Janice C. Pedersen, Dennis A. Senne, Rene Alvarez, Melissa S. Scott, Daniel J. King, Qingzhong Yu, Darrell R. Kapczynski, Genomic sequences of low-virulence avian paramyxovirus-1 (Newcastle disease virus) isolates obtained from live-bird markets in North America not related to commonly utilized commercial vaccine strains, Veterinary Microbiology, Volume 106, Issues 1-2, 20 March 2005, Pages 7-16, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2004.11.013.
(http://www.sciencedirect.com/science/article/B6TD6-4FBWHBR-1/2/3b19f9777ee6bc1166546a548f9890e8)

Abstract:
Avian paramyxovirus 1 (APMV-1), also referred to as Newcastle disease virus (NDV), variants of low virulence were isolated from chickens, ducks and other unidentified species found in live-bird markets of the northeastern United States. These isolates were characterized as APMV-1 by the hemagglutination-inhibition (HI) assay utilizing NDV-specific polyclonal antisera. However, the isolates failed to react with a monoclonal antibody that has specificity for a wide variety of APMV-1 isolates. Although only highly virulent isolates require reporting to international regulatory agencies, the ability to correctly identify APMV-1 types is important for control and regulatory purposes. Protein gel patterns of the purified isolates resembled previously reported APMV-1 and anti-NDV polyclonal sera recognized the viral proteins. For three isolates oligonucleotide primers specific for the nucleoprotein, fusion protein and polymerase genes of NDV were utilized to synthesize cDNA using viral RNA as a template. Approximately 12 kb of the genome was subsequently sequenced for the three isolates that included the nucleoprotein, phosphoprotein, matrix protein, fusion (F) protein, hemagglutinin-neuraminidase protein genes and a 5' portion of the polymerase gene. The isolates had an F protein cleavage site sequence of ERQER/LVG indicating low-virulence viruses that phylogenetically separated with other unique NDV isolates designated as a lineage 6 genotype. Additionally, a four amino acid insert was detected in the predicted phosphoprotein which complies with the 'rule of six' among paramyxoviruses. These APMV-1 genotypes have not been previously reported in North America and further substantiate the heterogeneous genetic nature of these commercially important pathogens found worldwide.
Keywords: Veterinary medicine; Emerging diseases; Molecular epidemiology; Mononegavirales

M. Machackova-Kopecna, M. Bartos, M. Straka, V. Ludvik, P. Svastova, J. Alvarez, J. Lamka, I. Trcka, F. Treml, I. Parmova, I. Pavlik, Paratuberculosis and avian tuberculosis infections in one red deer farm studied by IS900 and IS901 RFLP analysis, Veterinary Microbiology, Volume 105, Issues 3-4, 25 February 2005, Pages 261-268, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2004.11.008.
(http://www.sciencedirect.com/science/article/B6TD6-4F9N6YK-1/2/6ff4c6dcc6cb484e51ec32219fa2cef0)
Abstract:
As the attempt to eradicate paratuberculosis in one red deer (Cervus elaphus) farm failed, all 167 red deer of different age groups were slaughtered and examined by culture for mycobacteria, and the farm was closed down. Spleen and hepatic lymph nodes, mediastinal lymph node, ileocecal lymph node, and ileum were collected from each animal and examined (a total of 835 organs). Neither tuberculosis lesions nor pathognomic signs of paratuberculosis were detected. Among all microscopically negative for mycobacteria organs, Mycobacterium avium subsp. paratuberculosis alone was isolated from 165 organs, M. a. avium alone from 41 organs, and both pathogens from four organs. M. a. paratuberculosis alone was detected in 71 red deer, M. a. avium alone in 13 red deer and both pathogens in 18 red deer. Using standardised RFLP methods, three IS900 RFLP types B-C1, B-C16, and B-C32 were identified among 40 M. a. paratuberculosis isolates and four IS901 RFLP types N-B1, N-B3, N-B4, and P-B3 among 17 M. a. avium isolates.
Keywords: Johne's disease; Zoonoses; Risk assessment; Epidemiology; Small terrestrial vertebrates

Markus Rahaus, Manfred H. Wolff, A survey to detect subclinical polyomavirus infections of captive psittacine birds in Germany, Veterinary Microbiology, Volume 105, Issue 1, 5 January 2005, Pages 75-78, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2004.09.016.
(http://www.sciencedirect.com/science/article/B6TD6-4DV1K2S-3/2/6a77c1bbb95ca1eecaf2b0291e2469d0)
Abstract:

Infections of avian polyomavirus (APV) are known to cause fatal disease in a wide range of psittacine and non-psittacine birds. Here, we present a survey to investigate the existence of subpopulation of persistent or subclinically infected parrots inside the population of captive psittacine birds in Germany. DNA was isolated from feathers of 85 symptom-free birds from 20 different genera (all psittaciformes) taken from 30 different breeders from all over Germany. The presence of APV was analysed by performing polymerase chain reaction assays (PCR). APV was detected in none of the samples, indicating that the existence of a subpopulation of captive psittacine birds having a persistent APV infection in Germany seems to be relatively low.
Keywords: APV; PCR; Psittaciformes; Epidemiological study

Esther Shihmanter, A. Panshin, M. Lipkind, Nucleotide sequence of the matrix protein gene of avian paramyxovirus, serotype 3b: evidence on another member of the suggested new genus of the subfamily Paramyxovirinae, Comparative Immunology, Microbiology and Infectious Diseases, Volume 28, Issue 1, January 2005, Pages 37-51, ISSN 0147-9571, DOI: 10.1016/j.cimid.2004.03.010.
(http://www.sciencedirect.com/science/article/B6T5H-4CGNRDN-1/2/747db3a20da769c23f61849479927c58)
Abstract:
The complete nucleotide sequence of the gene encoding the matrix protein (M) of the avian paramyxovirus, serotype 3b (APMV-3b), has been determined by means of the direct sequencing of viral RNA using reverse transcriptase reaction. The adjacent portions of the neighboring phosphoprotein (P) and fusion (F) protein genes were also sequenced that permitted to determine the consensus sequence of the viral genome, the poly(A) tract, downstream and upstream non-coding portions of the P and F genes, respectively, as well as the corresponding intergenic regions. The gene is 1478 nucleotides long with a protein-coding sequence of 1194 nucleotides. The deduced protein consists of 398 amino acids with a calculated MW 44,465. According to the multalignment and phylogenetic analyses, the APMV-3b M protein has shown the closest relatedness towards Newcastle disease virus (NDV) which has recently been suggested to be excluded from the Rubulavirus genus and assigned (together with APMV-6) to a new Avulavirus genus within the subfamily Paramyxovirinae of the Paramyxoviridae family. On the basis of the M protein genetic multalignment, phylogenetic relationships, bipartite nuclear localization signal identification in combination with the cysteine residues distribution, and by the degree of intrageneric heterogeneity, the APMV-3b is proposed to be another member (together with NDV and APMV-6) of the new genus.
Keywords: Avian paramyxovirus; Matrix protein gene; Sequencing; Avulavirus

O. A. Fischer, L. Matlova, L. Dvorska, P. Svastova, D. L. Peral, R. T. Weston, M. Bartos, I. Pavlik, Beetles as possible vectors of infections caused by Mycobacterium avium species, Veterinary Microbiology, Volume 102, Issues 3-4, 8 September 2004, Pages 247-255, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2004.06.005.
(http://www.sciencedirect.com/science/article/B6TD6-4D0NJC9-2/2/c59a034471ab244c9ea57895de9ca220)
Abstract:
Mycobacteria were not isolated from any of 229 beetle imagoes of 29 species originating from 14 distinct localities in the Czech and Slovak Republics: 186 imagoes (34 samples) and 43 imagoes (12 samples) from the wild and herds with paratuberculosis infected ruminants, respectively. From 75 environmental samples taken from barns with infected ruminants, Mycobacterium avium subsp. paratuberculosis was isolated from five scrapings of the floors in barns and a feed processing room. From bran and peat taken from pig farms, M. a. hominissuis was diagnosed in 13% of 72 samples and in 69% of 70 samples, respectively. M. a. avium was isolated from 2 (2.9%) and atypical mycobacteria from 12 (17.1%) peat samples. In the respective experiments, larvae of

Tenebrio molitor Linnaeus and Zophobas atratus Fabricius were infected in vitro with isolates of M. a. paratuberculosis of IS900 RFLP type B-C1 and M. a. avium of IS901 RFLP type F-C3. T. molitor larvae were also infected with M. a. hominissuis by naturally contaminated bran and peat. M. a. paratuberculosis and M. a. avium were diagnosed in larvae of both species on days 1 to 3 post infection (p.i.). M. a. hominissuis was isolated from T. molitor larvae fed by bran on days 4 to 9 p.i. and from imagoes on day 35 p.i. and from larvae fed by peat on days 4 to 14 p.i. RFLP types of all the isolates identified before infection and after isolation from larvae were identical. Thus, beetles could mechanically transmit mycobacteria, this hazard should be considered for both the implementation of control measures and feeding captive animals with larvae.
Keywords: Zoonoses; Avian tuberculosis; Johne's disease; Mycobacterium avium complex

F. J. Vandemaele, S. M. Hensen, B. M. Goddeeris, Conservation of deduced amino acid sequence of FimH among Escherichia coli of bovine, porcine and avian disease origin, Veterinary Microbiology, Volume 101, Issue 2, 21 June 2004, Pages 147-152, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2004.03.013.
(http://www.sciencedirect.com/science/article/B6TD6-4CDJF89-1/2/a38745b97933dc7a38bdccc128c92a39)
Abstract:
The FimH subunit of type 1 pili mediates adhesion of Escherichia coli to epithelium in different animal hosts. In this study, we sequenced and analyzed the fimH genes of 24 E. coli strains from bovine and porcine clinical cases. The obtained sequences were compared among each other and also with 24 known fimH sequences from avian E. coli strains. This comparison revealed a substantial homology (>99%) among strains from the different animal species origins. Moreover, specific mutations were found, some of which were present more frequently in avian strains or in bovine and porcine strains.
Keywords: Escherichia coli; FimH; Cattle-bacteria; Pig-bacteria; Species

A. K. Tiwari, R. S. Kataria, T. Nanthakumar, B. B. Dash, G. Desai, Differential detection of Newcastle disease virus strains by degenerate primers based RT-PCR, Comparative Immunology, Microbiology and Infectious Diseases, Volume 27, Issue 3, May 2004, Pages 163-169, ISSN 0147-9571, DOI: 10.1016/j.cimid.2003.09.002.
(http://www.sciencedirect.com/science/article/B6T5H-4B0WG01-2/2/728fed91eaef9723286f4fdc7605ee67)
Abstract:
Degenerate primers based RT-PCR (previously described by [Avian Dis 26 (1997) 837]) has been used for the detection and differentiation of Newcastle disease (ND) viruses. Two sets of primers (A+B and A+C), with common forward primer and distinct reverse degenerate primers, designed from fusion protein gene encoding for cleavage site, could differentiate virulent and avirulent Newcastle disease viruses (NDV). Both sets of primers amplified `F' gene sequence of virulent (velogenic and mesogenic) viruses, whereas in avirulent strains, amplification was only with primer set A+C. Total 10 NDV isolates and two clinical samples including both known and unknown pathotypes, were checked. Based on amplification results 5 viruses were found to be virulent type and 6 as avirulent with one of the two clinical samples, earlier positive by RT-PCR using non-degenerate `F' gene specific primers was found negative in this study. The technique has been found to be a simple and quick for the detection and differentiation of virulent and avirulent NDV, which is important for control of the disease in the events of the outbreaks.
Keywords: Newcastle disease virus; Differentiation; F gene; Degenerate primers; RT-PCR

Robert L. Davies, Roslyn MacCorquodale, Sharon Reilly, Characterisation of bovine strains of Pasteurella multocida and comparison with isolates of avian, ovine and porcine origin, Veterinary

Microbiology, Volume 99, Issue 2, 5 April 2004, Pages 145-158, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2003.11.013.
(http://www.sciencedirect.com/science/article/B6TD6-4CT19H6-1/2/87ce739b4ee775028c4b356e5025c41f)
Abstract:
One hundred and fifty-three bovine Pasteurella multocida strains recovered primarily from cases of pneumonia and mastitis in England and Wales over an 11-year period were characterised by capsular PCR typing, comparison of outer membrane protein (OMP) profiles, and multilocus sequence analysis. All of the strains were of capsular type A with the exception of a single capsular type F isolate. Thirteen distinct OMP profiles (OMP-types) were identified based mainly on molecular mass heterogeneity of the heat-modifiable (OmpA) and porin (OmpH) proteins. However, 85% of the isolates were represented by just five OMP-types and 39% of the strains were of a single OMP-type. Multilocus sequence analysis revealed a limited degree of genetic diversity among bovine P. multocida isolates; strains of the same OMP-type have identical genetic backgrounds and represent distinct clones. Analysis of OMP variation was more discriminating than multilocus sequence analysis because strains of different OMP-types had the same, or similar, genetic backgrounds. The association of a small number of clones with the majority of cases of bovine pneumonia suggests that these clones have an increased capacity to cause disease compared to less frequently recovered clones. Molecular mass heterogeneity of OmpA and OmpH, in strains of the same or similar genetic background, suggests that these proteins are subject to diversifying selection within the host and might play important roles in host-pathogen interactions. Comparison of the OMP profiles of bovine isolates with those of avian, ovine and porcine strains showed that a high proportion of the respiratory tract infections in each of these species are caused by different strains of P. multocida. However, the presence of small numbers of closely related strains in more than one host species suggests that transmission of bacteria between different host species is also a factor in the population biology of P. multocida.
Keywords: Pasteurella multocida; Outer membrane proteins; Multilocus sequence analysis

Daniel Todd, Avian circovirus diseases: lessons for the study of PMWS, Veterinary Microbiology, Volume 98, Issue 2, ssDNA Viruses of Plants, Birds, Pigs and Primates, 4 February 2004, Pages 169-174, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2003.10.010.
(http://www.sciencedirect.com/science/article/B6TD6-4BBMTSJ-2/2/5432e34542522f94988d115aa25f45f4)
Abstract:
The diseases associated with psittacine beak and feather disease virus (BFDV), pigeon circovirus (PiCV) and goose circovirus (GoCV), which can be classified with porcine circovirus type 2 (PCV2) as members of the genus Circovirus of the family Circoviridae, have clinico-pathological features in common with post-weaning multisystemic wasting syndrome (PMWS), with which PCV2 infection is causally associated. Intracytoplasmic botryoid inclusions within macrophages and depletion of T and B lymphocytes are common histopathological features, and, in each case, affected animals usually exhibit ill-thrift and a predisposition to secondary infections, that is suggestive of an underlying immunosuppression. Although these avian diseases have been the subjects of relatively little research, their study can provide directly applicable lessons in the areas of diagnosis, epidemiology, pathogenesis and disease control for those charged with investigating PMWS. In keeping with its taxonomic separation as the only member of the genus Gyrovirus, the disease caused by chicken anaemia virus (CAV) differs histopathologically from the other circovirus-associated diseases. Most notably, the target cells of CAV have been identified as haemocytoblasts and precursor T lymphocytes, with lymphocyte depletion, which affects T cells only, occurring in cells directly infected with the virus. Nonetheless, CAV is the best-researched circovirus and provides excellent examples of both virus-induced immunosuppression and virus-

virus interactions. The study of CAV-induced disease can therefore provide valuable, if less directly applicable lessons.
Keywords: Circoviruses; Avian circoviruses; Porcine circovirus; Pigeon circovirus; Goose circovirus; BFDV; CAV; PMWS

S. Kariyawasam, B. N. Wilkie, C. L. Gyles, Resistance of broiler chickens to Escherichia coli respiratory tract infection induced by passively transferred egg-yolk antibodies, Veterinary Microbiology, Volume 98, Issues 3-4, 5 March 2004, Pages 273-284, ISSN 0378-1135, DOI: 10.1016/j.vetmic.2003.10.022.
(http://www.sciencedirect.com/science/article/B6TD6-4BBHBP0-2/2/06f8929f98e99a1f5981ad4977aece06)
Abstract:
Egg-yolk antibodies induced by immunizing hens with selected Escherichia coli antigens were evaluated for their ability to protect broiler chickens against respiratory/septicemic disease caused by avian pathogenic E. coli (APEC). Seven groups of broiler breeder hens were vaccinated three times, 1 week apart with live E. coli, killed E. coli, E. coli antigens [lipopolysaccharide (LPS), type 1 pilus adhesin (FimH), P pilus adhesin (PapG), aerobactin outer membrane receptor (IutA)] or phosphate buffered saline (PBS). An O78 APEC strain was used for preparation of all the antigens. Egg yolk immunoglobulins (IgY) were purified from eggs of each group and antibody activity in serum and purified IgY was determined by enzyme-linked immunosorbent assay (ELISA). IgY (100 mg) was injected intramuscularly into 11-day-old broiler chickens, which were challenged 3 days later with homologous (O78) or heterologous (O1 or O2) E. coli by the intra-air sac route. Mortality was recorded and surviving chickens were euthanized 1 week after the challenge and examined for macroscopic lesions. Passive antibodies against all antigens except FimH were protective (90-100%) against the homologous challenge, but only anti-PapG and anti-IutA were effective against heterologous challenge. Anti-PapG IgY provided the greatest protection against the three serogroups of E. coli used for challenge. Hence vaccination of broiler breeders to induce anti-PapG and anti-IutA antibodies may provide passive protection of progeny chicks against respiratory/septicemic disease caused by APEC.
Keywords: Escherichia coli; Chickens; FimH; PapG; IutA; LPS; Egg; Antibodies; Vaccine