

RICERCHE EFFETTUATE SANITÀ ANIMALE

Alborali°GL, Varisco°G

Diagnostic monitoring in veterinary medicine in zoonotic agents

43rd National congress of the Italian Society of Microbiology : Naples, Italy, 27-30 September 2015 : abstract book / [s.l. : s.n., 2015]. - p 5 [Nr. Estr. 7032]

National congress of the Italian Society of Microbiology (SIM 2015) (43rd : Naples : 27-30 September 2015)

Introduction: Zoonoses are infections and diseases that are naturally transmissible directly, or indirectly via contaminated foodstuffs, between animals and humans. Zoonoses monitoring programmes and antimicrobial resistance surveillance are regulated by DL 191/2006 (2003/99/CE). *Campylobacter* spp., *Salmonella* spp., verocytotoxigenic *Escherichia coli* (VTEC), *Mycobacterium bovis*, *Brucella* control programmes and the diagnostic monitoring in Veterinary Medicine are reported Materials and Methods: European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC) reported in 2014 data on the occurrence of zoonoses and foodborne outbreaks in 2012. Diagnostic and control are related to the official methodology used by Official Veterinary Services (OVS) and Istituti Zooprofilattici Sperimentali (IZZSS). Results: Successful *Salmonella* spp. control programmes in poultry, through serology, microbiology tests and PCR in breeders in meat and eggs, has been leading to a decreasing trend in confirmed salmonellosis cases in humans with a total of 91,034 cases reported in 2012. As well as for *Salmonella* spp. *C. jejuni* and *C. coli* are monitored in specific control programme and samples are analyzed with microbiological specific medium and Polymerase Chain Reaction (PCR). Nevertheless the occurrence of *Campylobacter* continued to be high in broiler meat and *Campylobacteriosis* is still the most commonly reported zoonosis, with 214,268 confirmed human cases. VTEC infections affected humans as well as domestic and wild ruminants with a total of 5,671 cases is monitored in animal samples and food by microbiology, PCR and other methods (e.g. microarray, sequencing) and positivity are investigated to identify VTX genes. The serogroups considered important regarding pathogenicity in humans and cattle are O26, O91, O103, O111, O145 and O157. Tuberculosis and Brucellosis are monitored at farms level for their eradication. The programmes are based on intra vitam diagnosis; isolation and identification of *M. bovis* by PCR and serological tests in blood and milk (Complement fixation, agglutination test, ELISA) for *Brucella* antibody detection. The number of human tuberculosis cases due to *Mycobacterium bovis* was 125, and 328 of brucellosis in humans. The prevalence of tuberculosis in cattle increased while brucellosis prevalence in ruminants is decreased. Discussion and Conclusions: *Campylobacter* spp. and *Salmonella* spp. control programmes in poultry, Brucellosis and tuberculosis eradication programmes, VTEC monitoring in ruminants diagnostic and antimicrobial resistance monitoring by OVS are the focal point for the containment of the transmission of the main zoonotic agents from animals to human in Italy.

Amadori°M, Fusi°F, Bilato°D, Archetti°IL, Lorenzi°V, Bertocchi°L

Disease risk assessment by clinical immunology analyses in periparturient dairy cows

Res Vet Sci. - Vol. 102 (2015). - p 25-26. - 11 bib ref [Nr. Estr. 7034]

A disease prediction system was investigated in a case-control study in the dry period of high-yielding dairy cows. Blood samples of 75 cows from 26 herds were collected before calving between - 23 and - 33 days (T1) and also between - 2 and - 6 days (T2) to investigate a panel of clinical immunology and chemistry parameters. Cows with abnormal serum lysozyme and interleukin-6 concentrations showed a greater disease prevalence until the 60th day in milk compared with non-responder cows ($P < 0.05$ and lower at T1). Differences in disease prevalence were observed on the basis of T1 data, and also by combining the results at T1 and T2. The other laboratory parameters under study were not predictive of a disease risk. Results indicate that

environmental stressors in the dry period may cause a negative imprinting of the innate immune response, underlying predisposition to later disease occurrence.

Amadori°M, Zanotti°C

Immunoprophylaxis in intensive farming systems : the way forward

Immunity to Veterinary Pathogens: Informing Vaccine Development : Keystone Symposia on Molecular and Cellular Biology, January 20-25, 2015 Colorado, USA / [Silverthorne, CO : Keystone Symposia, 2015]. - (The 2014-2015 Keystone Symposia Meeting Series ; p 35 [Nr. Estr. 5963]

Keystone Symposia on Molecular and Cellular Biology : Keystone, Colorado, USA : January 20-25, 2015)

High levels of production in intensive farming systems are associated with increased replacement rates as a result of multifactorial diseases. The so-called "production diseases" may include low-grade infection reducing profitability without increased morbidity. Such infections are sustained by low pathogenic viral and bacterial agents which give rise to full-blown disease in association with poor environmental conditions. In these farms, the results of vaccination may be disappointing. Therefore, fundamental issues should be dealt with toward successful immunoprophylaxis: High lean meat and milk production are associated with chronic inflammation and activation of the innate immune system vis-à-vis cellular stress. This may negatively affect adaptive immune responses. A negative modulation of the host microbiome by farm management practices and drug treatments is a further risk factor. The immune response to stressed cells questions the usual correlates of protection investigated after vaccination. In particular, there is evidence that specific and non-specific immune responses may overlap in vitro as a result of: 1) a high level of cellular immune responses to Damage-Associated Molecular Patterns (DAMPs), 2) the constitutive expression of stress antigens in the established cell lines used for virus propagation and immunoassays. The type of immune response: a vigorous adaptive immune response to microbial agents may be sometimes counterproductive, as shown e.g. in the PRRS mode). Alternative outcomes should be sometimes pursued: a better homeostatic control of the inflammatory response, effective and self-limiting innate immune responses, and even tolerance induction. On the whole, successful immunoprophylaxis in intensive farming systems demands coordinated and multi-disciplinary efforts in terms of animal breeding, farm management and hygiene, correct choice and harmonization of the prophylactic tools (vaccines, immunomodulators, pre- and probiotics). Finally, there is evidence that disease-predicting parameters of the innate immune response may greatly ease the identification of animals at risk and contribute to reduced antibiotic usage on farm.

Aqel AA, Hailat E, Serrecchia L, Aqel S, Campese E, Vicari°N, Fasanella A

Molecular characterization of the circulating Bacillus anthracis in Jordan

Trop Anim Health Prod. - Vol. 47 (2015). - p 1621-1624. - 14 bib ref [Nr. Estr. 7175]

To understand the biomolecular characteristics of Bacillus anthracis in Jordan, 20 blood smear slides from dead animals with suspected anthrax were analyzed using conventional and molecular approaches. All slides were positive for B. anthracis by conventional staining but no growth of the organism on selective media was detected. However, of the 20 samples, 16 were B. anthracis DNA-positive using polymerase chain reaction (PCR). Seven samples provided enough quantity and quality of DNA, and their multilocus variable tandem repeat analysis (MLVA)-15 loci analysis revealed two different genotypes. All genotypes were belonging to A.B..r. 008/009 which is very common in Asia and Europe. Single nucleotide repeat (SNR) analysis revealed that there were no sub genotypes. Molecular diagnosis of animal anthrax in Jordan is not used routinely; henceforth, official diagnosis of anthrax is based on the observation of the slides by optical microscope and this can often cause reading errors. Therefore, the prevalence of the disease in Jordan might be slightly lower than that reported by the official bodies.

Banco B, Avallone G, Grieco V, Gelmetti^oD, Giudice C

Unusual multifocal pulmonary neoplastic lesions in a cat

Atti del LXIX Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : XII Convegno AIPVet, II Convegno RNIV, XV Convegno SICV, XIII Convegno SIRA, XI Convegno So.Fi.Vet : Perugia, 15-17 Giugno 2015 / [s.l. : s.n., 2015]. - p 341 [Nr. Estr. 7016]

Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : 69 Convegno AIPVet : 12 Convegno RNIV : 2 Convegno SICV : 15 Convegno SIRA : 13 Convegno So.Fi.Vet : 11 : Perugia : 15-17 Giugno 2015)

An 8 years old castrated male stray cat, daily fed and looked after by feral cat caretakers was found death near the feline colony where it lived. The body was referred to the University of Milan for the necropsy. The cat was severely dehydrated, had lost incisors with severe gingivitis and abundant tartar accumulation and presented a shrunken, reduced in volume, left eye (phthisis bulbi). The most relevant alterations, affecting the abdominal and thoracic organs, were renal papillary erosion and necrosis associated to irregular renal profile with severe scarring and yellowish, pale cortex with numerous cortico-medullary strikes, and severe pulmonary atelectasis of the caudal lobes. Two pearly white, rounded, flat lesions, less than 1 cm in diameter, were detected in the left and right caudal lobes. Histologically, pulmonary lesions consisted of numerous, well circumscribed, not encapsulated nodules composed of irregularly arranged, tubular and/or dilated acinar structures, lined by a single layer of tall, columnar epithelial cells with abundant clear cytoplasm and basally located nuclei. Mitosis were less than 1 for HPF and anisokaryosis and anisocytosis were mild. Renal lesions were bilateral and diffuse. Histologically, they consisted of ulceration and necrosis of the papilla, numerous perivascular to interstitial aggregates of lymphocytes and plasmacells associated to severe interstitial fibrosis, glomerular synechiae/sclerosis and tubular degeneration, necrosis and mineralization. A diagnosis of end stage kidney, the most likely cause of death, was posed. Immunohistochemical investigation for thyroid transcription factor-1 (TTF-1), AE1/AE3 cytokeratins (CKs), CK5, smooth muscle actin (_-SMA) and histochemical staining with PAS and alcian blue (AB) (pH 2.5) was performed. Neoplastic glands were diffusely positive for CKAE1/AE3, CK5 and PAS. AB staining was faint and multifocal, while TTF-1 and _-SMA were negative. Based on histological and immunohistochemical findings, a diagnosis of mucus gland adenoma was formulated. Lung tumors, namely bronchial gland carcinoma, bronchiolo-alveolar tumors and squamous cell carcinoma, have been extensively reported in cats, even though they are overall considered rare tumors. Conversely, to the authors' best knowledge, pulmonary mucus gland adenoma has not been reported to date in the feline species. In human beings, mucus gland adenomas are extremely rare tumors, arising mostly within the main, lobar or segmental bronchi and more rarely in the lung periphery. They are often endobronchial and multicystic, causing signs and symptoms of obstruction. The present report described the first case of peripheral lung nodules arising from the submucosal mucinous gland in a peripheral small airway in a cat, an unusual and rare benign lesion that shares many similarities with the human counterpart.

Barbero R, Canale G, Bergagna S, Dezzutto D, Falzone R, Tarello V, Boniotti^oMB, Lombardi^oG, Tagliabue^oS, Gennero MS

Leptospirosi bovina : case reports di Leptospira hardjo in Piemonte

XVI Congresso Nazionale SIDI^oLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDI^oLV), 2015]. - p 206-207. - 4 bib ref [Nr. Estr. 7061]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDI^oLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Leptospira borgpetersenii is a bacterial pathogen of cattle le that causes zoonotic infections in

humans. It is important because is a significant public health problem and because causes organ failure in the liver, lungs, kidney, and brain. *L. borgpetersenii* serovar Hardjo type hardjobovis is the most common cause of leptospirosis in bovine, in addition, hardjo-bovis is the most common serovars because cattle are maintenance hosts. Moreover, it is costly contributors to reproductive loss in the beef and dairy industries. In the case report, we refer a cluster of two cases of leptospirosis in Piedmont farms, with regard to clinical, laboratory, environmental findings and pharmacological therapy. In Italy there are not vaccines for *Leptospira* in cattle, so autovaccines were prepared in five months with hardjo-bovis strains from urine samples from the two outbreaks. The antibiotic treatment and the vaccination allowed to close the outbreaks after several months.

Bassi°S, Formato G, Milito M, Trevisiol K, Salogni °C, Carra°E

Phenotypic characterization and ERIC-PCR based genotyping of *Paenibacillus larvae* isolates recovered from American foulbrood outbreaks in honey bees from Italy

Vet Q. - Vol. 35 no 1 (2015). - p 27-32. - 20 bib ref [Nr. Estr. 5998]

Background: *Paenibacillus larvae* is the etiological agent of American foulbrood (AFB), a widespread and severe bacterial brood disease of honey bees. The genomic characterization of *P. larvae* strains by enterobacterial repetitive intergenic consensus–polymerase chain reaction (ERIC–PCR) is able to differentiate four genotypes (ERIC I, ERIC II, ERIC III, ERIC IV). The information on the presence of *P. larvae* ERIC genotypes worldwide is few. Objectives: We have characterized *P. larvae* strains isolated in Italy from AFB outbreaks to obtain information on ERIC genotypes and phenotypes of the strains circulating in the country. Methods: A total of 117 *P. larvae* isolates from 115 AFB outbreaks occurring in 2008–2012 were subjected to phenotypic and genetic characterization. Results: The genomic characterization allowed the identification of ERIC I and ERIC II genotypes. Examining the data of Northern and Central Italy separately it was noted that in Northern Italy most outbreaks were caused by the ERIC I genotype (78.6%), followed by the ERIC II genotype (18.6%) and by co-infections (ERIC I + ERIC II) (2.6%). In Central Italy, only outbreaks caused by the ERIC I genotype were observed. With regard to phenotypic characteristics all examined strains of ERIC II genotype fermented fructose while no strains of ERIC I genotype possessed this ability. Conclusion: Both *P. larvae* ERIC I and ERIC II genotypes were isolated from the AFB outbreaks, but ERIC II genotype was isolated only in Northern Italy. The fermentation of fructose seems to be a genotype-specific biochemical marker.

Belardo V, Pietropaoli M, Mancuso E, Bassi°S, Artese F, Formato G

***Aethina tumida* : conoscere il nuovo parassita degli alveari**

Apimondia Italia. - Vol. no 1/2 (2015). - p 19-24. - 21 bib ref [Nr. Estr. 7146]

Bertocchi°L

Il benessere animale nella messa in asciutta

Convegno Nazionale SIVAR "Gestione della messa in asciutta: punti critici e possibili strategie di intervento" : 29 Ottobre 2015, Cremona / [Cremona : Società Italiana Veterinari per Animali da Reddito (SIVAR), 2015]. - 2 p. - 8 bib ref [Nr. Estr. 7212]

Convegno Nazionale SIVAR "Gestione della messa in asciutta: punti critici e possibili strategie di intervento" : Cremona : 29 Ottobre 2015)

Bertocchi°L

Il benessere animale nella messa in asciutta

Gestione della messa in asciutta : punti critici e possibili strategie di intervento : atti congressuali, Cremona, 29 Ottobre 2015 / [Agrate Brianza (MB) : CEVA, 2015]. - p 21-43. - 8 bib ref [Nr. Estr.

7252]

Convegno "Gestione della messa in asciutta : punti critici e possibili strategie di intervento" :
Cremona : 29 Ottobre 2015)

Bertoletti° M, Chiari° M, Avisani° D, Cerioli° MP, Alborali° LG, Moreno_Martin° MA,
Lavazza° A, Farioli M, Brenzoni LG, Zanoni° MG

Influence of geographical and swine herds' features on Aujeszky's disease seropositivity in Northern Italy

Society for Veterinary Epidemiology and Preventive Medicine : proceedings : Ghent, Belgium,
25th-27th March 2015 / [s.l. : Society for Veterinary Epidemiology and Preventive Medicine, 2015]. -
1 p. (ultimo accesso 10/03/2016 <http://www.svepm.org.uk/posters.html>) [Nr. Estr. 7178]

Society for Veterinary Epidemiology and Preventive Medicine : Ghent, Belgium : 25th-27th March,
2015)

Bertone I, Bellino C, Alborali° GL, Cagnasso A, Cagnotti G, Dappiano E, Lizzi M,
Miciletta M, Ramacciotti A, Gianella P, D'Angelo A

Clinical-pathological findings of otitis media and media-interna in calves and (clinical) evaluation of a standardized therapeutic protocol

BMC Vet Res. - Vol. 11 no 297 (2015). - 9 p. - 36 bib ref (ultimo accesso 10/12/2015
<http://www.biomedcentral.com/content/pdf/s12917-015-0606-3.pdf>) [Nr. Estr. 7137]

Background The aims of this field trial were to describe the clinical-pathologic findings in calves with otitis media (OM) and media-interna (OMI), to evaluate, through the development of a scoring system, the effectiveness of a standardized therapeutic protocol, and to identify the causative pathogens and their possible correlation with concurrent respiratory disease. All animals underwent physical and neurological examinations at three experimental time points: at diagnosis/beginning of treatment (T0), 1 week (T1) and 2 weeks (T2) after therapy was started, respectively. Follow-up telephone interviews with animal owners were conducted 1 month later. The therapeutic protocol consisted of tulathromycin (Draxxin®; Zoetis), oxytetracycline hydrochloride (Terramicina 100®; Zoetis), and carprofen (Rimadyl®; Zoetis). **Results** Twenty-two calves were enrolled. Physical and otoscopic examination at T0 revealed monolateral and bilateral otorrhea in 16 and 6 calves, respectively, with peripheral vestibular system involvement in calves presenting with neurological signs (n = 17; 77 %). A significant improvement of clinical and neurological scores was observed in 20 (90 %) calves, a full recovery in only 1 (5 %). One calf worsened between T0 and T1 and it was removed from the study. None of the other animals showed a worsening of clinical conditions and/or required further treatments at one month follow up. *Mycoplasma bovis* was isolated in 89 % of the affected ears either alone or together with *P. multocida* (n = 5), *Streptococcus* spp. (n = 1), *Staphylococcus* spp. (n = 1), and *Pseudomonas* spp. (n = 1). *M. bovis* either alone or together with these bacteria was also isolated from the upper and/or lower respiratory tract in 19 (86 %) calves. **Conclusions** This is the first prospective study to evaluate the effectiveness of a standardized therapeutic protocol for the treatment of OM/OMI in calves. The therapy led to clinical improvement in the majority of the calves. Persistence of mild clinical-neurological signs did not compromise productive performance. The numerical scoring system for clinical and neurological signs permitted objective evaluation of response to therapy. *M. bovis* was the pathogen most often isolated. This finding should be considered in the treatment of OM/OMI in calves. Moreover, respiratory tract infection should not be underrated, since it is one of the major risk factors for the development of OM/OMI.

Bianchi° A, Giacomelli° S, Ferloni M, Milani F, Pas serini A, Redaelli K, Bertoletti° I
Dysmorphology in wildlife and the role of rehabilitation centers

IX International Symposium on Wild Fauna : Kosice, Slovakia, September 15-19, 2015 / [Kosice,

Slovakia : University of Veterinary medicine and Pharmacy, 2015]. - 3 p. - 5 bib ref [Nr. Estr. 7187]
International Symposium on Wild Fauna (9. : Kosice, Slovakia : September 15-19, 2015)

Dysmorphism is the generic name for abnormalities of form and structure of an animal's body. In this work we describe 7 selected cases related to dysmorphological diseases as the results of 255 examined cases in diagnostic activities on alpine ungulates. Animals were found dead or recovered in wildlife rescue center (CRAS) of the Provincial Administration of Sondrio located in the central Italian Alps.

Bianchini°V, Recordati C, Borella°L, Gualdi V, Sc anziani E, Selvatico°E, Luini°M
Helicobacteraceae in bulk tank milk of dairy herds from Northern Italy

BioMed Res Int. - Vol. Article ID 639521 (2015). - 4 p. - 29 bib ref (Ultimo accesso 29/06/2015 : <http://dx.doi.org/10.1155/2015/639521>) [Nr. Estr. 6078]

Helicobacter pylori is responsible for gastritis and gastric adenocarcinoma in humans, but the routes of transmission of this bacterium have not been clearly defined. Few studies led to supposing that *H. pylori* could be transmitted through raw milk, and no one investigated the presence of other Helicobacteraceae in milk. In the current work, the presence of Helicobacteraceae was investigated in the bulk tank milk of dairy cattle herds located in northern Italy both by direct plating onto *H. pylori* selective medium and by screening PCR for Helicobacteraceae, followed by specific PCRs for *H. pylori*, *Wolinella* spp., and "Candidatus *Helicobacter bovis*." Three out of 163 bulk milk samples tested positive for Helicobacteraceae, but not for the subsequent PCRs. *H. pylori* was not isolated in any case. However, given similar growth conditions, *Arcobacter butzleri*, *A. cryaerophilus*, and *A. skirrowii* were recovered. In conclusion, the prevalence of Helicobacteraceae in raw milk was negligible (1.8%), and *H. pylori* was not identified in any of the positive samples, suggesting that, at least in the farming conditions of the investigated area, bovine milk does not represent a potential source of infection.

Bianchini°V, Romanò°A, Cremonesi P, Cortimiglia C , Barbieri°I, Gualdi V, Luini°M

Genotipizzazione di *Staphylococcus aureus* isolato da latte di massa bovino e caprino della Lombardia

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 64 [Nr. Estr. 7049]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

To get an overview of S. aureus genotypes isolated from bulk tank milk (BTM) in North of Italy, 16S-23S rRNA intergenic spacer PCR (RS-PCR) was applied to 1104 and 295 S. aureus isolated from 398 bovine and 65 caprine BTM samples, respectively. Based on the results of RS-PCR, 54 bovine and 42 caprine representative strains were further selected for genotyping by MLST. Genotyping showed a great variability of strains, both from cow and goat milk samples, with little overlap between the two species. Cluster B (ST8), reported in the literature as particularly pathogenic and diffusive, was by far the most frequent in bovine. Genotyping, together with new knowledge about pathogenicity and diffusiveness of the strains, could give the possibility to modulate actions in mastitis control in relation to the genotypes circulating in the farm.

Bianco C, Sarli G, Panarese S, Bacci ML, Galeati G, Dottori°M, Bonilauri°P,

Lelli°D, Leotti G, Vila T, Joisel F, Ostanello F

PCV2 infection in vaccinated conventional gilts inseminated with PCV2b-Spiked semen

Pakistan Vet J. - Vol. 35 no 3 (2015). - p 293-298. - 21 bib ref [Nr. Estr. 6094]

The present trial investigated the effect of PCV2 vaccination on viremia, virus shedding and viral load in maternal tissues and foetuses of conventional gilts inseminated with PCV2b-spiked semen. Twelve gilts were randomly divided into two groups of six animals each (vaccinated infected, VI; non-vaccinated infected, NVI). Estrus synchronization was followed by artificial insemination (AI) with a single PCV2 negative semen dose supplemented with 0.2 mL of a PCV2b suspension containing 104.4 TCID₅₀/50 µL (total viral dose: 105 TCID₅₀). Vaginal, nasal and faecal swabs, and blood samples were collected weekly from two days before artificial insemination till the end of the experimental period (55 days post AI; DPAI) and tested by real-time PCR (qPCR) for PCV2; sera were tested for anti-PCV2 antibodies. During necropsy foetal and maternal tissues were collected for qPCR and histopathology. In each of the VI and NVI groups three out of the six gilts were pregnant at 29 DPAI. The VI group showed a significantly lower proportion of PCR-positive swabs: 24.6% VI vs 71.3% NVI. PCV2 clearance was demonstrated by qPCR in lymphoid tissue during the trial in the VI group. Only one foetus was PCV2-positive (in the NVI group) and three amniotic fluids of the NVI group. PCV2 was found in a significantly lower proportion of the placenta of foetuses in the VI group (39%) than the NVI group (77%). The PCV2 vaccine seems to play an active role in reducing virus shedding, tissue viral load and foeto-placental infection.

Bilato°D, Tosi°G, Parini M, Paoli A, Fiorentini° L, Cantini F, Massi°P, Amadori°M

Applicazione di modelli di valutazione in vitro dell'attività antibatterica di monogliceridi degli acidi grassi a corta e media catena nei confronti di Salmonella spp.

Atti della Societa' Italiana di Patologia Aviare (SIPA) 2015 : LIV Convegno annuale : Forli, 16-17 Aprile 2015 / [s.l. : s.n., 2015]. - p 112-116. - 6 bib ref [Nr. Estr. 6099]

Convegno annuale Societa' Italiana Patologia Aviare (SIPA) (54. : Forli : 16-17 Aprile 2015)

Antibiotic resistance and, in particular, the generation of multidrug resistant bacteria among zoonotic agents highlights the importance to develop research on new disease control strategies on farm. In this scenario, organic acid monoglycerides proved to be valid products in terms of antibacterial potency, cost-benefit profile and absence of withdrawal periods. In order to define reliable parameters of efficacy, an integrated potency score of such monoglycerides was developed in vitro in Salmonella enterica serovar enteritidis (SE) and S. typhimurium (ST) models, based on inhibition of bacterial growth in medium, inhibition of intracellular invasion in Porcine Jejunal Epithelial Cells (IPEC-J2), and a killing test evaluated by flow cytometry. The above tests enabled us to detect significant differences in the activity of some monoglycerides. Results indicate that our panel of tests can be the foundation of a potency score system. This could be adopted to select proper monoglycerides for field trials in the target species. Further studies in vivo are necessary to confirm the predictive data in vitro. Moreover, the impact of monoglycerides on the innate and adaptive immune system and the development of assays on cell lines of poultry origin for pro-inflammatory cytokines should be further investigated.

Bolzoni°L, Pugliese A, Rosa R

The role of heterogeneity on the invasion probability of mosquito-borne diseases in multihost models

Ecology at the interface : 21-25 September 2015, Rome : abstract book / [s.l. : s.n., 2015]. - p 211 [Nr. Estr. 7160]

Ecology at the interface : Rome : 21-25 September 2015)

Stochastic events play a significant role in vector-borne epidemics, especially in the initial phase of an outbreak. Here, we use multi-type branching process approximations to assess how

heterogeneities in transmission among a large number of host groups can affect the probability of major outbreaks occurrence in mosquito-borne diseases. We show that heterogeneities in transmission affect the probability of major outbreaks occurrence in different ways than the basic reproduction number (R_0). While R_0 always increases with the heterogeneity, the probability of major outbreaks after the introduction of infected hosts can decrease with the increase of the heterogeneity, even approaching zero when the number of host groups is large. In addition, we show that the probability of major outbreaks via infected vectors is always larger than via infected hosts when heterogeneous transmission is sufficiently high. Our findings suggest that, for multi-species infections or for single-species infections with patchy host distribution, the introduction of primary infected vectors may represent a higher risk for major outbreaks occurrence than introductions of infected hosts.

Bolzoni^oL, Pugliese A, Rosà R

The role of heterogeneity on the invasion probability of mosquito borne diseases in multi-host models

J Theor Biol. - Vol. 377 (2015). - p 25-35. - 55 bib ref [Nr. Estr. 7132]

Heterogeneity in transmission and stochastic events can play a significant role in shaping the epidemic dynamics of vector-borne infections, especially in the initial phase of an outbreak. In this work, by using multi-type branching process methodologies, we assess how heterogeneities in transmission among a large number of host groups can affect the invasion probabilities of a mosquito-borne disease. We show with both analytical and numerical methods that heterogeneities in transmission can shape the invasion probabilities differently from how they affect the basic reproduction number (R_0). In particular, we find that, while R_0 always increases with the heterogeneity, the invasion probability after the introduction of infected hosts can decrease with the increase of transmission heterogeneity, even approaching zero when the number of host groups is very large. In addition, we show that the invasion probability via infected vectors is always larger than via infected hosts when heterogeneous transmission is sufficiently high. Our findings suggest that, for multi-species infections (e.g. West Nile fever and Rift Valley fever) or for single-species infections with patchy host distribution, the introduction of primary infected vectors may represent a higher risk for major outbreaks occurrence than introductions of infected hosts.

Bonilauri^oP, Forlenza J, Andrea^oL [i.e. Luppi^o, A], Torri^oD, Barbieri^oI, Martelli P

Use of phylogenetic analysis of PRRSV to monitor of the efficacy of the acclimatization of replacement gilts in a pyramid production system

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 166 (Poster P075) [Nr. Estr. 7091]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Introduction. In area of high pig density the eradication of PRRSV is challenging because of a high probability of reinfection . The control of the disease pass through a proper management of replacement gilts and a good acclimation help in the achievement of herd stability. Material and method. This study was carried out in a pyramid system of 1,500 females of three productive units: Grand-parent sows are reared in unit B and gilts are moved to farrow-to-finish units identified as M and L, a portion of growers of units M and L are moved in separate finishing units. Before spring 2013 the replacement females were introduced at 20kg to 40kg b.w. and quarantine were not applied. The gilts were vaccinated with a PRRSV MLV but acclimation to the resident strain of PRRSV before the introduction in productive units was not applied. M, B and L herds, were not stable and reproductive disorders were constantly observed. Starting from April 2013 an acclimatization protocol was implemented and gilts from unit B were moved to units M and L at 6kg

of b.w. After that, the replacement breeding females received a longer period of time to get exposed to the resident virus, to develop an appropriate immunity and to eliminate viremia and the shedding of the virus. At 130kg the replacement gilts were tested both by ELISA and PCR to evaluate the success of the natural exposure to PRRSV and the "freezing" of the infection (no shedders). Since 2010, ORF7 sequences were constantly obtained. The alignment and phylogenetic analysis was performed using MEGA6. Time scaled phylogenetic analysis and estimation of nucleotide substitution rates were generated using BEAST v1.8.1. A model of relaxed molecular clock was used (HKY with gamma distribution). A chain length of 8M was used to generate a clade credibility trees from 80k trees. Results. From farm M, B and L between 2010 and 2014 a total of 14 ORF7 nucleotide sequence data was obtained. The degree of nucleotide identity ranged from 100% to 84.6%. The phylogenetic analysis revealed 4 well separated clades. In clade A, B and C were spanned only sequences obtained from herd M, B and L, respectively. In clade D were grouped sequence from farms M, B and L obtained before the decision to change the system designed to acclimatize the replacement gilts. The substitution rate was estimated as $1.99E-3$ (95% HPD [3.69E-4, 4.02E-3]) and the maximum rate of diversity observed within a clade was 2.1% acquired in 14 months. Conclusion. The implemented acclimatization strategy induced PRRS stabilization among farms so that only one resident PRRSV was present. Phylogenetic analysis contributes to evaluate the efficiency of acclimation system.

Bonilauri°P, Torri°D, Defilippo°F, Calzolari°M, Luppi°A, Dottori°M

The detection of West Nile virus in veterinary surveillance : how to overcome the flavivirus similarity and control the absence of inhibition in RNA extracted

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 203-204 [Nr. Estr. 7038]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Boniotti°MB, Papetti°A, D'Incau°M, Tagliabue°S

Leptospiral infections in pigs from Northern Italy during the period 2002-2014

2nd ELS meeting on leptospirosis and other rodent borne haemorrhagic fevers : 16-18 April 2015 Amsterdam, the Netherlands / [s.l. : s.n., 2015]. - 1 p [Nr. Estr. 6053]

ELS meeting on leptospirosis and other rodent borne haemorrhagic fevers (2nd : Amsterdam, the Netherlands : 16-18 April 2015)

Swine are one of the most significant reservoir and source of *Leptospira* infections for man. Endemic infections in swine farms generally remain subclinical and they are mainly caused by serovars Pomona, Bratislava and Tarassovi while other serovars tend to occur only incidentally. The aim of this study was to investigate the leptospiral infections of the most important serovars in pig population and to understand the genetic characteristic of serogroup Pomona circulating in Northern Italy in the period 2002-2014. Microscopic agglutination test (MAT) with use of serovars Ballum, Bratislava, Canicola, Copenhageni, Grippotyphosa, Hardjo, Pomona, Tarassovi, was performed on a total of 117136 swine serum samples collected from 2002 to 2014. *Leptospira* DNA detection was carried out on 155 samples by a Real time PCR directed against the 14302 gene. Culture isolation was attempted on 272 kidney samples. The isolates were serotyped by MAT using a panel of reference hyperimmune sera. Moreover, 36 isolates collected from 2002 to 2014 from 36 different farms were identified and genotyped by molecular methods as Multi Locus Sequence Typing and Multi Locus Variable Number Tandem Repeat Analysis (MLVA) (loti: 4, 7, 10, Lb4, Lb5). Out of 117136 collected sera examined by MAT, 14685 (12,5%) samples were positive. Positive titers against more than one serovar were detected in 21,4% positive samples (3143/14685). Among MAT positive samples, 9,31% of sera demonstrated titers with serovar Bratislava, 4,23% with Pomona and less than 1% with Ballum, Canicola, Copenhageni, Grippotyphosa, Hardjo and Tarassovi. *Leptospira* detection by lipL32 Real time PCR revealed 53 positive samples out of 155. During this

study, 111 strains were isolated and all of them were serotyped as serogroup Pomona. Genotyping by MLST showed that 35 out of 36 isolates had the same profile as the reference strains serovar Pomona (ST 140) and one isolate showed a profile with 99,9% of nucleotide identity with serovar Mozdok (ST 117). By MLVA, the 35 Pomona isolates showed the same profile as the Italian reference strain (Mezzano I) but they differed from the international one (Pomona). Among the tested serovars, Bratislava remains the most prevalent while Tarassovi, unlike in the past, has become negligible. Culture isolation was successful only with Pomona infected kidneys showing interstitial nephritis. The genotype of Pomona isolates showed to be very stable over a long period of time (2002-2014). In fact, with the exception of one Mozdok isolate, a unique MLST and MLVA profile was detected in our study. These results are very important to design and develop new vaccines that could be used on the local pig population.

Boniotti[°]MB, Papetti[°]A, Lavazza[°]A, Sozzi[°]E, Cor dioli[°]P, Alborali[°]GL

Detection and genetic characterization of porcine epidemic diarrhea virus circulating in Northern Italy

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 164 (Poster P072) [Nr. Estr. 6050]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Introduction: Porcine epidemic diarrhea (PED) causes watery diarrhea, dehydration and a high death rate among suckling pigs. Nowadays, PED is considered an emergent infectious disease in United States and Asia, causing important economic losses. In Europe, the last reported outbreak occurred in 2005-2006 in Italy. Since then, PED detection is included in the diagnostic procedure of swine enteric diseases and only sporadic outbreaks with mild clinical signs were observed in Northern Italy. In this study, we report the presence of PEDV infection in pig farms and the genetic characterization of PEDV variants circulating in Italy from 2007 to 2014. Materials and Methods: A total of 1563 samples collected from clinical cases of pig enteritis were investigated through electron microscopy, ELISA and PCR. Fifty-four positive samples were molecularly characterized by sequencing of one to four regions of the genome, including 349 nt of the RNA-dependent RNA Polymerase (RdRp), 553 or 2581 nt of the spike S1 gene, 439 nt of the matrix (M) and 360-599 nt of the ORF3 gene. The nucleotide and amino acid sequences were aligned and compared to selected PEDV sequences available from the GenBank database. Phylogenetic trees were generated by the neighbor-joining method by MEGA 5. Results: PEDV was diagnosed in 61 outbreaks and a total of 54 were then confirmed by RT-PCR, using PEDV specific primers. Twenty-eight, 21, 22 and 5 sequences were obtained for the S1, RdRp, M and ORF3 regions, respectively. The phylogenetic analysis evidenced that genetically distant coronaviruses entered pig farms during the period 2007-2014. In particular 3 independent entries occurred in 2007, 2009 and 2014. Moreover, the virus detected in 2014 showed more than 99% nt identity with the U.S. "Ohio" variant considered less pathogenic. Conclusion: These results indicate an endemic presence of PEDV in Northern Italy. The PEDV strains circulating since 2007 showed a high genetic variability. The characterization of the circulating strains is important to keep updated the diagnostic tools that are in use for PED diagnosis and to understand the cross-protection ability of the different strains.

Busi[°]C, Lavazza[°]A, Canelli[°]E, Monini[°]M, Ruggeri[°]FM, Boniotti[°]MB, Falcone[°]E

Epidemiological and phylogenetic analysis of avian rotaviruses in Italy

6th European Rotavirus Meeting : 17-20 May, 2015 Dijon, France : programme and abstract book / [s.l. : s.n., 2015]. - p 28 [Nr. Estr. 6066]

European Rotavirus Meeting (6th : Dijon, France : 17-20 May, 2015)

Calzolari°M, Lelli°D, Bellini R, Bonilauri°P, De filippo°F, Maioli°G, Moreno_Martin°A, Tamba°M, Chiari°M, Angelini P, Natalini S, Farioli M, Lavazza°A, Prosperi°A, Faccin°F, Zanoni°M, Dottori°M

The entomological surveillance of West Nile virus in Lombardia and Emilia-Romagna regions, Northern Italy, 2014

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 48-49 [Nr. Estr. 7024]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Calzolari°M, Pautasso A, Montarsi F, Albieri A, Bellini R, Bonilauri°P, Defilippo°F, Lelli°D, Moreno°A, Chiari°M, Tamba°M, Zanoni°M G, Varisco°G, Bertolini S, Modesto P, Radaelli MC, Iulini B, Prearo M, Ravagnan S, Cazzin S, Mulatti P, Monne I, Bonfanti L, Marangon S, Goffredo M, Savini G, Martini S, Mosca A, Farioli M, Brenzoni LG, Palei M, Russo F, Natalini S, Angelini P, Casalone C, Dottori°M, Capelli G

West Nile Virus surveillance in 2013 via mosquito screening in Northern Italy and the influence of weather on virus circulation

PLoS One. - Vol. 10 no 10 (2015). - p e0140915 (14 p). - 49 bib ref (Ultimo accesso 23/10/2015 : <http://www.plosone.org/article/fetchObject.action?uri=info:doi/10.1371/journal.pone.0140915&representation=PDF>) [Nr. Estr. 7067]

West Nile virus (WNV) is a recently re-emerged health problem in Europe. In Italy, an increasing number of outbreaks of West Nile disease, with occurrences of human cases, have been reported since 2008. This is particularly true in northern Italy, where entomological surveillance systems have been implemented at a regional level. The aim of this study was to use, for the first time, all the entomological data collected in the five regions undergoing surveillance for WNV in northern Italy to characterize the viral circulation (at a spatial and temporal scale), identify potential mosquito vectors, and specify relationships between virus circulation and meteorological conditions. In 2013, 286 sites covering the entire Pianura Padana area were monitored. A total of 757,461 mosquitoes were sampled. Of these, 562,079 were tested by real-time PCR in 9,268 pools, of which 180 (1.9%) were positive for WNV. The largest part of the detected WNV sequences belonged to lineage II, demonstrating that, unlike those in the past, the 2013 outbreak was mainly sustained by this WNV lineage. This surveillance also detected the Usutu virus, a WNV-related flavivirus, in 241 (2.6%) pools. The WNV surveillance systems precisely identified the area affected by the virus and detected the viral circulation approximately two weeks before the occurrence of onset of human cases. Ninety percent of the sampled mosquitoes were *Culex pipiens*, and 178/180 WNV-positive pools were composed of only this species, suggesting this mosquito is the main WNV vector in northern Italy. A significantly higher abundance of the vector was recorded in the WNV circulation area, which was characterized by warmer and less rainy conditions and greater evapotranspiration compared to the rest of the Pianura Padana, suggesting that areas exposed to these conditions are more suitable for WNV circulation. This observation highlights warmer and less rainy conditions as factors able to enhance WNV circulation and cause virus spillover outside the sylvatic cycle.

Cavadini°P, Molinari°S, Pezzoni°G, Chiari°M, Brocchi°E, Lavazza°A, Capucci°L

Identification of a new non-pathogenic lagovirus in *Lepus europeus*

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 76-77. - 4 bib ref [Nr. Estr. 7025]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Cerutti F, Ebranati E, Luzzago C, Lauzi S, Caruso C, Masoero L, Giammarioli M, Moreno_Martin°AM, Cannella V, Guercio A, Ciccozzi M, De_Mia GM, Acutis PL, Zehender G, Peletto S

Filodinamica, filogeografia e caratterizzazione molecolare full genome di bovine viral diarrhoea virus (BVDV)

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 180-182. - 5 bib ref [Nr. Estr. 7060]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

BVDV-1 is a Pestivirus with large impact on cattle worldwide. 5'-UTR sequences of the three main Italian BVDV-1 subtypes were considered for phylogeography. High similarity clusters were identified, and the relative sequences used to simulate transmission chains. No significant geographic structure was observed in BVDV-1b tree; BVDV-1e tree branched into three main clades, with Piedmontese sequences clustered together, either due to later sample collection or to a recent introduction of BVDV-1e. BVDV-1f sequences clustered into three significant clades: all Piedmont sequences clustered in two subclades, one including Aosta Valley sequences. Viruses with identical 5'-UTRs, suggesting transmission between farms, were identified, and their Npro sequences were used to select clusters for further epidemiological investigations. Finally, full genome sequences were generated by massive parallel sequencing (MPS) to study viral quasispecies from mucosal disease cases

Chiapponi°C, Affanni P, Pariani E, Baioni°L, Lupp i°A, Faccini°S, Veronesi L, Colucci ME, Amendola A, Zanetti A, Foni°E

Comparative whole genome characterization of swine and human influenza A viruses isolated during surveillance activity in Northern Italy (2010-2014) : preliminary results

3rd International One Health Congress : 15-18 March, 2015 Amsterdam / [s.l. : s.n., 2015]. - 2 p. (Abstract no. 515) [Nr. Estr. 7155]

International One Health Congress (3rd : Amsterdam : 15-18 March, 2015)

Chiari°M, Ferrari N, Bertoletti°M, Avisani°D, Cerrioli°M, Zanoni°MG, Alborali°LG, Lanfranchi P, Lelli°D, Moreno_Martin°A, Lavazza° A

Long-term surveillance of Aujeszky's disease in the Alpine Wild Boar (Sus scrofa)

EcoHealth. - Vol. 12 (2015). - p 563-570. - 28 bib ref [Nr. Estr. 7173]

Although wild boar can act as a persistent Aujeszky's disease (AD) reservoir, limited data are available on long-term epidemiology in free-ranging wild boar living in areas where industrial swine herds are limited. Hence, this study provides crucial information, which fills this knowledge gap, on the natural dynamics of AD infection. From 3260 sera sampled during eight hunting seasons, 162 (4.97%) were tested positive. Factors, including the animal's age class, and the sampling year, had significant effects on the probability of the wild boar being seropositive, while wild boar mean abundance per area, yearly abundance and the total number of pig farms, as well as interactions among age, year and sex, were not significant. In particular, a positive trend of seroprevalence was observed over the years, with values ranging from 2.1 to 10.8%. This long-term surveillance showed an increase in seroprevalence with a higher probability of being seropositive in older individuals and the independence of wild boar seropositivity from the likelihood of contact with pigs in the area.

Chiari°M, Figarolli°BM, Bertoletti°M, D'Incau°M , Alborali°GL, Tagliabue°S, Zanoni°M, Boniotti°MB

Isolation and identification of a *Leptospira interrogans* serovar bratislava strain in wild boar in Lombardy Region, Northern Italy

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 365. - 5 bib ref [Nr. Estr. 7055]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Even if Leptospira species are zoonotic bacteria able to infect humans, livestock and wildlife, little is known about the temporal dynamics of Leptospira spp. infections in wildlife. Therefore, the aim of the study was to determine the spatio-temporal dynamic of Leptospira spp. infections in wild boars through serological MAT testing. Sera of 2101 wild boar hunted during 5 hunting seasons in 8 hunting districts were analysed and age and sex have been reported for each animal. 359 (17%) sera resulted positive at MAT (cut-off : (maggiore/minore)100) with the most frequent and higher antibody titers detected against serovar Bratislava (14.6%). Antibody titers against Grippotyphosa, Copenhageni and Pomona were sporadically detected. Serovar Bratislava showed a significant trend along years and a multilevel model revealed a higher presence in older wild boar, while abundance and sex were not influential. Age-class effect on seroprevalence resulted to be independent from the year of sampling.

Chiari°M, Moreno_Martin°A, Ferrari N, Bertoletti M, Avisani°D, Zanoni°M, Cerioli°M, Alborali°LG, Lanfranchi P, Lelli°D, Lavazza°A

Long term surveillance on Aujeszky's disease in wild boar of Central Italian Alps

Harmonized approaches in monitoring wildlife population health, and ecology and abundance : APHAEA - Final meeting, 17-18 March 2015, Amsterdam & Utrecht, The Netherlands : programme and abstract book / [s.l. : s.n., 2015]. - p 14 [Nr. Estr. 6006]

APHAEA - Final meeting : Amsterdam & Utrecht, The Netherlands : 17-18 March 2015)

BACKGROUND: Aujeszky's disease (AD) is one of the most economically important diseases of pigs. Despite wild boar can serve as a persistent reservoir, few data are available on the long term epidemiology in free ranging wild boar living in absence of industrial swine herds, even though these data may be useful to provide information on the natural dynamics of AD infection. **METHODS:** 3260 sera samples were collected from 2006 to 2014 from 4007 hunted free-living wild boar in the alpine footstep mountains (6 hunting districts, Brescia, IT) and tested for anti-AD total gB antibodies. Variables regarding pig farms (Total number of farms; Density; Average number of animals) and wild boar (Age; Sex; Abundance) were recorded. Differences in the composition of wild boar populations among areas (districts?) and factors affecting sero-positivity were investigated. Pig farms in the study area had limited size with usually a small number of pigs bred for a limited period of the year. **RESULTS:** A total of 162 (4.97%) out of 3260 wild boar sera resulted positive for anti-AD antibodies. Age, Year and Average number of pigs per farm resulted significant while wild boar Abundance and Total number of pig farms as well as interactions among Age, Year and Sex turned out not to be significant. The odds of being positive increased almost three times for adults with respect to young boars. In addition, for each individual pig increase (on average) per farm, the odds of wild boar being positive decreased by 9%. A positive trend of seropositivity in wild boars was observed along the considered interval, with an increase in positivity of 20% each year. **CONCLUSION:** The present long term surveillance showed an increase in AD seroprevalence in wild boar with higher probability of being seropositive among older individuals. In addition, AD sero-positivity in wild boar was tested as independent from the area's likelihood of contact with pigs.

Chiari°M, Moreno_Martin°A, Ferrari N, Bertoletti° M, Avisani°D, Zanoni°MG, Cerioli°M, Alborali°LG, Lanfranchi P, Lelli°D, Lavazza°A

Long term surveillance on Aujeszky's disease in wild boar of Central Italian Alps

Society for Veterinary Epidemiology and Preventive Medicine : 25th-27th March 2015, Ghent Belgium : Proceedings / [s.l. : Society for Veterinary Epidemiology and Preventive Medicine, 2015]. - 1 p. (ultimo accesso 10/03/2016 <http://www.svepm.org.uk/posters.html>) [Nr. Estr. 7179]

Society for Veterinary Epidemiology and Preventive Medicine : Ghent, Belgium : 25th-27th March, 2015)

Chiari°M, Prosperi°A, Faccin°F, Avisani°D, Cerioli°M, Zanoni°M, Bertoletti°M, Moreno°AM, Bruno R, Monaco F, Farioli M, Lelli°D, Lavazza°A

West Nile Virus surveillance in Lombardy Region, Northern Italy

Transbound Emerg Dis. - Vol. 62 (2015). - p 343-349 - 22 bib ref [Nr. Estr. 6044]

In 2013, the circulation of West Nile virus (WNV) was detected in the Lombardy region and the following year a surveillance programme was activated with the aim of early identification of the viral distribution in mosquitoes and wild birds. A total of 50 959 Culex spp. mosquitoes grouped in six hundred and forty-seven pools as well as 1400 birds were screened by RT-PCR for the presence of West Nile virus leading to the identification of the viral genome in 32 mosquito pools and 13 wild birds. The surveillance was able to detect the WNV circulation on an average of 42 days (CI 95% 29.98–53.86; Student's t-distribution) before the occurrence of human West Nile disease (WND) cases in the same area. These results demonstrate the presence of WNV in the Lombardy region and confirm entomological and wild birds surveillance as an effective measure for the early identification of WNV circulation in infected areas, thus providing a useful and cost-effective tool for the public health authorities in the application of measures to prevent human infection.

Chiari°M, Prosperi°A, Faccin°F, Lelli°D, Moreno _Martin°A, Sozzi°E, Tironi°M, Avisani°D, Cerioli°M, Zanoni°M, Farioli M, Piatti A, Lavazza°A

West Nile Virus surveillance in Lombardy Region, North Italy

3rd International One Health Congress : 15-18 March, 2015 Amsterdam / [s.l. : s.n., 2015]. - 2 p (Abstract 498) [Nr. Estr. 6009]

International One Health Congress (3rd : Amsterdam : 15-18 March, 2015)

Chirullo B, Pesciaroli M, Drumo R, Pistoia C, Petrucci P, Ruggeri°J, Razzuoli E, Mancinelli°N, Tentellini M, Antolini A, Moscati L, Magistrali C, Amadori°M, Alborali°G, Pasquali P

Salmonella typhimurium exploits gut inflammation in piglets

Atti del LXIX Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : XII Convegno AIPVet, Il Convegno RNIV, XV Convegno SICV, XIII Convegno SIRA, XI Convegno So.Fi.Vet : Perugia, 15-17 Giugno 2015 / [s.l. : s.n., 2015]. - p 359-360. - 3 bib ref [Nr. Estr. 7017]

Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : 69 Convegno AIPVet : 12 Convegno RNIV : 2 Convegno SICV : 15 Convegno SIRA : 13 Convegno So.Fi.Vet : 11 : Perugia : 15-17 Giugno 2015)

Salmonella Typhimurium (STM) is responsible for foodborne zoonotic infections. The human disease is characterized by self-limiting gastroenteritis that occasionally can cause fever and severe gut inflammation (1). Most of the current studies about STM infection have been conducted on murine

models that naturally do not develop gastroenteritis. These models are also based on the lack of an intact microbiota, caused by antibiotic treatment, which limits a comprehensive evaluation of the complex interactions of STM within the gastrointestinal environment (2). STM acquires an evolutionary adaptation to overcome antimicrobial defences in the lumen of the inflamed intestine and to exploit inflammation in order to outcompete the intestinal microbiota in mice (3). Since STM is able to naturally infect pigs, inducing a disease closely resemble those in humans, it is reasonable to hypothesize that pigs can be proposed as the model of choice for salmonellosis and gastrointestinal research. The aim of the study was to evaluate whether STM is able to exploit inflammation, favoring an active infection, using an experimental model of infection in piglets, as a paradigm of the pathogenic mechanisms occurring in humans during salmonellosis. For in vitro studies macrophage cells were isolated by adherence from porcine peripheral blood mononuclear cells. Macrophages and porcine intestinal columnar epithelial cells (IPEC-J2 cell line) were primed overnight with LPS and/or the antagonist of TLR-4/MD-2 complex (RS-LPS), the natural ligand of LPS, infected with wild type *S. Typhimurium* (STM14028), and then analyzed for intracellular colonization. For in vivo studies piglets, pre-treated with LPS, were orally infected with STM14028 and euthanized 24-48 hours. Innate immune response was assessed by FACS and ELISA; STM14028 colonization was evaluated in ceca, spleens and tonsils. We showed that STM14028 was able to efficiently colonize mono-macrophages and IPEC-J2 cells. However, a pre-treatment with LPS makes these cells more susceptible to infection with STM14028 resulting in a significant increase of the STM14028 colonization compared to the LPS-untreated group. This result was confirmed and strengthened by the use of the LPS-antagonist, which inhibited the LPS stimulation and significantly reduced the STM14028-intracellular colonization, restoring them to the values of the STM14028 colonization alone. Moreover, in vivo study indicated that, after infection of piglets by oral route with STM14028, the immune response rapidly react involving the innate compartment with a marked increase of granulocytes, mono-macrophages and neutrophils populations. Finally, the induction of inflammation, by LPS-treated piglets, influenced the colonization of STM14028 inducing a significant increase of the production of the pro-inflammatory IL-1beta and TNF-alpha cytokines in the blood, accompanied by a marked increase of STM14028-colonization in tonsils, cecum and spleens, compared to the control groups. As a whole, these findings suggest that STM is able to exploit inflammation for its own benefit in a model of porcine gastroenteritis.

Chirullo B, Pesciaroli M, Drumo R, Ruggeri^oJ, Razz uoli E, Pistoia C, Petrucci P, Martinelli^oN, Cucco L, Moscati L, Amadori^oM, Magi strali CF, Alborali^oGL, Pasquali P

Salmonella typhimurium exploits inflammation to its own advantage in piglets

Frontiers Microbiol. - Vol. 6, Article 985 (2015). - p 1-8. - 33 bib ref [Nr. Estr. 7028]

Salmonella Typhimurium (*S. Typhimurium*) is responsible for foodborne zoonotic infections that, in humans, induce self-limiting gastroenteritis. The aim of this study was to evaluate whether the wild-type strain *S. Typhimurium* (STM14028) is able to exploit inflammation fostering an active infection. Due to the similarity between human and porcine diseases induced by *S. Typhimurium*, we used piglets as a model for salmonellosis and gastrointestinal research. This study showed that STM14028 is able to efficiently colonize in vitro porcine mono-macrophages and intestinal columnar epithelial (IPEC-J2) cells, and that the colonization significantly increases with LPS pre-treatment. This increase was then reversed by inhibiting the LPS stimulation through LPS antagonist, confirming an active role of LPS stimulation in STM14028-intracellular colonization. Moreover, LPS in vivo treatment increased cytokines blood level and body temperature at 4 h post infection, which is consistent with an acute inflammatory stimulus, capable to influence the colonization of STM14028 in different organs and tissues. The present study proves for the first time that in acute enteric salmonellosis, *S. Typhimurium* exploits inflammation for its benefit in piglets.

Corlatti L, Rempfler T, Gugiatti A, Bianchi^oA, Fil li F, Silvestri GB, Pedrotti L

Monitoring of an infective keratoconjunctivitis outbreak in Alpine ibex populations within the Stelvio National Park and the Swiss National Park

23rd Meeting of the Alpine Ibex European Specialist Group (GSE- AIESG) : 29-31 October 2015, Kals Am Grossglockner (A) / [s.l. : s.n., 2015]. - 1 p [Nr. Estr. 7191]

Meeting of the Alpine Ibex European Specialist Group (GSE- AIESG) (23 : Kals Am Grossglockner (A) : 29-31 October 2015)

Cortimiglia°C, Bianchini°V, Franco A, Caprioli A, Battisti A, Colombo L, Stradiotto K, Vezzoli°F, Luini°M

Prevalence of Staphylococcus aureus and methicillin-resistant S. aureus in bulk tank milk from dairy goat farms in Northern Italy

J Dairy Sci. - Vol. 98 no 4 (2015). - p 2307-2311. - 32 bib ref [Nr. Estr. 6040]

Staphylococcus aureus is regarded as a leading cause of mastitis in goats. However, few data are available on the presence of methicillin-resistant S. aureus (MRSA) in this species. The aim of this study was to assess the prevalence of S. aureus and MRSA in bulk tank milk samples from dairy goat farms in Northern Italy. Eighty-five out of 197 samples (43.1%) tested positive for S. aureus with counts ranging from 10 to more than 1.5×10^4 cfu/mL. The MRSA was screened by both direct plating followed by a disk diffusion test to evaluate methicillin resistance and a selective enrichment method. Methicillin-resistance was confirmed by mecA-specific PCR. Methicillin-resistant S. aureus was identified in 4 samples (2.0%) and multilocus sequence typing (MLST) showed the presence of livestock-associated MRSA belonging to lineages ST398 (n = 3) and ST1 (n = 1). In one case we demonstrated that the same MRSA strain was able to persist over time on the farm, being isolated from both bulk tank milk and the udder of 3 goats 1 yr after the first isolation. The high prevalence of S. aureus-positive herds detected in this study and the presence of MRSA strains belonging to livestock-associated genotypes is of concern, and represents a novel finding in the Italian dairy goat production system. The application of stringent measures for the control of S. aureus mastitis at the farm level seems appropriate to reduce the economic losses, and to minimize the risk of foodborne illness and the transmission of MRSA to humans by occupational exposure.

Cremonesi P, Pozzi°F, Raschetti M, Bignoli G, Capra E, Graber HU, Vezzoli°F, Piccinini R, Bertasi°B, Biffani S, Castiglioni B, Luini°M

Genomic characteristics of Staphylococcus aureus strains associated with high within-herd prevalence of intramammary infections in dairy cows

J Dairy Sci. - Vol. 98 no 10 (2015). - p 6828-6838. - 45 bib ref [Nr. Estr. 7169]

Staphylococcus aureus is one of the most important causes of mastitis in dairy cattle. Based on previous research, Staph. aureus genotypes with different pathogenic and contagious properties can cause intramammary infection (IMI) and coexist in the same herd. Our study aimed to compare Staph. aureus strains from herds that differed in IMI prevalence using different molecular approaches such as ribosomal spacer (RS)-PCR, multilocus sequence typing (MLST), spa typing, ribotyping, pulsed-field gel electrophoresis (PFGE), and multiplex PCR. For this purpose, 31 dairy herds with Staph. aureus IMI were selected, and 16 of these were chosen for a comparison study: the 8 high-prevalence (HP) herds had Staph. aureus IMI prevalence >28% and the 8 low-prevalence (LP) herds had an IMI prevalence <4%. A total of 650 isolates of Staph. aureus from mammary quarters of all positive cows were genotyped with RS-PCR, a technique based on amplification of a portion of the intergenic spacer 16S-23S rRNA, and a subset of 54 strains was also analyzed by multiplex PCR, ribotyping, PFGE, MLST, and spa typing. The RS-PCR analysis revealed 12 different profiles. Staphylococcus aureus strains isolated from 5 out of 8 HP herds showed a profile identical to the genotype B (GTB), described in previous studies as being strongly associated with high within-herd prevalence of Staph. aureus mastitis and the presence of the genes coding for enterotoxins sea, sed, and sej, a long x-region of spa gene, and 3 lukE fragments. Moreover, all

strains isolated in the HP herds possessed genes coding for staphylococcal enterotoxins. In LP herds, a limited number of strains of 6 genotypes, different from those isolated in HP herds, were identified and GTB was not found. Within these genotypes, 4 strains were positive for the *mecA* gene. Preliminary results and comparison with other genotyping methods confirmed that genotyping by RS-PCR is an accurate, rapid, and inexpensive tool for future field studies on *Staph. aureus* mastitis strains and generates clinically relevant results.

Dayhum A, Eldaghayes I, Kammon A, Sharif M, Ferrari G, Conchedda G, Cinardi G, Sumption K, King D, Grazioli^oS, Brocchi^oE

FMD serological survey in Libya and the circulating viruses

Global Foot-and-Mouth Disease Research alliance (GFRA) Scientific Workshop : Hanoi, Vietnam, October 20-22, 2015 : abstract book / [s.l. : s.n., 2015]. - p 89 [Nr. Estr. 7176]

Global Foot-and-Mouth Disease Research alliance (GFRA) Scientific Workshop : Hanoi, Vietnam : October 20-22, 2015)

FMD is known to be present in Libya (currently qualified in stage 1 of the Progressive Control Pathway). Late 2012, mass vaccination of large ruminants (LR) using trivalent vaccine 0, A and SAT2, and small ruminants (SR) using bivalent vaccine 0 and A was carried out. A collaboration with Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER) in Brescia, Italy, was established in 2012. In the framework of this collaboration serological surveys have been undertaken to assess the level of virus circulation and identify serotypes. During spring 2013 a country-wide serosurvey has been carried out through which a total of 4,221 serum samples were collected from SR and LR in Libya. 2,793 samples from 141 farms for SR were collected from 39 cities and 1428 samples from 357 farms for LR were collected from 29 cities. Sera were tested by NSP and SP ELISA (against 0, A and SAT2) using IZSLER kits. Serotypes prevalence and between-serotype cross-reactivity was studied through the evaluation of both antibody titers against the three serotypes and a stratified Odds Ratio. Results of the nation-wide serosurvey stratified in each of the following age-category: 0-12, 12-24 and >24 months. Overall NSP antibodies prevalence was 15.4% (649/4221) with 95% CI (from 14.3 to 16.5). FMD sero-prevalence in SR and LR was 13.5% (378/2793) with 95%CI (12.3 — 14.8) and 19.0% (271/1428) with 95% CI (16.9— 21.0) respectively. The age standardized sero-prevalence of FMD in the two species was 18.3 and 15.5 for LR and SR respectively. The NSP serologic profile observed in both SR and LR supports the hypothesis of an endemic level of FMDV. All samples were then tested for SP antibodies (ELISA) for 0, A and SAT2 serotypes. Serotype 0 was the dominant circulating serotype followed by serotype A. There were significant differences in the sero-prevalence estimated among the age group in SR ($X^2= 118.1$, $P= 0.000$). The sero-prevalence of FMD in SR was 3.7, 13.6 and 21.3 for age group 5 1 year, 1 — 2 year and year respectively. Also in LR, there were significant differences in the sero-prevalence estimated among the age group ($X^2= 4.95$, $P= 0.026$). The sero-prevalence of FMD was 12.3 and 19.8 for age group 1 year and 1 year respectively with risk ratio 1.6 with 95%CI (1.04 — 2.5). Evidence of SAT2 presence was not found and most of the SAT2-positive results can be explained as cross-reactivity of type 0-antibody with SAT2 antigens. Only serotype 0 was found in suspect samples, phylogenetic analyses carried out in Pirbright lab indicated first detection in Libya of a strain belonging to 0/ME-SA/Ind-2001 lineage. Vaccine matching estimates suggested that the vaccine strain 0-3039 should provide protection against it better than vaccine strain 0-Manisa. Despite isolation of only serotype 0 from clinical samples, the results of SP-antibody titers suggests for the concurrent circulation of serotype A in some areas of the country.

De_Rensis FR, Mazzoni C, Scolo A, Bonilauri^oB

Distribution of regular and irregular inter-oestrus interval in sow during different period of the year in Northern Italy

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes,

France : proceedings / [s.l. : s.n., 2015]. - p 118 (Oral Presentation 047) [Nr. Estr. 7089]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Introduction. seasonal infertility in sow includes reduced farrowing rate, prolonged wean-to-oestrus interval, delayed onset of puberty, and autumn abortion syndrome. sows that experienced a conception failure or very early embryonic losses will return to oestrus at a regular interval (18-24 days), while animals that are pregnant but subsequently show a complete embryo loss return at irregular intervals (25-36 days). the aim of this study has been to determine the pattern of regular or irregular inter-oestrus interval during different months of the year to better understand the effect of temperature and/or photoperiodism on fertility. materials and methods insemination data for 51,048 sows from 20 farms located in the northern italy from january to december 2009 were extracted. during the year 2009 a significant increase in temperature were observed in june, july and august. the sows that returned-to-oestrus after weaning were divided into three groups: 1) rint-1 (regular inter-oestrus interval type 1): sows with inter-oestrus interval between 18 and 23 days. 2) rint-2 (regular inter-oestrus interval type 2): sows with inter-oestrus interval between 36 and 48 days. 3) irint (irregular inter-oestrus interval): inter-oestrus interval between 24 and 35 days. results. the total number of successful insemination at first oestrus after weaning was 44,275 out of 51,048 inseminated animals (86,7%). the number of not pregnant sows at ultrasound pregnancy exam was 6,773 of which, 5,103 (75%) returned in oestrus. the rate of successful insemination was reduced (83,6%) during the month of june, july and august compared the rest of the year was (87.7%) ($p < 0.05$). between june and august the proportion of sows with rint-1 was increased ($p < 0.05$) respect to the rest of the year. conversely an increase of irint was observed between september and october. no differences were observed in the fraction of rint-2 throughout the year. discussion. the observation that a greater proportion of sows present regular inter-oestrus interval during the period of june-august suggest a failure of the insemination or very early embryos losses during this period of the year. the increased of irregular inter-oestrus interval during the period of september and october suggests that insemination was successful but then embryos were lost. to know these patterns of reproductive losses is useful from a clinical point of view because suggest that, during the high temperature months of the year, the focus should be on insemination management while during the period of september-october the focus should be mainly on pregnancy maintenance.

Deni D, Caminiti^o A, Lai O, Alfieri L, Casati D, Sciarri M, Scaramozzino P, Brocherel G

Effect of a homeopathic complex on reproductive performance in a commercial pig farm

Homeopathy. - Vol. 104 (2015). - p 9-14. - 37 bib ref [Nr. Estr. 5911]

Background and aim Alternative therapies based on homeopathy can be effective in improving reproductive performance in intensive pig breeding. In this study, the effect of a homeopathic complex on reproductive performance of sows under intensive farming has been investigated. Material and methods Over period of three years, 186 sows were recruited from a farm where a large proportion of animals were suffering from prolonged weaning-to-oestrus intervals (WEI) and weaning-to-service intervals (WSI). Sows were allocated to two groups; once per month, one group was given a homeopathic complex (Borax 10 mK plus Lycopodium 10 mK), while the other group was given a hydro-alcoholic solution (placebo). The follow-up period started one week before the expected date of oestrus, continued for two pregnancies and ended after the weaning of the second farrowing. To evaluate reproductive performance, during the follow-up we collected data on quantitative parameters such as the average number of stillbirths, newborns, and repeat services per farrowing. Time-related data such as WEI, WSI, length of the two pregnancies and weaning periods were also collected to measure the length of the follow-up of each sow. Differences in quantitative parameters between the two groups were evaluated using parametric and non-parametric statistics. Time-related data were used to plot Kaplan–Meier curves and in Cox regression models to evaluate whether treated sows had a higher probability of experiencing a shorter follow-up in comparison to untreated sows. Results We did not found significant differences in the number of newborns, while the number of stillbirths was higher in the treatment group, even if

the difference was slightly significant (p-value = 0.03). The number of repeat services was lower in the treatment group, and this difference was highly significant (p-value < 0.001). Results from the Cox regression models suggest that the end of the follow-up was reached by sows of the treatment group at about twice the rate of sows of the control group (model 2, Hazard Ratio = 2.27; 95%CI: 1.56–3.24).

Di_Francesco A, Donati M, Laroucau K, Balboni A, Galuppi R, Meriardi°G, Salvatore D, Renzi°M

Chlamydiae in corvid birds

Proceedings of the third European meeting on animal chlamydioses and zoonotic aspects : Maisons-Alfort, France, September 24-25, 2015 / edited by Karine Laroucau and Marie-France Devaux. - [s.l. : s.n., 2015]. - p 63 [Nr. Estr. 7041]

European Meeting on Animal Chlamydia and Zoonotic Aspects (3rd : Anses, Maisons-Alfort, France : September 24-25, 2015)

Di_Francesco A, Donati M, Laroucau K, Balboni A, Galuppi R, Meriardi°G, Salvatore D, Renzi°M

Chlamydiae in corvids

Vet Rec. - Vol. 177 no 18 (2015). - p 466 (2 p). -17 bib ref [Nr. Estr. 7042]

Di_Francesco CE, Gentile L, Di_Pirro V, Ladiana L, Tagliabue°S, Marsilio F

Serologic evidence for selected infectious diseases in Marsican brown bears (*Ursus arctos marsicanus*) in Italy (2004–09)

J Wild Dis. - Vol. 51 no 1 (2015). - p 209-213. - 27 bib ref [Nr. Estr. 5985]

We tested 30 serum samples collected during 2004–09 from 22 free-ranging Marsican brown bears (*Ursus arctos marsicanus*) in the National Park of Abruzzo, Lazio, and Molise, Italy, for antibodies against canine distemper virus (CDV), canine adenovirus type 2 (CAV-2), canine parvovirus type 2 (CPV-2), *Brucella* spp., and eight *Leptospira interrogans sensu lato* serovars. Antibody to CDV was detected in 11 samples (37%); only two bears (10%) had detectable CAV-2 and *Brucella* spp. antibodies; three bears were positive for *L. interrogans* serovar Bratislava; and one sample had antibody against *L. interrogans* serovar Copenhageni. All samples were positive for CPV-2 antibody. The CPV-2 antibody titers varied from 1:640 to 1:10,240, suggesting that transmission was still active. Fifty percent of bears were positive for antibody to two or more pathogens. Our results highlight the need to consider infectious diseases as a potential risk for Marsican brown bear conservation.

Di_Marco P, Russotto L, Puleio R, Buttaci C, Gucciardi F, Antoci F, Agnello S, Vicari D, Cannella V, Purpari G, Lavazza°A, Scagliarini A, Guercio A

Ricerca corrente IZS SI 14/11 - Papillomavirus animali : diversità genetica, epidemiologia ed implicazioni patogenetiche

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 195-196. - 9 bib ref [Nr. Estr. 7047]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Papillomavirus (PV) is a circular DNA double-stranded virus, non-enveloped, belonging to Papillomaviridae Family, who infects several species of vertebrates. Up to now, at least 13 types of Bovine Papillomavirus (BPV 1-13) have been characterized. BPV 1 and 2 usually cause fibro — papilloma characterized by single or multiple proliferative lesions, hyperkeratotic or ulcerative. Productive lesions localized at the teats and udder can cause mastitis and economic damage. Aim of this research was to study the epidemiology and pathogenesis of PV infections in ruminants. Histopathological studies to characterize skin lesions were performed and biomolecular investigations were applied to identify the virus and make differential diagnosis with other epitheliotropic viruses as Orthopox and Parapox often cause of multiple infections.

Di_Martino B, Di_Profio F, Lanave G, De_Grazia S, Giammanco GM, Lavazza^o A, Buonavoglia C, Marsilio F, Bányai K, Martella V

Antibodies for strain 2117-like vesiviruses (caliciviruses) in humans

Virus Res. - Vol. 210 (2015). - p 279-282. - 21 bib ref [Nr. Estr. 7120]

The vesivirus strain 2117 has been identified as contaminant of bioreactors used for production of human drugs, due to possible contamination of the reagents used for cell cultivation. Using an ELISA assay, antibodies specific for 2117-like viruses were detected in 32/410 (7.8%) human sera, indicating exposure to these viruses.

Di_Martino F, Di_Profio F, Lanave G, De_Grazia S, Giammanco GM, Lavazza^o A, Buonavoglia C, Marsilio F, Banyai K, Martella V

Antibodies for strain 2117-like vesiviruses (caliciviruses) in humans

13th National Congress of the Italian Society for Virology (SIV) : Orvieto (TR), 14-16 September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 57 [Nr. Estr. 7285]

National Congress of the Italian Society of Virology (SIV) (13th : Orvieto (TR) : 14-16 September 2015)

In 2003, a novel calicivirus, the vesivirus (VeV) strain 2117, was identified incidentally as a contaminant in Chinese Hamster Ovary (CHO) cell cultures in Germany. Possible sources of contamination included reagents used for cell cultivation of bovine or porcine origin. Contamination of CHO cell cultures by the VeV strain 2117 was documented in three additional episodes, in 2008 and 2009 in Allston, Massachusetts, USA, and in 2008 in Geel, Belgium. More recently, screening of faecal specimens from household and shelter dogs in Europe has led to the identification of novel canine VeVs genetically similar in their genome (89-90% nt) to the vesivirus strain 2117. The 2117-like VeVs were detected at high prevalence (64.8%) in healthy dogs. Accordingly, it may be hypothesized that faecal contamination of canine origin may also be a major source of exposure to these VeVs for humans. An age-stratified collection of human sera (n=410) was screened for the presence of IgG antibodies by using an ELISA assay based on the capsid protein (VP1) of a 2117-like virus, the canine strain Bari/212/07/ITA, expressed in baculovirus. Also, a total of 611 serum samples from pigs of various age groups was included in the screening. The antigenicity of the recombinant VP1 was confirmed in Western blotting (WB), using sera collected from dogs naturally infected by a 2117-like VeV. The cut-off point of the test (OD405 > 0.5) was established as the mean of the OD405 readings of 50 human -serum samples negative in WB for the presence of VeV-specific antibodies, plus 2 standard deviations. Out of 410 human sera, a total of 32 sera (7.8%) reacted with the VeV antigen at a dilution of 1:100 with an OD405, ranging from 0.5 to 1.2 (mean OD405 of 0.8). None of the tested porcine sera showed reactivity to the VeV antigen. Overall, these findings seem to indicate that humans are exposed to 2117-like VeVs. At the same time, our results suggest that 2117-like VeVs are not common in pigs, at least in the population examined, and raise doubts on the hypothesis that porcine trypsin was the source of CHO contamination. The role of 2117-like viruses of canine origin in the repeated CHO contamination events should be considered.

Di_Paolo A, Corneli S, Arrigoni°N, Biagetti M, Ca giola M, Ciullo M, Mangili P, Maresca C, Papa P, Pezzotti G, Ricchi°M, Vitale N, Mazzone P

Bovine paratuberculosis and gamma interferon test

Atti del LXIX Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : XII Convegno AIPVet, Il Convegno RNIV, XV Convegno SICV, XIII Convegno SIRA, XI Convegno So.Fi.Vet : Perugia, 15-17 Giugno 2015 / [s.l. : s.n., 2015]. - p 370. - 2 bib ref [Nr. Estr. 7020]

Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : 69 Convegno AIPVet : 12 Convegno RNIV : 2 Convegno SICV : 15 Convegno SIRA : 13 Convegno So.Fi.Vet : 11 : Perugia : 15-17 Giugno 2015)

Traditional diagnosis of bovine Paratuberculosis (PTB), due to *M. avium* subsp. *paratuberculosis* (MAP), is based on serology and fecal culture. Gamma Interferon (γ -IFN) test, already used for ante-mortem diagnosis of bovine Tuberculosis (bTB) (1), is able to detect cytokine production by T lymphocytes after stimulation with mycobacterial antigens. γ -IFN test could be also useful for PTB diagnosis (2) and, at the same time, for detection of animals exposed to other mycobacteria belonging to the *Mycobacterium avium* complex. Istituto Zooprofilattico Sperimentale of Umbria and Marche, by permission of Italian Ministry of Health, since 1981 produces purified protein derivatives (PPDs) from *Mycobacterium bovis* (PPDB), from *Mycobacterium avium* (PPDA) and recently, for experimental use only, from MAP (PPDJ). In order to identify animals infected by mycobacteria, and particularly for early detection of subjects exposed to MAP infection, in the last decade we performed, in different cattle herds, a γ -IFN assay which provides the use of PPDB, PPDA and experimental PPDJs in the lymphocyte stimulation phase. At first, 391 sera of cattle older than 24 months, from officially bTB-free herds in Central Italy, collected during monitoring programs, were processed with PTB ELISA (IDVet), as screening test and then confirmed by PCR and cultural assays. For the γ -IFN test, 1 ml whole blood aliquots were stimulated respectively with PBS (blank), PPDs supplied by BOVIGAM kit (Prionics) and Italian PPDs. At the later time 3 new PPDJs extracted from culture of MAP field isolates were produced and compared to classic PPDs in the γ -IFN test. In this second study, 68 cattle, older than 12 months, from officially bTB-free herds, with previous PTB clinical cases, were included. All cattle were screened as previously described twice a year. PPDJs were added in γ -IFN test at dilutions 1:5 and 1:10. Samples have been considered positive when Optical Density (OD) value was, at least, twice the OD obtained after stimulation with PBS alone (blank). In the first study, 50/391 sera reacted in the screening test and 48 cattle were confirmed PTB positive by PCR and/or fecal cultures; out of these 48 PTB positive animals, Avian PPDs identified 43 subjects as *M. avium* infected cattle. In the later study, 55/68 animals were PTB positive, and 46 reacted to both PPDA and PPDJ, while only four to PPDJ. The sensitivity in PTB diagnosis of PPDJs was around 78%, but this value could be influenced by the poor sensitivity of the tests used as gold standard, which are able to detect only advanced stages of disease. In fact four of nine subjects, previously classified as PTB negative, but positive to PPDJ, became positive eight months later to serology and culture. Our preliminary results highlight the ability of γ -IFN test to avoid false positivity for bTB; for detection of MAP infection we obtained encouraging results, but more subjects should be included in the study to increase the robustness of γ -IFN with PPDJ, especially young animals with a suitable follow up. Projects RCIZSUM 11/2008 and RCIZSUM 04/2011 funded by Italian Ministry of Health.

Dondo A, Caruso C, Cerrina P, Giorgi I, Prato R, Masoero L, Grindatto A, Capucci° L, Cavadini°P, Di_Blasio A, Lavazza°A

Utilizzo di un protocollo diagnostico integrato per la prevenzione e gestione di focolai della malattia emorragica virale e della mixomatosi del coniglio

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 175-177. - 5

bib ref [Nr. Estr. 7058]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. :
Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Aim of this work is to realize an integrated diagnostic protocol for prevention and management of Myxomatosis and Rabbit Hemorrhagic Disease outbreaks, through the identification of suitable and achievable actions including vaccination, introduction of animals sentinel, serological testing and interpretation of antibody titers in fattening and reproductive categories.

Dore S, Liciardi M, Amatiste S, Bergagna S, Bolzoni°G, Caligiuri V, Cerrone A,
Farina G, Montagna C, Saletti MA, Cannas EA

Epidemiology of small ruminant mastitis in Italy

XXII International Congress of Mediterranean Federation for Health and Production of Ruminants :
Sassari June 17th-20th, 2015 / [s.l. : s.n., 2015]. - p 346-350. - 7 bib ref [Nr. Estr. 7183]

International Congress of Mediterranean Federation for Health and Production of Ruminants
(Fe.Me.S.P.Rum.) (22 : Sassari : June 17th-20th, 2015)

Small ruminant dairy sector represents the main agricultural activity in rural Mediterranean areas and mastitis is the most relevant disease affecting animal welfare and causing economic losses. Until now, only few investigations about the local epidemiology of udder infections were performed. Aim of the study was to describe the national epidemiology of bacterial mastitis in small ruminant dairy herds in Italy. An ad hoc electronic data collection module was created in 2014 by C.Re.N.M.O.C. To assess the methodological reliability of the electronic tool, a pilot study, enrolling the Istituti Zooprofilattici Sperimentali, was carried out. The selected items related to milk samples and herds were placed in 3 different sections: 1) general information; 2) microbiology other than mycoplasma spp.; 3) mycoplasma spp. 8/10 (80%) Institutes participated; however, 7/8 (87.5%) provided a full report. 15,861 sheep and goat milk samples from 982 herds were microbiologically tested in 2013. Most of them (65%) were collected in Sardinia, followed by Emilia Romagna (12%), Tuscany (9%), Lazio (9%), and Molise (4%). 5,910/15,861 (37.3%) milk samples were positive. Coagulase-negative staphylococci (CNS) were the most frequently isolated in dairy sheep (45.0% milk samples; 34.0% herds) and goats (19.0% milk samples; 36.0% herds), followed by Staphylococcus aureus (12.6% sheep milk samples; 25.9% sheep herds) (9.8% goat milk samples; 27.3% goat herds); other bacteria specie isolated were Pseudomonas spp. (4.6 % sheep milk samples; 7.3% sheep herds) (0.7 % goat milk samples; 2.9 % goat herds), Streptococcus uberis (4.4 % sheep milk samples; 8.5 % sheep herds) (0.9 % goat milk samples; 2.2 % goat herds), enterobacteriaceae (3.5 % sheep milk samples; 10.7 % sheep herds) (1.7 % goat milk samples; 10.8 % goat herds), etc. Data on mycoplasma spp. were insufficient. These preliminary results confirm previous findings detected in other countries where the small ruminant dairy sector is relevant; CNS are the most important aetiology probably because of subclinical symptoms. The present survey is the first standardized data electronic collection focused on small ruminant mastitis carried out in Italy. It can represent the backbone for future control and preventive strategies.

Dotti°S, Ferrari°M, Lombardi°G, Cinotti°S, Caloni F

Stato dell'arte sulle metodologie alternative

Benessere e animal care dell'animale da laboratorio / autori, A. Berry ... [et al.] a cura di Silvio Garattini ... [et al.]. - 1. ed. - Milano : Edizioni PVI, 2015. - p 43-51. - 12 bib ref [Nr. Estr. 7157]

Drumo R, Magistrali CF, Napolioni V, Ruggeri°J, Picciolini M, Tabarrini F, Cucco L,
Pesciaroli M, Battistoni A, Ammendola S, Alborali° G.L, Pasquali R, Pezzotti G

Gut porcine microbiota modifications upon infection with attenuated or virulent Salmonella typhimurium strains

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 240 (Poster P222) [Nr. Estr. 7094]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Pork has been considered the source of about 70% of human cases of salmonellosis in Italy. On that account, there is an urgent need for new methods for Salmonella control in pigs. The intestinal microbiota is an efficient barrier against pathogen colonization and plays a role in the progression of salmonellosis. The aim of this study was to investigate the relation between Salmonella Typhimurium virulence and gut microbiota in infected pigs. Materials and Methods Bacterial cultures Virulent S. Typhimurium ATCC14028 and its isogenic attenuated mutant strain denominated Salmonella Typhimurium AznuABC were used throughout the study. Experimental design Thirty-one weaned piglets, 20-25 days old, were divided in a group of 9 (Group A) and two groups of 11 (Groups B and C). Group A was used as control, Groups B and C were orally infected with 2x10⁹ CFU of S. Typhimurium znuABC (Group B) or 2x10⁹ CFU of S. Typhimurium ATCC 14028 (Group C). Faecal samples were collected at different time points (T0, challenge; T2 two days and T4, 12 days after infection). 16S rRNA Metagenomics Sequencing Extracted DNA was used to amplify by PCR the hypervariable V3-V4 regions of the 16S rRNA [3]. PCR amplicons underwent sequencing library prep (Illumina,US). All the libraries were normalized and pooled by 24 prior to sequencing on Illumina MiSeq using a 2x250 paired-end setting. Bioinformatics and statistical analysis The Lederhosen pipeline was used to create the operational taxonomic unit (OTU) table for each sample. Kruskal-Wallis Test was used to test significant differences among the groups. Benjamini-Hochberg False Discovery Rate (FDR) method was applied to correct for multiple testing. Statistical significance was set at P<0.05. Results Piglets infected either with fully virulent or attenuated S. Typhimurium shed bacteria through faeces with different patterns in the two groups. Metagenomics analyses revealed no significant differences among the three groups at T0. At T2, 7 phyla, 112 families and 404 genera resulted differentially present among the three groups. Notably, the hierarchical clustering of the most represented genera displayed a perfect clusterization of each single sample into its belonging study group. Discussion and conclusions At T2 and T4, pigs belonging to different groups clustered together; this difference was more evident at T4, when the excretion of Salmonella was significantly lower in group B than in group C. Salmonella infection caused a shift of porcine gut microbiota composition. The extent of the shift was correlated to the virulence, since the effect was more pronounced in S. Typhimurium ATCC14028 infected pigs than in S. Typhimurium AznuABC infected animals.

Eldaghayes I, Dayhum A, Kammon A, Sharif M, Ferrari G, Sumption K, King D, Grazioli S, Brocchi E

Control Strategy of FMD In Libya And post-vaccination monitoring

GFRA (Global Foot-and-Mouth Disease Research alliance) Congress 2015 : Hanoi, 20-22 October 2015 : abstract book / [s.l. : s.n., 2015]. - 49 p [Nr. Estr. 7177]

GFRA (Global Foot-and-Mouth Disease Research alliance) Congress : Hanoi : 20-22 October 2015)

Libya is currently qualified in stage 1 of the Progressive Control Pathway (PCP-FMD). FMD mass vaccination campaigns in Libya, once per year, for small ruminants (SR) and large ruminants (LR) have been carried out since 2012. A cooperation agreement was signed with the Italian Government in 2012 to gain a better understanding of the epidemiological situation and specific activities designed and conducted in collaboration with IZSLER. Since early 2013 a surveillance system has been designed and implemented structured into three main components: Collection of samples from clinically affected animals in FMD suspected outbreaks. Evaluation of immune response of vaccinated animals by collecting blood samples at the vaccination day and 30 days post-vaccination. Investigation on the level of FMD virus circulation (anti-NSP antibodies) and the serotypes present (anti-SP serotype-specific antibodies). Most of the lab work for the 3 components was carried out in IZSLER, Italy. For field diagnosis, the Veterinary Rapid Response Teams (RST) are using the

Pen-Side tests provided by EuFMD as part of the component 2.3 of EuFMD workplan (REMESA). For post-vaccination monitoring, a total of 164 from SR and 30 serum samples from LR were randomly collected during 2013 to assess the immune response at 30 days post-vaccination. Animals were ear tagged and vaccinated at day 0, and blood samples were collected at the same day of vaccination (day 0) and at 30 days post-vaccination. In SR immunity (seroconversion) at 30 DPV was 82% and 93% against type 0 and A respectively while in LR the proportion of seroconversion was 100% for both type 0 and A, and 97% against SAT2. Since 2014, the National Center of Animal Health (NCAH) has decided to vaccinate LR twice per year. Post-vaccination evaluation has been designed and started in January 2015. A total of 99 heads of LR were vaccinated and ear tagged. Blood samples were collected every two months. At 6 months post-vaccination, 70 heads were booster vaccinated. Blood samples will be collected 2, 4 and 6 months following the booster vaccination. Despite the instability of the country, lots of activities from Libyan vets in order to control FMD were carried out. To further progress along the PCP and with the objective of reaching stage 2 additional studies should be done to better characterize risk hotspots and transmission pathways.

Esteves PJ, Abrantes J, Bertagnoli S, Cavadini P, Gavier-Widén D, Guitton JS, Lavazza A, Lemaitre E, Letty J, Lopes AM, Neimanis AS, Ruvoën-Clouet N, Le_Pendu J, Marchandeu S, Le_Gall-Reculé G

Emergence of pathogenicity in lagoviruses : evolution from pre-existing nonpathogenic strains or through a species jump?

PLoS Pathog. - Vol. 11 no 11 (2015). - p e1005087 (8 p). - 97 bib ref (ultimo accesso 27/11/2015 <http://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1005087>) [Nr. Estr. 7097]

Fabbi M, Prati P, Vicari N, Manfredini A, Sacchi L, Clementi E, Bandi C, Epis S, Genchi M

No evidence of transovarial transmission of Francisella tularensis by tick vectors Dermacentor reticulatus and Ixodes ricinus

8th International Conference on Tularemia : September 28 - October 1, 2015, Opatija, Croatia : program agenda and abstract book / editor, Marina Santic. - [Rijeka : Faculty of Medicine, University of Rijeka, 2015]. - p 153 [Nr. Estr. 7072]

International Conference on Tularemia (8th : Opatija, Croatia : September 28 - October 1, 2015)

Due to its easy dissemination, multiple routes of infection, high environmental contamination and morbidity and mortality rates, Francisella tularensis is considered a potential bioterrorism threat and classified as a category A select agent by the CDC. Tick bites are among the most prevalent modes of transmission, and ticks have been indicated as a possible reservoir, although their reservoir competence has yet to be defined. Tick-borne transmission of E tularensis has been recognized since 1923, and transstadial transmission has been demonstrated in several tick species. Studies on transovarial transmission, conducted between 1920 and 1960, when molecular techniques had not been developed nor E tularensis subspecies had been defined yet, have produced conflicting results. The aim of this study was to evaluate the role of ticks as reservoirs for Francisella, assessing the transovarial transmission of fully virulent E tularensis subsp. holarctica in experimentally-infected females of Dermacentor reticulatus and Ixodes ricinus. The experimental design was performed in 6 replicates. A total of 150 D. reticulatus and 150 I. ricinus unfed questing adult female ticks were used. For each replicate, 2 guinea pigs were used. On Day -3, all animals were infected with 25 female ticks and 35 male ticks and on Day 0, the tick-infested guinea pigs were inoculated subcutaneously with 500 CFU of the bacterium suspended in 0.3 ml of sterile saline solution. After completion of the tick blood feeding, bacterial culture and real-time PCR confirmed the infection by E tularensis subsp. holarctica in all animals. All ticks examined during and/or at the end of oviposition were positive by PCR and culture. PCR, culture, transmission electron microscopy and fluorescence in situ hybridization showed E tularensis within tick oocytes. However, cultures and bioassays of eggs and larvae were negative; in addition, electron microscopy techniques revealed bacterial

degeneration/death in the oocytes. These results suggest that bacterial death might occur in oocytes, preventing the transovarial transmission of Francisella. We can speculate that Francisella does not have a defined reservoir, but rather various biological niches (e.g. ticks, mosquitoes, rodents, lagomorphs, amoebae) that allow the bacterium to persist in the environment. Our results suggest that ticks are not competent for the vertical transmission of the bacterium and are congruent with this view. However, even in the absence of a transovarial transmission, ticks are able to maintain the infection in the environment during the inter-epizootic period and can be identified as long-term vectors of *E. tularensis*.

Faccini°S, Barbieri°I, Franzini°G, Rosignoli°C, Caleffi A, Nigrelli°AD

Focolai del genotipo emergente PCV2d in allevamenti suini italiani

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 46-47. - 10 bib ref [Nr. Estr. 7057]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Porcine Circovirus Type 2 (PCV2) is an important pathogen related to several disease syndromes in pigs, collectively named PCVAD (PCV associated disease). PCV2 strains are currently classified into four genotypes: PCV2a, PCV2b, PCV2c and PCV2d. The latter is considered an emergent genotype since it has been increasingly isolated worldwide, mainly in cases of suspected vaccine failure. In this work we report recent outbreaks of PCVAD due to PCV2d infection in five Italian pig farms. Data strengthen the hypothesis of PCV2d as an emergent genotype. The role of vaccination pressure and natural selection is not clear and must be further investigated. Sustaining diagnostic data with sequence analysis is extremely important in this context.

Faccini°S, De_Mattia A, Barbieri°I, Chiapponi°C, Rosignoli°C, Franzini°G, Foni°E, Nigrelli°AD

Prima segnalazione della presenza del virus dell'influenza D in Italia

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 43-44. - 6 bib ref [Nr. Estr. 7043]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

In 2011 in Oklahoma a new strain of Influenza virus, distantly related to human influenza C virus, was isolated from a pig with respiratory symptoms and provisionally designated C/swine/Oklahoma/1334/2011(C/OK). Similar viruses have been subsequently isolated from cattle in the USA, China and France. Genetic, biological, and antigenic characterization suggested that C/OK-like viruses represent a new genus in the Orthomyxoviridae family, tentatively named Influenza D virus (IDV). The distribution and prevalence of IDV is still unknown and only few studies have been performed. Here we report the results of a pilot survey on IDV in clinical samples from cattle with respiratory symptoms in Italy. More than 100 nasal swabs and lung tissues have been tested by Real-Time PCR. Five positive samples from 4 herds have been demonstrated. Sequencing and phylogenetic analysis, confirmed the classification in Influenza D genus. These results represent the first evidence of IDV occurrence in Italy.

Falcone E, Busi°C, Lavazza°A, Monini M, Bertolett i°M, Canelli°E, Vignolo E, Ruggeri FM, Boniotti°MB

Molecular characterization of avian rotaviruses circulating in Italian poultry flocks

Avian Pathol. - Vol. 44 no 6 (2015). - p 509-515. - 39 bib ref [Nr. Estr. 7131]

Avian rotaviruses are still largely undefined despite being widespread in several avian species and despite the economic impact of rotavirus (RV) enteritis in poultry flocks. In this study, the presence of different avian RV groups was investigated in commercial poultry flocks reared in Northern and Central Italy and with a history of enteric diseases. Faeces or intestinal contents from different avian species previously found to contain RV particles by electron microscopy (EM) were analysed by both RNA-polyacrylamide gel electrophoresis and reverse transcription-polymerase chain reaction specific for groups A, D, F and G RVs. Group D avian RV was detected in 107 of 117 samples tested (91.5%), whereas groups A, F and G avian RVs were present in 70 (59%), 61 (52.1%) and 31 (26.5%) samples, respectively. Multiple presence of different RV groups was detected in 83% of samples. This study provides novel data on the prevalence of genetically different avian RVs in Italian poultry flocks. This information is useful to elucidate the epidemiology of avian RVs circulating in Italy.

Fanelli A, Agazzi A, Alborali°GL, Pilotto A, Bontempo V, Dell'Orto V, Demey V, Caputo JM, Savoini G

Prevalence reduction of pathogens in poultry fed with *Saccharomyces cerevisiae*

Biotechnol Agron Soc Environ. - Vol. 19 no 1 (2015). - p 3-10. - 29 bib ref [Nr. Estr. 7224]

Fink M, Schleicher C, Gonano M, Proding WM, Pacciarini°M, Glawischnig W, Ryser_Degiorgis MP, Walzer C, Stalder GL, Lombardo D, Schobesberger H, Winter P, Buettner M

Red deer as maintenance host for bovine tuberculosis, Alpine Region

Emerg Infect Dis. - Vol. 21 no 3 (2015). - p 464-467. - 14 bib ref [Nr. Estr. 6012]

To estimate the prevalence of bovine tuberculosis in the Alpine region, we studied the epidemiology of *Mycobacterium caprae* in wildlife during the 2009–2012 hunting seasons. Free-ranging red deer (*Cervus elaphus*) were a maintenance host in a hot-spot area, mainly located in Austria.

Fiorentini°L, Taddei°R, Casadio°M, Parigi°M, Vicari°N, Massi°P, Tosi°G

Valutazione della sensibilità antibiotica di ceppi di *Escherichia coli* isolati da specie avicole allevate e da avifauna selvatica

Atti della Società Italiana di Patologia Aviare (SIPA) 2015 : LIV Convegno annuale : Forlì, 16-17 Aprile 2015 / [s.l. : s.n., 2015]. - p 152-161. - 9 bib ref [Nr. Estr. 7000]

Convegno annuale Società Italiana Patologia Aviare (SIPA) (54. : Forlì : 16-17 Aprile 2015)

The in vitro susceptibility to 18 antibiotics of 85 Escherichia coli strains (50 strains recovered from different wild bird species and 35 strains recovered from poultry farms) isolated in Emilia Romagna region in the period 2013-2014 was studied. Resistances to 16 antibiotics was observed (both in poultry species than in wild birds) and the following percentages of resistance (respectively for domestic and wild species) were obtained: penicillin G (100% and 100%), amoxicillin (68% and 21%), enrofloxacin (62% and 13%), ceftiofur (54% and 16%), tylosin (97% and 100%), tetracycline (84% and 30%), trimethoprim (100% and 100%), neomycin (16% and 5%), lincomycin/ spectinomycin (81% and 70%), trimethoprim/sulfamethoxazole (38% and 12%), oxacillin (97% and 100%), erythromycin 97% and 100%), tiamulin (100% and 100%), lincomycin (100% and 100%), streptomycin (30% and 8%) and spectinomycin (69% and 64%). A significant correlation of the resistance of E.coli strains isolated from poultry was noted towards amoxicillin, ceftiofur, enrofloxacin

oxacin and tetracycline. The intestinal tract of wild birds is a reservoir of antibiotic resistance E.coli strains and it is also remarkable that multiresistant E.coli isolates were detected both in poultry species than in wild birds.

Fogola T, Leone A, Teodori L, Ronchi F, Lelli°D, L orusso A, Savini G

Indagine sierologica per Pteropine orthoreovirus (Genere Orthoreovirus, Famiglia Reoviridae) in animali domestici e selvatici

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 350-351. - 4 bib ref [Nr. Estr. 7064]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Indonesia/2010, a novel member of the Pteropine Orthoreovirus (PRV) species was recently discovered and isolated at the IZSAM from fruit bats (genus Pteropus, family Pteropodidae) -the biological reservoir of PRV- legally imported to Italy from Indonesia. Therefore we decided to investigate whether PRVs had the chance to circulate in animals in Italy and in selected countries, including Namibia and Mauritania. A total number of 1180 serum samples collected from wild and domestic animals were tested for the presence of PRV antibodies. Serum-neutralization was employed as read-out assay and, based on the samples tested so far, there is no evidence of PRV antibodies. Certainly, it is necessary to test more se-rum samples from different areas and animal species and -more importantly from humans. PRVs indeed are able to cause respiratory tract infections in humans and these infections have been linked to exposure with fruit bats.

Fogola T, Leone A, Teodori L, Ronchi F, Lelli°D, L orusso GA

Absence of serological evidente of Pteropine Orthoreoviruses (genus Orthoreovirus, family Reoviridae) from domestic and wild animals in Italy

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 253-254 [Nr. Estr. 7021]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Foni°E, Chiapponi°C, Baioni°L, Merenda°M, Luppi °A, Rugna°G, Mandalari°C, Tamba°M, Pellacini M, Forlenza J

High genetic variability of swine influenza virus in a confined area of Northern Italy

3rd International Symposium on Neglected Influenza Viruses : 15th — 17th April 2015, Athens, Georgia USA / International Society for Influenza and other respiratory virus diseases (ISIRV). - [s.l. : s.n., 2015]. - p 63 [Nr. Estr. 6033]

International Symposium on Neglected Influenza Viruses (3rd : Athens, Georgia USA : 15th — 17th April 2015)

Swine influenza A virus (SIAV) circulates actively in the Italian pig population and subtypes H1 avN1, H1 huN2, H3N2 and H1N1pdm are mainly detected, but also reassortant (r) strains are occasionally isolated. Considering a limited number of herds in a confined area high genetic variability of SIAVs was detectable. In a confined area in Northern Italy (388 Km²), where 65 pig farms were located, 37 sets of clinical samples (n.119) were collected from 3 different pig farms. A: a farrow to feeder farm, B: a finishing pig farm and C: a farrow to finish farm. The farms were monitored respectively for one year (2014), one year and half (2013-2014) and four years (2009-2011-2012-2014) according to the respiratory outbreaks occurrence. Virological and biomolecular investigations for SIAV were performed and 17 isolates were selected for genetic studies. A: 15 groups of samples (n.34) were examined and 4 H1N2 subtype SIAVs were obtained. Genetic studies characterized 2 SIAVs as

H1N2r pdm strains (German Papenburg lineage) and 2 SIAVs as H1N2r pdm strains showing H1N1 pdm internal genes but HA and NA clustering with H1huN2 Italian SIAV. B: 8 sets of samples (n.46) were examined and 8 SIAVs were isolated. Four strains were characterized as H1avN1, 2 strains as H1huN2 while 2 strains showed to be r strains H1avN2sw. C: 39 samples were examined and 10 SIAVs belonging to different genetic lineages were detected: H1avN1, H1huN2, H3N2, H1avN2r and also H1N2r strain clustering with the German lineage. A very high variability of gene constellation of SIAVs was described in three pig farms: 2, 3, and 5 SIAV lineages were detected respectively. The study underlines the increasing genetic diversity of Italian SIAVs also considering a confined area and also in absence of animal introduction. These differences cannot be explained easily; however the area is regarded as major node of trading network of swine and pork and this feature must be considered. Continuous surveillance of SIAV infections should be further reinforced to provide a baseline for updating and interpretation of the role of SIAV in zoonotic events and also to focus on relatedness to currently used vaccines.

Foni°E, Chiapponi°C, Baioni°L, Merenda°M, Mandarini°C, Luppi°A, Rugna°G, Tamba°M, Pellacini M, Forlenza J

Elevata variabilità genetica di virus influenzale suino in una delimitata area della Pianura padana = High genetic variability of swine influenza virus in a confined area of Northern Italy

Atti Convegno SIPAS. - Vol. 41 (2015). - p 231-239. - 19 bib ref [Nr. Estr. 7007]

Meeting Annuale della Società Italiana di Patologia ed Allevamento dei Suini (SIPAS) (41. : Montichiari (BS) : 19-20 Marzo 2015)

Il virus dell'influenza A suina (SIAV) circola attivamente nella popolazione suina italiana e i sottotipi H1avN1, H1huN2hu, H3N2 and H1N1pdm sono riscontrati con maggior frequenza anche se occasionalmente vengono isolati stipiti riassortanti (r). Sono stati condotti accertamenti virologici e biomolecolari nei confronti di SIAV su 3 allevamenti, per complessive 5 unità produttive, in una delimitata area del Nord Italia. Complessivamente sono stati isolati 35 sottotipi di SIAV da cui sono stati selezionati 17 SIAV per la caratterizzazione genetica. Nell'allevamento a ciclo aperto A, 4 SIAV sono stati isolati, 2 SIAV sono stati caratterizzati come virus h1N2r appartenenti al lineage Papenburg circolante in Germania mentre 2 SIAV sono risultati virus h1N1 pdm riassortanti con virus h1huN2hu circolanti nella popolazione suina italiana. Nell'allevamento di suini all'ingrasso B sono stati caratterizzati 4 SIAV riferibili al sottotipo H1avN1, mentre 2 isolati sono stati caratterizzati come h1huN2hu e, gli ultimi 2 come stipiti riassortanti H1avN2sw. Nell'allevamento a ciclo chiuso C (C1, C2 e C3 le tre unità produttive) è stata identificata la circolazione dei sottotipi H1avN1, H1huN2, h3N2, h1avN2r ed anche di uno stipite h1N2r riferibile al lineage Papenburg. Questo studio, se pur condotto su un numero limitato di aziende che circoscrivono un' area geografica ridotta, ha messo in evidenza una elevata variabilità nella composizione genetica dei SIAV coinvolti.

Swine influenza A virus (SIAV) circulates actively in the Italian pig population and mainly subtypes h1avN1, h1huN2hu, h3N2 and h1N1pdm are detected, but also reassortant (r) strains are occasionally isolated. Considering a limited number of herds (n. 5) in a confined area of North Italy a high genetic variability of SIAVs was detectable. Farm A: a farrow to feeder farm, farm B: a finishing pig farm and farm C: a farrow to finish farm (C1, C2 and C3). Virological and biomolecular investigations for SIAV were performed and 17 isolates were selected for genetic studies. A: 4 h1N2 SIAVs were obtained. Genetic studies characterized 2 h1N2r pdm strains (German Papenburg lineage) and 2 h1N2r pdm strains showing h1N1pdm internal genes but hA and NA clustering with h1huN2hu Italian SIAV. B: 8 SIAVs were isolated. four strains were characterized as h1avN1, 2 strains as h1huN2hu while 2 strains showed to be r strains h1avN2sw. C: 10 SIAVs belonging to different genetic lineages were detected: h1avN1, h1huN2hu, h3N2, h1avN2r and also h1N2r strain clustering with the German lineage. The study underlines the increasing genetic diversity of Italian SIAVs even in a limited number of herds and even in those that did not introduce animals, in confined area of North Italy. Continuous surveillance of SIAV infections should be further reinforced to provide a baseline for updating and interpreting the role of SIAV in zoonotic events and to focus on relatedness to currently used vaccines.

Formenti N, Ferrari N, Trogu T, Partesana ST, Pedrotti Luca, Gaffuri°A, Lanfranchi P

Toxoplasma gondii in gatti e cervi simpatrici: diffusione e ruolo dell'ospite definitivo sull'infezione di quello intermedio

33emes Recontres du GEEFSM : Balme : Recueil des resumes / [s.l. : s.n, 2015]. - 7182]

Recontres du GEEFSM (33emes : Balme : 21 au 24 Mai 2015)

Le popolazioni a vita libera sono soggette a processi epidemiologici complessi a causa della loro interazione con diversi fattori, biotici e abiotici, alla dinamica delle loro infezioni e alla crescente antropizzazione del territorio. L'indagine epidemiologica nelle popolazioni selvatiche si complica in caso di parassiti il cui ciclo può coinvolgere diverse specie ospiti, così come nel caso di *Toxoplasma gondii*. *T. gondii*, protozoo a diffusione ubiquitaria e caratterizzato da diverse vie di trasmissione, può infettare numerose specie domestiche e selvatiche. Tuttavia la sua diffusione e la dinamica dell'infezione in ecosistemi naturali deve essere tutt'ora approfondita e, in particolare, il ruolo che può avere l'ospite definitivo nella diffusione dell'infezione di quello intermedio. Pertanto è stata condotta un'indagine sierologica di *T. gondii* su cervi (*Cervus elaphus*) e gatti (*Felis catus*) simpatrici provenienti da due aree all'interno del Parco Nazionale dello Stelvio per valutare (i) i fattori epidemiologici che influenzano la diffusione del protozoo nelle due specie e per definire (ii) il ruolo dell'ospite definitivo sull'infezione di quello intermedio. Complessivamente sono stati campionati 137 sieri di cervo durante due campagne di abbattimento (Novembre e Dicembre 2012 e 2014) previste nel piano di contenimento numerico della specie all'interno del Parco. Per ogni soggetto sono stati rilevati età, sesso, località e misure morfobiometriche. Da Dicembre 2013 a Luglio 2014, sono stati raccolti un totale di 51 campioni di siero di gatti provenienti dalle stesse aree. I soggetti campionati sono gatti domestici, che trascorrono la maggior parte della loro giornata fuori dall'abitazione, gatti semi-domestici o gatti di stalla. Per ogni Soggetto sono stati rilevati età, sesso e località. I campioni sono stati analizzati con un kit ELISA commerciale (ID screen Toxoplasmosis Indirect multi-species). Tramite Modelli Lineari Generalizzati è stato indagato l'effetto di sesso, classe di età (piccoli, animali di un anno, adulti), Indice di Grasso Renale (Kidney Fat Index, KFI), area e anno di studio sulla probabilità che i cervi fossero infetti. Inoltre modellizzando i titoli sierologici dei soggetti sieropositivi sono stati valutati gli effetti delle stesse variabili sulla dinamica dell'infezione. Nell'analisi dei gatti è stato indagato l'effetto di sesso, classe di età (piccoli, animali di un anno, adulti) e area sulla probabilità di essere infetto. L'analisi sui cervi ha messo in evidenza una prevalenza (p) totale del 32.8%. È stato riscontrato un effetto significativo della classe di età: gli animali di un anno (p=42%) e gli adulti (p=43.7%) sono risultati significativamente più infetti rispetto ai piccoli (una femmina positiva su 35 analizzati). Inoltre è stata osservata una differenza significativa tra i due anni di studio: nel 2012 (p=39.5%), infatti, i soggetti sono risultati significativamente più infetti rispetto a quelli del 2014 (p=23.2%). I titoli sierologici degli animali di un anno sono risultati significativamente maggiori rispetto a quelli degli adulti.

Formenti N, Trogu T, Pedrotti L, Gaffuri°A, Lanfranchi P, Ferrari N

Toxoplasma gondii infection in Alpine red deer (Cervus elaphus) : its spread and effects on fertility

PLoS One. - Vol. 10 no 9 (2015). - p e0138472 (11 p). - 55 bib ref (ultimo controllo 02/10/2015 : <http://www.plosone.org/article/fetchObject.action?uri=info:doi/10.1371/journal.pone.0138472&representation=PDF>) [Nr. Estr. 7033]

In contrast to the depth of knowledge on the pathological effects of parasitism in domestic animals, the impact of the vast majority of parasites on wildlife hosts is poorly understood and, besides, information from domestics is rarely usable to disclose the parasites' impact on free-ranging populations' dynamics. Here we use Toxoplasmosis as a study model since, until now, the infection process and the protozoan's effects in natural conditions has received little attention. We analysed 81 sera from red deer (*Cervus elaphus*) sampled in Italian Alps and through generalized linear models we evaluated (1) the epidemiological factors influencing *T. gondii* infection dynamics; (2) its

impact on female fertility. High seroprevalence of *T. gondii* infection was recorded in yearling (1 year-old; prevalence = 52.4%) and adult (>2 year-old; prevalence = 51.3%) red deer, while calves (<1 year-old) did not contract the infection suggesting horizontal transmission as the main route of infection. The stable prevalence between yearlings and adults and the higher serological titres of younger individuals lead to two alternative infection processes suggesting a difference between age classes or in acquiring the infection or in responding to the pathogen. No associations between *T. gondii* serological titres and pregnancy status was observed indicating no direct effect on the probability of being pregnant; nevertheless a relation between females' higher serological titres and lower foetal development emerged, suggesting potential effects of the parasite infection on deer reproduction. The results demonstrate high seroprevalence of *T. gondii* infection in free-ranging red deer and, furthermore, the effect on foetal development suggests the potential impact of the parasite on red deer fertility and thus on its population dynamics.

Fusi°F, Lorenzi°V, Angelucci°A, Donati°M, Bertocchi°L

IZSLER/CRenBA on-farm dairy cow welfare assessment protocol : cause-effect association between management and housing factors and lameness prevalence : a retrospective study in Italy

Proceedings of the Second DairyCare Conference 2015 : Cordoba March 3rd and 4th 2015 / editor, C.H. Knight. - [s.l. : DairyCare COST Action FA1308, 2015]. - p 30 (P1.7) [Nr. Estr. 7208]

DairyCare Conference (2nd : Cordoba : March 3rd and 4th, 2015)

In 2011, the Italian National Animal Welfare Reference Centre (CRenBA) decided to develop a protocol to assess and compare the level of animal welfare and biosecurity in dairy herds, drawing a picture of the Italian situation. The protocol was applied at first to Northern Italian dairy herds; since then in 2012 it has been extended to the entire national territory. The IZSLER/CRenBA protocol comprises of 89 different indicators, both animal-based (ABMs) and non-animal-based measures (N-ABMs), divided into 5 areas: Area A - Management and personnel; Area B - Structures and equipment; Area C - ABMs; Area D - Exposure to environmental hazards; Area E - Biosecurity. The total amount of scores given to Areas A-B-C-D provides the overall level of animal welfare on-farm, ranging from 51.45 to 199.35 points; the score given to Area E (min 14.5 –max 52 points) provides the overall level of biosecurity on farm. From 2011 to January 2015, 922 Italian loose-housed dairy herds were assessed. Herds were randomly selected in different Italian regions and assessments were carried out by 74 veterinary assessors, who all attended a specific training course in IZSLER/CRenBA in order to ensure consistent and repeatable welfare assessment outcomes. Herd size ranged from 7 to 2736 animals (259.54 on average) and from 4 to 1135 lactating cows (119 on average); average milk production was 27.8 kg per cow/day (range 10-41 kg). The overall welfare score recorded on average was 154.53 points (69.69% of the available score). The aim of this study was to identify and compare management (n=21) and housing (n=28) factors associated with the prevalence of lameness " 8% (DairyCo Mobility Scoring system was used; both lactating and dry cows with a Mobility Score 2 or 3 were considered lame). The most significant (P<0.05) and strongest (OR>1.6) associations are reported in Table 1. In conclusion, the managerial factors that seem to be more associated with lameness are the number of stockpeople taking care of cows, the number of daily inspections and the overall cleanliness of the barn; while the housing factors are the lying area provided for dry cows and the type of floor.

Gaffuri°A, Formenti N, Vicari°N, Paterlini°F, Lanfranchi P

Can Sarcocystis spp. interfere in molecular diagnosis of Toxoplasma gondii in wild ungulates?

Harmonized approaches in monitoring wildlife population health, and ecology and abundance :

APHAEA - Final meeting, 17-18 March 2015, Amsterdam & Utrecht, The Netherlands : programme and abstract book / [s.l. : s.n., 2015]. - p 17 [Nr. Estr. 6005]

APHAEA - Final meeting : Amsterdam & Utrecht, The Netherlands : 17-18 March 2015)

BACKGROUND: The protozoan *Toxoplasma gondii* affects worldwide several mammalian and avian host species raising public health, economic and conservation concerns. As wild ungulates can be source of *T. gondii* human infection and this protozoan could affect their reproductive performances, a reliable diagnostic trial to monitoring the infection should be defined. Following previous positive serological results in Italian Central Alps, we investigated the reliability of different PCR protocols in wild ungulates. **METHODS:** We sampled heart muscles of 58 wild boar, 104 roe deer, 10 mouflon and brain samples of, 50 chamois and 159 red deer. Then the diagnostic trial was defined using a PCR targeting a 529 bp non-coding region (protocol 1), a single tube nested PCR (protocol 2) and a PCR-RFLP (protocol 3) using primers that identify also *Neospora caninum* and *Sarcocystis* spp.. **RESULTS:** *T. gondii* DNA was clearly detected in a chamois and in a mouflon by protocol 1. In 15 red deer samples, weak PCR products resulted from the protocol 1 and thus they were submitted to other PCRs. The *T. gondii* negativity was confirmed with protocols 2 and 3, but the 3 detected *Sarcocystis* spp. DNA in a calf. By the same protocol, *Sarcocystis* DNA was identified also in 34 wild boar and in 37 roe deer. Sequencing analysis discriminated *Sarcocystis hjorti*, *Sarcocystis miescheriana* and *S. cruzi* and/ or *S. gracilis*, respectively in red deer, wild boar and roe deer. **CONCLUSIONS:** Protocol 1 is useful in chamois and mouflon but can have a lower specificity than two others in red deer. On the contrary protocol 2 is recommended for the direct *T. gondii* diagnosis. Protocol 3 is useful to differentiate the three protozoa infections, but in latent toxoplasmosis and pauciparasitism infections with the simultaneous presence of *Sarcocystis* the detection of *T. gondii* may fail.

Garbarino°C, Merialdi°G, Arrigoni°N, Natalini S, Zanangeli A, Cammi M, Modenesi R, Finazzi°G, Fontana°MC, Rosignoli°C

Due focolai di botulismo in allevamenti di vacche da latte in regione Emilia Romagna

Buiatria. - Vol. 2015). - 6 p. - 7 bib ref [Nr. Estr. 7163]

Vengono descritti due focolai di botulismo che hanno coinvolto nel 2014 due allevamenti di vacche da latte della pianura emiliano-romagnola, causando rispettivamente la morte del 61% (allevamento A) e del 15% (allevamento B) degli animali in lattazione. La diagnosi è stata effettuata mettendo in evidenza la tossina botulinica e/o le spore di *Clostridium botulinum* nel contenuto ruminale ed intestinale degli animali deceduti dopo aver manifestato la classica sintomatologia paralitica. Le spore di *Clostridium botulinum* tipo D sono state dimostrate anche nell'alimento (unifeed) del focolaio B. Relativamente alle misure precauzionali di sanità pubblica adottate, gli animali deceduti ed abbattuti con sintomatologia clinica sono stati destinati ad un impianto di rendering. Il latte di tutte le bovine in lattazione, indipendentemente dalla sintomatologia clinica, è stato distrutto nel focolaio A, mentre nel focolaio B è stato distrutto solo il latte delle vacche con sintomatologia clinica e pastorizzato quello delle rimanenti. La durata dell'episodio è stata rispettivamente di 25 giorni nell'allevamento A e di 16 giorni nell'allevamento B. L'elevato danno economico per l'allevatore ha portato alla chiusura dell'allevamento A, dove la prevalenza è risultata più elevata. In relazione al fatto che in questi ultimi anni si è registrato un aumento del numero di focolai di botulismo nelle vacche da latte nei paesi a vocazione zootecnica, vengono presi in considerazione i fattori di rischio, che possono favorire la crescita e la tossinogenesi da parte di *C. botulinum* e la conseguente insorgenza di focolai, quali l'utilizzo di foraggio in rotoballe fasciate e la presenza di carcasse di animali selvatici (nutrie, ungulati, anatidi) che possono accidentalmente venire "inglobate" e contaminare l'alimento somministrato agli animali.

Garbarino°CA, Savi°R, Leo°S, Cammi°G, Bianchi° A, Gaffuri°A, Giacomelli°S, Ricchi°M, Bertolotti°I, Arrigoni°N

Sub-tipizzazione di ceppi di *Mycobacterium avium* subsp. *paratuberculosis* isolati da cervi (*Cervus elaphus*) selvatici

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 84-85. - 8 bib ref [Nr. Estr. 7045]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

*The role of wild ruminants as reservoir for *Mycobacterium avium* subsp. *paratuberculosis* (MAP) is still not clear. However, some studies have reported that the same genotypic MAP profiles can be shared by domestic and wild ruminants. The aim of our study was sub-typing MAP field strains isolated from red deer in the Stelvio National Park (collected from 2011 to 2014). All 11 field strains isolated in the study showed the same profile INMV1 (<http://mac-inmv.tours.inrafr>), which is also the most diffused in Europe both in domestic and wild species.*

Gasparrini°S, Pitozzi°A, Ruggeri°J, Nigrelli°AD , Alborali°L, Boniotti°MB

Characterization of *Brachyspira hyodysenteriae* from Italy by multilocus sequence typing and multiple locus variable number tandem repeat analysis

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 112 (Poster P042) [Nr. Estr. 7130]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Introduction: *Brachyspira hyodysenteriae* is an anaerobic intestinal spirochaete and the aetiological agent of swine dysentery (SD). The disease is characterized by severe mucohemorrhagic diarrhoeal and affects pigs primarily during the growing-finishing period. The increased resistance to antimicrobials observed in many countries induces to understand the dynamics of SD. The development of more effective measures to counter its spread depends also on the ability to characterize *B. hyodysenteriae* variants and trace relationships of epidemic strains through reliable strain typing methods. Materials and method: One hundred and four *B. hyodysenteriae* isolates were collected during a period of three years (2012-2014) from 75 Italian farms placed in 13 different administrative areas. The typing of every single strain was conducted using both multilocus sequence typing (MLST) and multiple locus variable number tandem repeat analysis (MLVA) to understand the better tool for their characterization. In particular, the MLST approach analyzes the allelic variation in nucleotide sequences of seven housekeeping gene loci (*adh*, *alp*, *est*, *gdh*, *glpK*, *pgm* and *thi*). Whereas, MLVA technique is based on the detection of the number of tandem repeats at seven multiple variable number tandem repeat (VNTR) loci within the genome (*Bhyo6*, *Bhyo7*, *Bhyo12*, *Bhyo17*, *Bhyo21*, *Bhyo22* and *Bhyo23*). Results: The study conducted with the MLST method described 19 different sequence type (ST), 8 clusters and 11 unique. One predominant ST (ST83) was observed in 54 strains isolated from 36 different farms located in 9 areas. In addition, the amino acid analysis recognized the presence of 12 amino acid type (AAT) parted in 2 clonal complex e 1 singleton. Phylogenetic analysis of the concatenated nucleotide sequences showed the presence of three major groups. The MLVA approach allowed to characterize completely 86 strains on a total of 104. The isolates were then gathered into 13 different VNTR profiles, 6 clusters and 7 unique. The VNTR profiles included all the STs previously recognized. Only in one case the analysis of VNTR gave a different and more specific characterization. The calculation of Diversity Index (DI) showed that MLST (DI=0,720) is a more discriminatory method than MLVA (DI=0,663). Conclusion: In conclusion, MLST approach is a reliable and discriminant method to characterize *Brachyspira hyodysenteriae* strains and to establish epidemiological correlation among different outbreaks..

Gazzonis AL, Veronesi F, Di_Cerbo AR, Zanzani SA, Molineri G, Moretta I, Moretti A, Fioretti DP, Invernizzi°A, Manfredi MT

Toxoplasma gondii in small ruminants in Northern Italy - prevalence and risk factors

Ann Agric Environ Med. - Vol. 22 no 1 (2015). - p 62-68. - 31 bib ref [Nr. Estr. 6007]

Objective. The aim of the survey was to evaluate *Toxoplasma gondii* seroprevalence in small ruminants and possible risk factors associated with the infection. **Materials and methods.** Sera from 474 goats and 502 sheep reared on 42 farms in northern Italy were collected and tested for IgG antibodies to *T. gondii* by IFAT (indirect immunofluorescence antibody test). To identify risk factors, a binary logistic regression analysis of the variables was performed. An audit form about farm management was used. **Results.** Antibodies to *T. gondii* were found in 96.6% of goat farms and in 87.5% of sheep farms; 41.7% goats and 59.3% sheep resulted positive. Seroprevalence was significantly higher in sheep than in goats. Seroprevalence values were similar in goats from eastern and western areas, whereas goats from the southern area were at lower risk of infection. Saanen goats presented the lowest seroprevalence (30.7 %), whereas cross-breed exhibited the highest rate (48.7%). Goats from farms housing both sheep and goats had an infection risk 1.39 times higher than goats from farms that did not house sheep. Animals bred on intensive farms showed lower prevalence (22.1%) in comparison with those from extensive (45.6%) or semi-intensive farms (60%). Sampling area was one of the strongest predictors of *T. gondii* infection in sheep flocks. Transhumant flocks showed a higher risk of infection by *T. gondii* compared with semi-intensive farms (66.8% vs. 38.4%). **Conclusions.** The highest *T. gondii* seroprevalence values were registered in transhumant flocks of sheep and in family businesses rearing goats. As these traditional activities represent an important resource for the conservation of the territory and its economy, management practices for a better control of the disease should be improved.

Genchi°M, Prati°P, Andreoli°G, Barzetti C, Bassa nini L, Ciraulo G, Bellotti°M, Petasecca°D, Rigamonti°S, Vicari°N

Sarcocystis spp.: indagini preliminari su un parassita negletto

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 334-335. - 8 bib ref [Nr. Estr. 7062]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Sarcocystis spp. is an intracellular protozoan belonging to the phylum Apicomplexa. It can infect mammals, birds and cold-blooded animals. Four Sarcocystis species infect cattle: S. cruzi, S. hirsuta, S. hominis (which is zoonotic), and the recently described S. rommeli. In humans, clinical signs vary depending on the species of Sarcocystis causing infection and the organ parasitized. The affected animals are usually clinically normal and eosinophilic myositis lesions induced by the parasite are only discovered at post-mortem inspection of carcasses. We analyzed 15 carcasses of cattle that had suspicious muscle lesions. Samples of muscle, heart, and (in some cases) diaphragm were collected from each carcass and investigated for the presence of Sarcocystis spp. by PCR-RFLP. All carcasses tested positive and genome sequencing led to the detection of S. cruzi, S. hominis, S. rommeli, and S. hirsuta in 40.0%, 26.7%, 20.0% and 13.3% of samples, respectively.

Genchi°M, Prati°P, Vicari°N, Manfredini°A, Sacc hi L, Clementi E, Bandi C, Epis S, Fabbì°M

Francisella tularensis : no evidence for transovarial transmission in the tularemia tick vectors Dermacentor reticulatus and Ixodes ricinus

PLoS One. - Vol. 10 no 8 (2015). - p e133593 (13 p). - 41 bib ref (Ultimo accesso: 07/09/2015 - <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0133593>) [Nr. Estr. 6088]

Background Tularemia is a zoonosis caused by the *Francisella tularensis*, a highly infectious Gram-negative coccobacillus. Due to easy dissemination, multiple routes of infection, high

environmental contamination and morbidity and mortality rates, *Francisella* is considered a potential bioterrorism threat and classified as a category A select agent by the CDC. Tick bites are among the most prevalent modes of transmission, and ticks have been indicated as a possible reservoir, although their reservoir competence has yet to be defined. Tickborne transmission of *F. tularensis* was recognized in 1923, and transstadial transmission has been demonstrated in several tick species. Studies on transovarial transmission, however, have reported conflicting results. Objective The aim of this study was to evaluate the role of ticks as reservoirs for *Francisella*, assessing the transovarial transmission of *F. tularensis* subsp. *holarctica* in ticks, using experimentally- infected females of *Dermacentor reticulatus* and *Ixodes ricinus*. Results Transmission electron microscopy and fluorescence in situ hybridization showed *F. tularensis* within oocytes. However, cultures and bioassays of eggs and larvae were negative; in addition, microscopy techniques revealed bacterial degeneration/death in the oocytes. Conclusions These results suggest that bacterial death might occur in oocytes, preventing the transovarial transmission of *Francisella*. We can speculate that *Francisella* does not have a defined reservoir, but that rather various biological niches (e.g. ticks, rodents), that allow the bacterium to persist in the environment. Our results, suggesting that ticks are not competent for the bacterium vertical transmission, are congruent with this view.

Gennero MS, Barbero R, Canale G, Bergagna S, Dezzutto D, Falzone R, Tarello V, Boniotti MB, Lombardi G, Tagliabue S

Leptospirosis in bovine : case reports of *Leptospira Hardjo* in Piedmont Region

2nd ELS meeting on leptospirosis and other rodent borne haemorrhagic fevers : 16-18 April 2015
Amsterdam, the Netherlands / [s.l. : s.n., 2015]. - p 92 [Nr. Estr. 6051]

ELS meeting on leptospirosis and other rodent borne haemorrhagic fevers (2nd : Amsterdam, the Netherlands : 16-18 April 2015)

Introduction *Leptospira borgpetersenii* is a bacterial pathogen of cattle and it also causes zoonotic infections in humans. It is important because is a significant public health problem and because causes organ failure in the liver, lungs, kidney, and brain. (Naiman, Brion M. et. al., 2002). *L. borgpetersenii* serovar *Hardjo* type *hardjo-bovis* is the most common cause of leptospirosis in bovine, in addition, *hardjo-bovis* is one of the most common serovars because cattle are maintenance hosts. **Materials and Methods** We report a cluster of two cases of leptospirosis in Italian farms, with regard to clinical, laboratory, environmental findings and pharmacological therapy: a beef farm of Piedmontese cows with 100 cows and 38 sheep, outbreak on 2013; a dairy farm of Pezzata Rossa d'Oropa with 70 cows, outbreak on 2014. The two cases were investigated by case interview and review of clinical and laboratory information. A site visit was made to the farm to assess environmental risk. Different methods of laboratory diagnosis were used with each case: microagglutination test MAT to reveal antibody in serum, microbiological techniques and PCR Real Time LipL32 to detect leptospiral DNA in tissue samples including urine and milk. The isolates were serotyped by MAT using a panel of reference hyperimmune sera. Moreover, serovar identification was performed by Multilocus Sequence Typing (MLST). Auto-vaccines whole cell bacterins were manufactured from *Leptospira* isolates of the two outbreaks. **Results and Conclusions** The two outbreaks were confirmed as leptospirosis by MAT (increasing Ab titers against serogroup Sejroe) and in both cases the isolated causative agent was identified as *L. borgpetersenii* serovar *Hardjo* type *hardjo-bovis* by MLST (ST 152). By PCR all the urine samples (9) and 8 out 12 urine samples examined were positive respectively in the first and in the second case. Laboratory tests showed the presence of *Leptospira* spp. antibodies in individual cow serum and *Leptospira* spp. organisms in urine. *L. borgpetersenii* serovar *Hardjo* type *hardjo-bovis* is one of the most important and costly contributors to reproductive loss in the beef and dairy industries. In Italy there are not vaccines for *Leptospira* in cattle, so auto-vaccines were prepared in five months with *hardjo-bovis* strains from urine samples from the two outbreaks. The antibiotic treatment and the vaccination allowed to dose the outbreaks after several months. On the basis of these data, vaccination of farm livestock for leptospirosis is an integral factor in preventing new infection and human cases. Particularly, in bovine livestock, auto-vaccines are extremely useful in case of animal movements to pasture.

Giacomelli°S, Bianchi°A, Bertoletti°I, Nicastro M, Ferrari N, Gallazzi D, Grilli G

Infestazione da Phthiraptera nell'avifauna italiana

Atti della Societa' Italiana di Patologia Aviaria (SIPA) 2015 : LIV Convegno annuale : Forli, 16-17 Aprile 2015 / [s.l. : s.n., 2015]. - p 171-179. - 21 bib ref [Nr. Estr. 7001]

Convegno annuale Societa' Italiana Patologia Aviaria (SIPA) (54. : Forli : 16-17 Aprile 2015)

The present work intend to expose the results of a 9 year long parasitological survey on wild avian fauna. The main goal is to update the checklist of the Italian fauna for the Phthiraptera order with the first signalement of Myrsidea quadrimaculata in Italy. Moreover in this publication we try to explain the differences found in prevalence from species specific and generalist parasites. In the meta-population studied it seems that generalist lice have a greater chance to colonize a single species. Some example are presented as a validation of this theory (Streptopelia decaocto and Parus major) and the example of Turdus merula as a exception to this paradigm. Lastly we show the poor parasitological situation of Erithacus rubecula in Italy.

Giacomelli°S, Polloni°A, Bianchi°A, Rota_Nodari° S, Pedrotti L, Gugiatti A, Archetti°IL, Bertoletti°I, Lombardi°G

Ferogramma sieroproteico in cervi (Cervus elaphus) viventi nelle Alpi Centrali italiane

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 105-106. - 6 bib ref [Nr. Estr. 7046]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Serum protein electrophoresis is a valuable ancillary test. its use has proven to be useful on the behalf of diagnosis and screening of pathologies (4) and, moreover, in animal welfare monitoring (1). Recent papers have applied this technique to wildlife investigating trade off between innate and adaptive immunity (2). The application of this method need a certain grade of experience, mostly when the investigation concerns a species rarely considered by blood tests in general. Reference intervals are a rapid consultation tool for a more accurate evaluation of the results returned by the method. The definition of such values, determined from a reference population with valid and widely accepted statistical methods, is therefore a way to validate any future study that includes this method and red deer species (Cervus elaphus). Defining reference intervals, in this publication, we provide some cornerstones for the availment of this technique on free-living red deer.

Giacomini°E, Boniotti°MB, Lavazza°A, Lazzaro°M, Papetti°A, Salogni°C, Giovannini°S, Luppi°A, Nigrelli°A, Alborali°GL

Focolai di diarrea epidemica del suino (PED) in 3 allevamenti a ciclo chiuso del nord Italia = Outbreaks of porcine epidemic diarrhea (PED) in 3 farrow-to-finish farms

Atti Convegno SIPAS. - Vol. 41 (2015). - p 217-222. - 9 bib ref [Nr. Estr. 7006]

Meeting Annuale della Societa' Italiana di Patologia ed Allevamento dei Suini (SIPAS) (41. : Montichiari (BS) : 19-20 Marzo 2015)

La Diarrea Epidemica del Suino (PED è l'acronimo di Porcine Epidemic Diarrhea) è una patologia sostenuta da coronavirus, caratterizzata da elevata morbilità e bassa mortalità, che si manifesta clinicamente con diarrea e disidratazione. Lo studio descrive tre episodi di PED che si sono verificati in aziende a ciclo chiuso della Lombardia segnalati nel volgere di pochi giorni a gennaio 2015. La sintomatologia era caratterizzata da anoressia e diarrea acquosa che ha interessato i riproduttori, i suinetti in sala parto e i suini in svezzamento, magronaggio ed ingrasso. Nei tre episodi la morbilità è stata del 80-100% e la mortalità assente in tutti i settori tranne nei suinetti sottoscrofa dove è stata del 25-50%. La diagnosi è stata fatta sia in PCR che in MAb-ELISA e l'analisi genomica preliminare

dei ceppi identificati ha permesso di determinare che essi presentano un'elevata percentuale di identità con il ceppo USA Oh851 considerato a moderata patogenicità. Le indagini epidemiologiche hanno evidenziato nei tre episodi la carenza di misure di biosicurezza esterna, in particolare riferite alla modalità di carico e scarico di animali vivi, della circolazione, pulizia e disinfezione dei mezzi di trasporto.

Porcine Epidemic Diarrhea (PED) is a disease caused by coronavirus characterized by high morbidity, low mortality and clinically by diarrhea and dehydration. The study describes three outbreaks of PED occurred in farrow-to-inish farms located in Lombardy, which occurred within few days on January 2015. The clinical signs in breeders, piglets growing and fattening pigs were characterized by anorexia and watery diarrhea. In the three PED outbreaks morbidity was 80-100% and mortality missing in all categories but piglets in which it was 25-50%. The diagnosis was performed by PCR and MAb-ELISA and preliminary genomic analysis of the strains showed a high percentage of identity with the mild strain USA Oh851. Epidemiological investigations in the three outbreaks have shown failure of external biosecurity measures related to the animal loading and unloading, movement, cleaning and disinfection of vehicles.

Giacomini°E, Boniotti°MB, Pitozzi°A, Gasparri° S, Remistani°M, Dottori°M, Alborali°GL

Mycoplasma hyopneumoniae detection in tracheobronchial swabs, oral fluid and lung

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 107 (Oral Presentation 037) [Nr. Estr. 7082]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Introduction. Detection of *M. hyopneumoniae* (*M.hyo*) by quantitative polymerase chain reaction (qPCR) can be used to identify the beginning of an infection and its variations according to the age of the animal. The collection of OF showed advantages over the collection of blood samples and tracheobronchial swabs (TBS) regarding animal welfare, as it is less intrusive and pigs are more cooperative. The aim of this study was to compare the *M. hyo* titers in TBS and OF specimen by quantitative Real Time PCR (qPCR) in vaccinated and unvaccinated animals. Materials and Methods. The study was carried out in a three-site herd in the North of Italy with endemic *M. hyo* infection. The animals were bred in the first site until a month of life, in the second site from one month to three months and in the third site from three months until slaughterhouse. Different *M. hyo* vaccination schemes were applied in three groups: 1) 30 pigs were vaccinated at 7 days of life, 2) 30 pigs were vaccinated at 26 days old and 3) 30 pigs were used as controls. Blood, TBS and OF samples were taken from each pig at the first week of life (T1) and once a month until 9 months old (T2-T10). Blood samples were tested by HerdChek® *M. hyo* antibody test kit while TBS and OF were analyzed by qPCR directed against the p102 gene of *M. hyo*. Samples were considered positive when the n° of genomic copies was equal or above $1,9 \times 10^3$ copies/ml. Results. Both in TBS and OF of all groups, *M. hyo* infection was detected by qPCR when the animals were moved to the third site (T5) till the last sampling (T10). In TBS the percentage of positive animals at T5 was 30, 35, and 42% in group 1, 2 and 3, respectively. The higher number of positive pigs occurred at T6 in group 1 and T9 in group 2 and 3. Overall, TBS were positive for 52% out of 90 while OF for 8% samples. Copies/ml values were in the range of $1,9 \times 10^3$ - $1,7 \times 10^8$ in TBS samples and $1,9 \times 10^9$ - $6,4 \times 10^5$ in OF samples. ELISA results showed a maternal immunity at T1 in all groups. At T3, vaccinated animals developed antibodies against *M. hyo* while unvaccinated animals seroconverted when infection started (T5).

Gibellini M, Bonilauri°P, Gherpelli°Y, Giovanardi D, Marzani°K, Torri°D, Dottori°M, Ferro P, Scandurra S, Maioli°G, Hidalgo A, Lupp i°A

Prevalenza dei fattori di virulenza associati a E. coli isolati da suini con diarrea post svezzamento (PWD) in Italia = Prevalence of virulence factors associated with post weaning

diarrhoea (PWD) in pigs in Italy

Atti Convegno SIPAS. - Vol. 41 (2015). - p 199-207. - 15 bib ref [Nr. Estr. 7005]

Meeting Annuale della Societa' Italiana di Patologia ed Allevamento dei Suini (SIPAS) (41. : Montichiari (BS) : 19-20 Marzo 2015)

In questo studio è stata valutata la prevalenza di *Sarcoptes scabiei* var. *suis* in partite di suini macellati provenienti da allevamenti del nord Italia. Nel periodo agosto 2014 – gennaio 2015 sono state campionate 219 partite di suini macellati, provenienti da 112 allevamenti di 20 province suddivise su 6 regioni diverse (Emilia Romagna, Lombardia, Veneto, Piemonte, Marche e Friuli-Venezia Giulia). Sono stati analizzati pool costituiti da 30 scaricati auricolari di suino attraverso una metodica di chiarificazione e concentrazione. La prevalenza totale in tutte le partite campionate è risultata del 13,7% (IC 95%: 9,1%- 18,3%), mentre gli allevamenti positivi sono risultati essere il 19,6% (IC 95%: 12,2%- 27%). Questo lavoro evidenzia che la rogna sarcoptica nel suino è una problematica attuale ed importante nell'allevamento industriale, sia per le perdite economiche ad essa correlate sia per la difficile diagnosi ed eliminazione.

From 2012 to 2014, 159 E. coli isolates were obtained from diagnostic samples (rectal swabs, faeces and small intestine) collected from pigs with post weaning diarrhoea (PWD), belonging to 84 herds located in Northern Italy, using standardized bacteriological methods. To evaluate the prevalence of virulence factors, a multiplex PCR (Casey and Bosworth, 2009) for f4 (K88), f5 (K99), f6 (987P), f18, f41, STa, STb, LT and Stx2e genes was performed on E. coli isolates. The prevalence of imbric genes was: F4 (54,8%), f18 (33,3%) and f6 (1,2%). In 5 cases, the strains isolated harboured more than one imbric gene: F4+F18 (4,8%) and F5+F41 (1,2%). The prevalence of toxin genes was: LT (55,9%), STa (63,1%), STb (71,4%) and STx2e (9,5%). ETEC isolates were detected in 68 of the herds (80,9%), with 98,8% of them being haemolytic. ETEC-f4 were isolated in 57,6% of the outbreaks (39 out of 68), whilst 36,8% (25 out of 68) were classified as ETEC-F18. The two most common ETEC serotypes were F4, STb, LT (25%) and f4, STa, STb, LT (22,1%). This study confirms that ETEC-F4 is most commonly associated with PWD in Italy and the most prevalent serotype was f4, STb, LT. Information about the prevalence of ETEC in cases of PWD is relevant when measures of control of the disease such as vaccination must be taken. Alternative approaches to antibiotic therapy are needed, since very high rates of antimicrobial resistance are reported in ETEC isolated from cases of PWD.

Giorda F, Ballardini M, Mignone W, Iulini B, Pintore MD, Petrella A, Pintore A, Toffan A, Scholl F, Terracciano G, Latini M, Ferri N, Caracappa G, Rubini S, Di_Nocera F, Mazzariol S, Di_Guardo G, Casalone C, Pautasso A

The Italian diagnostic network on stranded cetaceans : "from local to global" approach

29th Conference of the European Cetacean Society (ECS) "Marine mammal conservation from local to global" : 23rd to 25th March, 2015, Malta / [s.l. : s.n., 2015]. - p 12 [Nr. Estr. 7147]

Conference of the European Cetacean Society (ECS) (29th : Malta : 23rd to 25th March, 2015)

Liguria Region is an important commercial and touristic area located in the north west of Italy on the Ligurian Sea, in the middle of the Pelagos Sanctuary. The 'Istituto Zooprofilattico Sperimentale (IZS) del Piemonte, Liguria e Valle d'Aosta', a Public Health Research Institute, in Imperia District, has been involved in the health and epidemiologic surveillance of cetaceans stranded in this area since 1985, with more than 130 animals submitted to diagnostic investigations. Since 2009, thanks to a project promoted by the Italian Ministry of Health, its' diagnostic approach has been expanded to Tuscany and Lazio regions and progressively adopted by all other IZS. Such diagnostic network has been integrated in the national marine mammal strandings' network, which uses a multidisciplinary approach involving several institutions and experts. By doing so, standardization of diagnostic post mortem protocols, traceability of reports, sampling and sharing of the results were obtained. Thanks to these achievements, it was also possible to manage with efficiency and coordination an unusual mortality event (UME), which occurred along the Tyrrhenian coast of Italy between January and March 2013, which should be regarded as the fourth dolphin morbillivirus outbreak in the western Mediterranean basin (Casalone et al., 2014), along with a mass stranding of 7 sperm whales (*Physeter macrocephalus*), whose investigations are still ongoing, which occurred in September

2014 along the Adriatic Sea coast. The Italian experience permitted to realize how a joint activity leads to an optimization of the efforts. A similar approach, standardized across all the European countries of the Mediterranean basin, would allow improvement of the health and epidemiologic surveillance on stranded cetaceans, with the result of monitoring the aquatic environment, as well as the animal and public health, in the long-term and on a larger geographic scale.

Gradassi°M, Caminiti°A, Galletti°G, Santi°A, Pa ternoster°G, Tamba°M, Zanoni°M, Tagliabue°S, Alborali°GL, Trevisani M

Suitability of a Salmonella control programme based on serology in slaughter heavy pigs

Res Vet Sci. - Vol. 101 (2015). - p 154-160. - 47 bib ref [Nr. Estr. 6082]

The key component of most European pig Salmonella control programmes is the classification of herds according to seroprevalence at slaughter. The objectives of this study were to estimate the true Salmonella seroprevalence, and investigate the association between the true status of infection and serology in slaughter heavy pigs. Blood of 3340 pigs was collected and tested with ELISA. From 385 pigs, also lymph nodes and cecal content were collected for bacteriology. Analysis was performed in a Bayesian framework. Results showed that a large proportion of pigs was serologically positive (herd seroprevalence 93% and within-herd seroprevalence higher than 81% in half of herds at cut-off 10 OD%). The association between the true status of infection and serology was not significant, and therefore the classification of heavy pig herds according to seroprevalence at slaughter would not be suitable to reduce the risk of introducing Salmonella into the food chain.

Hocking T, Veldkamp L, Vinco°LJ, Woodward P

High water intake is associated with soya compared with non-soya protein sources and may be associated with foot pad dermatitis in growing turkeys

Br Poult Abstr. - Vol. 11 no 1 (2015). - p 33-34. - 1 bib ref [Nr. Estr. 7189]

Jacob D, Fabbi°M, Prati°P, Becker S, Lochau P, Gr unow R

Results on antimicrobial susceptibility testing of Francisella tularensis using minimal inhibitory concentration with two methods, gradient diffusion and broth dilution

8th International Conference on Tularemia : September 28 - October 1, 2015, Opatija, Croatia : program agenda and abstract book / editor, Marina Santic. - [Rijeka : Faculty of Medicine, University of Rijeka, 2015]. - p 110 [Nr. Estr. 7070]

International Conference on Tularemia (8th : Opatija, Croatia : September 28 - October 1, 2015)

Francisella tularensis is the causative agent of tularemia. In Europe only F. tularensis ssp. holarctica (F.t.h.) was found to cause tularemia in humans so far. The infection is quite often induced through the contact with infected European brown hares (Lepus europaeus). Although F.t.h. causes a relative mild form of tularemia in humans, an adequate antibiotic treatment is indispensable. Among the guidelines of the European Committee on Antimicrobial Susceptibility Testing (EUCAST) no recommendations of minimal inhibitory concentration (MIC) testing and interpretation of data on F. tularensis are given. For the further evaluation of protocols for Antimicrobial Susceptibility Testing developed in the framework of the JointAction "Quality Assurance Exercises and Networking on the Detection of Highly Infectious Pathogens" (QUANDHIP), we used 16 isolates of F.t.h. collected from 1964 until 2010 mostly from hares. The developed standard operation procedure (SOP) considers the special requirements for growth of these fastidious bacteria. The MIC was tested by gradient diffusion using LiofilchemD stripes and broth microdilution on commercial test plates from Merlin, MICRONAUT, comprising a panel of 12 freeze-dried antimicrobial agents (penicillin, vancomycin, clindamycine, imipenem, ciprofloxacin, levofloxacin, gentamicin, tigecycline, doxycycline, rifampicin,

chloramphenicol, and linezolid). The results of both methods were compared and the MIC data were interpreted according to the American Clinical and Laboratory Standards Institute (CLSI) criteria, when available. Both methods showed a good performance and are applicable for highly infectious fastidious bacteria under appropriate biosafety conditions.

Kreizinger Z, Erdélyi K, Fabbi^oM, Gyuranecz M

**Detection of virulence difference between B.13 ("RED") and FTNF002-00 ("PURPLE")
Francisella tularensis ssp. *holarctica* genotypes**

8th International Conference on Tularemia : September 28 - October 1, 2015, Opatija, Croatia : program agenda and abstract book / editor, Marina Santic. - [Rijeka : Faculty of Medicine, University of Rijeka, 2015]. - p 154 [Nr. Estr. 7073]

International Conference on Tularemia (8th : Opatija, Croatia : September 28 - October 1, 2015)

The *Francisella tularensis* ssp. *holarctica* population in Europe is classified into two main genetic subclades. The B.13 subclade predominates in central and eastern Europe while the FTNF002-00 is the only native subclade in the western part of the continent. The European brown hare (*Lepus europaeus*) is considered the main reservoir species of tularemia in central Europe. The B.13 type strains from this region cause subacute/chronic disease in hares with typical granulomatous lesions in the lung, pericardium and kidney. However, European brown hares dying from tularemia caused by the FTNF002-00 strain in western Europe generally show signs of septicaemia with enlarged spleen and liver during necropsy. The aim of this study was to examine whether there is a difference in the virulence of B.13 and FTNF002-00 genotypes of *Francisella tularensis* ssp. *holarctica* strains. Groups of six age-matched (7 weeks) Fisher rats were infected intraperitoneally with 10⁶, 10⁷ and 10⁸ CFU of the B.13 genotype (Hungarian strain) and FTNF002-00 genotype strains (Italian strain). Six rats served as negative controls. Clinical signs and body weights of the rats were checked daily, and after 21 days all the rats that did not succumb to the infection were euthanized. Samples from the dead rats were submitted for serological, pathological and histopathological examinations. No significant difference was detected between the different inoculation doses. However, rats infected with the FTNF002-00 genotype strain developed a more severe disease than those infected with the B.13 genotype isolate. Seven out of the 18 rats inoculated with the FTNF002-00 genotype strain died (3-5 days post inoculation /pi./) while only 3 of the 18 rats infected with the B.13 genotype strain succumbed to the infection (3-4 days pi.). Clinical signs were similar in both groups: decreased appetite, water consumption and weight loss between days 4-13 pi., accumulated porphyrin around the eyes and nose and diarrhea. The deceased rats were seronegative while all surviving animals showed positive reaction in slide agglutination test on day 21 pi. The only macroscopic finding was the enlarged spleen in both deceased and euthanized rats. Histopathological examination is in progress. Based on these results it seems that FTNF002-00 *Francisella tularensis* ssp. *holarctica* isolates are indeed more virulent than B.13 strains. We hypothesize that this difference in the virulence could be behind the different pathological picture observed in *Francisella tularensis* ssp. *holarctica* infected European brown hares at the western and central-eastern part of the continent.

Lanave G, Martella V, Farkas SL, Marton S, Fehér E, Bodnar L, Lavazza^oA, Decaro N, Buonavoglia C, Bányai K

Novel bocaparvoviruses in rabbits

Vet J. - Vol. 206 (2015). - p 131-135. - 27 bib ref [Nr. Estr. 7119]

Bocaparvovirus is a newly established genus within the family Parvoviridae and has been identified as a possible cause of enteric, respiratory, reproductive/neonatal and neurological disease in humans and several animal species. In this study, metagenomic analysis was used to identify and characterise a novel bocaparvovirus in the faeces of rabbits with enteric disease. To assess the prevalence of the novel virus, rectal swabs and faecal samples obtained from rabbits with and

without diarrhoea were screened with a specific PCR assay. The complete genome sequence of the novel parvovirus was reconstructed. The virus was distantly related to other bocaparvoviruses; the three ORFs shared 53%, 53% and 50% nucleotide identity, respectively, to homologous genes of porcine bocaparvoviruses. The virus was detected in 8/29 (28%) and 16/95 (17%) samples of rabbits with and without diarrhoea, respectively. Sequencing of the capsid protein fragment targeted by the diagnostic PCR identified two distinct bocaparvovirus populations/sub-types, with 91.7–94.5% nucleotide identity to each other. Including these novel parvoviruses in diagnostic algorithms of rabbit diseases might help inform their potential pathogenic role and impact on rabbit production and the virological profiles of laboratory rabbits.

Lanave G, Martella V, Farkas SL, Marton S, Fehér E, Bodnar L, Lavazza^o A, Decaro N, Buonavoglia C, Bényai K

Identificazione e caratterizzazione del genoma di un nuovo parvovirus nei conigli

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 226-227. - 6 bib ref [Nr. Estr. 7050]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Bocaparvovirus (family Parvoviridae) have been identified as a possible cause of enteric, respiratory, reproductive/neonatal and neurological disease, in humans and several animal species. In this study the complete genome sequence of a novel parvovirus identified in rabbits was determined. The virus was distantly related, genetically, to other bocaparvoviruses. Rectal swabs and faecal samples obtained from symptomatic and asymptomatic animals were screened by a PCR assay with specific primers. The virus was detected in 8/29 (28%) and 16/95 (17%) samples of diarrheal and non-diarrheal animals, respectively, indicating that it is a common component of the faecal viroma of these animals. Including this novel parvovirus in the diagnostic algorithms of rabbit diseases will be helpful to assess more in depth their pathogenic role and potential impact on rabbit productions. Also, it will be important to define the virological profile of animals used in laboratory experiments.

Lanza G, Faccini F, Valdonio M, Arrigoni^oN, Pattarini P, Grilli B, Cabrini E, Boccellino M, Delledonne M

Consumo e modalità d'impiego degli antibatterici nell'allevamento di bovine da latte della provincia di Piacenza = Consumption and methods of use of antibacterial agents in the breeding of dairy cattle in the province of Piacenza

Large Anim Rev. - Vol. 21 no 2 (2015). - p 51-58. - 9 bib ref [Nr. Estr. 6063]

La conoscenza dei dati reali sul consumo di antibiotici è essenziale per impostare una strategia mirata, attraverso un uso razionale e prudente, ad una efficace riduzione dei quantitativi impiegati. Questo studio è stato condotto nel corso del 2012 per determinare il consumo di antibatterici in un campione di 50 allevamenti di bovini da latte della provincia di Piacenza. Attraverso il controllo delle ricette medicow veterinarie, dei registri aziendali di scorta e trattamento ed utilizzando le liste di riscontro in uso in Regione Emilia Romagna per le ispezioni di farmaco sorveglianza, è stato ricavato il consumo delle varie categorie di antibatterici e la relativa conformità d'impiego. Sono stati analizzati i dati ottenuti per le classi di antibatterici considerati critici in medicina umana (cefalosporine di III e IV generazione, fluorochinoloni, macrolidi e polipeptidi). Nel 72% degli allevamenti le terapie venivano effettuate unicamente a seguito di diagnosi clinica, mentre esami batteriologici ed antibio-grammi venivano effettuati in maniera sistematica solo nel 18% degli allevamenti. Il mancato rispetto delle indicazioni (dosi e durata) contenute nei foglietti illustrativi rappresenta un altro punto critico emerso dalla ricerca. La raccolta manuale dei dati sul consumo degli antibatterici richiede un impegno di risorse non sostenibile nel tempo; è quindi fondamentale poter disporre di un sistema di raccolta dati informatizzato delle prescrizioni veterinarie, che possa permettere ai vari attori coinvolti di conoscere i reali consumi di antibatterici nelle diverse tipologie di

allevamento. Altri aspetti da considerare sono la gestione sanitaria della mandria, il rispetto del benessere animale e delle norme di biosicurezza, il grado di selezione genetica, la formazione del personale.

Introduction - The problem of antimicrobial resistance is considered by the international scientific community one of the main public health topics, both in human and veterinary medicine. Knowledge about the real antimicrobial consumption is essential for setting an efficient strategy focused on their rational and prudent use. In fact, only starting from the real consumption data in different zootechnical sectors, will it be possible to build strategies for an effective reduction of antibiotic use in animals. Aim - This study was carried out to determine the antibiotic consumption during 2012 in a sample of 50 dairy cattle farms in the province of Piacenza. Since the collection of data through an informative system was not available, we checked all the veterinary prescriptions collected in the selected farms. Materials and methods - Through the verification of recorded treatments and using the official checklists for drug surveillance in the Emilia Romagna region, we calculated the total consumption of the different classes of antibiotics, and compliance with leaflet prescriptions. Finally, we analyzed the data obtained for the CIA (Critically Important Antimicrobials) for human medicine (third and fourth generation cephalosporins, fluoroquinolones, macrolides and polypeptides). Results and discussion - Data collected didn't show any statistically significant correlation neither between antibacterial amount per head and herd consistency, nor between antibacterial amount and milk production per cow. In 72% of the inspected farms, antibacterial therapies were established only on the basis of a clinical diagnosis, while bacteriological exams and antibiograms were systematically performed in only 18% of farms. For this reason it's possible to conclude that, in most farms, the breeder was not aware of the real health state of his herd. From the results of this research, a frequent failure in compliance to leaflet instructions regarding doses and treatment duration was evident, although it is well known that this could lead to emergence of resistant bacterial strains. Conclusions - The availability of data on the consumption of antibacterial drugs is a key element for surveillance of their correct use and for setting objectives; however, manual collection requires a significant commitment of resources, unsustainable over time. It would be essential in the future to have an informative system about the real antimicrobial consumption, to make the data promptly available to the Veterinary Health Service and to all the stakeholders. Other aspects, however, should be taken into consideration for a comprehensive assessment of the problem, such as proper health management of the herd, compliance to animal welfare and bio-security standards, genetic selection and managerial aspects such as staff training.

Lavazza[°]A, Cavadini[°]P, Barbieri[°]I, Tizzani P, Pí nheiro A, Abrantes J, Esteves PJ, Grilli G, Gioia E, Zanoni[°]M, Meneguz PG, Guitton J S, Marchandean S, Chiari[°]M, Capucci[°]L

Field and experimental data indicate that the eastern cottontail (*Sylvilagus floridanus*) is susceptible to infection with European brown hare syndrome (EBHS) virus and not with rabbit haemorrhagic disease (RHD) virus

Vet Res. - Vol. 46 (2015). - no 13 (10 p). - 42 bib ref (ultimo accesso 12/02/2015
<http://www.veterinaryresearch.org/content/46/1/13>) [Nr. Estr. 5995]

The eastern cottontail (*Sylvilagus floridanus*) is an American lagomorph. In 1966, it was introduced to Italy, where it is currently widespread. Its ecological niche is similar to those of native rabbits and hares and increasing overlap in distribution brings these species into ever closer contact. Therefore, cottontails are at risk of infection with the two lagoviruses endemically present in Italy: Rabbit Haemorrhagic Disease virus (RHDV) and European Brown Hare Syndrome Virus (EBHSV). To verify the susceptibility of *Sylvilagus* to these viruses, we analyzed 471 sera and 108 individuals from cottontail populations in 9 provinces of north-central Italy from 1999 to 2012. In total, 15–20% of the cottontails tested seropositive for EBHSV; most titres were low, but some were as high as 1/1280. All the cottontails virologically tested for RHDV and EBHSV were negative with the exception of one individual found dead with hares during a natural EBHS outbreak in December 2009. The cottontail and the hares showed typical EBHS lesions, and the EBHSV strain identified was the same in both species (99.9% identity). To experimentally confirm the diagnosis, we performed two trials in which we infected cottontails with both EBHSV and RHDV. One out of four cottontails infected with EBHSV died of an EBHS-like disease, and the three surviving animals

developed high EBHSV antibody titres. In contrast, neither mortality nor seroconversion was detected after infection with RHDV. Taken together, these results suggest that *Sylvilagus* is susceptible to EBHSV infection, which occasionally evolves to EBHS-like disease; the eastern cottontail could therefore be considered a “spill over” or “dead end” host for EBHSV unless further evidence is found to confirm that it plays an active role in the epidemiology of EBHSV.

Lavazza°A, Tittarelli C, Cerioli°M

The use of convalescent sera in immune-electron microscopy to detect non-suspected/new viral agents

Viruses. - Vol. 7 (2015). - p 2683-2703. - 47 bib ref [Nr. Estr. 6046]

Negative staining electron microscopy methods can be employed for the diagnosis of viral particles in animal samples. In fact, negative staining electron microscopy methods are used to identify viruses, especially in minor species and wild animals, when no other methods are available and in cases of rare, emerging or re-emerging infections. In particular, immune-electron-microscopy with convalescent sera is employed to detect etiological agents when there are undiagnosed clinical outbreaks, when alternative diagnostic methods fail due to the lack of immunological reagents and primers, and when there is no indicative clinical suspect. An overview of immune-electron-microscopy with convalescent sera's use in the diagnosis of new and unsuspected viruses in animals of domestic and wild species is provided through the descriptions of the following four diagnostic veterinary cases: (I) enteric viruses of pigs: Porcine Rotavirus, Porcine Epidemic Diarrhea Virus, Porcine Circovirus and Porcine Torovirus; (II) Rotavirus and astrovirus in young turkeys with enteritis; (III) Parvovirus-like particles in pheasants; and (IV) Lagoviruses: Rabbit Hemorrhagic Disease Virus and European Brown Hare Syndrome Virus.

Lazzara F, Amadori°M, Bilato°D, Ferraris M, Ferrari A, Razzuoli E

Salmonella serovar specific modulation of inflammation in a jejunal epithelial cell line

Atti del LXIX Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : XII Convegno AIPVet, II Convegno RNIV, XV Convegno SICV, XIII Convegno SIRA, XI Convegno So.Fi.Vet : Perugia, 15-17 Giugno 2015 / [s.l. : s.n., 2015]. - p 363-364. - 4 bib ref [Nr. Estr. 7018]

Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : 69 Convegno AIPVet : 12 Convegno RNIV : 2 Convegno SICV : 15 Convegno SIRA : 13 Convegno So.Fi.Vet : 11 : Perugia : 15-17 Giugno 2015)

Salmonella infections are an important source of food-borne illnesses and therefore a major public health concern. In Liguria, this pathogen have a prevalence of 9.8% in wild boars liver and the 85.1% of isolated were characterized by resistance of antibiotic(1). These evidence outline a possible risk for public health. However, no all these strain are associated to salmonellosis in animals and/or humans (2). Owing to the above, the aim of our study was to evaluate the effect of Salmonella infection on inflammatory regulation in the porcine GI-tract using IPEC-J2 cell line, that represent a good model to study salmonella infection (3). An overnight culture of 6 different Salmonella enterica strain: S. Coeln, S. Ablogame, S. Enterica subspecie Diarizonae (Strain 1), S. Veneziana, S. Enterica sub-specie Diarizonae (strain 2) and S. Thompson was sub-cultured for 2 h at 37°_C in BHI. Each Bacteria cultured, re-suspended at 100 million CFU/ml in DMEM/F12 medium (4) was used to treated IPEC-J2 cell; untreated wells were employed as negative control. After 1 hours of incubation at 37°_C with 5% of CO2 monolayers were washed three time; than 2 ml/wells of plain medium were added and cell were incubate for 4 hours at 37°_C with 5% of CO2. Supernatants were harvested to evaluate IL-8 release by ELISA and the gene expression of IL-8 and NF-Kb1 was investigated by RT Real-time PCR (4). A Kolmogorov-Smirnov test was conducted to check Gaussian distributions, than differences between data sets were checked for significant differences by Kruskal-Wallis test, followed by a Dunn's test. The significance threshold was set at

$P < 0.05$ with a correction for multiple comparisons. Porcine intestinal epithelial cells more closely mimic human physiology than analogous rodent cell lines, which is important in studies of zoonotic infections. Moreover this cell line give information about pathogenicity of salmonella spp. (3). In our study we demonstrated that *S. Coeln* determine a significant increase both of IL-8 release ($P=0.005$; +527 pg/ml) that a gene expression ($P<0.0001$) with respect to control cells; also NF-Kb1 was up-regulated by this strain ($P=0.059$). *S. Veneziana*, like *S. Coeln*, determine a significant increase both of IL-8 release ($P=0.0037$; + 2898 pg/ml) that a gene expression ($P<0.04$) with respect to control cells; also NF-Kb1 was up-regulated by this strain ($P=0.0168$). Regarding *S. Enterica* sub-specie *Diarizonae* (strain 2) and *S. Thompson* caused a significant increase of IL-8 secretion ($P=0.0021$ + 3148 pg/ml and $P=0.0007$ + 3374 pg/ml; respectively) and up-regulation of IL-8 gene expression ($P=0.0098$ and $P=0.0010$); whilst, *S. Ablogame* and *S. Enterica* sub-specie *Diarizonae* (Strain 1) no modulated significantly any parameter under study. These data suggest a potential pathogenic of *S. Coeln*, *S. Veneziana*, *S. Enterica* sub-specie *Diarizonae* (strain 2) and *S. Thompson*. In particular, *S. Coeln* and *S. Thompson* data are in according with EFSA report (2). Moreover, *S. Enterica* sub-specie *Diarizonae* are usually found the environment and only occasionally are associated with human disease; however, one of our strain may be associated with disease. These evidence outline a possible risk for public health associated with the consumption of wild boars livers.

Le_Normand I, Chatellier S, Devaud I, Delvecchio A, Lavazza°A, Capucci°L

Evaluation de l'immunité humorale consecutive a la vaccination avec Dervaximyxo SG33 chez des lapines reproductrices vaccinees a differents stades du cycle productif

16ernes Journees de la Recherche Cunicole : 24 et 25 novembre 2015, Le Mans France / [s.l. : s.n., 2015]. - p 17-20. - 5 bib ref [Nr. Estr. 7204]

Journees de la Recherche Cunicole (16 : Le Mans, France : 24 et 25 novembre 2015)

L'efficacite d'une vaccination est liee A la qualite de l'immunité qu'elle induit. Cette qualite repose sur la reactivite et l'activite du systeme immunitaire au moment de la vaccination. En elevage, les vaccinations sont souvent realisees au moment oil l'eleveur a le plus de temps et en dehors des periodes reputees les plus sensibles (semaine precedant et suivant l'insemination artificielle [IA]). Neanmoins, aucune etude n'a ete conduite sur le developpement de l'immunité post vaccinale scion le moment de la vaccination durant le cycle de production : nous avons souhaite approfondir ce point concernant la vaccination contre la myxomatose (Dervaximyxo SG330, voie intra-dermique).

Evaluation of humoral immunity after vaccination with Dervaximyxo SG33® at differents states of the production cycle in rabbit does. Multiparous does of different ages received a v accinal booster Dervaximyxo SG 33 ® at various moments of breeding cycle. Blood samples were analyzed by ELISA for myxomatosis antibodies kinetics before and after vaccination. The study reveals that the does which receive a vaccinal booster after parturition and artificial insemination show a significant decrease in antibodies titers: they have to deal with two major stressful steps which is negative for optimal post-vaccinal immunity. Also, ELISA for myxomatosis carried out on young "vaccine-naïve" does allowed to exclude any viral infection in the breeding during the study.

Lecchi C, Marques AT, Redegalli M, Carisetti M, Rota_Nodari°S, Vinco°LJ, Ceciliani F

Circulating extracellular miR-22, miR-155, and miR-365 as potential biomarkers to assess the turkey (Meleagris gallopavo) welfare

5th European veterinary immunology workshop (EVIW) : Vienna, Austria, 2nd-4th September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 169 [Nr. Estr. 7108]

European veterinary immunology workshop (EVIW) (5th : Vienna, Austria : 2nd-4th September 2015)

MicroRNAs (miRNAs) are small 21-25 nucleotide regulatory non-coding RNAs that modulate gene

expression in animals. miRNAs are complementary to the 3'-untranslated regions of mRNA and act as post-transcriptional regulators of gene expression, exhibiting remarkable stability in extracellular fluids such as blood. Turkey (*Meleagris gallopavo*) farming is a species economically relevant but the lack of efficient protocols for the evaluation of commercial turkeys prevents to assess the impact of industry practices on birds productivity and welfare. In order to measure potential molecular biomarkers for monitoring stress in turkey's handling, we investigated by TaqMan qPCR the abundance of five circulating miRNA, namely miR-22, miR-155, miR-181a, miR-204 and miR-365, previously demonstrated to be involved in stress in chicken due to feed deprivation. Road transportation is regarded as one of the most stressful event in the turkeys' lifetime and it was selected as stressful model for this study. The serum of twenty healthy animals was collected before and after 2h transportation. Our results demonstrated that miR-22, miR-155 and miR-365 are statistically more expressed after road transportation. Receiver-operator characteristics (ROC) analysis was used to estimate the diagnostic value of these miRNAs to evaluate the stress in animals. The serum level of miR-22, miR-155 and miR-365 can discriminate stressed from non-stressed animals with a AUC=0.763, 0.710 and 0.704, respectively, and the average expression of their combination has the same specificity (AUC=0.745). miR-22, miR-155 and miR-365 are stress-specific markers and can be considered as suitable biomarkers to identify turkeys stressed by road transportation.

Lelli°D, Moreno°A, Lavazza°A

Virus Ebola e mondo animale = Ebola virus in animals

Prax Vet. - Vol. 36 no 1 (2015). - p 7-12. - 33 bib ref [Nr. Estr. 6010]

Ebola è una malattia trasmissibile dagli animali selvatici all'uomo attraverso lo stretto contatto con il sangue, gli organi, le secrezioni e altri fluidi di animali infetti. Mentre i pipistrelli della frutta sono considerati gli ospiti naturali dell'infezione, il coinvolgimento di altre specie animali nel ciclo di trasmissione di Ebola virus non è chiaro. Obiettivo dell'articolo è quindi quello di fornire informazioni utili per una migliore comprensione degli aspetti legati al ruolo degli animali domestici e selvatici nell'epidemiologia dell'infezione da virus Ebola. Verranno riportate le caratteristiche generali del virus e della malattia con particolare riferimento agli aspetti zoonotici. L'infezione da virus Ebola sarà affrontata, per le diverse specie animali domestiche e selvatiche, nel contesto dell'attuale epidemia in Africa occidentale e alla luce delle conoscenze ad oggi disponibili. Saranno inoltre presi in considerazione i fattori di rischio d'interesse veterinario per l'introduzione e la diffusione di Ebolavirus in Paesi indenni quali importazione di animali esotici e alimenti di origine animale.

Ebola is a disease potentially transmitted from wild animals to humans through dose contact with blood, secretions and other fluids of infected animals. Fruit bats are considered the natural hosts of the infection, but the involvement of other animal species in the transmission cycle of Ebola virus is still unclear. The purpose of this article is to provide useful information for a better understanding of the issues related to the role of domestic and wild animals in the epidemiology of Ebola virus. The virus and disease characteristics will be described with particular reference to the zoonotic features. The Ebola virus infection will be addressed in the different domestic and wild animal species in the context of the West Africa epidemic and in the light of the knowledge currently available. The risk factors for the introduction and spread of Ebolavirus in free country countries such as import of exotic animals and bushmeat, will also be taken into account.

Lelli°D, Moreno°A, Steyer A, Naglic T, Chiapponi° C, Prosperi°A, Faccin°F, Sozzi°E, Lavazza°A

Detection and characterization of a novel reassortant mammalian orthoreovirus in bats in Europe

Viruses. - Vol. 7 (2015). - p 5844-5854. - 38 bib ref [Nr. Estr. 7096]

A renewed interest in mammalian orthoreoviruses (MRVs) has emerged since new viruses related to

bat MRV type 3, detected in Europe, were identified in humans and pigs with gastroenteritis. This study reports the isolation and characterization of a novel reassortant MRV from the lesser horseshoe bat (*Rhinolophus hipposideros*). The isolate, here designated BatMRV1-IT2011, was first identified by electron microscopy and confirmed using PCR and virus-neutralization tests. The full genome sequence was obtained by next-generation sequencing. Molecular and antigenic characterizations revealed that BatMRV1-IT2011 belonged to serotype 1, which had not previously been identified in bats. Phylogenetic and recombination detection program analyses suggested that BatMRV1-IT2011 was a reassortant strain containing an S1 genome segment similar to those of MRV T1/bovine/Maryland/Clone23/59 and C/bovine/ Indiana/MRV00304/2014, while other segments were more similar to MRVs of different hosts, origins and serotypes. The presence of neutralizing antibodies against MRVs has also been investigated in animals (dogs, pigs, bovines and horses). Preliminary results suggested that MRVs are widespread in animals and that infections containing multiple serotypes, including MRVs of serotype 1 with an S1 gene similar to BatMRV1-IT2011, are common. This paper extends the current knowledge of MRVs and stresses the importance to continue and improve MRV surveillance in bats and other mammals through the development and standardization of specific diagnostic tools.

Lelli[°]D, Moreno[°]A, Steyer A, Naglic T, Prosperio[°] A, Faccin[°]F, Lavazza[°]A

Detection and characterization of a novel reassortant Mammalian Orthoreovirus of bats in Europe

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 97-99. - 8 bib ref [Nr. Estr. 7037]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Lelli[°]D, Moreno[°]A, Steyer A, Naglic T, Rosti E, Chiapponi[°]C, Prosperio[°]A, Faccin[°]F, Sozzi[°]E, Lavazza[°]A

Insectivorous bats as carriers of a variety of mammalian Orthoreoviruses

13th National Congress of the Italian Society for Virology (SIV) : Orvieto (TR) 14-16 September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 23-24 [Nr. Estr. 7281]

National Congress of the Italian Society of Virology (SIV) (13th : Orvieto (TR) : 14-16 September 2015)

Bats are being increasingly recognized as reservoir hosts of highly pathogenic and zoonotic emerging viruses in tropical regions but little is known on human-pathogenic viruses that may be present in bats in Europe. A renewed interest in Mammalian Orthoreoviruses (MRVs) has recently grown since new viruses related to Bat-MRVs detected in Europe have been identified in humans and pigs with gastroenteritis. Here, we report the results of MRVs surveillance in bats in Italy and the full-genome characterization of representative isolates belonging to different serotypes. During the period 2009-2015 bat samples were collected in Northern Italy from rehabilitation centres or from known roost sites. Virus isolation and identification were performed using cells culture, electron microscopy and PCRs for LI and S1 genes. Selected representative bat-MRVs were fully sequenced by NGS approach. Phylogenetic and molecular analyses were performed. Virus neutralization (VNT) was carried out for serotype identification. A total of 394 faecal and tissue samples belonging to 8 different bat species were analysed. 27 MRVs (6.9%) were isolated on cell culture and for 21 of them it was succeeded to type as MRVs type 3 by PCR targeting the S1 gene. Representative strains denominated BatMRV1-191797/1T2011, BatMRV2-5515/3/1T2012 and BatMRV3-5515/2/1T2012, belonging to serotype 1, 2 and 3 respectively, were selected and fully sequenced. Bat-MRVs appeared genetically widely differentiated. Particularly, BatMRV3-5515/2/1T2012 showed high similarity with T3/Bat/Germany/342/08 detected in Germany and SL-MRVO1 detected from a child with acute gastroenteritis in Slovenia. BatMRV1-IT2011 was a reassortant strain of serotype 1, never identified in bats before, with the S1 gene similar to T1/bovine/Maryland/Clone23/59 and

C/bovine/Indiana/MRV00304/2014 and the other segments similar to MR.Vs of different host, origin and serotype. This research provides evidence that insectivorous bats carry a wide variety of MRVs with members of the type 3 most represented. This finding extends the current knowledge on bat-MRVs, and stresses the importance to continue and improve the MRV surveillance in bats and other mammals even through the development and standardization of specific diagnostic tools.

Leo°S, Paternoster°G, Tamba°M, Bontempi°G, Arri goni°N

iRAMP: uno strumento per la valutazione del rischio e la gestione sanitaria degli allevamenti nei confronti della paratubercolosi

Buiatria. - Vol. 2015). - 9 p. - 13 bib ref [Nr. Estr. 7164]

Nel 2013 il Ministero della Salute ha approvato le Linee Guida per l'adozione di piani di controllo e per l'assegnazione della qualifica sanitaria degli allevamenti nei confronti della paratubercolosi bovina. Il controllo della paratubercolosi si basa sull'adozione volontaria di misure di biosicurezza associate ad un adeguato programma diagnostico. Il Centro di Referenza Nazionale per la paratubercolosi ha messo a punto un'applicazione web (app) per la valutazione del rischio e per l'individuazione delle misure gestionali idonee a ridurre la diffusione dell'infezione in allevamento, da mettere a disposizione dei veterinari pubblici e liberi professionisti. Tale strumento è strutturato in modo da essere anche utile alla formazione e informazione di veterinari e allevatori sulla problematica della paratubercolosi, con lo scopo ultimo di promuovere l'adozione volontaria e a lungo termine di piani di gestione sanitaria. Lo scopo del presente lavoro è di illustrare il funzionamento della app iRAMP (Italian Risk Assessment and Management Planning) per tablet (Android, iOS, Windows), da utilizzare direttamente in campo. iRAMP è un'applicazione che i) semplifica e standardizza la raccolta dei dati aziendali e l'esecuzione della valutazione del rischio, ii) comprende uno strumento di programmazione gestionale che facilita la stesura di piani di gestione sanitaria e iii) fornisce nozioni chiave e approfondimenti sulla paratubercolosi. La app elabora automaticamente un file scaricabile in formato Excel, che riporta i dati aziendali registrati, la distribuzione del rischio nell'ambito delle varie aree dell'allevamento e un elenco di raccomandazioni specifiche che, concordate con l'allevatore, costituiscono il piano di gestione sanitaria dell'allevamento. I dati possono essere integrati nel tempo per valutare il successo e le criticità del piano implementato.

Lo_Vecchio C, Rizzo F, Chiapponi°C, Sona B, Origli a S, Zoppi S, Bertolini S, Ru G, Foni°E, Mandola ML

Reassortant Swine Influenza A detected in a detection of a divergent Alpha Coronavirus in bats in Piedmont (Italy) [i.e. Reassortant Swine Influenza A detected in a pig-farm in Piedmont (Italy)]

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 226-227. - 9 bib ref [Nr. Estr. 7027]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Lo_Vecchio C, Rizzo F, Chiapponi°C, Sona B, Origli a S, Zoppi S, Dondo A, Bertolini S, Ru G, Foni°E, Mandola ML

Influenza suina : sorveglianza epidemiologica nella provincia di Cuneo

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 212-213. - 5 bib ref [Nr. Estr. 7048]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Swine influenza viruses (SIVs) are endemic in pig populations in America, Asia, and Europe. The viruses cause few deaths in pigs but substantial economic impact for farmers due to secondary infections and reduced weight gain in affected pigs. Moreover the capacity of SIV strains to recombine from gene segments originating from multiple species (swine, humans and avian), also pose implications for human health. The project aims to investigate the circulation of SIVs in pig farms of the Cuneo province. At present 43 out of the 60 selected farms have been sampled and a total of 989 nasal swabs and sera have been analysed for an active surveillance. So far, five out twelve positive swabs were identified as H1N2 SIV subtype, A/sw/It/240307/2014, originated from the reassortment of an avian H1N1 for the HA gene and a swine H3N2 for the NA gene. The seroprevalence obtained in the study, 86%, and the higher seroprevalences in breeding than fattening pigs is in accordance with other studies.

Lombardo^oT, Chiapponi^oC, Baioni^oL, Cinotti^oS, Ferrari^oM

Protein mutations following adaptation of avian influenza viruses in different biological systems

Res Vet Sci. - Vol. 103 (2015). - p 176-178. - 12 bib ref [Nr. Estr. 7136]

Traditionally, embryonated chicken eggs (ECE) are considered the gold standard for Influenza virus isolation and vaccine production. Nowadays, different biological systems have been improved and performed, in order to evaluate a feasible alternative to ECE. In fact, in a previous study, mammalian and avian cell cultures were successfully used for avian influenza viruses primary isolation from target tissues and virus propagation. This research is focused on the investigation of adaptive mutations that occur after influenza A virus amplification in ECE and cell cultures. The results of the study shows that avian influenza viruses after multiple passages in different biological systems undergo mutations, in particular, the largest number of amino acid substitutions occurred in all biological substrates in the hemagglutinin.

Lorenzi^oV, Fusi^oF, Angelucci^oA, Donati^oM, Bertocchi^oL

On-farm dairy cow welfare assessment: what's going on in Italy?

Proceedings of the Second DairyCare Conference 2015 : Cordoba March 3rd and 4th 2015 / editor, C.H. Knight. - [s.l. : DairyCare COST Action FA1308, 2015]. - p 43-44 (P1.27) [Nr. Estr. 7209]

DairyCare Conference (2nd : Cordoba : March 3rd and 4th, 2015)

The Italian Reference Centre for Animal Welfare (CReNBA) has set-up a system to assess loosely housed dairy cows welfare. CReNBA method fundamentals are the European research projects (WQ@), publications (EFSA) and laws, and the scientific literature. CReNBA on-farm assessment system, developed in 2011, includes both animal based measures (ABMs) and non-animal based measures (N-ABMs) and examines all the animals present within the farm (lactating and dry cows, young animals). The system is organized in four areas: A, B, C and D (see Figure). The method also includes the analysis of biosecurity parameters (Area E 15 indicators). Within a specific area, each single indicator is weighed basing on its importance in relation to welfare or biosecurity. The final outcome reports the scores of the five areas (A, B, C, D, E). The sum of the scores obtained in areas A, B, C and D gives the farm level of welfare. Legislative non-compliances are also reported. Before the on-field application, the system was validated for inter-observers agreement. From 2011 to January 2015, 922 dairy farms (size: 7 2736 total animals; milk production: 10 41 kg) were assessed by trained veterinarians. System on-farm application took maximum half a day. The examined farms covered the entire National territory. Since 2013, the method has included also biosecurity assessment, which has been applied to 527 out of 922 currently examined herds. Analysis of the collected data (922 farms) reveals a good level of welfare in the

majority of the evaluated farms: 881 farms (95.6%) showed a welfare level over the achievable mean score. Despite this result, in 527 farms (57.2%) legislative non-compliances were recorded. The most frequent non-compliances were related to calves lack of contact in individual pens (36.8%) and disbudding over three weeks of age (24.3%). Concerning biosecurity assessment 362 out of 527 (68.7%) evaluated farms resulted under the achievable mean score. Relationship between the scores obtained in N-ABMs areas (A, B, D) and the score achieved in Area C (ABMs) was analysed by multivariate linear regression (results in the Table). The analysis demonstrated that improvements in areas A and B can positively affect Area C result.

Luini^oM, Cremonesi P, Magro G, Bianchini^oV, Minozzi G, Castiglioni B, Piccinini R

Methicillin-resistant Staphylococcus aureus (MRSA) is associated with low within-herd prevalence of intra-mammary infections in dairy cows : genotyping of isolates

Vet Microbiol. - Vol. 178 (2015). - p 270-274. - 25 bib ref [Nr. Estr. 7133]

Staphylococcus aureus is one of the most common mastitis-causing pathogens worldwide. In the last decade, livestock-associated methicillin-resistant S. aureus (LA-MRSA) infections have been described in several species, included the bovines. Hence, this paper investigates the diffusion of MRSA within Italian dairy herds; the strains were further characterized using a DNA microarray, which detects 330 different sequences, including the methicillin-resistance genes mecA and mecC and SCCmec typing. The analysis of overall patterns allows the assignment to Clonal Complexes (CC). Overall 163 S. aureus isolates, collected from quarter milk samples in 61 herds, were tested. MRSA strains were further processed using spa typing. Fifteen strains (9.2%), isolated in 9 herds (14.75%), carried mecA, but none harboured mecC. MRSA detection was significantly associated ($P < 0.011$) with a within-herd prevalence of S. aureus intra-mammary infections (IMI) \approx 5%. Ten MRSA strains were assigned to CC398, the remaining ones to CC97 (n = 2), CC1 (n = 2) or CC8 (n = 1). In 3 herds, MRSA and MSSA co-existed: CC97-MRSA with CC398-MSSA, CC1-MRSA with CC8-MSSA and CC398-MRSA with CC126-MSSA. The results of spa typing showed an overall similar profile of the strains belonging to the same CC: t127-CC1, t1730-CC97, t899 in 8 out of 10 CC398. In the remaining 2 isolates a new spa type, t14644, was identified. The single CC8 was a t3092. The SCCmec cassettes were classified as type IV, type V or type IV/V composite. All or most strains harboured the genes encoding the β -lactamase operon and the tetracycline resistance. Streptogramin resistance gene was related to CC398. Enterotoxin and leukocidin genes were carried only by CC1, CC8 and CC97- MRSA. The persistence of MRSA clones characterized by broader host range, in epidemiologically unrelated areas and in dairy herds with low prevalence of S. aureus IMI, might enhance the risk for adaptation to human species.

Luppi^oA, Bonilauri^oP, Casappa G, Rugna^oG, Merialdi^oM, Dottori^oM

Monitoraggio alla macellazione delle pleuriti dorso-caudali del suino mediante griglia di valutazione SPES

Riv Med Vet. - Vol. 53 no 2 (2015). - p 39-43. - 15 bib ref [Nr. Estr. 7198]

Le patologie respiratorie sono un elemento di grande importanza sanitaria ed economica nell'allevamento suinicolo. Il loro monitoraggio rappresenta un ausilio importante per il clinico e per l'allevatore per verificare, correggere o implementare le strategie di controllo. Utilizzo di griglie di valutazione delle lesioni polmonari consente di valutare entità, diffusione e gravità delle lesioni classificando i lotti di polmoni esaminati alla macellazione. Tutto ciò è in particolare legato alle lesioni da Actinobacillus pleuropneumoniae, relativamente alle quali si propongono i risultati di uno studio effettuato su 24 partite di suini macellati all'inizio del 2014, confrontandoli con i risultati di precedenti studi.

Respiratory diseases are an important sanitary and economical aspect for swine breeding. Furthermore, the possibility to keep them monitored is helpful for clinical examination and also to

veirify, correct or implement control strategies at farm level. The use of grids to evaluate lung lesions allow to evaluate entity, diffusion and severity of these lesions giving a classification for examined lung batches. This aspect is linked to several respiratory pathogens and especially to Actinobacillus pleuropneumoniae lesions: the results of a study run during the beginning of 2014 on 24 batches of lungs are presented and compared to data from previous experiences.

Luppi° A, Bonilauri° P, Dottori° M, GherPELLI° Y, Biasi° G, MeriALDI° G, Maioli° G, Martelli P

Antimicrobial resistance of F4+ Escherichia coli isolated from swine in Italy

Transbound Emerg Dis. - Vol. 62 (2015). - p 67-71. - 22 bib ref [Nr. Estr. 5622]

Four-hundred and forty-two F4+ pathogenic Escherichia coli were isolated in a period of 10 years (2002–2011), from pigs that were suffering from diarrhoea belonging to Italian swine herds. The strains were analysed for their susceptibility to 12 antimicrobials using the disc diffusion method. During the study period, a statistically significant proportion of isolates resistant to enrofloxacin (14.5–89.3%), marbofloxacin (5.4–60.7%), flumequine (49.1–92.9%), danofloxacin (21.6–80%), florfenicol (9.8–64.3%), thiamphenicol (50–92%) and cefquinome (3.8–44%) was recorded. An increase in resistance (not statistically significant) to gentamicin (63.6–85.7%), apramycin (61.8–82.1%), trimethoprim-sulphamethoxazole (75–89.3%), tetracycline (97–100%) and erythromycin (92.4–100%) was also observed. Based on antimicrobial multiresistance, the strains were collected into three groups: I. resistant to 2–5 antimicrobials; II. resistant to 6–8 antimicrobials; III. resistant to 9–12 antimicrobials. The number of isolates belonging to the first group showed a statistically significant decrease ($P < 0.05$; $R_2 = 0.896$; $r = -0.9608$), while the isolates belonging to the second and third groups showed a statistically significant increase in resistance ($P < 0.05$; $R_2 = 0.753$; $r = 0.8890$ and $P < 0.05$; $R_2 = 0.727$; $r = 0.8701$, respectively) over the period of study. The results of this study suggest the need for continued monitoring of the development of resistance..

Luppi° A, Gibellini M, Bonilauri° P, GherPELLI° Y, Giovanardi D, Marzani° K, Torri° D, Dottori° M, Ferro P, Scandurra S, Hidalgo A

Prevalence of virulence factors associated with post weaning diarrhoea (PWD) in pigs in Italy

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 223 (Poster P188) [Nr. Estr. 7093]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Introduction Post weaning diarrhoea (PWD) caused by enterotoxigenic Escherichia coli (ETEC) is globally distributed disease. PWD has a great economic impact on pig production, leading to reduction on performance and increased mortality. Porcine ETEC strains typically express F4 (K88) or F18 fimbria and heat-labile (LT) and/or heat-stable (STa, STb) enterotoxins This study investigates the prevalence of virulence factors of ETEC isolated from PWD cases in Italy. Materials and methods In total, 159 E. coli isolates from 84 herds located in Northern Italy were obtained from nursery pigs with PWD from 2012 to 2014 using standardized bacteriological methods from diagnostic samples (rectal swabs, faeces and small intestine). To evaluate the prevalence of virulence factors, a multiplex PCR (Casey and Bosworth, 2009) for F4 (K88), F5 (K99), F6 (987P), F18, F41, STa, STb, LT and Stx2e genes was performed on E. coli isolates. When more than one isolate per herd resulted in the same virotype being detected, it was counted only once for prevalence calculations. E.coli strains were classified as ETEC when isolates carried both fimbrial and toxin genes. Results In 98.8% of the cases, only one strain of E. coli was involved in the PWD outbreak. In addition, haemolytic activity was detected in 95.24% of the isolates. The prevalence of fimbriae genes was: F4 (54.76%), F18 (33.33%) and F6 (1.19%). In 5 cases, the strains isolated harboured more than one fimbrial gene: F4+F18 (4.76%) and F5+F41 (1.19%). The prevalence of toxin genes was: LT (55.95%), STa (63.10%), STb (71.43%) and STx2e (9.52%). ETEC isolates were detected in 68 of the herds (80.95%), with 98.83% of them being haemolytic. In 16 herds

(19.05%) the isolates were negative for fimbrial or toxin genes in this assay. The role of these strains in the development of diarrhoea needs further investigations. 57.57% of ETEC isolates (39 out of 68) were ETEC-F4, whilst 36.76% (25 out of 68) were classified as ETEC-F18. In 4 cases (5.88%), ETEC carrying F4 and F18 genes were detected. The two most common ETEC virotypes were F4, STb, LT (25%) and F4, STa, STb, LT (22.06%). Conclusion This study confirms that ETEC-F4 is most commonly associated with PWD in Italy, similarly to the situation previously described from 2002 to 2012 (Luppi et al., 2014), resulting more prevalent than ETEC-F18. The most prevalent virotype was F4, STb, LT. Information about the prevalence of ETEC in cases of PWD is relevant when measures of control of the disease such as vaccination must be taken. Alternative approaches to antibiotic therapy are needed, since very high rates of antimicrobial resistance are reported in ETEC isolated from cases of PWD.

Magistrali CF, Cucco L, Pezzotti G, Farneti S, Cambiotti V, Catania S, Prati°P, Fabbi°M, Lollai S, Mangili P, Sebastiani C, Bano L, Dionisi AM, Luzzi I

Characterisation of *Yersinia pseudotuberculosis* isolated from animals with yersiniosis during 1996–2013 indicates the presence of pathogenic and Far Eastern strains in Italy

Vet Microbiol. - Vol. 180 (2015). - p 161-166. - 31 bib ref [Nr. Estr. 7127]

Yersinia pseudotuberculosis is a pathogen that infects both animals and humans worldwide. The epidemiology of infection caused by *Y. pseudotuberculosis* is poorly understood; however, its outbreaks have been traced back to a probable source in wildlife. This study aimed to characterise *Y. pseudotuberculosis* isolates collected from animals with yersiniosis. This study included 90 isolates of *Y. pseudotuberculosis* collected from different animals with yersiniosis between 1996 and 2013 in Italy. The isolates were tested for antimicrobial susceptibility and were biotyped. Genes associated with virulence plasmid pYV and those encoding O-antigen, high pathogenicity island (HPI), and super-antigenic toxin (YPM) were determined by performing PCR. Pulsed-field gel electrophoresis (PFGE) was performed using NotI and SpeI enzymes, and 3 dendrograms were generated. No antibiotic resistance was found. The presence of pYV was shown in 57 out of 90 isolates. Virulence profiles of majority of the isolates indicated that they belonged to O:1a and O:1b serotypes, biotype 1, and genetic type 2. Isolates belonging to O:2a serotype were detected in sheep and cattle and were found to be associated (for the first time) with septicemia in hares. *Y. pseudotuberculosis* isolates belonging to O:5a and O:12–O13 serotypes were also detected in hares. To our knowledge, this is the first study to detect *Y. pseudotuberculosis* isolates belonging to the O:12–O13 serotype from a clinical case in Europe. Results of PFGE indicated that it was a reliable method for investigating the genetic relatedness of *Y. pseudotuberculosis* isolates. Thus, characterisation of *Y. pseudotuberculosis* infection in animals should be considered a possible tool for the surveillance of pseudotuberculosis.

Maioli°G, Scollo A, Leotti G, Defilippo°F, Veloci M, Bonilauri°P, Dottori°M, Luppi°A

Prevalenza di rogna sarcoptica in partite di suini macellati = Prevalence of sarcoptic mange in swine at slaughterhouse

Atti Convegno SIPAS. - Vol. 41 (2015). - p 129-134. - 9 bib ref [Nr. Estr. 7004]

Meeting Annuale della Societa' Italiana di Patologia ed Allevamento dei Suini (SIPAS) (41. : Montichiari (BS) : 19-20 Marzo 2015)

In questo studio è stata valutata la prevalenza di *Sarcoptes scabiei* var. *suis* in partite di suini macellati provenienti da allevamenti del nord Italia. Nel periodo agosto 2014 – gennaio 2015 sono state campionate 219 partite di suini macellati, provenienti da 112 allevamenti di 20 province suddivise su 6 regioni diverse (Emilia Romagna, Lombardia, Veneto, Piemonte, Marche e friuli-Venezia Giulia). Sono stati analizzati pool costituiti da 30 scaricati auricolari di suino attraverso

una metodica di chiarificazione e concentrazione. La prevalenza totale in tutte le partite campionate è risultata del 13,7% (IC 95%: 9,1%- 18,3%), mentre gli allevamenti positivi sono risultati essere il 19,6% (IC 95%: 12,2%- 27%). Questo lavoro evidenzia che la rogna sarcoptica nel suino è una problematica attuale ed importante nell'allevamento industriale, sia per le perdite economiche ad essa correlate sia per la difficile diagnosi ed eliminazione.

*In this study we evaluated the prevalence of *Sarcoptes scabiei* var. *suis* mite in pigs at slaughterhouse in northern Italy. From August 2014 to January 2015 we sampled 219 pigs batches at slaughterhouse belonging to 112 farms from 20 different provinces. We analysed pools from 30 swine ear scrapings with a clarification/concentration method. Sarcoptic mange overall prevalence in herds was 13,7% (IC 95%: 9,1%-18,3%), while positive farms were 19,6% (IC 95%: 12,2%-27%) of 112 farm sampled. Sarcoptic mange is still present in swine industry in northern Italy representing an important cause of economic losses in pig breeding and a problem for difficult diagnosis and managing.*

Maisano AM°, Luini°M, Attanasio G, Vezzoli°F

Il benessere animale del suino grasso italiano in allevamento : valutazione al macello = The animal welfare of fattening Italian pig in breeding : assessment at slaughterhouse

Atti Convegno SIPAS. - Vol. 41 (2015). - p 85-94. - 16 bib ref [Nr. Estr. 7165]

Meeting Annuale della Società Italiana di Patologia ed Allevamento dei Suini (SIPAS) (41. : Montichiari (BS) : 19-20 Marzo 2015)

Lo scopo di questo lavoro è stato quello di indagare sulla possibilità di valutare al macello il Benessere Animato (BA) in allevamento nella specie suina. Vengono esposti i dati osservati su 10.085 suini grassi al macello, provenienti da 54 allevamenti della pianura padana. Le osservazioni sono state registrate durante le visite ante-mortem e post-mortem, secondo i principi delle Animal Based Measures (ABM). La valutazione di 28 osservazioni per ciascuna partita (62) di macellazione, raggruppate in 5 principi, ha generato un punteggio generale, come descritto dal protocollo Welfare Quality® (WQ). I relativi calcoli sono stati sviluppati seguendo gli algoritmi del WQ, riadattati in base, al modello di allevamento intensivo nazionale, ed alle caratteristiche del suino pesante italiano. In 15 allevamenti di provenienza è stato valutato anche il BA in azienda e i relativi punteggi sono stati calcolati in modo analogo a quelli del macello ma tenendo conto sia delle ABM sia delle misure indirette. Le prevalenze medie delle ABM rilevate al macello, mettono in evidenza principalmente le problematiche riconducibili all'inadeguatezza delle strutture (Imbrattamento fecale 1 e 2 47,7% e Bursiti 1 e 2 23,7%) ed alla elevata prevalenza di segni riferibili a parassitosi (White spot 25,4% e Dermatiti ad eziologia varia 28%). Infine dal confronto dei punteggi di BA ottenuti al macello e nei rispettivi allevamenti di provenienza, l'analisi, conferma che gli tutti gli score, tranne quello riguardante le lesioni, risultano correlati in maniera statisticamente significativa; suggerendo la possibilità di valutare il BA in allevamento attraverso osservazioni al macello, mantenendo un costante monitoraggio con specifici indicatori.

The aim of this work was to investigate on the possibility of assessing the Animal Welfare (AW) in swine farming at slaughterhouse. Here, are presented the observed data on 10.085 fattening pigs at slaughterhouse, coming from 54 farms in Pianura Padana. This data were collected during ante-mortem and post-mortem, according to the principles of Animal Based Measures (ABM). The assessment of 28 observations for each batch (62) of slaughter, grouped into five principles, has generated an overall score, as described by the Welfare Quality® protocol (WQ). The results have been developed following the algorithms of WQ and they were adapted according to the model of intensive national farming, and the characteristics of Italian fattening pigs. It was also studied in 15 farms of origin the AW in farmhouse and their scores were calculated in a similar way to the slaughterhouse result but taking into account the ABM and structural measures. The measured mean value of ABM recorded at slaughter, highlights problems mainly due to the structure's inadequacy (Manure on the body 1 and 2 47.7% and bursitis 1 and 2 23.7%) and to the high prevalence of signs related to parasites (White spot 25.4% and Dermatitis etiology varies 28%). Excepted those carried out on lesion, the AW compared scores obtained at slaughter and farms are correlated in a statistically significant way. It suggests the possibility of evaluating the AW of breeding through observations at the slaughterhouse, maintaining a constant monitoring through

specific indicators.

Mamberti S, Prati^oP, Cremaschi P, Seppi C, Morelli CF, Galizzi A, Fabbi^oM, Calvio C

[γ]-PGA hydrolases of phage origin in *Bacillus subtilis* and other microbial genomes

PLoS One. - Vol. 10 no 7 (2015). - p e130810 (17 p). - 55 bib ref (Ultimo accesso: 07/09/2015 - <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0130810>) [Nr. Estr. 6091]

Poly-γ-glutamate (γ-PGA) is an industrially interesting polymer secreted mainly by members of the class Bacilli which forms a shield able to protect bacteria from phagocytosis and phages. Few enzymes are known to degrade γ-PGA; among them is a phage-encoded γ-PGA hydrolase, PghP. The supposed role of PghP in phages is to ensure access to the surface of bacterial cells by dismantling the γ-PGA barrier. We identified four unannotated *B. subtilis* genes through similarity of their encoded products to PghP; in fact these genes reside in prophage elements of *B. subtilis* genome. The recombinant products of two of them demonstrate efficient polymer degradation, confirming that sequence similarity reflects functional homology. Genes encoding similar γ-PGA hydrolases were identified in phages specific for the order Bacillales and in numerous microbial genomes, not only belonging to that order. The distribution of the γ-PGA biosynthesis operon was also investigated with a bioinformatics approach; it was found that the list of organisms endowed with γ-PGA biosynthetic functions is larger than expected and includes several pathogenic species. Moreover in non-Bacillales bacteria the predicted γ-PGA hydrolase genes are preferentially found in species that do not have the genetic asset for polymer production. Our findings suggest that γ-PGA hydrolase genes might have spread across microbial genomes via horizontal exchanges rather than via phage infection. We hypothesize that, in natural habitats rich in γ-PGA supplied by producer organisms, the availability of hydrolases that release glutamate oligomers from γ-PGA might be a beneficial trait under positive selection.

Mancini G, Calzolari^oM, Capelli G, Lelli^oD, Montarsi F, Chiari^oM, Santilli A, Quaglia M, Federici V, Catalani M, Monaco F, Goffredo M, Savini G

Mosquito species involved in West Nile and Usutu viruses transmission in Italy between 2008 and 2014

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 204-205 [Nr. Estr. 7029]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Mancini R, Ferlizza E, Fasoli S, Isani G, Giacomelli^oS, Bianchi^oA, Archetti^oI

Serum protein electrophoresis from clinically healthy mouflons (*Ovis ammon musimon*)

Congresso Internazionale SCIVAC : 29-31 Maggio 2015 Rimini : atti congressuali, comunicazioni brevi, poster, sessioni ad ingresso libero, sessioni avanzate / [s.l. : SCIVAC, 2015]. - p 489. - 3 bib ref [Nr. Estr. 7159]

Congresso Internazionale SCIVAC : Rimini : 29-31 Maggio 2015)

The aim of the present study was to determine the electrophoretic pattern of serum proteins in mouflons (*Ovis ammon musimon*) using agarose gel electrophoresis. We included 30 clinically healthy mouflons living in a natural park in Rome, Italy. Serum was analyzed for total protein and albumin concentration by an automated biochemical analyzer (Olympus AU400). Serum proteins were separated on a 0.8% agarose gel with an automated system (Hydrasis, Sebia, Lisses, France). Gels were stained by amido black and digitalized with a scanner yielding the densitometric profile

(software Phoresis 6.1.2, Sebia). Total protein and albumin concentrations were 7.33 ± 0.61 and 3.49 ± 0.34 g/dL respectively. After gel electrophoresis, we identified six fractions including albumin, α_1 , α_2 , β_1 , β_2 and γ -globulins. Mean concentrations of serum protein fractions in mouflons were: 4.16 ± 0.49 g/dL for albumin, 0.47 ± 0.08 g/dL for α_1 -globulins, 0.83 ± 0.07 g/dL for α_2 -globulins, 0.26 ± 0.04 g/dL for β_1 -globulins, 1.13 ± 0.18 g/dL for β_2 -globulins, 0.47 ± 0.19 g/dL for γ -globulins. Data regarding reference intervals for serum protein fractions are lacking in mouflons; therefore the values reported in the present research can be considered a useful tool for clinical pathologists, clinicians, and researchers working in wild ruminant medicine and conservation..

Marianelli C, Armas F, Boniotti^oMB, Mazzone P, Pac ciarini^oML, Di_Marco Lo_Presti V

Multiple drug-susceptibility screening in Mycobacterium bovis : new nucleotide polymorphisms in the embB gene among ethambutol susceptible strains

Int J Infect Dis. - Vol. 33 (2015). - p e39-e44. - 42 bib ref [Nr. Estr. 6015]

Objectives: Pyrazinamide-resistant Mycobacterium bovis isolates of animal origin were assessed for drug susceptibility to five antituberculosis drugs by the agar based Middlebrook 7H11 method as gold standard as well as by a simplified, dichotomous resazurin microtitre assay (d-REMA). Methods: A total of 53 M. bovis isolates were typed and tested against isoniazid, rifampin, streptomycin, ethambutol, kanamycin and the control drug pyrazinamide. On the basis of the results obtained, pncA and embB genes were PCR-amplified and DNA-sequenced for all isolates. Results: All M. bovis isolates, classified into 21 spoligotype/MIRU-VNTR profiles, were resistant to pyrazinamide by both methods, as expected. The pncA gene sequencing confirmed the presence of the resistance-conferring H57D mutation. All strains were found to be susceptible to the other five drugs by the agar based gold standard method. The d-REMA was in agreement with these results for all five drugs, with the exception of 12 isolates, which showed ambiguous and therefore inconclusive results in ethambutol testing. Mutations in the embB gene were observed in all 53 isolates: four new single- nucleotide polymorphisms were identified. No association was found between embB genetic profiles and ethambutol resistance results by the gold standard. Conclusion: All M. bovis isolates were sensitive to the most common antituberculosis drugs used for treatment. There was a good agreement between the d-REMA assay and the agar based reference method. Among ethambutol susceptible isolates, four new embB mutations were found 2015 The Authors. Published by Elsevier Ltd on behalf of International Society for Infectious Diseases. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Marques AT, Lecchi C, Grilli G, Giudice C, Restelli L, Rota_Nodari^oS, Vinco^oLJ, Cecilian F

Response to road transportation in turkey (Meleagris gallopavo) : the acute phase protein expression in liver and adipose tissue

Atti della Societa' Italiana di Patologia Aviaria (SIPA) 2015 : LIV Convegno annuale : Forli, 16-17 Aprile 2015 / [s.l. : s.n., 2015]. - p 215-219. - 13 bib ref [Nr. Estr. 7002]

Convegno annuale Societa' Italiana Patologia Aviaria (SIPA) (54. : Forli : 16-17 Aprile 2015)

Road transportation is one of the most stressful events during the turkeys' lifetime and is associated with economic losses. Beside their use as biomarkers of inflammation, acute phase proteins (APP) have been also used as biomarkers of animal welfare, including stress due to transport, but no information is available in turkey species. The aim of the present study was to evaluate whether the gene expression of four APP, namely α_1 -acid glycoprotein (AGP), C-Reactive Protein (CRP), Serum Amyloid A (SAA) and PIT54, as potential indicators of transport stress in turkey (Meleagris gallopavo), by qualitative and quantitative real time (qPCR) in liver and adipose tissue. Fourteen healthy animals were divided into two groups: a group subject to road transport and a control group

not subject to road transport. The expression of AGP and CRP mRNA was found to be increased in animals slaughtered after road transport. AGP mRNA expression was increased in both liver and adipose tissue, and identified as one of the major stress indicators. The presence of AGP protein in liver and adipose tissue was also confirmed by immunohistochemistry. CRP mRNA expression was found to be increased in liver alone. The results of this study suggest that AGP.

Martinelli °N, Pavoni°E, Filogari D, Ferrari°N, Chiari°M, Canelli°E, Lombardi°G
Hepatitis E virus in wild boar in the Central Northern part of Italy

Transbound Emerg Dis. - Vol. 62 (2015). - p 217-222. - 36 bib ref [Nr. Estr. 5532]

Hepatitis E virus (HEV) is responsible for sporadic acute hepatitis in developed countries, where the infection is acquired probably through ingestion of contaminated food, in addition to travel-related cases. In this study, the circulation of HEV in wild boar from nine Italian provinces was evaluated. An overall seroprevalence of 10.2% was found, although there were differences among the provinces, while no samples were positive for HEV RNA detection. This study indicates an active circulation of HEV in the Italian wild boar populations and suggests to consider the zoonotic risk in handling and eating meat from this animal.

Massi°P, Barbieri°I, Fiorentini°L, Casadio°M, Parigi°M, Tosi°G

Analisi molecolare di ceppi del virus della bronchite infettiva aviare negli anni 2013 e 2014 : considerazioni sui genotipi circolanti in Italia e in altri paesi europei ed extra-europei

Atti della Societa' Italiana di Patologia Aviare (SIPA) 2015 : LIV Convegno annuale : Forli, 16-17 Aprile 2015 / [s.l. : s.n., 2015]. - p 220-228. - 8 bib ref [Nr. Estr. 7003]

Convegno annuale Societa' Italiana Patologia Aviare (SIPA) (54. : Forli : 18-19 Aprile 2015)

Infectious bronchitis virus (IBV) is a coronavirus that causes upper respiratory, renal and/or reproductive diseases with high morbidity in poultry. Classification of IBV is important for implementation of vaccination strategies to control the disease in commercial poultry. Currently, the sequence analysis of the IBV S1 gene is considered the gold standard for IBV strain identification, with a high nucleotide identity (e.g.= 95%) indicating related strains. A study was carried out on 545 Infectious Bronchitis virus identified in Italy and European Countries and extra European Countries between 2013 and 2014. A portion of the S1 gene was amplified and sequenced in order to explore the genetic variability of the IBV strains circulating in the late two years. Genotypes QX-like, 793B, Q1 and M41 are prevalent in Italy. Genotypes EG/CLEVB-2, 793B, QX-like and Q1 are prevalent in European and extra European Countries.

Mazzoni C, Scollo A, GherPELLI M, Bonilauri°P, Kirkwood R, De_Rensis F

Effetto della somministrazione di alliltrembolone per un periodo ridotto rispetto a quello standard sulla sincronizzazione dell'estro e sulla fertilità di scrofette puberi = Effect of alliltrembolone administration for a shorter compared a standard period on oestrus synchronization and fertility in pubertal gilts

Atti Convegno SIPAS. - Vol. 41 (2015). - p 71-75. - 14 bib ref [Nr. Estr. 7008]

Meeting Annuale della Societa' Italiana di Patologia ed Allevamento dei Suini (SIPAS) (41. : Montichiari (BS) : 19-20 Marzo 2015)

Per un periodo di 10, 12, 14 o 18 giorni sono stati somministrati a 501 scrofette puberi 20 mg/ giorno di Alliltrembolone per via orale. Negli animali trattati per 10 e 12 giorni, la somministrazione di Alliltrembolone è stata seguita dalla somministrazione di una doppia dose di 75 µg Dclopustenolo, un analogo delle PGf2alfa. I risultati di questo studio indicano che, nella scrofetta, il trattamento con Alliltrembolone per 10 o 12gg, non comporta differenze sulla sincronizzazione degli estri, la fertilità e

la prolificità. rispetto alla somministrazione standard per 14 o 18 gg.

Allyl trenbolone was administered for 10, 12, 14, or 18 days, at 20 mg per day followed by the administration of 2x75 µg D-cloprostenol at last feeding at 10 or 12 days, to synchronize estrus in gilts. There were no differences in the number of gilts in oestrus, on farrowing rate or subsequent litter sizes.

Meriardi°G, Giacometti F, Bardasi°L, Stancampiano L, Taddei°R, Serratore P, Serraino A

Fecal shedding of thermophilic Campylobacter in a dairy herd producing raw milk for direct human consumption

J Food Prot. - Vol. 78 no 3 (2015). - p 579-584. - 32 bib ref [Nr. Estr. 6002]

Factors affecting the fecal shedding of thermophilic Campylobacter in Italian dairy farms were investigated in a 12-month longitudinal study performed on a dairy farm authorized to sell raw milk in Italy. Fifty animals were randomly selected from 140 adult and young animals, and fecal samples were collected six times at 2-month intervals. At each sampling time, three trough water samples and two trough feed samples also were collected for both adult and young animals. Samples were analyzed with real-time PCR assay and culture examination. Overall, 33 samples (9.7%) were positive for thermophilic Campylobacter by real-time PCR: 26 (9.2%) of 280 fecal samples, 6 (16.6%) of 36 water samples, and 1 (4.2%) of 24 feed samples. Campylobacter jejuni was isolated from 6 of 280 samples; no other Campylobacter species was isolated. A higher (but not significantly) number of positive fecal samples were found in younger animals (11.33 versus 6.92% of adult animals), and a significantly higher number of positive water samples were collected from the water troughs of young animals. A distinct temporal trend was observed during the study period for both cows and calves, with two prevalence peaks between November and December and between May and July. Several factors such as calving, housing practices, herd size, management practices forcing together a higher number of animals, and variations in feed or water sources (previously reported as a cause of temporal variation in different farming conditions) were excluded as the cause of the two seasonal peaks in this study. The factors affecting the seasonality of Campylobacter shedding in the dairy herds remain unclear and warrant further investigation. The results of the present study indicate that special attention should be paid to farm hygiene management on farms authorized to produce and sell raw milk, with increased surveillance by the authorities at certain times of the year.

Molinari°S, Cavadini°P, Pezzoni°G, Chiari°M, Brocchi°E, Lavazza°A, Capucci°L

Identification of a new non-pathogenic lagovirus in brown hare (Lepus europeus)

13th National Congress of the Italian Society for Virology (SIV) : Orvieto (TR), 14-16 September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 35 [Nr. Estr. 7040]

National Congress of the Italian Society of Virology (SIV) (13th : Orvieto, Italy : 14-16 September 2015)

European Brown Hare Syndrome (EBHS) is a viral disease mainly observed in brown hares (*L. europeus*). The causative agent of EBHS is a calicivirus belonging to the Lagovirus genus, highly related to another lagovirus of rabbits (*Oryctolagus cuniculus*) i.e. Rabbit Hemorrhagic Disease Virus (RHDV). A third member of Lagovirus genus, named Rabbit Calicivirus (RCV), causes a silent infection of intestine without inducing clinical signs. The existence of a non-pathogenic EBHSV-like virus in hares has been put forward for explaining some "unexpected" positive serological results obtained either from brown hares and other *Lepus* species, living in areas where the disease has never been detected (e.g. Australia, Africa and South America). The aim of this work is to report the results of investigations performed to seek this putative virus. Faecal and blood samples from 30 young healthy hares (30-60 days of age) reared in cages in a breeding farm of Brescia province

(North Italy), were collected during the summer of 2014. The total RNA was extracted and analyzed by RT-PCR using the universal primers for lagoviruses. The entire vp60 gene was completely amplified and sequenced. The entire vp60 of this "new" lagovirus was expressed in the baculovirus system. Western blotting analysis, electron microscopy and ELISA were performed on supernatant of infected sf9 cells. Serological analysis was performed on blood samples using two ELISAs with different levels of specificity and sensitivity towards EBHSV and other lagoviruses. Three hares resulted RT-PCR positive for the presence of a lagovirus. The sequence analysis of the vp60 gene showed that the identified virus is phylogenetically distinct from all previously described members of the Lagovirus genus and forms a new genetic group. Moreover most animals resulted seropositive by ELISA test detecting cross-specific antibodies, thus suggesting that the virus was probably present since some time in the farm. This aspect and the lack of any sign of disease among the hares, show that the viral infection has a subclinical course and thus the virus could be considered non pathogenic. Based on these results we propose to name the virus as "Hare Calicivirus".
Acknowledgment: This research was supported by Italian Ministry of Health (PRC2012/015)..

Montarsi F, Drago A, Martini S, Calzolari M, De Filippis F, Bianchi A, Mazzucato M, Ciocchetta S, Arnoldi D, Baldacchino F, Rizzoli A, Capelli G

Current distribution of the invasive mosquito species, *Aedes koreicus* [*Hulecoeteomyia koreica*] in Northern Italy

Parasites & Vectors. - Vol. 8 (2015). - no 614 (5 p). - 23 bib ref (ultimo accesso 04/01/2016 <http://www.parasitesandvectors.com/content/pdf/s13071-015-1208-4.pdf>) [Nr. Estr. 7140]

The invasive species *Aedes (Finlaya) koreicus* was first identified in north-eastern Italy in 2011, during the ongoing surveillance activity of *Aedes albopictus*. Following this finding, a more intensive monitoring was carried out to assess the distribution of the species and to collect biological data. Herein, we report the new records obtained by four years of surveillance. **Findings** The presence of *Ae. koreicus* was checked using ovitraps, adults traps and by larval collections in all possible breeding sites from May 2011 to July 2015. The monitoring started in the site of the first detection (Province of Belluno) and was then extended in the neighbouring Provinces belonging to four Regions. *Aedes koreicus* was found in 73 municipalities out of 155 monitored (47.1 %), including 23 municipalities (14.8 %) previously not infested. The area of first detection of *Ae. koreicus* (Province of Belluno) was also the most infested (68 %). However the mosquito has also been found to the west (Province of Trento) and to the south and south-west (Provinces of Vicenza and Treviso) of the initially infested area. **Conclusions** The spread of *Ae. koreicus* is directed towards south and west from the original infested area, likely due to the dense road connections and the habitat suitability of the new areas. According to these records, northern Italy has a high probability to be invaded by *Ae. koreicus* in the next decade. These data can be useful to validate predictive models of potential distribution and dispersal of this species in Italy or in Europe.

Moreno A, Lelli D, Chiapponi C, Calzolari M, Prospero A, Sozzi E, Lavazza A

Complete genomic characterization and molecular analysis of Usutu virus in Italy

13th National Congress of the Italian Society for Virology (SIV) : Orvieto (TR) 14-16 September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 23 [Nr. Estr. 7282]

National Congress of the Italian Society of Virology (SIV) (13th : Orvieto (TR) : 14-16 September 2015)

Usutu virus (USUV) is a member of the Japanese encephalitis serocomplex within the family Flaviviridae, and is maintained in a typical enzootic cycle between mosquitoes and birds. USUV was identified in South Africa in 1959 and for the first time in Italy and Europe in 1996. Even though avian infections are reported to be not fatal in Africa, USUV was highly pathogenic for several avian species in Austria, and it was recently associated to two cases of human encephalitis in Italy. In this

study, we performed phylogenetic and molecular analyses of the complete genome of 14 USUV strains isolated in North Italy in 2010-2014. We considered 14 strains, originated respectively 3 from Lombardia (LOM) and 11 from Emilia Romagna (ER), and isolated in 2010 (1), 2011 (3), 2012 (4), 2013 (4) and 2014 (2). Two were isolated from black birds and 12 from Cx. Pipiens. Strains were propagated in Vero cells and their full genome was sequenced using Illumina NGS platform. Phylogenetic and molecular analyses were performed using MEGA5 including USUV reference strains from Europe and Africa. Phylogenetic tree showed six different clades, three originated from Africa and three from Europe. European clade 1 grouped strains from Austria and Hungary, while Italian isolates were distributed in the other two clades according to their origin. The 11 strains from ER formed a distinct clade 2 together with two published strains isolated in the same region in a black bird and a patient with neuroinvasive disease. The 3 strains from LOM grouped in clade 3 together with German strains originated from mosquitoes, bats and birds. Molecular analysis revealed five aa changes (G595S, E830G, I1324T, 11602V, N2304S) and seven aa changes (A231V, K1054R, D1062N, V12191, A1236L/V, 11602V, A3076T) within the polyprotein, which defined ER and LOM clades respectively. The results suggested the circulation of two different clades in Italy depending on the geographical origin with the Po River likely acting as a barrier between the two clade distributions. This could indicate different strategies of adaptation and evolution of USUV to spread into new areas and become established. Interestingly the clade present in LOM was closely related to German strains but different from the Austro-Hungarian clade.

Moreno^oA, Lelli^oD, Sozzi^oE, Tamba^oM, Brocchi^oE, Sambri V, Bonilauri^oP, Lavazza^oA

MAB-BASED competitive ELISA for detection of antibodies Anti-Chikungunya virus

13th National Congress of the Italian Society for Virology (SIV) : Orvieto (TR) 14-16 September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 37 [Nr. Estr. 7283]

National Congress of the Italian Society of Virology (SIV) (13th : Orvieto (TR) : 14-16 September 2015)

The Chikungunya fever epidemic, occurred in summer 2007 in Emilia-Romagna (Italy), was the first autochthonous European outbreak of a tropical vector-borne disease. In this study the Chikungunya virus (CHIKV) isolated at that time was used for the production of monoclonal antibodies (MAbs), which were then used in a competitive ELISA test for anti-CH.TKV antibodies detection. CHIKV Italy/209395/07 isolated from a mosquito (*Aedes albopictus*) pool was used for MAbs production and as antigen in the ELISA test. Characterization of MAbs was performed by indirect ELISA, immunoperoxidase, virus-neutralization (VN) and Western blotting (WB). 400 known human sera (200 positive and 200 negative in indirect immunofluorescence test) were used for ELISA validation through ROC curve approach. Moreover, 493 animals (256 dogs, 123 pigeons, 79 chicken, 28 coypus and 7 rabbits) sera were analysed. All these sera were collected in the area of the Emilia-Romagna outbreak. Forty five MAbs were produced, 9 with VN activity. Two neutralizing MAbs (1H7, 1A7) were selected and peroxidase-conjugated to be evaluated in a competitive ELISA for antibody detection. MAb 1H7, positive in WB, reacted against a linear epitope while 1A7 against a conformational epitope located both within the E2 protein. The ELISA test was developed using in parallel the two conjugated MAbs, and 1H7 was finally selected. Plates were coated with partially purified antigen, two serum dilutions (1/10; 1/20) were used, followed by addition of the selected MAb-conjugate. Results were expressed as % of inhibition. The ROC curve at 1/10 dilution showed that the ELISA is highly accurate (Area Under Curve=0.997; 95%CI 0.985-1.000) with optimal sensitivity (Se: 96.0; 95%CI 92.3-98.3) and specificity (Sp: 100; 95%CI 98.2-100) values using the cut-off >55%. All the 493 animal sera resulted negative for anti-CHIKV antibodies. Our MAb-based competitive ELISA seems a valid and easy-to-perform diagnostic tool for serological diagnosis in humans, the study of CHIKV epidemiology and of the effective role of animals in virus spreading. These results suggest that, during the Italian epidemic, the CHIKV presumably circulated in an urban cycle involving people and mosquitoes only.

Moreno^oA, Sozzi^oE, Grilli G, Gibelli^oLR, Gelmett i^oD, Lelli^oD, Chiari^oM, Prati^oP, Alborali^oGL, Boniotti^oMB, Lavazza^oA, Cordioli^oP

Detection and molecular analysis of Pseudorabies virus strains isolated from dogs and a wild boar in Italy

Vet Microbiol. - Vol. 177 (2015). - p 359-365 . - 25 bib ref [Nr. Estr. 6077]

Aujeszky's disease (AD) is one of the most economically important diseases of farmed pigs. Wild boars can act as reservoirs and might represent a potential threat for domestic animals, including dogs. The aim of this study was to report the results of an AD survey based on the Pseudorabies virus (PRV) genome detection in samples of dogs clinically suspected of AD and of wild boars collected during four consecutive hunting seasons in the period 2010–2014. Genomic characterization was based on the partial gC sequence of the Italian strains and the comparison with those from domestic pigs and European PRV strains circulating in wild boars. The Italian PRV strains were mainly distributed into three different clusters and revealed two interesting findings. First, there was a clear distinction between the viral strains that were isolated from dogs used for hunting and subsequently traced back to wild boars and the strains that were isolated from working dogs and subsequently found to be closely related to domestic pigs. Second, the Italian epidemiological situation was found to be different from those of European countries in that the Italian situation was characterized by the presence of both the typical Italian clades 1 and 2 and supported by new patterns of aa deletions/insertions. Italian clade 1 included strains from hunting dogs and two Italian wild boars, and Italian clade 2 grouped with recent strains from dogs that were unable to hunt and domestic pigs that were related to one old reference strain (S66) and not included elsewhere. Molecular and phylogenetic analyses of PRV strains are therefore necessary to improve the understanding of the distribution of the PRV clusters and their evolution.

Moreno^oA, Vaccari G, Chiapponi^oC, Zaccaria G, Lelli^oD, Foni^oE, Alborali^oGL, Baioni^oL Lavazza^oA, Cordioli^oP

Multiple reassortment events involving swine and human influenza viruses in the Italian pig farms

3rd International One Health Congress : 15-18 March, 2015 Amsterdam / [s.l. : s.n., 2015]. - 2 p (Abstract 518) [Nr. Estr. 6008]

International One Health Congress (3rd : Amsterdam : 15-18 March, 2015)

Orzi V, Scaglia B, Lonati S, Riva C, Boccasile G, Alborali^oGL, Adani F

The role of biological processes in reducing both odor impact and pathogen content during mesophilic anaerobic digestion

Sci Total Environ. - Vol. 526 (2015). - p 116-126. - 41 bib ref [Nr. Estr. 6043]

Mesophilic anaerobic digestion (MAD) produces renewable energy, but it also plays a role in reducing the impact of digestates, both by reducing odor and pathogen content. Ten full-scale biogas plants characterized by different plant designs (e.g. single digesters, parallel or serial digesters), plant powers (ranging from 180 to 999 kWe), hydraulic retention time (HRT) (ranging between 20 to 70 days) and feed mixes were monitored and odors and pathogens were observed in both ingestates and digestates. Results obtained indicated that MAD reduced odors (OU) from, on average, $OU_{ingestate} = 99,106 \pm 149,173 \text{ OU m}^{-2} \text{ h}^{-1}$ ($n = 15$) to $OU_{digestate} = 1106 \pm 771 \text{ OU m}^{-2} \text{ h}^{-1}$ ($n=15$). Pathogens were also reduced during MAD both because of ammonia production during the process and competition for substrate between pathogens and indigenous microflora, i.e. Enterobacteriaceae from $6.85 * 10^3 \pm 1.8 * 10^1$ to $1.82 * 10^1 \pm 3.82 * 10^1$; fecal Coliform from $1.82 * 10^4 \pm 9.09$ to $2.45 * 10^1 \pm 3.8 * 10^1$; Escherichia coli from $8.72 * 10^3 \pm 2.4 * 10^1$ to $1.8 * 10^1 \pm 2.94 * 10^1$; Clostridium perfringens from $6.4 * 10^4 \pm 7.7$ to $5.2 * 10^3 \pm 8.1$ (all data are expressed as CFU g⁻¹ ww). Plants showed different abilities to reduce pathogen indicators, depending on the pH value

and toxic ammonia content.

Ostanello F, Serraino A, Arrigoni°N, Ricchi°M, Bo nilauri°P, Giacometti F

Valutazione della prevalenza di aziende da latte infette da *Mycobacterium avium* subsp. paratuberculosis nel sud Italia = Prevalence of *Mycobacterium avium* subsp. paratuberculosis-infected dairy herds in Southern Italy

Large Anim Rev. - Vol. 21 no 1 (2015). - p 13-21. - 22 bib ref [Nr. Estr. 6004]

In questo lavoro è stata valutata la prevalenza di aziende di bovine da latte infette da *Mycobacterium avium* subsp. paratuberculosis (MAP) in tre Regioni dell'Italia meridionale attraverso una procedura di screening che prevedeva l'analisi ripetuta sia di campioni di latte di massa (esaminati mediante test ELISA), sia dei filtri dell'impianto di mungitura (esaminati mediante real-time PCR) e prelevati in 569 allevamenti da latte. Un totale di 121 allevamenti sono risultati positivi allo screening (21,3%; IC 95%: 18,0-24,9%). Per stimare la prevalenza apparente intra-aziendale (PA), in 102 dei 121 allevamenti risultati positivi allo screening è stato esaminato, mediante test ELISA, il latte individuale di tutti gli animali in lattazione. Il prelievo del latte individuale è stato realizzato anche in un campione casuale di 24 aziende risultate negative allo screening. Complessivamente, sono stati sottoposti a test ELISA 12312 campioni di latte individuale. La PA varia dallo 0,0% al 22,7% (media 5,7%). Il confronto tra i dati delle diverse Regioni non ha evidenziato differenze significative della prevalenza di aziende infette o della PA intra-aziendale. La procedura di screening è stata in grado di rilevare il 56,2% degli allevamenti con PA $\geq 2,00/0$ fino ad un massimo del 100% degli allevamenti con PA. Complessivamente, la procedura di screening è in grado di individuare l'85,6% degli allevamenti con almeno 1 capo positivo al test ELISA del latte individuale. La procedura di screening utilizzata è relativamente economica (circa 60 euro) e rappresenta un utile strumento per l'individuazione di allevamenti ad alto rischio di diffusione dell'infezione e contaminazione del latte. Potrebbe quindi essere applicata, nel contesto di piani volti a ridurre la prevalenza di infezione negli allevamenti da latte e/o a ridurre la contaminazione del latte, per assegnare una scala di priorità adeguata alle misure di controllo da adottare nei singoli allevamenti.

Mycobacterium avium subsp. paratuberculosis (MAP) is the etiological agent of paratuberculosis, a chronic contagious bacterial disease primarily affecting dairy cattle. Paratuberculosis represents a dual problem for the milk production chain: in addition to economic losses to affected herds, MAP may have zoonotic potential. Infected herds must be identified in order to implement programs designed to reduce the incidence of disease within and between herds and to prevent MAP from entering the food chain. The objective of this study was to evaluate the sensitivity and specificity of a screening sampling plan (SSP) to detect MAP-positive dairy cattle herds by repetitive analysis of bulk tank milk (BTM) samples by ELISA and in-line milk filter (ILMF) samples by real-time PCR. Samples from BTM and ILMF were collected twice from 569 dairy herds in southern Italy. Additionally, 12,312 individual milk samples were collected: 9,509 from 102 SSP-positive herds and 2,803 from 24 randomly selected SSP-negative herds. In our study we detected a total of 121 SSP-positive herds (i.e., 21.3%; 95% CI: 18.0-24.9%); the within-herd apparent prevalence (AP) ranged between 0.00 and 22.7% (mean 5.7%). A significant difference in within-herd AP was shown between SSP-positive herds and SSP-negative herds. A highly significant association was shown between the median AP herd status ($>5\%$) and positivity to at least one ILMF or BTM sample. The SSP detected a minimum of 56.2% of low AP herds (AP 2.0%) up to a maximum of 100% of herds with a within-herd AP $\geq 8.0\%$. Overall, the SSP detected 85.6% of herds in which at least one individual milk sample was positive by ELISA. The proposed SSP was an inexpensive and useful tool to detect MAP-positive herds with a higher risk of infection diffusion and milk contamination. Although the SSP cannot be used for MAP-free certification of herds, it could be useful to prioritize appropriate control measures aimed at reducing the prevalence of infection in dairy herds and milk contamination.

Papetti°A, Lavazza°A, Alborali°GL, Giacomini°E, Sozzi°E, Lazzaro°M,

Chiapponi°C, Faccini°S, Bonilauri°P, Cordioli°P , Boniotti°MB

Highly genetically distant and recombinant Swine Enteric Coronaviruses from Italy

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 257-258 [Nr. Estr. 7022]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Paternoster°G, Galletti°G, Santi°A, Renzi°M, Lombardini°A, Caminiti°A, Rugna°G, Tamba°M

Active surveillance for canine leishmaniasis in Emilia-Romagna public kennels : a web-based information system

Society for Veterinary Epidemiology and Preventive Medicine : 25th-27th March 2015, Ghent Belgium : proceedings / [s.l. : Society for Veterinary Epidemiology and Preventive Medicine, 2015]. - 1 p. (ultimo accesso 10/03/2016 <http://www.svepm.org.uk/posters.html>) [Nr. Estr. 7180]

Society for Veterinary Epidemiology and Preventive Medicine : Ghent, Belgium : 25th-27th March, 2015)

Pezzoni°G, Stercoli°L, Cavadini°P, Lavazza°A, Brocchi°E, Capucci°L

First expression in baculovirus of major capsid proteins belonging to two new lagoviruses

10th International Congress for Veterinary Virology, 9th Annual Epizone Meeting : "Changing Viruses in a Changing World" : August 31st - September 3rd 2015, Montpellier, France / [s.l. : s.n., 2015]. - p 110-112. - 5 bib ref [Nr. Estr. 7026]

International Congress for Veterinary Virology : 10th Annual meeting Epizone : 9th : Montpellier, France : August 31st - September 3rd 2015)

Piccinini R, Gosney F, Snel GGM, Luini°MV, Nicholas RAJ

Environmental survival of Mycoplasma bovis on a white veal farm

Vet Rec Case Rep. - Vol. 3 (2015). - p e000207 (3 p). - 15 bib ref [Nr. Estr. 7278]

Mycoplasma bovis is an emerging cause of bovine respiratory disease (BRD), particularly in intensive feedlots where disease is mainly spread by aerosol route over dose distances. The present study aimed to investigate the occurrence of mycoplasmas in the environment of barns housing white veal calves presenting BRD. The majority of calves seroconverted to *M bovis* three weeks after arrival; there was little evidence of respiratory virus activity, but *Mannheimia haemolytica* and *Pasteurella multocida* were isolated from clinically affected calves. *M bovis* was detected in nasal swabs of sick animals and also on cages and mangers. The isolates were mostly of the same molecular type, suggesting the possibility of infection from the environment. Environmental resistance conferred by biofilm formation might play a significant role in the continuous circulation of *M bovis* within the white veal herd, indicating the need for all-in, all-out replacement systems and effective disinfection.

Piccirillo A, Lavezzo E, Niero G, Moreno°A, Massi° P, Franchin E, Toppo S, Salata C, Palù G

High-throughput sequencing of avian infectious laryngotracheitis virus (ILTV)

13th National Congress of the Italian Society for Virology (SIV) : Orvieto (TR) 14-16 September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 37 [Nr. Estr. 7317]

Infectious laryngotracheitis (ILT) is an acute and highly contagious respiratory disease of chickens, caused by an alphaherpesvirus, named Infectious Laryngotracheitis virus (ILTV). Recently, full genome sequences of wild-type and vaccine strains have been analysed, but none was from Europe. The aim of this study was to determine and analyse the complete genome sequences of five Italian ILTV strains. Sequences were also compared to reveal the similarity of strains across time and to discriminate between wild-type and vaccine strains. Genomes of 3 ILTV field isolates from outbreaks occurred in Italy in 1980, 2007 and 2011, and 2 commercial chicken embryo origin (CEO) vaccines were sequenced using the 454 Life Sciences technology. Sequences were mapped on the reference sequence (Serva strain, GenBank accession no. HQ630064) using Roche gsMapper. The length of the five ILTV genomes ranged from 153,650 bp to 153,662 bp. The comparison with the Serva genome showed that 35 open reading frames (ORFs) differed across the five ILTV genomes. Overall, 54 single nucleotide polymorphisms (SNPs) and 27 amino acid differences in 19 ORFs and 2 insertions of 9 and 3 nucleotides in two different ILTV genes were identified. Similarity among the wild-type and between the wild-type and the vaccine strains ranged from 99.95% to 99.98%. Phylogenetic analysis of the five strains and all the ILTV complete genomes available within the NCBI GenBank database showed a dose relatedness of the three wild-type isolates, whereas the two vaccine strains grouped into separate clusters. This study generated data on genomic variation among Italian ILTV strains revealing that the genome is well conserved across time and between wild-type and vaccine strains. Results of this study may contribute to the understanding of the molecular bases of ILTV pathogenicity and the genetic differences between wild-type and vaccine ILTV strains.

Piralla A, Moreno^oA, Orlandi ME, Percivalle E, Chi apponi^oE, Vezzoli^oF, Baldanti F and the Influenza Surveillance Study Group

Swine influenza A (H3N2) virus infection in immunocompromised man, Italy, 2014

Emerg Infect Dis. - Vol. 21 no 7 (2015). - p 1189-1191. - 15 bib ref [Nr. Estr. 6086]

Because swine influenza virus infection is seldom diagnosed in humans, its frequency might be underestimated. We report a immunocompromised hematologic patient with swine influenza A(H3N2) virus in 2014 in Italy. Local pigs were the source of this human infection.

Piras C, Soggiu A, Bonizzi L, Greco V, Ricchi^oM, A rrigoni^oN, Bassols A, Urbani A, Roncada P

Identification of immunoreactive proteins of Mycobacterium avium subsp. paratuberculosis

Proteomics. - Vol. 15 (2015). - p 813-823. - 58 bib ref [Nr. Estr. 6013]

Mycobacterium avium subsp. paratuberculosis (MAP) is the cause of a chronic enteritis of ruminants (bovine paratuberculosis (PTB)—Johne's disease) that is associated with enormous worldwide economic losses for the animal production. Diagnosis is based on observation of clinical signs, the detection of antibodies in milk or serum, or evaluation of bacterial culture from feces. The limit of these methods is that they are not able to detect the disease in the subclinical stage and are applicable only when the disease is already advanced. For this reason, the main purpose of this study is to use the MAP proteome to detect novel immunoreactive proteins that may be helpful for PTB diagnoses. 2DE and 2D immunoblotting of MAP proteins were performed using sera of control cattle and PTB-infected cattle in order to highlight the specific immunoreactive proteins. Among the assigned identifiers to immunoreactive spots it was found that most of them correspond to surface-located proteins while three of them have never been described before as antigens. The identification of these proteins improves scientific knowledge that could be useful for PTB diagnoses.

The sequence of the identified protein can be used for the synthesis of immunoreactive peptides that could be screened for their immunoreaction against bovine sera infected with MAP. All MS data have been deposited in the ProteomeXchange consortium with identifier PXD001159 and DOI 10.6019/PXD001159.

Ponti MN, Palmas B, Noworol M, Falchi A, Pintore A, Ruiu A, Vannini A, Boniotti^o MB, Piras A, Picardeau M, Piredda I

A leptospirosis overview on wild fauna in Sardinia, Italy

2nd ELS meeting on leptospirosis and other rodent borne haemorrhagic fevers : 16-18 April 2015
Amsterdam, the Netherlands / [s.l. : s.n., 2015]. - p 46 [Nr. Estr. 6052]

ELS meeting on leptospirosis and other rodent borne haemorrhagic fevers (2nd : Amsterdam, the Netherlands : 16-18 April 2015)

INTRODUCTION: Leptospire are usually transmitted through contact with the urine of infected animals, either directly or through exposure to contaminated water or soil. Among wildlife species, rodents are the most important maintenance hosts for *Leptospira* spp. and may transfer infection to livestock, pets and humans. This study reports the prevalence of leptospirosis in wild animals such as deer, wild boar, rodent, rabbit, hare, marten, mouflon, shrew, nutria, fox and hedgehog circulating in Sardinia. **MATERIALS AND METHODS:** Between 2012-2014 were examined: 7608 sera by MAT using a reference panel of 9 serovars, and 466 organ, blood and urine samples used to inoculate four tubes of liquid EMJH medium. Cultures were incubated at 29°C and evaluated weekly by darkfield microscopy for up to 3 months. 451 of 466 were examined by PCR using the LigA/LigB primer pair amplifies an expected product of 331 bp. The PCR products were analyzed by agarose gel electrophoresis and visualized by staining with SYBR-green. The isolated *Leptospira* species were identified by Multi Locus Variable-number tandem repeat (VNTR) analysis (MLVA) and *rrs* gene sequencing. **RESULTS:** 563 (7,5%) of 7512 wild boar serum samples evaluated in our study presented anti-*Leptospira* spp. antibodies. 3,4% had agglutinating antibodies against *L. interrogans* serovar Pomona, 2,6% against Bratislava, and 1,5% against Grippotyphosa. 141 out of 563 (25%) have reported titres 1:800. 466 (99%) kidneys were tested by culture. *Leptospira* spp was isolated from 26 (5,6%) samples. Out of these, using molecular tools, such MLVA and MLST, 11 wild boar isolates were identified as *L. interrogans* serovar Pomona, 2 out of 9 from rodents as *L. borgpetersenii* and *L. interrogans*, 1 out of 4 from hedgehogs as *L. borgpetersenii*. A single isolate from foxes was typed as *L. interrogans* serovar Bratislava. 62 (54 kidneys and 8 livers of 451 organ samples) tested positive by PCR. Emerging technologies like MLVA and MLST facilitate the identification of infertile leptospire species, thereby contributing to the knowledge of the serovars circulating in our region. **CONCLUSIONS:** Our study indicates that pathogenic leptospire are widely distributed in Sardinia. The excretion of highly pathogenic serovars in the environment could represent an increased risk for humans and animals, especially those living in rural areas. Our data suggest a high level of environmental contamination and indicate that wild animals could become good sentinels for the monitoring of leptospirosis.

Posautz A, Loncaric I, Lundin M, Hoffmann D, Lavazza^o A, Kelemen Z, Beiglboeck C, Walzer C, Kuebber-Heiss A

Health screening of free-ranging European brown hares (*Lepus europaeus*) on the German North-Sea island Pellworm

Acta Vet Scand. - Vol. 57 no 43 (2015). - 9 p. - 48 bib ref [Nr. Estr. 6096]

Background: A sudden decline of the European brown hare (*Lepus europaeus*) population in one of the best hunting districts for small game species in northern Germany, the German North-Sea island Pellworm, in the years 2007/08 following marked habitat changes led to the implementation of a thorough health assessment program of the population. 110 animals were collected during the

normal hunting season in the years 2010 and 2011. A post-mortem examination and histopathological investigation was performed on all animals. Additionally, routine bacteriology of the small intestine and parasitology were carried out. Sera of hares were tested for European Brown Hare Syndrome (EBHS) by enzyme linked immunosorbent assay, and for *Treponema* sp. by indirect immunofluorescent test. Additional testing was performed when deemed necessary. Results: The most striking result was a shift in the intestinal bacterial flora towards Gram-negative nterobacteriaceae with a predominance of either *Escherichia coli*, or *Aeromonas* sp., or a high-grade double-infection with these two pathogens with subsequent catarrhal enteritis. Additionally, a marked coccidiosis, and varying infestations with the nematode *Trichostrongylus retortaeformis* were found. The sero-prevalence for EBHS was 78.1%, and for *Treponema* 43.9%. Conclusions: The shift and decrease in diversity of the intestinal flora was the main and most consistent result found. In the authors' opinion the change of the habitat combined with other stressors increased the animals' sensitivity to ubiquitous bacterial species and parasites which usually would not have such fatal effects.

Pravettoni D, Fantinato E, Luini^o M

Sindrome emorragica da BVDv tipo 2 in un vitello in Italia = BVD virus type 2: hemorrhagic syndrome in a calf in Italy

Large Anim Rev. - Vol. 21 no 6 (2015). - p 265-267. -13 bib ref [Nr. Estr. 7202]

A 5-month-old female calf hospitalized for diarrhea showed petechial bleedings on the oral, conjunctival and vaginal mucosa. Pulse- and respiratory-rate were respectively 76 bpm and 44 breaths/min. The mental status of the calf was alert, although the appetite was bad. The calf was born in Italy through Ovum Pick Up and in vitro embryo production starting from a donor cow coming from Netherlands. Laboratory analysis were characterized by leucopenia, thrombocytopenia and altered coagulation times. Differential diagnosis consisted in coccidiosis, poisoning by Warfarin, septicemia and type 2 BVDv infection. Other causes of hemorrhagic diathesis such as hemophilia and bovine neonatal pancytopenia were not considered among differential diagnosis due to the age of the subject. After fluid and electrolyte therapy and antibiotic administration, the calf got better, but 5 days later the clinical status worsened. The clinical condition was characterized by mental status depressed, sternal recumbence, severe bloody diarrhea and pete-chial hemorrhages. The calf died few hours later. BVDv-2 was detected by means of PCR-RT; virus isolation failed due to a low-level viremia. The absence of NS 2-3 antibodies in serum (ELISA) can be explained as sign of immune tolerance or as a first stage of an acute infection; symptoms observed were consistent with a BVDv-2 acute hemorrhagic syn-drome. To further confirm the diagnosis, a seroconversion test would have been useful. Data concerning the oocyte donor are not available; oocytes employed for in vitro embryo production have been demonstrated to contain BVDv when they come from infected or persistently infected animals. A few months before, in the same farm, an apparently healthy heifer was found to be positive for BVDv-2. Due to the economic loss related to BVDv infection, many european countries underwent BVDv eradication. BVDv-2 has a lower pre-alence than type-1, but the detection of BVDv-2 throughout Europe is increasing. To conclude, BVDv-2 should be now considered among differential diagnosis in case not only of hemorrhagic syndrome but even in case of mild or subclinical disease.

Nell'agosto del 2015 e stata ricoverata una vitella di 5 mesi di eta affetta da diarrea che presentava petecchie emorragiche a carico delle mucose esplorabili. Il paziente presentava sensorio vigile, appetito assente; la frequenza cardiaca era di 76 bpm, quella respiratoria di 44 atti/min. Gli esami ematologici evidenziavano una marcata trombocitopenia e leucopenia associate ad una grave deplezione neutrofilica. Le diagnosi differenziali comprendevano la coccidiosi intestinale, l'avvelenamento da cumarini-ci, la setticemia e l'infezione da BVDv tipo 2. In quinta giornata il vitello moriva per un aggravamento del quadro clinico, caratterizzato da petecchie emorragiche diffuse ed enterorragia gravissima. Gli esami diagnostici confermavano la positivita del soggetto nei confronti di BVDv tipo 2 (PCR Real Time). Il tentativo di isolamento del virus su colture cellulari e risultato pero negativo a causa del basso titolo virale. La ricerca su siero di anticorpi anti-NS 2-3 dava esito negativo lasciando presupporre che si trattasse di un soggetto immunotollerante o con infezione acuta in fase precoce. Per confermare questa ipotesi sarebbe stato necessario verificare la

sieroconversione. Non è stato possibile risalire allo stato sanitario della madre: è stata comunque dimostrata la presenza del virus della BVD in ovociti prelevati da donatrici infette o immunotolleranti. Qualche mese prima, nello stesso allevamento, una manna apparentemente sana era risultata positiva a BVDv-2. Negli ultimi anni le segnalazioni di BVDv-2 in Europa stanno aumentando, con manifestazioni cliniche più o meno apparenti che vanno da forme cliniche evidenti, come nel presente caso, a forme subcliniche più subdole, con soggetti apparentemente asintomatici.

Pruckner S, Kovacs A, Vandi L, Massi° P, Tosi° G

Effects of enhanced acidifiers on the reduction of E. coli in challenged turkeys

20th European Symposium on Poultry Nutrition (ESPN) : 24-27 August 2015, Prague, Czech Republic : proceedings / [s.l. : s.n., 2015]. - p 162 (P-057) [Nr. Estr. 7150]

European Symposium on Poultry Nutrition (ESPN) (20th : Prague, Czech Republic : 24-27 August 2015)

A combination of synergistically acting organic acids and a permeabilizing substance in water application can reduce the microbial contamination in turkeys. An experiment was conducted to confirm these effects using water application with a blend of formic, acetic and propionic acid and a permeabilizing substance (Biotronic0 Top liquid, BIOMIN, Austria). 60 day-old female turkey poults were randomly assigned to three groups with 20 turkeys each. A control group (NC) received a commercial diet with no antibiotic or NGP, trial group (NGP) received water supplemented with Biotronic0 Top liquid 1.25 ml/l of water and positive control group (PC) received water supplemented with Enrofloxacin 0.5 ml/l of water. On day 10 the animals in all groups were challenged with E. coli 078. The trial lasted for 30 days. Bacterial counts of the intestinal tract were recorded on day 20 and 30. On day 20, E. coli counts of NGP group ($5.42a \pm 1.07$) were significantly ($p < 0.05$) lower than NC ($7.42b \pm 0.78$) and PC group ($7.24b \pm 1.18$). On day 30, E. coli counts of NGP group ($5.12a \pm 0.44$) were as well significantly ($p < 0.05$) lower compared to NC ($8.09b \pm 0.21$) and PC group ($7.89b \pm 0.31$). The results of the NGP group showed a significant ($p < 0.05$) reduction of E. coli counts in the intestinal tract compared to NC and PC group.

Pruckner S, Kovacs A, Vandi L, Massi° P, Tosi° G

Reducing Escherichia coli colonization in artificially challenged turkey using a feed supplemented natural growth promoter product

20th European Symposium on Poultry Nutrition (ESPN) : 24-27 August 2015, Prague, Czech Republic : proceedings / [s.l. : s.n., 2015]. - p163 (P-058) [Nr. Estr. 7151]

European Symposium on Poultry Nutrition (ESPN) (20th : Prague, Czech Republic : 24-27 August 2015)

Supplementing feed with a natural growth promoter product can reduce E. coli counts in turkey intestinal tract. A trial was conducted to study the effects of dietary supplementation with a blend of formic, propionic and acetic acids combined with cinnamaldehyde and a permeabilizing substance (NGP, BiotronicO Top3, BIOMIN, Austria) on the reduction of E. coli counts in turkey intestinal tract. 60 day-old BUT female turkey chicks were randomly assigned to 3 treatments of 20 chicks each and placed in isolators. A control group (NC) received a commercial diet with no antibiotic or NGP, trial group (NGP) received 2 kg NGP/ton of feed and positive control group (PC) received water supplemented with Enrofloxacin 0.5 ml/l of water. On day 10 the animals in all groups were challenged with E. coli 078. The trial lasted for 30 days. Bacterial counts of the intestinal tract were recorded on day 20 and 30. On day 20, E. coli counts of NGP group ($6.22b \pm 0.83$) were significantly ($p < 0.05$) lower than NC ($7.42a \pm 0.78$) and PC group ($7.24a \pm 1.18$). On day 30, E. coli counts of NGP group ($6.01 b \pm 0.40$) were as well significantly ($p < 0.05$) lower compared to NC ($8.09a \pm 0.21$) and PC group ($7.89a \pm 0.31$). This results show that NGP supplemented diet significantly reduces E. coli counts in the intestinal tract of turkey.

Quirino A, Torti C, Strazzulla A, Nisticò S, Galati L, Barreca GS, Lamberti AG, Berardelli G, Pacciarini M, Gasparini G, Pisani V, Gambardella A, Liberto MC, Focà A

Professional acquisition of *M. bovis* in Calabria Region (Southern Italy) : a challenging case of osteomyelitis in a migrant patient from Bulgaria

Case Reports Infect Dis. - Vol. ID 794715 (2015). - 4 p. - 13 bib ref [Nr. Estr. 6095]

Razzuoli E, Amadori M, Lazzara F, Bilato D, Ferraris M, Ferrari A

Salmonella serovar specific modulation of innate immunity in a jejunal epithelial cell line

5th European veterinary immunology workshop (EVIW) : Vienna, Austria, 2nd-4th September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 74 [Nr. Estr. 7106]

European veterinary immunology workshop (EVIW) (5th : Vienna, Austria : 2nd-4th September 2015)

Salmonella infections are an important source of food-borne illnesses and a major public health concern. In this study we evaluated the effect of Salmonella infection on innate immunity using intestinal IPEC-J2 cells. Overnight cultures of 6 different Salmonella enterica strains (S. Coeln, S. Ablogame, S. Enterica sub-specie Diarizone 1, S. Veneziana, S. Enterica sub-specie Diarizone 2 and S. Thompson) were sub-cultured for 2 h at 37 °C in Brain Heart Infusion (BHI) medium. Each bacterial strain resuspended at 1 x 10⁸ CFU/ml in DMEM/F12 medium, was used to infect IPEC-J2 cells. After 5 hours of incubation, supernatants were harvested to evaluate IL-8 release by ELISA and the expression of IL-8, IL-113, TNF- α , IFN- γ , IL-8, IL-6, IL-4, bD1, bD2, bD3, bD4, IL-18, TLR4, SOCS1 and NF-KB1 genes by RT Real-time PCR. S. Coeln, S. Enterica sub-specie Diarizone 2, S. Thompson and S. Veneziana determined a significant (P[It] 0.05) increase of both IL-8 release and gene expression with respect to control cells; also NF-KB1 was up-regulated by S. Coeln and S. Veneziana. S. Ablogame and S. Enterica sub-specie Diarizone 1, did not significantly modulate these parameters. Moreover, S. Thompson down-regulated the expression of IL-6 (P[It] 0.05) and IL-4 (P[It] 0.05) genes, whilst TNF- α gene expression was up-regulated. Also, S. Thompson, S. Veneziana and S. Enterica 2 caused a significant (P[It] 0.05) up-regulation of bD1 and bD2, while S. Coeln, S. Veneziana and S. Ablogame modulated bD4 likewise. However, no significant differences were found in terms of protein release. TLR4 and IFN- γ genes were down-regulated by S. Coeln and S. Ablogame. These findings outline a different modulation of innate immunity by different salmonella spp strains.

Razzuoli E, Montoya M, Foni E, Baratelli M, Bilato D, Córdoba L, Del_Burgo MAM, Martinez J, Martinez J, Martinez-Orellana P, Chiapponi C, Perlin DS, Del_Real G, Ferrari A, Amadori M

Innate immune responses in broncho-alveolar fluids after infection with swine-adapted or non-adapted influenza virus strains

Atti del LXIX Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : XII Convegno AIPVet, Il Convegno RNIV, XV Convegno SICV, XIII Convegno SIRA, XI Convegno So.Fi.Vet : Perugia, 15-17 Giugno 2015 / [s.l. : s.n., 2015]. - p 368-369. - 6 bib ref [Nr. Estr. 7019]

Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : 69 Convegno AIPVet : 12 Convegno RNIV : 2 Convegno SICV : 15 Convegno SIRA : 13 Convegno So.Fi.Vet : 11 : Perugia : 15-17 Giugno 2015)

Three IV subtypes (H1N1, H1N2 and H3N2) are currently circulating in swine herds in Europe (1), and have been associated with disease occurrence and gross lesions in swine (2). Also, pigs are susceptible to infection with low pathogenic and high pathogenic avian influenza viruses (LPAIV and

HPAIV, respectively) (3). However, pigs have been shown to be susceptible to other IV strains that are able to cross the species barrier. Besides, it is well known that some influenza viruses are able to infect humans and pigs, as it was the case in the last H1N1 2009 pandemic infection (1). Additionally, the pig has been proposed as an animal model for human influenza as the anatomy and physiology of the porcine respiratory tract exhibit more similar features to humans than those of rodents (4). Owing to the above, the aim of our study was to investigate the modulation of innate immune responses in bronchoalveolar fluids (BALF) after infection with swine-adapted or non-adapted IV strains. 6 groups of healthy pigs each were set up. One was the uninfected control group (group 1, six pigs). 12 other pigs were infected with a H3N2 Swine IV (Group 2). Four different H3N8 IV strains circulating in different animal species (dogs, horses, wild aquatic birds and seals) were administered to groups 3 to 6 (12 pigs each). At day 0, each pig in groups 2, 3, 4, 5, 6 was intratracheally infected with 2 ml of virus, containing 200,000 Doses (EID)₅₀ of the corresponding virus strain. Animals were clinically inspected on a daily basis. Four pigs of each virus-infected group were euthanized at day 3, 6 and 21 post infection (p.i.), respectively. BALF were harvest to perform Real time PCR to evaluate the expression of the following genes: porcine IFN- γ , IL-8, IL-6, bD1, bD2, IL-1b, TNF- α , IFN- β , IFN- γ , IFN- δ , IFN- ϵ , IFN- ζ and IFN- η (5-6). All infected groups exhibited Ab responses to Influenza virus NP protein. Also, no antibody response was observed in mock-infected animals. The gene expression profile was the following. MOCK group: there was no significant difference between the different sampling times for each cytokine gene under study. SWINE group: only tendencies ($P < 0.10$) were shown for IL-8, IL-10 and IFN- genes. EQUINE group: significant differences were shown for IFN- γ , IFN- δ and IL-10 genes. CANINE group: significant differences were shown for IFN- β , IFN- γ and IFN- genes. AVIAN group: there were significant differences for IFN- β , IFN- δ , IFN- η and IFN- gene expression, and tendencies for IFN- γ and IFN- δ genes. SEAL group: significant differences were observed for IFN- β , IFN- δ and IL-10 genes. In all groups infected with non-adapted strains there was a significant modulation of IFN- gene expression characterized by down regulation at day 21 after infection. Moreover, different influenza virus strains activated different IFN- genes; in particular, genes of IFN- subtypes with little if any antiviral activity were activated by the canine and seal strains. Also, each virus strain could be associated to an expression pattern of cytokine genes in BALF cells.

Ricchi^oM, Mazzarelli A, Di_Caro A, Savi^oR, Leo^oS , Russo^oS, Garbarino^oCA, Cammi^oG, Arrigoni^oN

La tecnologia MALDI-TOF nell'identificazione rapida di *Mycobacterium avium* subsp. paratuberculosis (MAP) : risultati preliminari

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 240-241. - 5 bib ref [Nr. Estr. 7051]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

*The identification and sub-typing of *Mycobacterium avium* subsp. paratuberculosis (MAP) is based on DNA fingerprinting methods, while no methods are currently available based on protein profile. We report here preliminary data about the use of MALDI-TOF (Matrix-assisted laser desorption/ionization, coupled with time-of-flight mass spectrometer) for exploring MAP identification and sub-typing.*

Rizzoli A, Bolzoni^oL, Chadwick EA, Capelli G, Mont arsi F, Grisenti M, Puente JM, Muñoz J, Figuerola J, Soriguer R, Anfora G, Di_Luca M, Rosà R

Understanding West Nile virus ecology in Europe : *Culex pipiens* host feeding preference in a hotspot of virus emergence

Parasites & Vectors. - Vol. 8 (2015). - no 213 (28 p). - 69 bib ref (ultimo accesso 23/04/2015 <http://www.parasitesandvectors.com/content/pdf/s13071-015-0831-4.pdf>) [Nr. Estr. 6031]

Background Understanding wildlife disease ecology is becoming an urgent need due to the continuous emergence and spread of several wildlife zoonotic diseases. West Nile Virus (WNV) is the most widespread arthropod-borne virus in the world, and in recent decades there has been an increase both in geographic range, and in the frequency of symptomatic infections in humans and wildlife. The principal vector for WNV in Europe is the common house *Culex pipiens* mosquito, which feeds on a wide variety of vertebrate host species. Variation in mosquito feeding preference has been described as one of the most influential parameters driving intensity and timing of WNV infection in the United States, but feeding preferences for this species have been little studied in Europe. Methods Here, we estimated feeding preference for wild *Cx. pipiens* in northern Italy, using molecular analysis to identify the origin of blood meals, and avian census to control host abundance variations. Additionally, we used host bird odour extracts to test experimentally mosquito preferences in the absence of environmental variations. Results For the first time, we demonstrate a clear feeding preference for the common blackbird (*Turdus merula*), both for wild collected specimens and in the lab, suggesting a potential important role for this species in the WNV epidemiology in Europe. A seasonal decrease in abundance of blackbirds is associated with increased feeding on Eurasian magpies (*Pica pica*), and this may be linked to seasonal emergence of WNV in humans. Feeding preferences on blackbirds are more marked in rural areas, while preference for magpies is higher in peridomestic areas. Other species, such as the house sparrow (*Passer domesticus*) appear to be selected by mosquitoes opportunistically in relation to its abundance. Conclusions Our findings provide new insights into the ecology of *Cx. pipiens* in Europe and may give useful indications in terms of implementing targeted WNV surveillance plans. However, a clearer understanding of spatio-temporal variations of *Cx. pipiens* feeding preferences, and targeted studies on reservoir competence for WNV for these species are therefore now urgently needed as this is essential to describe disease dynamics and quantify virus transmission risk.

Rizzoli A, Jiménez-Clavero MA, Barzon L, Cordioli P, Figuerola J, Koraka P, Martina B, Moreno A, Nowotny N, Pardigon N, Sander S, Ulbert S, Tenorio A

The challenge of West Nile virus in Europe : knowledge gaps and research priorities

EuroSurveillance. - Vol. 20 no 20 (2015). - p 28-42. - 118 bib ref (Ultimo controllo 26/05/2015 : <http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=21135> - <http://www.eurosurveillance.org/images/dynamic/EE/V20N20/V20N20.pdf>) [Nr. Estr. 6048]

West Nile virus (WNV) is continuously spreading across Europe, and other continents, i.e. North and South America and many other regions of the world. Despite the overall sporadic nature of outbreaks with cases of West Nile neuroinvasive disease (WNND) in Europe, the spillover events have increased and the virus has been introduced into new areas. The high genetic diversity of the virus, with remarkable phenotypic variation, and its endemic circulation in several countries, require an intensification of the integrated and multidisciplinary research efforts built under the 7th Framework Programme of the European Union (FP7). It is important to better clarify several aspects of WNV circulation in Europe, including its ecology, genomic diversity, pathogenicity, transmissibility, diagnosis and control options, under different environmental and socio-economic scenarios. Identifying WNV endemic as well as infection-free areas is becoming a need for the development of human vaccines and therapeutics and the application of blood and organs safety regulations. This review, produced as a joint initiative among European experts and based on analysis of 118 scientific papers published between 2004 and 2014, provides the state of knowledge on WNV and highlights the existing knowledge and research gaps that need to be addressed with high priority in Europe and neighbouring countries.

Rosà R, Bolzoni L, Cagnacci F, Hauffe H, Tagliapietra V, Ferreri L, Giacobini M, Kazimirova M, Henttonen H, Rizzoli A

Modelling the effects of tick-host interaction on pathogen dynamics : TBE as a case study

Ecology at the interface : 21-25 September 2015, Rome : abstract book / [s.l. : s.n., 2015]. - p 213 [Nr. Estr. 7161]

Ecology at the interface : Rome : 21-25 September 2015)

Tick-borne encephalitis (TBE) is an emerging vector-borne zoonosis reported in Europe with complex transmission routes that involve key vertebrate host species and a major tick vector. Understanding interactions between ticks and main hosts involved in TBE virus (TBEv) cycle is crucial to quantify TBEv emergence and spread. We used eco-epidemiological models to explore the dynamics of ticks and TBEv infection in relation to the density of two key hosts, deer and rodents. Both hosts may act as tick amplifiers, but at high densities may also dilute pathogen transmission. Results were validated with empirical data from selected foci in Italy and Slovakia. In addition, we explored the effect on TBEv dynamics when using various distributions to describe tick aggregation on rodents. We modelled the number of ticks per rodent observed in Trentino (Northern Italy) with different theoretical distributions. Power Law (PL) distribution better described the heterogeneity observed in our data. Using a stochastic model, we observed that TBEv infection is highly dependent on the capability of the implemented model to describe tick burden on rodents. We found that the epidemic threshold and equilibria obtained with PL distribution are a good approximation of those observed in simulations feed with empirical distribution.

Rosignoli°C

Aggiornamenti sulla diagnosi e il controllo delle infezioni enteriche neonatali del suinetto

17° Congresso Internazionale SIVAR : 13-15 Maggio 2015 Cremona : estratti, relazioni / [Cremona : Societa' Italiana Veterinari per Animali da Reddito (SIVAR), 2015]. - p 34-35 [Nr. Estr. 7207]

Congresso Internazionale SIVAR (17. : Cremona : 13-15 Maggio 2015)

Rosignoli°C, Faccini°S, Franzini°G, Nigrelli°A

Resistenza agli antimicrobici in ceppi di pasteurilla multocida isolati da bovini con patologia respiratoria dal 2005 al 2014

Buiatria. - Vol. 2015). - 5 p. - 4 bib ref [Nr. Estr. 7203]

Scopo del presente studio retrospettivo è stato quello di rilevare il tasso e valutare il trend della resistenza di ceppi di Pasteurella multocida isolati da bovini con patologia respiratoria nei confronti di 15 antimicrobici. Nell'indagine sono stati analizzati i dati relativi a 10 anni, dal 2005 al 2014. Considerando la globalità dei ceppi esaminati sono emersi i seguenti tassi di resistenza: sulfadiazina 64,6%, tetraciclina 39,5%, tilosina 34,9%, penicillina G 33,2%, trimetoprim-sulfametossazolo 26,1%, tiamfenicolo 25,4%, ampicillina 23,7%, enrofloxacin 22,6%, danofloxacin 17,6%, cefalexina 15,7%, ceftiofur 15,6%, amoxicillina 15,3%, marbofloxacin 13,7%, florfenicolo 11,5% e amoxicillina/acido clavulanico 9,9%. Il tasso annuale di resistenza dei ceppi di P. multocida ha mostrato un aumento statisticamente significativo del trend per cefalexina e florfenicolo e una diminuzione per penicillina G e sulfadiazina. Per gli altri antimicrobici il trend della resistenza è rimasto stabile.

Rossi G, De_Leo GA, Pongolini°S, Natalini S, Vincenzi S, Bolzoni°L

Epidemiological modelling for the assessment of bovine tuberculosis surveillance in the dairy farm network in Emilia-Romagna (Italy)

Epidemics. - Vol. 11 (2015). - p 62-70. - 51 bib ref [Nr. Estr. 6057]

Assessing the performance of a surveillance system for infectious diseases of domestic animals is a challenging task for health authorities. Therefore, it is important to assess what strategy is the most

effective in identifying the onset of an epidemic and in minimizing the number of infected farms. The aim of the present work was to evaluate the performance of the bovine tuberculosis (bTB) surveillance system in the network of dairy farms in the Emilia-Romagna (ER) Region, Italy. A bTB-free Region since 2007, ER implements an integrated surveillance strategy based on three components, namely routine on-farm tuberculin skin-testing performed every 3 years, tuberculin skin-testing of cattle exchanged between farms, and post-mortem inspection at slaughterhouses. We assessed the effectiveness of surveillance by means of a stochastic network model of both within-farm and between-farm bTB dynamics calibrated on data available for ER dairy farms. Epidemic dynamics were simulated for five scenarios: the current ER surveillance system, a no surveillance scenario that we used as the benchmark to characterize epidemic dynamics, three additional scenarios in which one of the surveillance components was removed at a time so as to outline its significance in detecting the infection. For each scenario we ran Monte Carlo simulations of bTB epidemics following the random introduction of an infected individual in the network. System performances were assessed through the comparative analysis of a number of statistics, including the time required for epidemic detection and the total number of infected farms during the epidemic. Our analysis showed that slaughterhouse inspection is the most effective surveillance component in reducing the time for disease detection, while routine surveillance in reducing the number of multi-farms epidemics. On the other hand, testing exchanged cattle improved the performance of the surveillance system only marginally.

Rovida F, Sarasini A, Campanini G, Percivalle E, Gorini G, Mariani B, Pan A, Cuzzoli A, Possenti S, Manzini L, Castelli F, Bossini N, Grossi PA, Castilletti C, Calzolari M, Lelli D, Piatti A, Baldanti F and West Nile Virus Task Force (Calzolari M, Lelli D, Lavazza A)

West Nile virus outbreak in the Lombardy region, Northern Italy, Summer 2013

Vector Borne Zoonotic Dis. - Vol. 15 no 4 (2015). - p 278-283. - 26 bib ref [Nr. Estr. 6036]

In the summer of 2013, an outbreak of West Nile virus (WNV) infection occurred in the Lombardy, a region of northern Italy to the west of districts affected by WNV in previous years. Eighteen cases of human WNV infection were diagnosed—10 cases of acute WNV neuroinvasive disease and eight of WNV fever. In the same period, WNV was detected in birds (one crow) in horses (11 cases) and from mosquitoes (six pools).

Rubini S, Tosi G, Pari S, Angelini V, Ambrosio E, Vallini C, Tarricone L, Scaravelli D, Rinaldi A, Ferrari C, Raffaelli K, Lombardini A, Delogu M

Risultati delle attività della rete regionale Emilia Romagna per la conservazione e la tutela delle tartarughe marine a 3 anni dalla sua istituzione

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 242-243. - 8 bib ref [Nr. Estr. 7059]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

All sea turtles species are affected by a range of different conservation problems caused by human activities and primarily due to fishing activities. As a result sea turtles are now considered to be threatened or endangered. The purpose of this paper is to illustrate the results of three years of activity of the Regional Network for the Conservation and Protection of Sea Turtles established by the Emilia Romagna Region. During the last three years the IZLER laboratories received 104 sea turtles to determine death causes. The 38,5% of the animals had traumatic lesions, the 26% showed signs of drowning and in the 35,6% of the carcasses it was not possible determine the cause of

death.

Ruggeri° J, Pesciaroli M, Foresti F, Giacomini° E, Lazzaro° M, Ossiprandi M, Corradi A, Pasquali P, Alborali° GL

Autogenous Salmonella Typhimurium monophasic variant bacterin is effective in two endemic farms of the North of Italy

Atti del LXIX Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : XII Convegno AIPVet, II Convegno RNIV, XV Convegno SICV, XIII Convegno SIRA, XI Convegno So.Fi.Vet : Perugia, 15-17 Giugno 2015 / [s.l. : s.n., 2015]. - p 57. - 1 bib ref [Nr. Estr. 7014]

Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : 69 Convegno AIPVet : 12 Convegno RNIV : 2 Convegno SICV : 15 Convegno SIRA : 13 Convegno So.Fi.Vet : 11 : Perugia : 15-17 Giugno 2015)

Salmonella enterica serovar Typhimurium monophasic variant (S.T. 1,4,[5],12:i-) is increasingly responsible of human salmonellosis (EFSA, 2014) and pork represents the first source of infection. Salmonella can sub-clinically colonize pigs, principally during the finishing phase, and hence being introduced in the slaughterhouse, contaminating pork products destined to human consumption (Boyen et al., 2008). The biosecurity activities and management effectively decrease the prevalence in farms. However, other tools are envisaged for controlling Salmonella in endemic areas. Of these vaccination represents an efficient solution to decrease the infection in pig farms (Pesciaroli et al., 2013). Live vaccines are more effective than inactivated ones, inducing a cellular immune response that better enhances the clearance of Salmonella (Coward et al., 2014). The limitation is represented by the availability of attenuated vaccines whose protection versus different serovars, frequently diagnosed in pig farms, is not completely disclosed. In this scenario, immunization with autogenous bacterin could be more effective in endemic Salmonella farrowto- finish or multisite pig farms (Roesler et al., 2006). The efficacy of two autogenous vaccines versus S.T. 1,4,[5],12:i- was evaluated in two multisite pig production systems of the North of Italy. Forty sows were divided in vaccinated (V) or not vaccinated and intramuscular injection of 2x10⁹ CFU/ml of inactivated S. Typhimurium 1,4,[5],12:i- was performed at 6 and 2 weeks before the delivery. Sixty piglets from sows of group V (three from each sow) were divided into 2 groups: vaccinated group (VV) and not vaccinated group (VnV). Also, the 60 piglets born from unvaccinated sows (nV) were divided in 2 groups: vaccinated group (nVV) and not vaccinated group (nVnV). Piglets were primed and boosted at 4 and 8 weeks after birth with the same immunization protocol of sows. Microbiological and serological exams of sows were performed during pregnancy and suckling phase, conversely, piglets were monitored throughout the production cycle. Data related to weight gain, fecal shedding of bacteria, organs colonization and humoral immune response were recorded. The results indicate that the administration of inactivated vaccines in breeding and/or growing phase is differently able to improve the growth of animals and hence the productivity of farms, and to reduce the load of bacteria carried into the food processing. Vaccination of sows does not affect Salmonella shedding in sows faeces, but tends to reduce the percentage of shedder piglets. Furthermore, the antibody titers of pigs born from vaccinated sows were reduced (V/V) or remained constant (V/nV) during the observational period, while antibody titers of pigs born from unvaccinated sows had a sharp increase close the slaughtering. Particularly, a combined vaccination of sows and their piglets is the best protocol to improve the weight gain of growing pigs, to limit Salmonella colonization of organs and to reduce carrier pigs.

Ruggeri° J, Pesciaroli M, Foresti F, Giacomini° E, Lazzaro° M, Ossiprandi MC, Corradi A, Lombardi° G, Pasquali P, Alborali° GL

Inactivated Salmonella enterica serovar Typhimurium monophasic variant (S. Typhimurium 1,4,[5],12:i-) in sows is effective to control infection in piglets under field condition

Vet Microbiol. - Vol. 180 (2015). - p 82-89. - 26 bib ref [Nr. Estr. 7135]

The monophasic variant of Salmonella enterica serovar Typhimurium, namely Salmonella

1,4,[5],12:i-, has been increasingly responsible for foodborne human cases of disease and is most frequently detected in pork, since the variant is widely spread in pig farms. The aim of this study was to assess the efficacy of an autologous vaccine in decreasing the prevalence of Salmonella 1,4,[5],12:i-, in pigs. The trial was performed in a multisite pig production system of Northern Italy. The autogenous vaccine was prepared from the Salmonella 1,4,[5],12:i- strain isolated from the clinical case occurring in the Farm. Different immunization protocols were applied, ranging from interventions only in sows or piglets, or both. Microbiological analysis was performed to assess faecal shedding in sows and their offspring from birth till end of the production cycle and organ colonization of slaughtered pigs. Body weight of pigs was recorded at different time-points. Humoral immune response was evaluated in serum samples of sows and piglets. S. Typhimurium 1,4,[5],12:i- determines reduction of animal growth and farm production, furthermore, contamination of carcasses at the slaughterhouse. The load of bacteria entering into the food processing chain is differently influenced by the regimen of administration of inactivated vaccine. In particular, a combined vaccination of sows and their offspring was able to improve the weight gain of growing pigs, to limit Salmonella colonization of organs and to reduce the number of carrier pigs, and hence lowering the risk of introducing Salmonella organisms in the slaughter process.

Ruggeri° J, Pesciaroli M, Gaetarelli° B, Pregel P, Scaglione FE, Bollo E, Alborali° L, Pasquali P, Pasquali P

An intramuscularly administered Salmonella typhimurium attenuated vaccine (S.typhimurium znuabc) induces protection versus S. typhimurium infection in piglets

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 264 (Poster P271) [Nr. Estr. 7095]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Salmonella enterica serovar Typhimurium (S.Typhimurium) is the major cause of human salmonellosis due to consumption of pork products. Vaccination represents a complementary solution to control Salmonella spp. in positive farms. Recently, we had demonstrated that an orally administered mutant strain of S. Typhimurium (S.Typhimurium AznuABC) was protective versus salmonellosis in mice and pigs. Here, we have assessed if S.Typhimurium AznuABC, intramuscularly administered, is also safe and effective in piglets. MATERIALS AND METHODS: Twenty-five piglets were divided in 5 groups. Attenuated S. Typhimurium AznuABC strain was intramuscularly administered at concentration of 10⁴ CFU in group A and orally at 5x10⁷ and 5x10⁵ CFU in group B and C, respectively. Group D was the control group and group E was orally challenged with 4x10⁸ CFU of wild type S.Typhimurium at 6 weeks after vaccination of other piglets. Afterwards all groups were allocated in the same pen for two weeks to favor contact among uninfected and shedder animals (seeder mode)). Feces were collected once a week after vaccination and after contact to estimate the bacteria shedding. Four weeks after animals contact, samples of ileocecal lymph nodes, ileum, caecum, and colon, were collected during necropsy and then were submitted to microbiological and histological analyses. RESULTS: Attenuated S.Typhimurium AznuABC is safe because no clinical signs of salmonellosis was recorded after parenteral and ora) vaccination. In addition, it is isolated only in feces of orally vaccinated animals for a limited period of time. The attenuated strain is effective because it reduces fecal shedding, or9ans lesion and colonization of wild type S. Typhimurium in vaccinated groups. In particular, gross lesions, ileum wall thickening and reactivity of ileocecal lymph nodes, were recorded in group D and C. Histologically, villi conglutination and necrosis were associated to vasal congestion and lymph nodes depletion in 90:4 D. Similar lesions were observed in group C, that was the most affected of the vaccinated groups. DISCUSSION: In conclusion, intramuscular and high dose ora) administration of the S.Typhimurium AznuABC mutant strain is protective against infection with a virulenta S.Typhimurium strain. Vaccination is a method suggested to decrease Salmonella sp. prevalence in swine farms and to prevent its dissemination through the pork production chain.

Ruggeri° J, Pesciaroli M, Martinelli°N, Chirullo B , Ossiprandi M, Corradi A, Pasquali P, Alborali°GL

Efficacy of an immunization protocol based on an attenuated *Salmonella typhimurium* vaccine boosted with an inactivated *Salmonella choleraesuis* vaccine in piglets experimentally infected with *S. choleraesuis*

Atti del LXIX Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : XII Convegno AIPVet, Il Convegno RNIV, XV Convegno SICV, XIII Convegno SIRA, XI Convegno So.Fi.Vet : Perugia, 15-17 Giugno 2015 / [s.l. : s.n., 2015]. - p 55-56. - 5 bib ref [Nr. Estr. 7013]

Convegno Nazionale della Societa' Italiana delle Scienze Veterinarie (SISVET) : 69 Convegno AIPVet : 12 Convegno RNIV : 2 Convegno SICV : 15 Convegno SIRA : 13 Convegno So.Fi.Vet : 11 : Perugia : 15-17 Giugno 2015)

Salmonella Choleraesuis causes a systemic disease in pigs responsible of economic problems for farmers (Ku et al. 2005). *Salmonella Typhimurium* is the second important serovar, diagnosed in pig farms and is the principal responsible of salmonellosis in humans as a consequence of consumption of contaminated pork products (EFSA Journal, 2010). Vaccination is a decisive tool to control disease in countries with high prevalence of infection (Wales et al., 2011), unfortunately different serovars affect pigs and the cross-protection of available vaccines is not completely disclosed (Foss et al., 2013). *S.Typhimurium* ÎTznuABC is an attenuated vaccine and recently we tested its safety and efficacy in mice and pigs experimentally infected with virulent *S.Typhimurium* (Pesciaroli et al. 2011; Gradassi, et al. 2013). The aim of this study is to assess the efficacy of this attenuated vaccine, in comparison to an inactivated *S.Choleraesuis* vaccine, in piglets experimentally infected with *S.Choleraesuis*. Eighteen piglets were randomly divided in 3 groups. Group A was orally vaccinated with *S.Typhimurium* Î TznuABC and boosted with inactivated *S.Choleraesuis* vaccine, group B was intramuscularly vaccinated with inactivated *S. Choleraesuis* vaccine and group C was unvaccinated. All groups were challenged with 5x10⁸ CFU of virulent *S.Choleraesuis* at day 35 after vaccination. Animals were weighed at vaccination and before necropsy (day 47 from first vaccination). Tonsils, ileocecal lymph nodes, spleen, liver, intestinal content of ileum, cecum, colon and jejunum were collected during necropsy for microbiological analyses and gross lesions of organs were recorded. The results show that vaccination does not influence the weight gain; furthermore, the synergic action of attenuated vaccine followed by a boost with inactivated vaccine reduces fever, ileocecal lymph nodes and gut colonization caused by virulent *S. Choleraesuis* infection. Antibody titers of vaccinated groups (A and B) were statistically different from group C, indicating the capability of this new immunizing protocol in providing humoral response. These findings show that this new immunizing approach is more effective than the homologous inactivated vaccination protocol in controlling *S. Choleraesuis* infection.

Ruggeri° J, Pesciaroli M, Martinelli°N, Chirullo B , Scaglione FE, Pregel P, Ammendola S, Lazzaro°M, Giacomini°E, Ossiprandi M C, Battistoni A, Bollo E, Pasquali P, Alborali°GL

Controllo delle infezioni da *Salmonella* nel suino : strategie vaccinali = Controlling *Salmonella* infections in pigs : vaccination protocols

Atti Convegno SIPAS. - Vol. 41 (2015). - p 175-181. - 14 bib ref [Nr. Estr. 7272]

Meeting Annuale della Societa' Italiana di Patologia ed Allevamento dei Suini (SIPAS) (41. : Montichiari (BS) : 19-20 Marzo 2015)

Salmonella sp. è uno dei principali responsabili di tossinfezioni alimentari dovute al consumo di prodotti contaminati di origine animale. Il suino è la principale fonte d'infezione, determinando l'ingresso del patogeno nella fase di macellazione. La situazione italiana è caratterizzata da un'elevata percentuale di allevamenti suini infetti, e la vaccinazione avrebbe un ruolo decisivo nel controllo dell'infezione, ma nessun vaccino è disponibile in commercio per il suino. L'obiettivo del nostro lavoro è quello di descrivere i dati relativi alla valutazione della sicurezza ed efficacia di un

vaccino attenuato di *S.Typhimurium*, in condizioni sperimentali, e di un vaccino stabulogeno inattivato di *S.Typhimurium* var. Monofasica, testato in campo. Il ceppo attenuato è sicuro e protettivo, limitando l'eliminazione fecale e la colonizzazione degli organi del ceppo virulento e la sua efficacia è stata testata anche a seguito della somministrazione parenterale e in corso d'infezione eterologa con *S.Choleraesuis*. Il ceppo stabulogeno inattivato è stato somministrato in alcune scrofe in gestazione e/o nei loro suinetti. I buoni risultati ottenuti hanno confermato che la vaccinazione delle scrofe, e il trasferimento degli anticorpi tramite il colostro, è maggiormente protettiva rispetto alla diretta vaccinazione dei suini.

First results. Salmonella sp. is responsible of human infections due to consumption of contaminated pork products. Carrier pigs introduce bacteria in the slaughter process. Italian situation is characterized by a high percentage of infected farms, and vaccination could have a decisive role in controlling infection. Unfortunately, none vaccine, licensed for swine, is available in Italy. The aim of our work is to describe data related to efficacy and safety of an attenuated S.Typhimurium vaccine, tested in experimental conditions, and an inactivated autogenous vaccine, tested in field conditions. Attenuated strain is safe and protective, limiting fecal spread and organs colonization by virulent S.Typhimurium and it is also effective when intramuscularly administered or challenge is performed with S.Choleraesuis. Inactivated autogenous vaccine was administered in pregnant sows and their piglets of two farms. The results of this trial confirmed that sows vaccination, therefore antibody transfer with colostrum, is more protective than direct piglets vaccination.

Rugna°G, Bonilauri°P, Carra°E, Bergamini°F, Lup pi°A, Gherpelli°Y, Magistrali CF, Nigrelli°A, Alborali°GL, Martelli P, La T, Ha mpson DJ, Meriardi°G

Sequence types and pleuromutilin susceptibility of *Brachyspira hyodysenteriae* isolates from Italian pigs with swine dysentery : 2003-2012

Vet J. - Vol. 203 (2015). - p 115-119. - 22 bib ref [Nr. Estr. 5992]

Swine dysentery is a mucohaemorrhagic colitis of pigs caused by infection with *Brachyspira hyodysenteriae*. The disease can be controlled by treatment with antimicrobial agents, with the pleuromutilins tiamulin and valnemulin being widely used. In recent years, the occurrence of *B. hyodysenteriae* with reduced susceptibility to these drugs has been increasing. The aim of this study was to determine temporal changes in genetic groups and pleuromutilin susceptibility amongst *B. hyodysenteriae* isolates from Italy. Multilocus sequence typing (MLST) was performed on 108 isolates recovered from 87 farms in different regions of Italy from 2003 to 2012, and their minimum inhibitory concentrations (MICs) for tiamulin and valnemulin were determined. Logistic regression was performed to assess associations between susceptibility to the two antimicrobial agents and genetic group, year and region of isolation. The isolates were allocated to 23 sequence types (STs), with five clonal clusters (Ccs) and seven singletons. More than 50% of isolates were resistant to both pleuromutilins (MIC >2.0 µg/mL for tiamulin and >1.0 µg/mL for valnemulin). All 10 isolates in ST 83 were resistant; these were first isolated in 2011 and came from nine farms, suggesting recent widespread dissemination of a resistant strain. Significant associations were found between the proportion of pleuromutilin susceptible isolates and the genetic group and year of isolation. Although resistant isolates were found in all Ccs, isolates in Ccs 2 and 7 were over five times more likely to be susceptible than those in the other Ccs. A significant trend in the reduction of susceptibility over time also was observed.

Scaravelli D, Terregino C, Tosi°G, Massi°P

Indagini su *Streptopelia decaocto* conferite all'Istituto Zooprofilattico di Forlì negli anni 2011-2014

Atti della Società Italiana di Patologia Aviaria (SIPA) 2015 : LIV Convegno annuale : Forlì, 16-17 Aprile 2015 / [s.l. : s.n., 2015]. - p 254-258. - 16 bib ref [Nr. Estr. 6098]

Convegno annuale Società Italiana Patologia Aviaria (SIPA) (54. : Forlì : 16-17 Aprile 2015)

Collared dove Streptopelia decaocto (Frisvaldszky, 1838) is a widespread species in Europe, which typically lives in villages and towns, often nesting on trees and houses. It is well known for being a possible reservoir of zoonotic diseases, such as Trichomoniasis or other bacterial infections. This species are commonly affected by Avian Paramyxovirus 1 and are also proved to be sensitive to West Nile Disease with ascertained spill over cases. In order to investigate the causes of death and detect the presence of zoonotic agents affecting this important bioindicator, the Forlì section of the Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna implemented a surveillance on dead doves collected throughout its area of competence. Between 2011 and 2014, 143 dead doves were collected and tested, with a peak of findings at the end of winter. No positive cases for Avian Influenza, West Nile, Usutu, Flavivirus and Salmonella were found, whereas two cases of Trichomoniasis were identified. Avian Paramyxovirus type 1 (pigeon variant) were found in more than 80% of cases, with a high prevalence of the sublineage 4b, while sublineage 4a was only found in 2011 and 2012 in a lower percentage.

Scott MR, Gaele S, Loeffen W, Larsen L, Zohari S, Chiapponi C, Harder T, Gorin S, Krog JS, Foni E, Brookes SM, Brown IH

Development and validation of molecular tools for sub-typing swine influenza viruses

Influenza 2015 : one influenza, one world, one health : 08-10 September 2015, Oxford, UK / [s.l. : s.n., 2015]. - p 19-20 [Nr. Estr. 7156]

One influenza, one world, one health : Oxford, UK : 08-10 September 2015)

Swine influenza is a major economically important disease across Europe. Four major sub-types (H1auN1, H1N1pdm09, H1huN2 and H3N2) of swine influenza A viruses (swIAVs) plus various reassortant combinations have been isolated in pigs. Diagnostic tests capable of identifying the sub-types of the circulating strains rapidly within the pig population are crucial. Traditional serological methods for HA and NA sub-typing are laborious, costly, time-consuming and interpretation of results suffers from non-specific cross-reactions of test antigens. Furthermore, conventional assays are unable to detect novel viruses or distinguish the emergence of new reassortants. Real-time RT-PCR (rtRT-PCR) formats can improve the sensitivity and speed of swIAV sub-typing and overcome shortcomings with conventional formats. A panel of representative swIAV isolates was tested in an initial ring trial for comparison of the molecular and conventional sub-typing protocols employed across seven laboratories. The best-performing primers/probe sets and amplification protocols were then used in simplex rtRT-PCR assays specific for detection of H1 of the different genetic lineages (H1au, H1hu, H1pdm), for H3, and in duplex assays for detection of Ni (N1av and N1pdm) and N2. A second ring trial was then undertaken. These harmonized protocols enabled partners to achieve successful, sensitive and specific identification of HA and NA genes of swIAVs from enzootic European lineages. The assays provided fast results, enabled a semi-quantitative assessment of virus loads with differentiation between the pandemic and avian-like H1N1 virus strains and identification of HA/NA reassortant viruses. The harmonized protocols will enable partners to sub-type previously uncharacterized swIAV strains without having to depend on virus isolation and sequencing. Importantly the protocols might also facilitate sub-typing of swIAV RT-PCR-positive samples from clinical material which were negative by virus isolation.

Siarkou VI, Vorimore F, Vicari N, Magnino S, Rodolakis A, Pannekoek Y, Sachse K, Longbottom D, Laroucau K

Diversification and distribution of ruminant Chlamydia abortus clones assessed by MLST and MLVA

PLoS One. - Vol. 10 no 5 (2015). - p e0126433 (14 p). - 44 bib ref (ultimo accesso 10/06/2015 <http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0126433>) [Nr. Estr. 6065]

Chlamydia abortus, an obligate intracellular bacterium, is the most common infectious cause of abortion in small ruminants worldwide and has zoonotic potential. We applied multilocus sequence typing (MLST) together with multiple-locus variable-number tandem repeat analysis (MLVA) to

genotype 94 ruminant *C. abortus* strains, field isolates and samples collected from 1950 to 2011 in diverse geographic locations, with the aim of delineating *C. abortus* lineages and clones. MLST revealed the previously identified sequence types (STs) ST19, ST25, ST29 and ST30, plus ST86, a recently-assigned type on the Chlamydiales MLST website and ST87, a novel type harbouring the hemN_21 allele, whereas MLVA recognized seven types (MT1 to MT7). Minimum-spanning-tree analysis suggested that all STs but one (ST30) belonged to a single clonal complex, possibly reflecting the short evolutionary timescale over which the predicted ancestor (ST19) has diversified into three single-locus variants (ST86, ST87 and ST29) and further, through ST86 diversification, into one double-locus variant (ST25). ST descendants have probably arisen through a point mutation evolution mode. Interestingly, MLVA showed that in the ST19 population there was a greater genetic diversity than in other STs, most of which exhibited the same MT over time and geographical distribution. However, the evolutionary pathways of *C. abortus* STs seem to be diverse across geographic distances with individual STs restricted to particular geographic locations. The ST30 singleton clone displaying geographic specificity and represented by the Greek strains LLG and POS was effectively distinguished from the clonal complex lineage, supporting the notion that possibly two separate host adaptations and hence independent bottlenecks of *C. abortus* have occurred through time. The combination of MLST and MLVA assays provides an additional level of *C. abortus* discrimination and may prove useful for the investigation and surveillance of emergent *C. abortus* clonal populations.

Simon G, Larsen LE, Duerwald R, Foni^oE, Harder T, Van_Reeth K, Markowska_Daniel I, Dan A, Maldonado J, Huovilainen A, Billinis C, Davidson I, Reid SM, Brown IH, Loeffen W

Swine influenza viruses in circulation in European pigs exhibit an increasing genetic diversity since last pandemic in 2009

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 80 (Oral Presentation 014) [Nr. Estr. 7087]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Swine influenza causes concern for veterinary and public health. Thus, ongoing knowledge of influenza A viruses circulating in pigs is necessary for the prevention and control of the disease in pigs, but also to detect reassortant viruses that may pose a threat to humans, as was the case for the H1N1 virus responsible for the last pandemic in 2009 (H1N1pdm). In continuation to two previous coordination actions (2001-2008) that initiated the surveillance for swine influenza viruses (SIVs) circulating in European pigs, a third phase of the European Surveillance Network for Influenza in Pigs (ESNIP3) aimed to expand the knowledge of European SIVs from 2010 to 2013. ESNIP3 stimulated surveillance in European countries and supported the coordination of appropriate diagnostic tools and subtyping methods. Thus, in an extensive virological monitoring, mainly conducted through passive surveillance programs, more than 9 000 herds in 17 countries were examined over a period of three years. Influenza A viruses were detected in 31% of herds, from which 1887 viruses were subtyped preliminary. Viruses of the 3 subtypes enzootic in swine (H1N1, H3N2, H1N2) were identified but several genetic lineages were distinguished depending on the origin of genomic segments. Thus, the dominating lineages were identified to represent the 3 previously known European enzootic SIVs, i.e. the avian-like swine H1N1 (53.6%), the human-like reassortant swine H1N2 (13%) and the human-like reassortant swine H3N2 (9.1%), but also the H1N1pdm lineage (10.3%). Viruses from these four lineages co-circulated in several countries, but with very different relative levels of incidence. The H3N2 lineage was missing from some areas whereas it was still prevalent in other parts of Europe. Interestingly, regions free of H3N2 were those that exhibited the highest frequencies of H1N2 viruses in circulation. H1N1pdm viruses were detected at an increasing rate in some countries throughout the three year period, indicating that this subtype has become established in the European pig population. Finally, based on HA and NA identification, 13.9% of the viruses represented reassortants between these four lineages. Among them, reassortants between older enzootic SIVs and H1N1pdm emerged in several countries and were detected at an increasing frequency in 2012-2013. Surveillance of SIV infections on a

European scale revealed striking differences between countries participating in the ESNIP3 network regarding the prevalence of ancient and newly emerged SIV lineages. Some novel reassortants might become established in pig herds in the near future and potentially provide implications for zoonotic infections.

Sinclair A, Weber_Wyneken C, Veldkamp L, Vinco°LJ, Hocking PM

Behavioural assessment of pain in turkeys with foot pad dermatitis

Br Poult Abstr. - Vol. 11 no 1 (2015). - p 24-25. - 2 bib ref [Nr. Estr. 7190]

Sinclair A, Weber Wyneken C, Veldkamp T, Vinco°LJ, Hocking PM

Behavioural assessment of pain in commercial turkeys (*Meleagris gallopavo*) with foot pad dermatitis

Br Poult Sci. - Vol. 56 no 5 (2015). - p 511-521. - 40 bib ref [Nr. Estr. 7099]

1. Two experiments were conducted to investigate the differences in susceptibility to foot pad dermatitis (FPD) of two medium-heavy lines of turkeys, and whether FPD is painful, by detailed analysis of behaviour in birds with and without analgesic treatment (betamethasone).
2. Turkeys housed on dry litter in the first experiment generally had more frequent bouts of different behaviours that were of shorter duration than birds on wet litter. T-patterns (behavioural sequences) were more frequent, varied and complex on dry than on wet litter. Betamethasone-injected birds of line B, but not breed A, had shorter resting and longer standing durations on wet litter than saline-injected birds.
3. In the second experiment, turkeys on wet litter given saline stood less and rested more than all other treatment groups, suggesting that they experienced pain that was alleviated in birds receiving betamethasone. Turkeys on dry litter had more frequent, varied and complex patterns of behaviour than turkeys on wet litter and birds kept on intermediate litter wetness. Betamethasone provision increased pattern variety regardless of litter treatment.
4. Turkeys with low FPD scores transferred to wet litter and given saline injections had a longer total duration of resting and shorter duration of standing compared to betamethasone-treated birds. Low FPD birds transferred to wet litter had a similar number of patterns and total pattern occurrence as high FPD birds transferred to dry litter. Betamethasone increased pattern variety and frequency compared to saline injections whereas overall pattern complexity was similar.
5. It was concluded that wet litter affects the behaviour of turkey poults independently of FPD and that betamethasone may also change the behaviour of turkeys. There was some evidence from analgesic treatment and T-pattern analyses that FPD was painful. However, there was no evidence of differences in susceptibility to FPD of the two commercial hybrids.

Solórzano A, Foni°E, Cordoba L, Baratelli M, Razzu oli E, Bilato D, Del_Burgo MAM, Perlin DS, Martinez J, Martinez_Orellana P, Fraile L, Chiapponi°C, Del_Real G, Amadori°M, Montoya M

Immune response to influenza infection of swine, friend or foe?

Immunity to Veterinary Pathogens: Informing Vaccine Development : Keystone Symposia on Molecular and Cellular Biology, January 20-25, 2015 Colorado, USA / [Silverthorne, CO : Keystone Symposia, 2015]. - (The 2014-2015 Keystone Symposia Meeting Series ; p 36 [Nr. Estr. 5962]

Keystone Symposia on Molecular and Cellular Biology : Keystone, Colorado, USA : January 20-25, 2015)

Swine influenza (SwIV) is considered a zoonosis and the fact that swine may act as an intermediate reservoir for avian influenza virus, potentially infectious for humans, highlights its relevance and the

need to understand the interaction of different influenza viruses with the porcine immune system. Dendritic cells (DC) link innate and adaptive immune system, expressing specialized pattern-recognition receptors (PRRs) which recognise particular pathogen-associated molecular patterns (PAMPs). Furthermore, there is growing evidence that the so-called "early" cytokines play an important role in influenza virus (IV) infection. Thus, porcine DCs were exposed to different circulating IV in vitro showing a differential wave of cytokines released upon encountering different IV strains. This prompted us to investigate whether swine-adapted or non-adapted IV strains might give rise to peculiar innate immune responses that could be correlated with pathological lesions in pigs. In fact, each virus strain could be associated to cytokine gene and protein markers of infection. These markers were observed well beyond the period of virus replication, which suggests a prolonged homeostatic imbalance of the innate immune system following IV infection. Interestingly, our data indicated that viruses from birds and seals have the potential to cross the species barrier and establish successful infections in pigs. Interestingly, we could not detect antibodies against HA after infection with viruses from birds and seals, not only in pigs but also in infected mice. Therefore, increasing surveillance efforts must be directed to identifying novel viruses with the capability to cross the species barrier, as well as new diagnostic tools to detect these viruses in new hosts.

Solórzano A, Foni°E, Córdoba L, Baratelli M, Razzuoli E, Bilato D, Martín_Del_Burgo MA, Perlin DS, Martínez J, Martínez_Orellana P, Fraile L, Chiapponi°C, Amadori°M, Del_Reale G, Montoya M

Cross-species infectivity of H3N8 influenza virus in an experimental infection in swine

5th European veterinary immunology workshop (EVIW) : Vienna, Austria, 2nd-4th September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 124 [Nr. Estr. 7105]

European veterinary immunology workshop (EVIW) (5th : Vienna, Austria : 2nd-4th September 2015)

Avian influenza viruses have gained increasing attention due to their ability to cross the species barrier and cause severe disease in humans and other mammal species as pigs. H3 and particularly H3N8 viruses, are highly adaptive since they are found in multiple avian and mammal hosts. H3N8 viruses have not been isolated yet from humans; however a recent report showed that equine influenza viruses can be isolated from pigs, although a stable infection has not been observed yet in this host. To gain insight into the possibility of H3N8 avian influenza viruses to cross the species barrier into pigs, in vitro experiments and an experimental infection in pigs with four H3N8 viruses from different origins (equine, canine, avian and seal) were performed. As positive control, a H3N2 swine influenza virus was used. While equine and canine viruses hardly replicated in the respiratory apparatus of pigs, avian and seal viruses replicated substantially and caused detectable lesions in inoculated pigs without previous adaptation. Interestingly, antibodies against HA could not be detected after infection by hemagglutination inhibition test (HAI) with the avian and seal virus. This phenomenon was observed not only in pigs but also in mice immunized with those virus strains. Our data indicated that H3N8 viruses from wild aquatic birds have the potential to cross the species barrier and establish successful infections in pigs that might spread unnoticed using HAI as diagnostic tool.

Solórzano E, Foni°E, Córdoba L, Baratelli M, Razzuoli°E, Bilato°D, Del_Burgo MAM, Perlin DS, Martínez J, Martínez_Orellana P, Fraile L, Chiapponi°C, Amadori°M, Del_Real G, Montoya M

Cross-Species infectivity of H3N8 influenza virus in an experimental infection in swine

J Virol. - Vol. 89 no 22 (2015). - p 11190-11202. - 31 bib ref [Nr. Estr. 7129]

Avian influenza A viruses have gained increasing attention due to their ability to cross the species

barrier and cause severe disease in humans and other mammal species as pigs. H3 and particularly H3N8 viruses, are highly adaptive since they are found in multiple avian and mammal hosts. H3N8 viruses have not been isolated yet from humans; however, a recent report showed that equine influenza A viruses (IAVs) can be isolated from pigs, although an established infection has not been observed thus far in this host. To gain insight into the possibility of H3N8 avian IAVs to cross the species barrier into pigs, in vitro experiments and an experimental infection in pigs with four H3N8 viruses from different origins (equine, canine, avian, and seal) were performed. As a positive control, an H3N2 swine influenza virus A was used. Although equine and canine viruses hardly replicated in the respiratory systems of pigs, avian and seal viruses replicated substantially and caused detectable lesions in inoculated pigs without previous adaptation. Interestingly, antibodies against hemagglutinin could not be detected after infection by hemagglutination inhibition (HAI) test with avian and seal viruses. This phenomenon was observed not only in pigs but also in mice immunized with the same virus strains. Our data indicated that H3N8 IAVs from wild aquatic birds have the potential to cross the species barrier and establish successful infections in pigs that might spread unnoticed using the HAI test as diagnostic tool.

Stoppani°E, Bassi I, Dotti°S, Lizier M, Ferrari° M, Lucchini F

Expression of a single siRNA against a conserved region of NP gene strongly inhibits in vitro replication of different Influenza A virus strains of avian and swine origin

Antiviral Res. - Vol. 120 (2015). - p 16-22. - 25 bib ref [Nr. Estr. 6047]

Influenza A virus is the principal agent responsible of the respiratory tract's infections in humans. Every year, highly pathogenic and infectious strains with new antigenic assets appear, making ineffective vaccines so far developed. The discovery of RNA interference (RNAi) opened the way to the progress of new promising drugs against Influenza A virus and also to the introduction of disease resistance traits in genetically modified animals. In this paper, we show that Madin-Darby Canine Kidney (MDCK) cell line expressing short hairpin RNAs (shRNAs) cassette, designed on a specific conserved region of the nucleoprotein (NP) viral genome, can strongly inhibit the viral replication of four viral strains sharing the target sequence, reducing the viral mRNA respectively to 2.5×10^{-4} , 7.5×10^{-5} , 1.7×10^{-3} , 1.9×10^{-4} compared to the control, as assessed by real-time PCR. Moreover, we demonstrate that during the challenge with a viral strain bearing a single mismatch on the target sequence, although a weaker inhibition is observed, viral mRNA is still lowered down to 1.2×10^{-3} folds in the shRNA-expressing clone compared to the control, indicating a broad potential use of this approach. In addition, we developed a highly predictive and fast screening test of siRNA sequences based on dual-luciferase assay, useful for the in vitro prediction of the potential effect of viral inhibition. In conclusion, these findings reveal new siRNA sequences able to inhibit Influenza A virus replication and provide a basis for the development of siRNAs as prophylaxis and therapy for influenza infection both in humans and animals.

Tamba°M, Paternoster°G, Caminiti°A, Bellini°R, Bonilauri°P, Finarelli AC, Cagarelli R, Mattivi A, Angelini P, Natalini S, Velati C, Dottori°M

Six years of west nile virus surveillance in the Emilia-Romagna Region, Italy

Society for Veterinary Epidemiology and Preventive Medicine : 25th-27th March 2015, Ghent Belgium : Proceedings / [s.l. : Society for Veterinary Epidemiology and Preventive Medicine, 2015]. - 1 p. (ultimo accesso 10/03/2016 <http://www.svepm.org.uk/posters.html>) [Nr. Estr. 7181]

Society for Veterinary Epidemiology and Preventive Medicine : Ghent, Belgium : 25th-27th March, 2015)

Tamba°M, Paternoster°G, Caminiti°A, Santi°A, Gallotti°G, Bellini R, Bonilauri°P, Finarelli AC, Cagarelli R, Mattivi A, Angelini P, Gualanduzzi C, Natalini S, Velati C,

Calzolari^oM, Dottori^oM

West Nile virus integrated surveillance in Emilia-Romagna: an example of One Health approach in Italy

14th International Symposium on Veterinary Epidemiology and Economics : 3-7 November 2015
Merida, Yucatan, Mexico : Proceedings / [s.l. : s.n., 2015]. - 1 p (057) [Nr. Estr. 7213]

International Symposium of International Society for Veterinary Epidemiology and Economics (ISVEE) (14th : Merida, Yucatan, Mexico : 3-7 November 2015)

Purpose: West Nile virus (WNV) circulates in nature between mosquitoes and birds, and can cause neuroinvasive disease in humans. As iatrogenic transmission via blood transfusion is possible, the National Blood Centre has established that WNV Nucleic Acid Test (NAT-PCR) on blood donations shall be timely introduced in a province after the notification of West Nile neuroinvasive disease in humans (WNND). Testing shall be then continued until 30 November and repeated from 1 July to 30 November in the following year. In 2014, NAT-PCR testing started after the notification of WNV circulation detected by the integrated surveillance system for WNV in place in the Emilia Romagna region (ER), Italy. This work describes how the results of the integrated surveillance could be used to establish also the end of the testing period for blood donations. Methods: The ER integrated surveillance system includes: entomological monitoring; active and syndromic surveillance of wild birds; syndromic surveillance of horses; active surveillance on patients with neuroinvasive disease. Mosquitoes, birds and humans are tested by Real Time RT-PCR, while horses are tested by a commercial IgM ELISA. Positive samples are sent to the National Reference Centres for confirmation, sequencing and lineage determination. Results: In 2009 and 2010, the surveillance system detected the circulation of a lineage 1 WNV.

Tosi^oG, Massi^oP, Fiorentini^oL, Scozzoli M, Matta relli A

Oli essenziali in medicina veterinaria : saggi di alcuni oli essenziali e di una miscela nei confronti di ceppi di Escherichia coli multi-resistenti

SIROE (Società Italiana per la Ricerca sugli Oli Essenziali). - Vol. no 2 (2015). - p 28 - 5 bib ref [Nr. Estr. 7152]

Congresso Nazionale della Società Italiana per la Ricerca sugli Oli Essenziali (SIROE) (3. : Roma : 6-7-8 Novembre 2015)

Trovato A, Panelli S, Strozzi F, Cambulli C, Barbieri^oI, Martinelli^oN, Lombardi^oG, Capoferri R, Williams JL

Expression of genes involved in the T cell signalling pathway in circulating immune cells of cattle 24 months following oral challenge with Bovine Amyloidotic Spongiform Encephalopathy (BASE)

BMC Vet Res. - Vol. 11 no 105 (2015). - 9 p. - 47 bib ref (ultimo accesso 25/06/2015
<http://www.biomedcentral.com/1746-6148/11/105>) [Nr. Estr. 6058]

Background: Bovine Amyloidotic Spongiform Encephalopathy (BASE) is a variant of classical BSE that affects cows and can be transmitted to primates and mice. BASE is biochemically different from BSE and shares some molecular and histo-pathological features with the MV2 sub-type of human sporadic Creutzfeldt Jakob Disease (sCJD). Results: The present work examined the effects of BASE on gene expression in circulating immune cells. Ontology analysis of genes differentially expressed between cattle orally challenged with brain homogenate from cattle following intracranial inoculation with BASE and control cattle identified three main pathways which were affected. Within the immune function pathway, the most affected genes were related to the T cell receptor-mediated T cell activation pathways. The differential expression of these genes in BASE challenged animals at 10,12 and 24 months following challenge, vs unchallenged controls, was investigated by real time PCR. Conclusions: The results of this study show that the effects of prion diseases are not limited to the CNS, but involve the immune system and particularly T cell signalling during the early stage

following challenge, before the appearance of clinical signs.

Vangroenweghe E, Luppi^o A, Van_Driessche E, Vandenbroucke V, Hidalgo A

Prevalence of virulence factors in Escherichia coli isolated from pigs with post-weaning diarrhoea in Belgium and The Netherlands

ESPHM 2015 : 7th European Symposium of Porcine Health Management : 22-24 April, 2015 Nantes, France : proceedings / [s.l. : s.n., 2015]. - p 221 (Poster P184) [Nr. Estr. 7092]

European Symposium of Porcine Health Management (ESPHM) (7th : Nantes, France : 22-24 April, 2015)

Introduction Post-weaning diarrhoea (PWD) is a major cause of economic losses for the pig industry due mainly to increased mortality rates and poor weight gain in surviving piglets. PWD is usually caused by some strains of *E. coli*, known as enterotoxigenic *E. coli* (ETEC), with the ability to produce one or several enterotoxins and attach to intestinal cells. The most common adhesins found on ETEC from PWD in pigs are fimbriae F4 (previously called K88) and F18, while the predominant enterotoxins are heat-labile toxin (LT), heat-stable toxin a (STa), and heat-stable toxin b (STb). The objective of this study was to investigate the prevalence of virulence factors in *E. coli* isolated from pigs with PWD in Belgium and The Netherlands. Materials and methods A total of 88 pig herds in Belgium and the Netherlands showing typical clinical signs of PWD were selected for the study in 2014. Seventy piglets (3-5 weeks of age) from 70 Belgian farms were submitted to the laboratory (DGZ, Belgium) and faecal samples obtained during post mortem examination. In addition, rectal swabs were obtained from diarrheic pigs (n=5 per farm) in 18 Dutch farms. In both cases, samples were taken within 48 hours of the start of a clinical PWD outbreak and used for *E. coli* diagnostics according to the routine procedures of the laboratory. The presence of adhesin (F4, F5, F6, F18 and F41) and toxin (LT, STa, STb, Stx2e) genes in haemolytic *E. coli* isolates was investigated by multiplex PCR (IZSLER, Italy). Results In total, 123 *E. coli* isolates were obtained from 88 farms. The overall prevalence of adhesin and toxin genes was: F4 (50.4%), F5 (0.8%), F6 (0.8%), F18 (43.1%), F41 (0.0%), LT (20.3%), STa (25.2%), STb (35.8%) and Stx2e (4.9%). Only 1.6% of the isolates had mixed F4+F18 adhesins present. A total of 39.02% of isolates carried both adhesin and enterotoxin genes, being classified as ETEC. These ETEC isolates were recovered from 36.36% of the initial PWD outbreaks, of which 68.8% were ETEC-F4 and 31.2% ETEC-F18. No mixed infections of ETEC-F4 and ETEC-F18 were detected. The ETEC serotypes most frequently detected were F4, STb, LT (25.0%) and F4, STa, STb (18.7%). In 51 herds (57.9%) the isolates harboured only fimbriae or toxin genes in this assay. The role of these strains in the development of diarrhoea needs further investigations. Conclusion Among ETEC isolates involved in cases of PWD, ETEC-F4 is more widespread than ETEC-F18 in Belgian and Dutch farms. Laboratory diagnostics, including characterization of virulence factors, are essential to understand the role of different *E. coli* isolates in PWD outbreaks and initiate appropriate preventive and control measures.

Vicari^o N, Rizzo F, Manfredini^o A, Labalestra^o I, Prati^o P, Mandola ML, Magnino^o S

Investigation for novel chlamydial species in wild birds

Proceedings of the third European meeting on animal chlamydioses and zoonotic aspects : Maisons-Alfort, France, September 24-25, 2015 / edited by Karine Laroucau and Marie-France Devaux. - [s.l. : s.n., 2015]. - p 93 [Nr. Estr. 7158]

European meeting on animal chlamydioses and zoonotic aspects (3rd : Anses, Maisons-Alfort, France : September 24-25, 2015)

According to a recent taxonomic revision, the Chlamydiaceae family consists of the single genus *Chlamydia*, which currently includes nine species. However, diagnostic tests carried out in recent years in Italy, Germany and France for the detection of *Chlamydia* in some avian species (poultry and wild birds) yielded inconclusive results and provided evidence of microorganisms that do not

belong to any Chlamydia species known to date. Two new chlamydial species were recently proposed that can be identified by two different real-time PCRs, which are specific for two novel organisms, one infecting poultry (*C. gallinaceae* sp. nov.) and the other infecting pigeons and psittacine birds (*C. avium* sp. nov.), respectively. In order to investigate the presence of novel chlamydial species in wild birds, a retrospective study was carried out on archival samples stored in the Italian NRL for Animal Chlamydioses. Two different real-time PCRs were applied, one specific for atypical Chlamydiaceae from chickens (novel species: *C. gallinaceae*) and one specific for atypical Chlamydiaceae from pigeons (novel species: *C. avium*) on Chlamydiaceae-positive samples obtained from different wild birds from 2009 to 2013. Out of the 41 DNA samples, 28 tested positive with the Chlamydiaceae-specific real-time PCR, while 13 samples were not amplified, possibly due to DNA degradation. No sample tested positive for *C. psittaci* with the ompA-specific real-time PCR, nor the PCR-RFLP analysis of the 16S gene. Among the 28 Chlamydiaceae-positive samples, only 7 (six from pigeons, one from a magpie) tested positive with the *C. avium* real-time PCR, while no sample tested positive for *C. gallinaceae*. Microorganisms belonging to the Chlamydiaceae family were detected in the majority (21/28) of samples from other avian species (mallard, hooded crow, herring gull, green sandpiper, great tit, canary). In conclusion, we detected *C. avium* in a magpie, which suggests that this novel chlamydia may infect avian species other than pigeons and psittacine birds, but we never detected *C. gallinaceae*, which, to our knowledge, has been found only in poultry so far.

Vicari°N, Scaltriti°E, Chiapponi°C, Mandalari°C , Manfredini°A, Pongolini°S, Fabbi°M

Whole-genome sequencing of Italian isolates of *Francisella tularensis* subsp. *holarctica* : preliminary data

8th International Conference on Tularemia : September 28 - October 1, 2015, Opatija, Croatia : program agenda and abstract book / editor, Marina Santic. - [Rijeka : Faculty of Medicine, University of Rijeka, 2015]. - p 127 [Nr. Estr. 7071]

International Conference on Tularemia (8th : Opatija, Croatia : September 28 - October 1, 2015)

Tularemia is a zoonosis caused by *Francisella tularensis*. The bacterium infects lots of vertebrates and is either transmitted directly through dose contact with infected animals (tissues and body fluids) and via insect bites, or indirectly through inhalation/ingestion of contaminated aerosols, water and food. Currently only *Francisella tularensis* subsp. *holarctica* (F.t.h.) has been detected in Europe. In Italy the first confirmed cases of tularemia date back in 1964 when the disease was detected in European brown hares and humans. Since then, very rare outbreaks or sporadic cases of tularemia occurred, but infected hares have been detected almost every year. We performed whole-genome sequencing of 35 Italian isolates of F.t.h. recovered between 1964 and 2015 from different sources (animals, human and water). Our aim was to understand the genetic relationships among them and European isolates. The genomes were sequenced by MiSeq Illumina system and de-novo assembled. Core SNPs were identified with a MAUVE-based approach and used for phylogenetic studies with MrBayes and Beast softwares. Bayesian tree highlights that Italian field isolates are divided into two main clusters, one cluster encloses isolates from imported hares (East Europe n=16) and the other one includes isolates recovered from autochthonous hares (n=16), natural spring water (n=2) and human patient (n=1). Notably, strains belonging to this last cluster are very similar to West Europe isolates. These results confirm previous data obtained by MLVA subtyping carried out on the same isolates. Furthermore, molecular clock analysis suggests some possible dates for lineages separation.

Vinco°LJ

Crate height and turkey welfare during transport : field trial results in Italy

Abstracts of 8th "Hafez" International Symposium on turkey production : meeting of the Working

Group 10 (Turkey) of WPSA : Berlin, Germany, 28th - 30th May 2015 / [Berlin : organized and published by H.M. Hafez, 2015]. - 2 p [Nr. Estr. 7083/A]

"Hafez" International Symposium on turkey production (8th : Berlin, Germany : 28th - 30th May 2015)

Turkey transport practices at present are being debated with particular focus on design and dimensions of commercially available transport crates. In particular the height of the crates currently used is questioned as this is considered by some of the stakeholders involved, insufficient to fulfil the welfare needs of the turkeys during transport. Others, on the contrary, argue that the welfare of turkeys transported in higher crates would be even more compromised. The European Food Safety Authority (EFSA) highlighted the lack of scientific evidence supporting recommendations on the height of crates used for turkey transportation. In order to fill this gap by providing scientific knowledge on the impact of crate height on the welfare of turkeys during transport, a field trial was carried out analysing the animal welfare outcomes on a single commercial journey of 324 turkeys, comparing the welfare of birds transported in standard commercial crates with that of others transported in higher crates. Two types of higher crates were used one doubled in height which would guarantee less restriction to the birds movement and one tripled in height which would be able to comply with chapter II point 1.2 of Council Regulation EC 1/2005 stating: "Sufficient space shall be provided inside the animal's compartment and at each of its levels to ensure that there is adequate ventilation above the animals when they are in a naturally standing position without on any account hindering their natural movement". Animal welfare was evaluated through the use of animal based parameters such as behaviour, physiological variables, dead on arrivals and post mortem lesions observed at slaughter. None of the parameters assessed proved advantages of the higher crates over those currently used. On the other hand several parameters underlined favourable aspects of current crates towards the modified ones. Although based on the results of one single test, it appears from this trial that the suggestion to replace the transport crates commercially in use at present, with crates of the heights suggested and used in this trial is not supported by improvements in animal welfare. On the contrary this replacement would have a negative impact on the welfare of the turkeys transported.

Vinco^o LJ, Archetti^o IL, Meani S, Lombardi^o G

Influence of crate height on the welfare of Turkeys during transport

Turkey production and health : current and future perspectives : proceedings of 8th "Hafez" International Symposium on turkey production : meeting of the Working Group 10 (Turkey) of WPSA : Berlin, Germany, 28th - 30th May 2015 / organized and published by H.M. Hafez. - [Berlin : Institute of Poultry Diseases, Free University Berlin, 2015]. - p 73-79. - 16 bib ref [Nr. Estr. 7083]

"Hafez" International Symposium on turkey production (8th : Berlin, Germany : 28th - 30th May 2015)

Vitali A, Felici A, Esposito S, Bernabucci U, Bertocchi^o L, Maresca C, Nardone A, Lacetera N

The effect of heat waves on dairy cow mortality

J Dairy Sci. - Vol. 98 no 7 (2015). - p 4572-4579. - 31 bib ref [Nr. Estr. 6087]

This study investigated the mortality of dairy cows during heat waves. Mortality data (46,610 cases) referred to dairy cows older than 24 mo that died on a farm from all causes from May 1 to September 30 during a 6-yr period (2002–2007). Weather data were obtained from 12 weather stations located in different areas of Italy. Heat waves were defined for each weather station as a period of at least 3 consecutive days, from May 1 to September 30 (2002–2007), when the daily maximum temperature exceeded the 90th percentile of the reference distribution (1971–2000). Summer days were classified as days in heat wave (HW) or not in heat wave (nHW). Days in HW were numbered to evaluate the relationship between mortality and length of the wave. Finally, the first 3 nHW days after the end of a heat wave were also considered to account for potential

prolonged effects. The mortality risk was evaluated using a case-crossover design. A conditional logistic regression model was used to calculate odds ratio and 95% confidence interval for mortality recorded in HW compared with that recorded in nHW days pooled and stratified by duration of exposure, age of cows, and month of occurrence. Dairy cows mortality was greater during HW compared with nHW days. Furthermore, compared with nHW days, the risk of mortality continued to be higher during the 3 d after the end of HW. Mortality increased with the length of the HW. Considering deaths stratified by age, cows up to 28 mo were not affected by HW, whereas all the other age categories of older cows (29–60, 61–96, and >96 mo) showed a greater mortality when exposed to HW. The risk of death during HW was higher in early summer months. In particular, the highest risk of mortality was observed during June HW. Present results strongly support the implementation of adaptation strategies which may limit heat stress-related impairment of animal welfare and economic losses in dairy cow farm during HW.

Watson SJ, Langata P, Reid SM, Lam TT, Cotten M, Kelly M, Van_Reeth K, Qiu Y, Simone G, Bonin E, Foni[°]E, Chiapponi[°]C, Larseng L , Hjulsager C, Markowska-Daniel I, Urbaniak K, Dürrwald R, Schlegel M, Huovilainen A, Davidson I, Dán A, Loeffen W, Edward S, Bublot M, Vila T, Maldonado J, Valls L, ESNIP3 Consortium, Brown IH, Pybus OG; Kellam P

Molecular epidemiology and evolution of influenza viruses Circulating 2 within European swine between 2009 and 2013

J Virol. - Vol. 89 no 19 (2015). - p 9920-9931. - 55 bib ref [Nr. Estr. 7241]

The emergence in humans of the A(H1N1)pdm09 influenza virus, a complex reassortant virus of swine origin, highlighted the importance of worldwide influenza virus surveillance in swine. To date, large-scale surveillance studies have been reported for southern China and North America, but such data have not yet been described for Europe. We report the first large-scale genomic characterization of 290 swine influenza viruses collected from 14 European countries between 2009 and 2013. A total of 23 distinct genotypes were identified, with the 7 most common comprising 82% of the incidence. Contrasting epidemiological dynamics were observed for two of these genotypes, H1huN2 and H3N2, with the former showing multiple long-lived geographically isolated lineages, while the latter had short-lived geographically diffuse lineages. At least 32 human-swine transmission events have resulted in A(H1N1)pdm09 becoming established at a mean frequency of 8% across European countries. Notably, swine in the United Kingdom have largely had a replacement of the endemic Eurasian avian virus-like (“avian-like”) genotypes with A(H1N1)pdm09-derived genotypes. The high number of reassortant genotypes observed in European swine, combined with the identification of a genotype similar to the A(H3N2)v genotype in North America, underlines the importance of continued swine surveillance in Europe for the purposes of maintaining public health. This report further reveals that the emergences and drivers of virus evolution in swine differ at the global level.

Weber Wyneken C, Sinclair A, Veldkamp T, Vinco[°]LJ, Hocking PM

Footpad dermatitis and pain assessment in turkey poults using analgesia and objective gait analysis

Br Poult Sci. - Vol. 56 no 5 (2015). - p 522-530. - 31 bib ref [Nr. Estr. 7100]

1. The relationships between litter moisture, footpad dermatitis (FPD) and pain in medium-heavy turkey strains was studied by gait analysis in two medium-heavy with and without analgesia (betamethasone or bupivacaine).

2. The relationship between FPD and litter moisture was linear above a breakpoint of 49% litter moisture, and there were no differences between the two breeds in susceptibility to FPD.

3. Gait analysis showed higher impulse, single support time, stride time and stance time in breed A

compared to breed B. Significant interactions between breed, litter and analgesic for impulse, single support time and stride time were associated with higher means for breed A given saline injection on wet litter.

4. Data from betamethasone analgesia in Experiments 1 and 3 were combined for analysis. Peak vertical force was higher in saline- compared to betamethasone-treated birds. Compared to the wet (high FPD) litter treatments, birds on dry (low FPD) litter had greater speed and lower double support time and longer stride length. Turkeys kept on wet litter had a longer stride length compared to dry litter when given saline, whereas in betamethasone-treated birds the means were similar.

5. There were no differences between birds with or without bupivacaine analgesia. Peak vertical force was higher in breed A than B and in birds with a low FPD compared to a high FPD score.

6. It was concluded that breeds A and B did not differ in susceptibility to develop FPD when housed on wet litter but may have natural gait differences. Significant changes in gait parameters were associated with wet litter and with analgesic treatments. The results showed that FPD affected the gait of the turkeys and, combined with evidence of behavioural changes when given analgesia, suggest that footpad lesions are painful.

Wernike K, Brocchi°E, Cordioli°P, Sénéchal Y, Sch elp C, Wegelt A, Aebischer A, Roman-Sosa G, Reimann I, Beer M

A novel panel of monoclonal antibodies against Schmallenberg virus nucleoprotein and glycoprotein Gc allows specific orthobunyavirus detection and reveals antigenic differences

Vet Res. - Vol. 46 (2015). - no 27 (12 p). - 51 bib ref (ultimo accesso 22/04/2015
<http://www.veterinaryresearch.org/content/pdf/s13567-015-0165-4.pdf>) [Nr. Estr. 6030]

A panel of monoclonal antibodies (mAbs) specific for the nucleocapsid (N) protein or the glycoprotein Gc of Schmallenberg virus (SBV), a novel member of the Simbu serogroup (genus Orthobunyavirus, family Bunyaviridae), was produced and used to analyze antigenic differences among members of this serogroup. Reactivity with various SBV-isolates and other Simbu serogroup viruses was assessed by an indirect immunofluorescence test and by immunoblotting. The Gc-specific mAbs detected different SBV isolates as well as two closely related members of the Simbu serogroup. In addition, one mAb showed a highly specific reactivity with the homologous SBV strain only. Based on their differing reactivity with different SBV-strains, these antibodies represent a valuable novel tool to rapidly determine the phenotype of new SBV isolates. In contrast, the N-specific mAbs showed a broad reactivity spectrum and detected not only all the tested SBV-isolates, but also several other viruses of the Simbu serogroup. One out of these mAbs even recognized all of the tested Simbu serogroup viruses in the indirect immunofluorescence assay. In order to further characterize the N-specific antibodies, PepScan analysis was performed and a specific epitope could be identified. In summary, the newly generated mAbs showed differing pan-Simbu virus-, pan-SBV- as well as SBV-isolate-specific reactivity patterns. Thus, they represent valuable tools for the development of novel antigen and antibody detection systems either specific for SBV or, in a broader approach, for the pan-Simbu serogroup diagnostics.

Zanotti C, Amadori°M

Immune responses to different doses of PCV2 vaccines

Immunity to Veterinary Pathogens: Informing Vaccine Development : Keystone Symposia on Molecular and Cellular Biology, January 20-25, 2015 Colorado, USA / [Silverthorne, CO : Keystone Symposia, 2015]. - (The 2014-2015 Keystone Symposia Meeting Series ; p 45 [Nr. Estr. 5961]

Keystone Symposia on Molecular and Cellular Biology : Keystone, Colorado, USA : January 20-25, 2015)

Porcine Circovirus 2 (PCV2) fa associated with a number of syndromes collectively referred to as porcine Circovirus-associated disease (PCVAD). PCVAD incidence has been strongly reduced by

PCV2 vaccines worldwide. Because of the poor standardization of PCV2 vaccines, this study aimed (a) to correlate the inactivated virus mass content (measured by sucrose gradient analysis and UV spectroscopy) with in vivo vaccine potency, and (b) to define in vitro correlates of protection. Using the same oil emulsion, 22 pigs were vaccinated with three different doses of inactivated, whole-virus antigen (211 to 844 netosel; 4 animals were injected with a commercial vaccine (positive control), and 4 other pigs were mock-vaccinated with PBS. 4 weeks later, pigs were challenged intranasally with 2x10³ TC10₁ of a PCV2a strain. Antibody was measured in blood and oral fluids (OF) by ELISA and a neutralization assay; PCV2 was quantified in serum by Real-time PCR for ORF2 gene. PCV2-specific cell-mediated responses were investigated by an interferon- γ release assay in whole blood, IFN- γ ELISPOT and lymphocyte proliferation (KI-67 and BrDU incorporation assays). All the vaccines under study but mock protected animal from PCV2 infection in terms of post challenge viraemia, the lowest Ag payload performing even better than the others. A weak Ab response was observed in OF of vaccinated pigs. No correlation was observed between serum antibody titers (both ELISA and neutralizing and protection. Instead, cell-mediated immune (CMI) parameters showed a good correlation with vaccine efficacy. In particular, the IFN- γ release assay was a useful marker for predicting protection in vaccinated pigs. In agreement with the KI-67 and ELISPOT assays. All control pigs were always tested negative in all assays. Our results highlight an in vitro approach to potency testing of PCV2 vaccines towards a batch consistency policy. This may be conducive to effective control measures for veterinary vaccines, in the framework of the current 3R policies.

Zanotti[°]C, Amadori[°]M

A simple method for measuring porcine circovirus 2 whole virion particles and standardizing vaccine formulation

Biologicals. - Vol. 43 no 2 (2015). - p 79-83. - 14 bib ref [Nr. Estr. 5999]

Porcine Circovirus 2 (PCV2) is involved in porcine circovirus-associated disease, that causes great economic losses to the livestock industry worldwide. Vaccination against PCV2 proved to be very effective in reducing disease occurrence and it is currently performed on a large scale. Starting from a previous model concerning Foot-and Mouth Disease Virus antigens, we developed a rapid and simple method to quantify PCV2 whole virion particles in inactivated vaccines. This procedure, based on sucrose gradient analysis and fluorometric evaluation of viral genomic content, allows for a better standardization of the antigen payload in vaccine batches. It also provides a valid indication of virion integrity. Most important, such a method can be applied to whole virion vaccines regardless of the production procedures, thus enabling meaningful comparisons on a common basis. In a future batch consistency approach to PCV2 vaccine manufacture, our procedure represents a valuable tool to improve in-process controls and to guarantee conformity of the final product with passmarks for approval. This might have important repercussions in terms of reduced usage of animals for vaccine batch release, in the framework of the current 3Rs policy.

Zanotti[°]C, Martinelli[°]N, Lelli[°]D, Amadori[°]M

Correlates of protection following vaccination with inactivated Porcine Circovirus 2 vaccines

5th European veterinary immunology workshop (EVIW) : Vienna, Austria, 2nd-4th September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 127 [Nr. Estr. 7107]

European veterinary immunology workshop (EVIW) (5th : Vienna, Austria : 2nd-4th September 2015)

Porcine Circovirus type 2 (PCV2) is associated with a number of diseases and syndromes, collectively referred to as porcine Circovirus-associated disease. The main objective of this study was to define some in vitro correlates of protection after injection of inactivated PCV2 vaccines with a defined antigen mass. 12 pigs were vaccinated with three different doses of inactivated,

whole-virus antigen (211 to 844 ng), while 4 animals were injected with a commercial vaccine (positive control) and 4 other pigs were mock-vaccinated with PBS in the same oil emulsion. 4 weeks later, they were intranasally challenged with 2×10^5 TCID₅₀ of a PCV2a strain. Antibody was measured in blood and oral fluids by ELISA and a neutralization assay. PCV2 was quantified in serum by real-time PCR for ORF2 gene. PCV2-specific cell-mediated responses were investigated by an interferon- γ release assay in whole blood, IFN- γ ELISPOT and lymphocyte proliferation (Ki-67 and BrDU assays). All the vaccines under study but mock provided complete or incomplete protection from PCV2 infection in terms of post-challenge viremia. No correlation was observed between serum antibody titers (ELISA and neutralizing) and protection. Instead, cell-mediated immune parameters showed a good correlation with vaccine efficacy. In particular, the IFN- γ release assay was an effective marker for predicting protection in vaccinated pigs, in good agreement with the Ki-67 and ELISPOT assays. All control pigs always tested negative in assays of cell-mediated immunity. Our results outline in vitro testing procedures towards reduced animal usage in the control of PCV2 vaccine batches.

Zanotti[°]C, Martinelli[°]N, Lelli[°]D, Amadori[°]M

Correlates of protection following vaccination with inactivated Porcine Circovirus 2 vaccines

Viral Immunol. - Vol. 28 no 10 (2015). - p 600-608. - 37 bib ref (ultimo accesso 08/01/2016 <http://online.liebertpub.com/doi/10.1089/vim.2015.0021>) [Nr. Estr. 7124]

Porcine Circovirus type 2 (PCV2) is associated with a number of diseases and syndromes, collectively referred to as porcine Circovirus-associated disease. The main objective of this study was to define some in vitro correlates of protection after injection of inactivated PCV2 vaccines with a defined antigen mass. 12 pigs were vaccinated with three different doses of inactivated, whole-virus antigen (211 to 844 ng), while 4 animals were injected with a commercial vaccine (positive control) and 4 other pigs were mock-vaccinated with PBS in the same oil emulsion. 4 weeks later, they were intranasally challenged with 2×10^5 TCID₅₀ of a PCV2a strain. Antibody was measured in blood and oral fluids by ELISA and a neutralization assay. PCV2 was quantified in serum by real-time PCR for ORF2 gene. PCV2-specific cell-mediated responses were investigated by an interferon- γ release assay in whole blood, IFN- γ ELISPOT and lymphocyte proliferation (Ki-67 and BrDU assays). All the vaccines under study but mock provided complete or incomplete protection from PCV2 infection in terms of post-challenge viremia. No correlation was observed between serum antibody titers (ELISA and neutralizing) and protection. Instead, cell-mediated immune parameters showed a good correlation with vaccine efficacy. In particular, the IFN- γ release assay was an effective marker for predicting protection in vaccinated pigs, in good agreement with the Ki-67 and ELISPOT assays. All control pigs always tested negative in assays of cell-mediated immunity. Our results outline in vitro testing procedures towards reduced animal usage in the control of PCV2 vaccine batches.

Zanotti[°]C, Razzuoli E, Crooke H, Soule O, Pezzoni[°] G, Ferraris M, Ferrari A, Amadori[°]M

Differential biological activities of swine interferon-(ALFA) subtypes

J Interferon Cytokine Res. - Vol. 35 no 12 (2015). - p. 990-1002 - 35 bib ref [Nr. Estr. 7171]

Interferons (IFNs) play a crucial role in the host's immune response and other homeostatic control actions. Three IFN types and several IFN families within the types allow for a plethora of regulatory actions. The number of distinct IFN molecules is highest among type I IFNs and, in particular, within the IFN- α family. In pigs, there are 17 IFN- α subtypes with different antiviral activities and different expression profiles; however, no data are available about biological properties other than the antiviral effector activities. Therefore, 16 porcine IFN- α genes were cloned, expressed in mammalian Chinese hamster ovary cells, and characterized for antiviral, anti-inflammatory, and MHC-modulating

activities at a pre-established level of 10 IU/mL. Antiviral activity: IFN- α 2, - α 5, - α 9, and - α 10 showed the highest level of activity in a pseudorabies virus yield reduction assay. On the contrary, little, if any, activity was shown by IFN- α 3, - α 7, - α 13, - α 4, and - α 15. Anti-inflammatory activity: With the exception of IFNs- α 2, - α 7, - α 9, and - α 11, all IFN- α subtypes had significant anti-inflammatory control activity in an interleukin-8 (IL-8) yield reduction assay. Gene expression analyses showed that some IFN- α subtypes can significantly downregulate the expression of IL-8, tumor necrosis factor α (TNF- α), IL-6, Toll-like receptor 4 (TLR4), β D1, and nuclear factor- κ B (NF- κ B) genes, while maintaining or upregulating the expression of β D4. Immunomodulation: A significant upregulation of class I and/or class II MHC was induced by all the IFNs under study, with the exception of IFNs- α 11, - α 15, and - α 16, which instead significantly downregulated class I MHC. Our results indicate that gene duplications in the porcine IFN- α family underlie diverse effector and regulatory activities, being therefore instrumental in host survival and environmental adaptation. This role of IFN- α could be founded on fine-tuning and regulation of pro- and anti-inflammatory control actions after exposure to both infectious and noninfectious environmental stressors.

Zanotti[°]C, Razuoli E, Crooke H, Soule O, Pezzoni [°]G, Ferraris M, Ferrari A, Amadori[°]M

Differential biological activities of swine interferon-alpha subtypes

5th European veterinary immunology workshop (EVIW) : Vienna, Austria, 2nd-4th September 2015 : programme and abstract book / [s.l. : s.n., 2015]. - p 24 [Nr. Estr. 7109]

European veterinary immunology workshop (EVIW) (5th : Vienna, Austria : 2nd-4th September 2015)

Interferons (IFNs) play a crucial role in the host's immune response and other homeostatic control actions. The number of distinct IFN molecules is highest among Type I IFNs and, in particular, within the IFN- α family. In pigs, there are 17 IFN- α subtypes with different antiviral activity and different expression profiles, however, no data are available about biological properties other than the antiviral effector activities. Therefore, sixteen porcine IFN- α genes were cloned, expressed in mammalian CHO cells and characterized for antiviral, anti-inflammatory and MHC-modulating activities at a pre-established level of 10 IU/ml. The subtypes under study presented highly significant differences in the three profiles of activity. IFN- α 2, - α 5, - α 9 and - α 10 showed the highest level of antiviral activity in a Pseudorabies virus yield reduction assay. On the contrary, no such activity was shown by IFN- α 3, - α 7, - α 13, - α 4 and - α 15. With the exception of IFNs- α 2, - α 7, - α 9 and - α 11, all IFN- α subtypes had significant anti-inflammatory control activity in an IL-8 yield reduction assay. Gene expression analyses in the same cells showed that some IFN- α subtypes can significantly down-regulate the expression of IL-8, TNF- α , IL-6, TLR4, betaD1 and NF- κ B genes, while maintaining or up-regulating the expression of betaD4. Also, a significant up-regulation of class I and class II MHC was induced by all the IFNs under study, with the exception of IFNs- α 11, - α 15 and — α 16, which instead significantly down-regulated class I MHC. Our results indicate that gene duplications in the porcine IFN- α family underlie diverse effector and regulatory activities, being therefore instrumental in host survival and environmental adaptation.

Zarengi L, Bolzoni[°]L, Ferroni L, Filippin N, Menguzzato G

I gas tossici e i parametri ambientali negli allevamenti del suini : esperienze del controllo ufficiale = Toxic gases and environmental parameters in pig farms

Summa Anim Reddito. - Vol. 10 no 9 (2015). - p 55-62. - 6 bib ref [Nr. Estr. 7162]

Zema J, Caporali A, Mariotti C, Panzieri C, Pela M, Pellegrini C, Pezzoni[°]G, Costarelli S, Sensi M

Valutazione del “Pathogen spreading” in allevamenti backyard umbri

XVI Congresso Nazionale SIDiLV : 30 Settembre - 2 Ottobre 2015 Montesilvano (PE) : volume degli atti / [s.l. : Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV), 2015]. - p 249-250. - 4 bib ref [Nr. Estr. 7052]

Congresso Nazionale Societa' Italiana Diagnostica di Laboratorio Veterinaria (SIDiLV) (16. : Montesilvano (PE) : 30 Settembre - 2 Ottobre 2015)

Despite a huge reduction in the numbers during last five years, pig breeding represents one of the main activity in Umbria region. Exploiting sera sampled derived from SVD control Plan, a serological monitoring was performed with the aim to evaluate the “pathogens spreading” within “backyard” units. The results highlight the presence of some epidemiological interesting situations that could represent important risk factors especially for zoonotic agents such as Brucella spp. and HEV.