RICERCHE EFFETTUATE

ARGOMENTI VARI

Almugadam S, Bellini T, Contini C, Maritati M, Trentini A, Rugna°G, Dallocchio F, Hanau S

Effect of the antimetabolite 6-aminonicotinamide on Leishmania infantum promastigotes

58th National Meeting of the Italian Society of Biochemistry and Molecular Biology : Urbino, September 14 -16, 2015 / [s.l. : s.n., 2015]. - 7276]

National Meeting of the Italian Society of Biochemistry and Molecular Biology (58. : Urbino : September 14 -16, 2015)

Introduction Leishmaniasis is a major parasitic disease. WHO estimates that 1.3 million new cases and 20000 to 30000 deaths occur annually, and a population of 350 million is at risk. Available chemotherapy is far from satisfaction because antileishmanial drugs are costly with unpleasant side effects. The situation has further worsened with emergente of drug resistance in various regions of endemicity. The anti-metabolite 6-aminonicotinamide (6AN) is converted to 6-aminoNAD and 6-aminoNADP, the latter being a strong inhibitor of the pentose phosphate pathway. We tested 6AN ability to inhibit parasite growth. Methods L. infantum promastigotes were grown at 25℃ in RPMI with 15% FBS. The number of viable cells was measured either by Alamar Blue fluorescente or using a hemocytometer. 6-phosphogluconate dehydrogenase (6PGD) ac¬tivity was measured spectrophotometrically. Results Effect of 6AN on oxidative stress. Parasites incubated 48 h with 6AN, were treated with 100 uM H202 for 45 min. The number of viable parasites in control cultures decreased by 7.2% (±5), while in cultures preincubated with 100 or 250 uM 6AN decreased by 38.7% (±1.2) and 50% (±2.6). Effect of 6AN on the growth rate in absence of oxidative stress. When the parasites were grown in the presence of 200 uM 6AN, the growth rate, measured after 48 and 96 h, decreased by 33% ($p<0.05$). Effect of 6AN on 6PGD activity. 6PGD is the main target of 6-aminoNADP. The parasites, grown with or without 6AN, were lysed and the 6PGD activity was assayed. The enzymatic activity of 6AN treated cells was reduced to 30% of the activity of untreated cells. The inhibition extent does not change by changing the dilution of the cell extract, meaning that the inhibition is not due to the residual presence of the inhibitor. Conclusions 6AN shows good antileishmanial activity. In fact its effect on the parasites is not limited to an increased sensitivity to the oxidative stress. 6PGD is confirmed as main target of the inhibitor.

Biancardi°A, Dall'Asta C

Determinazione di sterigmatocistina (STC) in cereali e mangimi mediante LC-MS/MS

V Congresso nazionale "Le micotossine nella filiera agro-alimentare" : Istituto Superiore di Sanità Roma, Roma 28-30 Settembre 2015 : riassunti / a cura di Carlo Brera... [et al.]. - Roma : Istituto Superiore di Sanità, 2015. - (ISTISAN Congressi ; 15/C4) p 45 [Nr. Estr. 7118]

Congresso nazionale "Le micotossine nella filiera agro-alimentare" (5. : Roma : 28-30 Settembre 2015)

Prodotta principalmente da Aspergillus Versicolor, la sterigmatocistina (STC) è una micotossina strutturalmente correlata all'Aflatossina B1 (AFB1), di cui è il precursore biogenico. La sua tossicità sia acuta che cronica è in relazione sia a proprietà tossicologiche intrinseche che alla capacità di generare in vivo la AFB1. STC è stata riconosciuta dalla IARC come cancerogeno di classe 2B (possibile cancerogeno per l'uomo). Comunemente diffusa in substrati quali cereali e derivati, mangimi, spezie, semi di caffè e frutta secca, non è attualmente normata quanto a limite di tolleranza. Una recente raccomandazione EFSA suggerisce di avviare studi di monitoraggio sulla presenza di STC in alimenti e mangimi con metodi sensibili e accurati (LOQ consigliato 1,5 mg/kg. Nel presente lavoro è stato messo a punto un metodo veloce e affidabile per la determinazione di STC in cereali e mangimi mediante LC-MS/MS. Il campione è estratto con miscela idroacetonitrilica; una volta filtrato e opportunamente diluito è pronto per l'analisi LC-MS/MS (HPLC Agilent 1290

Infinity abbinato a triplo quadrupolo Agilent 6430). La colonna cromatografica è una Zorbax SB-C18 (5 cm; ID 2,1 mm; diametro medio delle particelle 1,8 mm). La fase mobile è costituita da un sistema binario (fase A acido formico 0,1%; fase B acetonitrile contenente acido formico 0,1%) combinati in una corsa cromatografica con gradiente di eluizione della durata di 6 minuti (flusso 0,4 mL/min). La quantificazione avviene mediante metodo dello standard esterno con acquisizione in MRM (ESI ioni negativi) delle due transizioni caratteristiche 325.1 à 310 (transizione di quantificazione Quantifier) e 325.1 à 281 (transizione di qualificazione Qualifier) tra 0 e 4.2 minuti (tempo di ritenzione dell'analita 3,61 minuti). Parametri strumentali: dwell time 200 msec, fragmentor 174 V, collision energy 25 V (transizione Quantifier), collision energy 40 V (transizione Qualifier), cell acceleration 7 V. Il metodo è stato validato. I parametri valutati sperimentalmente sono: linearità - specificità - LOQ 1 mg/kg (sei repliche indipendenti) - esattezza e precisione su tre diversi livelli di drogaggio in sei repliche indipendenti. Il recupero medio complessivo è 97,96% (N=24), con un CV% pari a 3,75%. L'incertezza estesa relativa è pari a 19% (gradi di libertà n=56, fattore di copertura k=2,00). È stata sperimentalmente verificata l'assenza di effetto matrice. Il metodo è stato applicato a 14 campioni naturalmente contaminati da AFB1 a diversi livelli (da un minimo di 28,75 mg/kg ad un massimo di 240,08 mg/kg). Effettivamente in tutti i campioni è stata constatata la presenza di STC da un valore minimo di 0,7 mg/Kg ad un massimo di 2,25 mg/kg.

Bregoli°A, Pezzoni°G, Brocchi°E

Expression of the three capsid proteins of Hepatitis A virus in E. coli

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 50 [Nr. Estr. 7039]

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

Hepatitis A virus (HAV) is classified within the genus Hepatovirus of Picornaviridae and causes acute hepatitis in human. The single-stranded positive sense RNA genome codes for a single polyprotein that is subsequently processed into structural and nonstructural proteins. The viral capsid is composed by the structural proteins VP1, VP2, VP3 and VP4. In endemic countries, despite a successful vaccination, HAV continues to be a source of mortality. In the European Union HAV infection rates are low and decreasing, however, a reduction in the circulation of HAV leads to an accumulation of susceptible individuals in a population and allows for outbreaks to occur. In recent years in Europe foodborne transmission of HAV has been associated with several outbreaks; the implicated foods included fish and seafood products, vegetables, juices, semi-dried tomatoes, berries and pomegranate seeds. For the control of foodborne viral infections, it is necessary to optimize and standardize methods for the detection of foodborne viruses. Monoclonal antibodies (MAbs) could be an important tool in this regard. Since HAV replication in cell culture is slow and has poor yields, we have expressed in E.coli system the HAV capsid proteins VP1, VP2 and VP3 to be used as immunogens for the production of MAbs. The coding region of VP1, VP2 and VP3 proteins has been cloned in a plasmid vector in fusion with small ubiquitin¬related modifier (SUMO) using the Champion pET SUMO Expression System (Life Technologies); VP1 was also cloned in a pQE30 vector (Qiagen) in fusion with a tag of six histidines. Selected clones of each protein have been expressed in E.coli. The recombinant proteins have been purified by NI-NTA affinity chromatography. Recombinant VP1sumo-His, VP2sumo-His, VP3sumo-His and VP1-His were successfully expressed as a single band in total protein extract of E.coli at the expected molecular masses of 44, 38, 41, 31 kDa respectively. All the proteins were purified from insoluble protein extracts. The purity and identities of the purified proteins were verified by SDS-page and Western blotting using an anti-His MAb. The three recombinant proteins will be used as immunogen for MAbs production.

Caloni F, Cortinovis C, Bertoletti°M, Alborali°L, Zanoni°M, Ferretti°E, Chiari°M

Cadmium concentrations in tissues of red deer from Northern Italy

J Vet Pharmacol Ther. - Vol. 38 Suppl 1 (2015). - p 139-140. - 3 bib ref (ultimo accesso 07/09/2015 http://onlinelibrary.wiley.com/doi/10.1111/jvp.2015.38.issue-S1/issuetoc) [Nr. Estr. 6093]

International Congress of the European Association for Veterinary Pharmacology and Toxicology (EAVPT 2015) (13th : Nantes, France : 19–22 July, 2015)

Caloni F, Mazzoleni G, Meloni M, Urani C, Ferrari° M, Dotti°S, Sambuy Y

Models on liver : alternative methods in hepatotoxicity

Altex Alternative Anim Exp. - Vol. 32 no 3 (2015). - p 228-229 [Nr. Estr. 7078]

Calzolari°M, Lombardi°G, Dottori°M

Preliminary study on the development of an anti-mosquito vaccine

Trop Med Int Health. - Vol. 20 Suppl 1 (2015). - p 403 (PS2.265) [Nr. Estr. 7036]

European Congress on Tropical Medicine and International Health (9th : Basel, Switzerald : 6-10 September 2015)

INTRODUCTION Different attempts to develop a vaccine against mosquito were performed in the past, with alternating results but without any concrete outcome. A mosquito vaccine could be an excellent way for decreasing transmission of mosquito-borne diseases, acting directly on blood fed insects. In this preliminary work, we tested the immunogenic capacity of the mosquito Malpighian tubules (MT) on mice. Since MT play the prominent excretory and osmoregulatory role in insect, we hypothesized that mouse antibody against these organs, ingested by blood meal, are able to affect mosquito lifespan. METHODS AND MATERIALS Five mice were treated intraperitoneally twice, at 2 weeks of interval, with ground MT from six tiger mosquitoes (Aedes albopictus). After 3 weeks about 30 host-seeking tiger mosquitoes, laboratory reared, were put in a single cage with every treated mouse; the same was done for the five control mice. A maximum of 12 engorged mosquitoes were collected for every treated and control mouse, and were placed, in groups of 3, in glass jars with a water container for oviposition, daily provided with sucrose solution by a cotton wool, and keep in controlled conditions (25 t 1℃, 70 ± 5% R.H., 14 h of light per day). Jars were daily monitored to check died mosquitoes and estimate mosquito lifespan. RESULTS A total of 108 mosquitoes were included (54 fed on treated mice and 54 on controls). Mosquitoes fed on treated had an average life of 48.7 days and an average hazard of 0.021; mosquitoes fed on the controls had an average life of 58.4 days and an average hazard of 0.017. The differente between the survíval probabilities, resumed by the Kaplan Meier curve, was evaluated by the log-rank test and was statistically significant ($P < 0.05$). CONCLUSION The result of this preliminary work is encouraging and proves that MT of mosquitoes have an immunogenic activity on mice, and that produced antibodies are able to affect lifespan of mosquitoes, with a decreasing of more than 16% in the average life of treated mosquitoes. Further experiments are needed to confirm obtained results; the next step could be the identification and characterization of the mosquito protein, or proteins, involved in this antigenic response and its engineering and testing in other trials. If the decreasing in the mosquito lifespan will be confirmed, this finding may lead to the development of an anti-mosquito vaccine, which would help in the control of several mosquito-borne diseases. DISCLOSURE Nothing to disclose.

Calzolari°M, Petrovic T, Petric D

Italian - Serbian joint development of a standardized mosquito-based health surveillance of West Nile virus

Serbia - Italia : Italian - Serbian Bilateral Cooperation on Science, Technology and Humanities : November 12, 2013 Belgrado / edited by P. Battinelli and J. Striber. - Belgrado : Associazione Italiani e Serbi Scienziati e Studiosi (AIS3), [2015]. - p 111-112. - 4 bib ref [Nr. Estr. 7199]

Italian - Serbian Bilateral Cooperation on Science, Technology and Humanities : Belgrado : November 12, 2013)

Close strains of the neurothopphic West Nile virus circulated in Serbia and Italy in recent years, causing several human cases. The entomological surveillance gives encouraging results in term of precocity and virus spread detection. The standardization of an Italian-Serbian mosquito-based surveillance in could constitute the foundation for a public health alert system targeting mosquito-borne viruses, and the base for a creation of a European network of Arbovirus surveillance.

Chiari°M, Cortinovis C, Bertoletti°M, Alborali°L , Zanoni°M, Ferretti°E, Caloni F

Lead, cadmium and organochlorine pesticide residues in hunted red deer and wild boar from northern Italy

Food Addit Contam Part A. - Vol. 32 no 11 (2015). - p 1867-1874. - 36 bib ref [Nr. Estr. 7142]

The objectives of the present study were to assess heavy metal cadmium (Cd), lead (Pb) and organochlorine pesticide concentrations in tissues of red deer (Cervus elaphus) and wild boar (Sus scrofa) from nine hunting areas and to evaluate related risk factors for the host animal. Over a period of 2 years, a total of 1055 and 210 masseters, 424 and 201 livers, 642 and 152 kidneys were collected from wild boar and red deer, respectively, and concentrations of Cd, Pb and organochlorine pesticides were determined. Comparing the two species, Cd concentration in the kidney (3.72 mg/kg), liver (0.67 mg/kg) and muscle (0.02 mg/kg) of wild boar was found to be significantly higher than in the organs of red deer (1.02 mg/kg in the kidneys, 0.07 mg/kg in the liver and 0.006 mg/kg in muscle). Mean Pb concentrations were found to be similar in both animals, with 0.39, 0.52 and 2.60 mg/kg detected in the wild boar kidney, liver and muscle, respectively, and 0.24, 0.21 and 2.04 mg/kg in the respective organs of the red deer. No difference in concentrations were found based on age class, location of tissue sample or contaminant in the case of wild boar. By contrast, a significantly lower Cd concentration was found in the kidney of the young red deer. The search for organochlorine pesticides in both red deer and wild boar produced negative results with values below the limits of detection. Due to the high levels of renal Cd and muscle Pb detected in wild boar and red deer, further research needs to be carried out in an effort to identify the source of contamination and preserve the health of animals and humans.

Cocchi°L, Basile°P, Lanzi°M

L'archivio storico dell'Istituto Zooprofilattico : una fonte per la storia della veterinaria

Atti del VI congresso nazionale di storia della medicina veterinaria / a cura di Elisabetta Lasagna ; Centro Italiano di Storia Sanitaria e Ospitaliera (CISO), Sezione di storia della medicina veterinaria, Fondazione Iniziative Zooprofilattiche e Zootecniche. - Brescia : Fondazione Iniziative Zooprofilattiche e Zootecniche, 2015. - (Atti delle giornate di studio Fondazione Iniziative Zooprofilattiche e Zootecniche ; 99) p 231 [Nr. Estr. 7074]

Congresso nazionale di storia della medicina veterinaria (6. : Brescia : 6-7-Ottobre 2011)

Cocchi°L, Tropea MF

Gli Istituti Zooprofilattici Sperimentali

La sicurezza alimentare : profili normativi e giurisprudenziali tra diritto interno, internazionale ed europeo / a cura di Carlo Bottari presentazione di Stefano Cinotti. - Santarcangelo di Romagna : Maggioli editore, 2015. - (Quaderni di sanità pubblica ; 9) p 175-199 [Nr. Estr. 7196]

Defilippo°F, Rubini°S, Dottori°M, Bonilauri°P

The use of forensic entomology in legal veterinary medicine : a case study in the North of Italy

J Forensic Sci & Criminol. - Vol. 3 no 5 (2015). - 5 p. - 22 bib ref [Nr. Estr. 7148]

During winter 2010 a forensic entomological study was undertaken in San Bartolomeo in Bosco (FE) Emilia-Romagna Region (North of Italy) on different animal carrion found in a farm several days after they died. The entomological evidence collected at the scene consisted of Calliphoridae (larvae of Calliphora vicina), Stratiomydae (larvae of Hermetia illucens), Dermestidae (larval exuviae of Dermestes maculatus). During diagnostic investigation the Diptera Larvae were taken from the carrion and were reared in the laboratory under constant temperature, humidity and fotoperiod. The minimum Post Mortem Interval (mPMI) was calculated using the quantity of thermal energy necessary for a given species to complete its life cycle from eggs to imago (accumulated degree-days-method). The results of the calculations were consistent with what the judicial investigation later showed. This case report illustrated the importance of using insects in legal veterinary medicine for define the time and circumstances of the death of an animal.

Gaiarsa S, Comandatore F, Gaibani P, Corbella M, Dalla_Valle C, Epis S, Scaltriti° E, Carretto E, Farina C, Labonia M, Land ini MP, Pongolini° S, Sambri V, Bandi C, Marone P, Sassera D

Genomic epidemiology of Klebsiella pneumoniae in Italy and novel insights into the origin and global evolution of its resistance to carbapenem antibiotics

Antimicrob Agents Chemother. - Vol. 59 no 1 (2015). - p 389-396. - 44 bib ref [Nr. Estr. 6011]

Klebsiella pneumoniae is at the forefront of antimicrobial resistance for Gram-negative pathogenic bacteria, as strains resistant to third-generation cephalosporins and carbapenems are widely reported. The worldwide diffusion of these strains is of great concern due to the high morbidity and mortality often associated with K. pneumoniae infections in nosocomial environments. We sequenced the genomes of 89 K. pneumoniae strains isolated in six Italian hospitals. Strains were selected based on antibiotypes, regardless of multilocus sequence type, to obtain a picture of the epidemiology of K. pneumoniae in Italy. Thirty-one strains were carbapenem-resistant K. pneumoniae carbapenemase producers, 29 were resistant to third-generation cephalosporins, and 29 were susceptible to the aforementioned antibiotics. The genomes were compared to all of the sequences available in the databases, obtaining a data set of 319 genomes spanning the known diversity of K. pneumoniae worldwide. Bioinformatic analyses of this global data set allowed us to construct a whole-species phylogeny, to detect patterns of antibiotic resistance distribution, and to date the differentiation between specific clades of interest. Finally, we detected an_1.3-Mb recombination that characterizes all of the isolates of clonal complex 258, the most widespread carbapenem-resistant group of K. pneumoniae. The evolution of this complex was modeled, dating the newly detected and the previously reported recombination events. The present study contributes to the understanding of K. pneumoniae evolution, providing novel insights into its global genomic characteristics and drawing a dated epidemiological scenario for this pathogen in Italy.

Gaibani P, Scaltriti° E, Foschi C, Baggio E, Tambur ini MV, Creti R, Pascucci MG, Fagioni M, Ambretti S, Comandatore F, Pongolini° S , Landini MP

Matrix-Assisted Laser Desorption Ionization : time of flight and comparative genomic analysis of M-18 group A Streptococcus strains associated with an acute rheumatic fever outbreak in Northeast Italy in 2012 and 2013

J Clin Microbiol. - Vol. 53 no 5 (2015). - p 1562-1572. - 34 bib ref [Nr. Estr. 7153]

Acute rheumatic fever (ARF) is a postsuppurative sequela caused by Streptococcus pyogenes

infections affecting school-age children. We describe here the occurrence of an ARF outbreak that occurred in Bologna province, northeastern Italy, between November 2012 and May 2013. Molecular analysis revealed that ARF-related group A Streptococcus (GAS) strains belonged to the M-18 serotype, including subtypes emm18.29 and emm18.32. All M-18 GAS strains shared the same antigenic profile, including SpeA, SpeB, SpeC, SpeL, SpeM, and SmeZ. Matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) analysis revealed that M-18 GAS strains grouped separately from other serotypes, suggesting a different S. pyogenes lineage. Single nucleotide polymorphisms and phylogenetic analysis based on whole-genome sequencing showed that emm18.29 and emm18.32 GAS strains clustered in two distinct groups, highlighting genetic variations between these subtypes. Comparative analysis revealed a similar genome architecture between emm18.29 and emm18.32 strains that differed from noninvasive emm18.0 strains. The major sources of differences between M-18 genomes were attributable to the prophage elements. Prophage regions contained several virulence factors that could have contributed to the pathogenic potential of emm18.29 and emm18.32 strains. Notably, phage FSPBO.1 carried erythrogenic toxin A gene (speA1) in six ARF-related M-18 GAS strains but not in emm18.0 strains. In addition, a phage-encoded hyaluronidase gene (hylP.2) presented different variants among M-18 GAS strains by showing internal deletions located in the a-helical and TSßH regions. In conclusion, our study yielded insights into the genome structure of M-18 GAS strains responsible for the ARF outbreak in Italy, thus expanding our knowledge of this serotype.

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 1 (2015). - p 40-43 [Nr. Estr. 5997]

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 2 (2015). - p 40-43 [Nr. Estr. 6003]

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 4 (2015). - p 40-43 [Nr. Estr. 6054]

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 6 (2015). - p 40-43 [Nr. Estr. 7111]

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 7 (2015). - p 40-43 [Nr. Estr. 7112]

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 8 (2015). - p 40-43 [Nr. Estr. 7113]

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 9 (2015). - p 40-43 [Nr. Estr. 7138]

Gatti°L, Bucca°M

Dieci percorsi FAD

30 giorni. - Vol. 8 no 10 (2015). - p 40-43 [Nr. Estr. 7172]

Grisendi A, Defilippo°F, Gatti F, Dottori°M, Boni lauri°P

Estimation of accumulated degree day value of six landmarks within the pupal stage of Lucilia sericata

J Life Sci. - Vol. 9 (2015). - p 311-317. - 23 bib ref [Nr. Estr. 7139]

The present paper investigates the pupal development times of Lucilia sericata which were studied in the laboratory at six different constant temperatures (20, 22, 24, 26, 28 ℃ each ± 1 ℃). Lower thresholds (tL) for development were estimated from the linear regression of the developmental rates on each temperature. These data have made it possible to calculate the ADD (Accumulated Degree-Days) necessary for L. sericata to complete the larval stage and to achieve adult emergence. The minimal duration of development from oviposition to adult emergence was found to be inversely related to temperature. Additionally, six landmarks in pupal development are showed and for each of the landmarks the ADD value was calculated for every rearing temperature involved. These data assist in calculating the duration of the pupal stage based on morphological characteristics and would be of great value for future forensic entomological casework.

Huedo P, Gori M, Scaltriti°E, Morganti°M, Casadei °G, Amato E, Pontello M

Draft genome sequence of Salmonella enterica subsp. enterica Serovar Napoli strain SN310, cause of a multischool outbreak in Milan, Italy, in 2014

Genome Announc. - Vol. 3 no 5 (2015). - p e01044-15 (1 p). - 6 bib [Nr. Estr. 7122]

We report the draft genome sequence of Salmonella enterica subsp. enterica serovar Napoli strain SN310, isolated from a stool sample of an affected pupil during a multischool outbreak in 2014 in Milan, Italy. This represents the first reported draft genome sequence of the emerging serovar Napoli.

Lombardo°T, D'incau°M, Villa°R, Ferrari°M, Cino tti°S

The development of the veterinary biobank network: present and future

Annual Conference ESSB : Biobanking for the Environment, Nature and Clinical Medicine : 29 September - 02 October 2015 London / [s.l. : s.n., 2015]. - p 98 [Nr. Estr. 7226]

Annual Conference ESSB : London : 29 September - 02 October 2015)

The lack of standardization and high quality samples from bio-repositories can delay the progress of research. It is difficult to get from other laboratories biological samples with known characteristics except for those that are obtained from certified Centres. The Italian Biobank of Veterinary Resources (IBVR) of the Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER) has the aim to collect all biological resources submitted to purity and identity controls. IBVR has been recently recognized as an OIE (Office International des Epizooties) Collaborating

Centre and aquired the status of International Depositary Authority under the Budapest Treaty (IDA). Biological resources can also be stored at IZSLER-BVR for the following categories of deposit: open collection (open deposit), as a second site or backup security system (safe deposit) and patent deposit under Budapest Treaty for viruses and bacteria. Another safe deposit service for go-vernment laboratories and other institutions will be provide in full compliance with current good manufacturing practices (GMP). The experience of IZSLER has allowed to create a network with other laboratories, in order to increase the types and facilitate the sharing of biological resources to optimise cooperation among the scientific community. Currently, four VS contribute to the network with biological resources collected during their activity performed as National Reference Centres and OIE Reference and Collaborating Laboratories. A further field of interest consists in the development of an international network in order to share "standard reference reagents", know their quality parameters evaluated through proficiency test according to the OIE guidelines.

/testestr/7226en.doc.

Lombardo°T, Dotti°S, Villa°R, Cinotti°S, Ferrar i°M

Veterinary biobank facility : development and management for diagnostic and research purposes

Veterinary infection biology : molecular diagnostics and high-throughput strategies / edited by Mónica V. Cunha, João Inácio. - New York : Humana Press Springer, 2015. - p 43-60. - 37 bib ref [Nr. Estr. 5947]

Biobanking is an essential tool for ensuring easy availability of high-quality biomaterial collections that combine essential samples and epidemiological, clinical, and research data for the scientific community. Specimen collection is an integral part of clinical research. Indeed, every year throughout the world, millions of biological samples are stored for diagnostica and research, but in many fields the Jack of biological material and models is a major hindrance for ongoing research. A biobank facility provides suitable samples for large-scale screening studies and database repositories. Software dedicated to biological banks simplify sample registration and identification, the cataloging of sample properties (type of sample/specimen, associated diseases and/or therapeutic protocols, environmental information, etc.), sample tracking, quality assurance, and specimen availability characterized by well-defined features. Biobank facilities must adopt good laboratory practices (GLPs) and a stringent quality control system and also comply with ethical issues, when required. The creation of a veterinary network can be useful under different aspects: the first one is related to the importance of animal sciences itself to improve research and strategies in the different branches of the veterinary area, and the second aspect is related to the possibility of data management harmonization to improve scientific cooperation.

Lombardo°T, Villa°R, Dotti°S, Stoppani°E, Lomba rdi°G, Ferrari°M, Cinotti°S

Biobank of veterinary resources and potential applications in veterinary medicine

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 279 [Nr. Estr. 7023]

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

Lombardo°T, Villa°R, Ferrari°M, Cinotti°S

The Italian veterinary biobank network

HandsOn: Biobanks 2015 : The EXPOnential relevance of Biobanking : Milano, July 29-31, 2015 / [s.l. : s.n., 2015]. - 1 p [Nr. Estr. 7123]

Biobanks 2015 : The EXPOnential relevance of Biobanking : Milano : July 29-31, 2015)

Luini°M

L'innovazione tecnologica nell'allevamento dei bovini da latte : il contributo della diagnostica veterinaria

Setting a model for a sustainable dairy chain : 22 luglio 2015, EXPO2015, Milano : book of abstract / a cura del Gruppo operativo del progetto "Spazi espositivi per la Ricerca - Padiglione Italia EXPO 2015". - [Milano : s.n., 2015]. - p 31-32 [Nr. Estr. 6090]

Setting a Model for a sustainable dairy chain : Milano : July 22nd, 2015)

Maritati M, Almugadam S, Hanau S, Bellini T, Dallocchio F, Rugna°G, Bonazza S, Govoni M, Contini C

Elevato riscontro di DNA circolante di Leishmania infantum in soggetti immunocompetenti affetti da malattie reumatologiche e trattati con farmaci biotecnologici

XIV Congresso Nazionale Societa' Italiana di Malattie Infettive e Tropicali (SIMIT) : 8-11 Novembre 2015, Catania / [s.l. : s.n., 2015]. - p 111 (abstract 63) [Nr. Estr. 7275]

Congresso Nazionale Societa' Italiana di Malattie Infettive e Tropicali (SIMIT) (14. : Catania : 8-11 Novembre 2015)

Introduzione. In Italia, casi di Leishmaniosi (L) si registrano più frequentemente al Sud, in zone rurali e peri-urbane. Recenti dati epidemiologici hanno dimostrato una diffusione del parassita e del vettore competente anche in alcune regioni Settentrionali, a causa dei recenti cambiamenti climatici con incremento della T°. In Emilia-Romagna, tra il 1999 e il 2011, sono stati diagnosticati 44 casi di L di cui 26 viscerale (Lv) e 18 cutanea (Lc). Nel 2013, l'incidenza è aumentata (30 casi Lv, 9 Lc). La provincia di Bologna è risultata la più interessata (20 casi), in particolare, Valle del Samoggia, Sasso Marconi, Monterenzio, Pianoro ed Imola. L'incremento potrebbe essere attribuito anche all'impiego di farmaci immunosoppressivi (chemioterapici, cortisonici, farmaci biotecnologici [FB]) per il trattamento di malattie autoimmuni, neoplasie e trapianti, arricchendo quindi la categoria dei soggetti potenzialmente vulnerabili nei confronti di questa parassitosi. Obiettivo dello studio è stato quello di attestare la prevalenza (DNA circolante) dell'infezione da L. infantum (LO in pazienti immunocornpetenti affetti da reumatismi infiammatori cronici in trattamento immunosoppressivo con FB, correlando l'eventuale positività genomica alla zona di residenza. Materiali e Metodi. Sono stati retrospettivamente analizzati PBMC di pazienti affetti da artrite reumatoide, spondilite anchilosante ed artrite psoriasica, in trattamento con FB da almeno 5 anni (2009-2014). Ciascun campione è stato sottoposto a PCR per Li presso la Sezione Malattie Infettive dell'Università di Ferrara. L'analisi statistica è stata condotta mediante Test del Chi Quadro corretto secondo Yates. Risultati. Dei 55 campioni analizzati, 38 erano donne (69%) e 17 uomini (30%) con età media di 53.2 (range 29-78 anni). In 21/55 (38`)/0) si riscontrava DNA circolante di Li; di essi 14 (66%) erano donne e 7 (33ªA) uomini. 15 pazienti (71%) risiedevano in zone rurali, mentre 6 (28%) in aree urbane, contro i 34 pazienti risultati negativi per Li DNA, di cui solo 9 risiedevano in aree rurali (26%) e 25 in aree urbane (73%) (p5.0.0028). Le province con più elevata incidenza sono risultate quelle di Ravenna (9 casi), Imola (7 casi) e Rovigo (3 casi), mentre solo 2 pazienti erano residenti a Ferrara, entrambi in zone rurali. Conclusioni. Riattivazioni di infezioni da L sono state sporadicamente descritte in pazienti con malattie reumatiche sottoposti a trattamento con FB anche se dati definitivi sulla loro reale incidenza non sono disponibili. Lo screening di routine non contempla attualmente, la ricerca preliminare di infezioni subcliniche da patogeni opportunisti e da L spesso difficilmente identificabili. In assenza di dati epidemiologici omogenei e di indicazioni sulla gestione di tali infezioni in pazienti esposti a FB ed esenti da deficit immunitari, potrebbe rivelarsi opportuna una sorveglianza capillare ed accurato screening, soprattutto in aree rurali ad elevata prevalenza di DNA.

Onori R, Gaiarsa S, Comandatore F, Pongolini°S, Br isse S, Colombo A, Cassani G, Marone P, Grossi P, Minoja G, Bandi C, Sassera D, Toniolo A

Tracking nosocomial Klebsiella pneumoniae infections and outbreaks by whole-genome analysis : small-scale Italian scenario within a single hospital

J Clin Microbiol. - Vol. 53 no 9 (2015). - p 2861-2868. - 43 bib ref [Nr. Estr. 7154]

Multidrug-resistant (MDR) Klebsiella pneumoniae is one of the most important causes of nosocomial infections worldwide. After the spread of strains resistant to beta-lactams at the end of the previous century, the diffusion of isolates resistant to carbapenems and colistin is now reducing treatment options and the containment of infections. Carbapenem-resistant K. pneumoniae strains have spread rapidly among Italian hospitals, with four subclades of pandemic clonal group 258 (CG258). Here we show that a single Italian hospital has been invaded by three of these subclades within 27 months, thus replicating on a small scale the "Italian scenario." We identified a single clone responsible for an epidemic outbreak involving seven patients, and we reconstructed its star-like pattern of diffusion within the intensive care unit. This epidemiological picture was obtained through phylogenomic analysis of 16 carbapenem-resistant K. pneumoniae isolates collected in the hospital during a 27-month period, which were added to a database of 319 genomes representing the available global diversity of K. pneumoniae strains. Phenotypic and molecular assays did not reveal virulence or resistance determinants specific for the outbreak isolates. Other factors, rather than selective advantages, might have caused the outbreak. Finally, analyses allowed us to identify a major subclade of CG258 composed of strains bearing the yersiniabactin virulence factor. Our work demonstrates how the use of combined phenotypic, molecular, and whole-genome sequencing techniques can help to identify quickly and to characterize accurately the spread of MDR pathogens.

Sorcinelli F, Tozzi R, Rubini° S, Zaccherini A

Maltrattamento di animali e pericolosità sociale : le attività di Link Italia

30 giorni. - Vol. 8 no 11 (2015). - p 22-25 [Nr. Estr. 7269]

Stacchiotti A, Favero G, Lavazza° A, Aleksic M, Gol ic I, Korac A, Rezzani R

Melatonin limits er stress in the obese mice liver through Sirtuin 1

Microscopy Conference MC 2015 : September 6-11, 2015, Goettingen, Germany : proceedings / organized by DGE - German Society for Electron Microscopy e. V.. - [Goettingen : Georg-August-University Goettingen, 2015]. - p 720-721 - 7 bib ref [Nr. Estr. 7084]

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Comment on : Retrospective study of human cystic echinococcosis in Italy based on the analysis of hospital discharge records between 2001 and 2012

Acta Trop. - Vol. 144 (2015). - p 50-51. - 7 bib ref [Nr. Estr. 6016]

Torre ML, Lucarelli E, Guidi S, Ferrari° M, Alessan dri G, De_Girolamo L, Pessina A, Ferrero I

Ex vivo expanded mesenchymal stromal cell minimal quality requirements for clinical application

Stem Cells Dev. - Vol. 24 no 6 (2015). - p 677-685. - 56 bib ref [Nr. Estr. 6014]

Mesenchymal stromal cells (MSCs), as advanced therapy products, must satisfy all the requirements for human use of medicinal products, aiming to maintain the quality and safety of the cells. The MSC manufacturing process for clinical use should comply with the principles of Good Manufacturing Practice (GMP). This ensures that cell preparations are produced and controlled, from the collection

and manipulation of raw materials, through the processing of intermediate products, to the quality controls, storage, labeling and packaging, and release. The objective of this document is to provide the minimal quality requirements for the MSC production and its delivery for clinical use, so that the safety of the final cell therapy product will not be compromised. For this purpose, the document evaluates the most important steps of GMP-compliant MSC production: the isolation and expansion process; the validation phase of the process, including all quality controls for the characterization, functionality, potency, and safety of MSCs; and the quality control at the batch release to guarantee the safety of patient infusion.