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<td>1</td>
<td>Assessment of Aflatoxin M1 Residues in Raw Cow Milk at Al-Riyadh Area with Reference to Some Detoxification Applications</td>
<td>Yosef, T.A.1*; Al-Julaifi, M.Z.2; Salah-El-Dein W.M.3 and AL-Rizqi, A.M.2</td>
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<td>2</td>
<td>First record of chewing louse Heterodoxus spiniger (Insecta, Phthiraptera, Boopidae) on stray dogs from northern region of Egypt</td>
<td>Sultan, K. and Khalafalla, R.E.</td>
<td>Tropical Biomedicine, vol, 31(2), p 378-380.</td>
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<td>Desalted and lyophilized bovine seminal plasma delays induction of the acrosome reaction in frozen-thawed bovine spermatozoa in response to calcium ionophore</td>
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<td>Elazab, Ghada M Gomaa and Walied Abdo</td>
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<td>Maged G. Hemida, IDaniel K.W. Chu, Leo L.M. Poon, Ranawaka A.P.M. Perera, Mohammad A. Alhammadi, Hoi-yee Ng, Lewis Y. Siu, Yi Guan, Abdelmohsen Alnaeem, and Malik Peiris</td>
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<td>Cells Tissues Organs, vol, 199(4):p278-93</td>
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<td>Mostafa Ali Elmadawy, Atushi Nagai, Ghada M. Gomaa, Hanaa M.R. Hegazy, Fawzy Eid Shaaban, Yasuo Bunai</td>
<td>Legal Medicine, vol,15, p338-341</td>
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ASSESSMENT OF AFLATOXIN M1 RESIDUES IN RAW COW MILK AT AL-RIYADH AREA WITH REFERENCE TO SOME DETOXIFICATION APPLICATIONS

Yosef, T.A.1; Al- Julaifi, M.Z.2; Salah-El-Dein W.M.3 and AL- Rizqi, A.M.2
1Dept. of Forensic Med. and Toxicology, Fac. of Vet. Med., Kafrelshiekh Univ., 33516, Egypt.
2Toxicology lab. Management of Vet. Laboratories, Min. of Agric, Riyadh, 11418, KSA.
3Animal Health Research Inst., Dept. of Food Hygiene, Zagazig Provincial Lab., 44516, Egypt.

ABSTRACT

This study was carried out to evaluate the levels of aflatoxin M1 (AFM1) in sixty raw cow milk samples collected from different farms at Al- Riyadh area, Saudi Arabia, besides reviewing the reduction effects of some detoxification methods on it. Results of the field study revealed that the mean concentration of AFM1 was 0.185 ±0.0181 ppb. On the other hand, 43 (71.7%), out of 60 examined samples, contained AFM1 residues in levels exceeded the EU maximum limit for raw milk (0.05 μg/l). Meanwhile 32 (53.3%), out of 60 samples, surpassed the Gulf maximum limit for raw milk (0.2 μg/l). For experimental study, negative milk samples for AFM1 were mixed and divided into 4 main groups which inoculated with 10, 5, 2.5 and 1.25 µg/l AFM1 standard respectively. Each group subdivided into 4 subgroups of 5 samples (100 ml each). The 1st subgroup let as control, the 2nd subgroup undergo pasteurization at 65°C for 30 minutes following by sudden cooling at 4°C, the 3rd subgroup treated by boiling at about 100°C for 10 minutes; while, the 4th one exposed to microwave radiation for 2 minutes in microwave oven at high energy level. The obtained results exhibited a significant reduction in AFM1 concentrations by all treatment methods comparing with the actual positive control levels. The reduction rate were ranked as follow: microwave radiation exposure (52.08%) > boiling treatment (23.93%) > pasteurization treatment (12.90%). Accordingly, microwave irradiation of AFM1 contaminated cow milk may be valuable to reduce its levels and subsequently minimize its hazardous on the public health.
FIRST RECORD OF CHEWING LOUSE *HETERODOXUS SPINIGER* (INSECTA, PHTHIRAPTERA, BOOPIDAE) ON STRAY DOGS FROM NORTHERN REGION OF EGYPT

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Department of Parasitology, Faculty of Veterinary Medicine, Kafrelsheikh University, 33516 Kafr El-Sheikh, Egypt

**ABSTRACT**

*Heterodoxus spiniger* is a rare chewing louse; infest dogs and occasionally cats with expanding geographical distribution. This preliminary report is aimed to record infestation of stray dogs in Kafr El-Sheikh city, Egypt by *H. spiniger*. Two dogs out of 10 were naturally infected with *H. spiniger*. This report is the first to demonstrate *H. spiniger* infestation on dogs in northern regions of Nile-delta of Egypt.
DESALTED AND LYOPHILIZED BOVINE SEMINAL PLASMA DELAYS INDUCTION OF THE ACROSOME REACTION IN FROZEN-THAWED BOVINE SPERMATOZOA IN RESPONSE TO CALCIUM IONOPHORE

Essam Almadaly\textsuperscript{a,b}, Youichiro Hoshino\textsuperscript{c}, Takuya Ueta\textsuperscript{c}, Koushi Mukoujima\textsuperscript{c}, Mostafa Shukry\textsuperscript{d}, Foad Farrag\textsuperscript{d}, Ismail El-Kon\textsuperscript{b}, Kazuo Kita\textsuperscript{c}, Tetsuma Murase\textsuperscript{a,*}

\textsuperscript{a} Laboratory of Theriogenology, Faculty of Applied Biological Sciences, Department of Veterinary Medicine, Gifu University, Gifu, Japan

\textsuperscript{b} Faculty of Veterinary Medicine, Department of Theriogenology, Kafrelsheikh University, Kafrelsheikh, Egypt

\textsuperscript{c} Hida Beef Cattle Research Department, Gifu Prefectural Livestock Research Institute, Takayama, Japan

\textsuperscript{d} Faculty of Veterinary Medicine, Kafrelsheikh University, Kafrelsheikh, Egypt

**ABSTRACT**

Cryopreservation is partially damaging and induces capacitation-like changes in spermatozoa. Seminal plasma (SP) contains a variety of biochemical components, such as protein and lipids, which are specific for the regulation of sperm cell function including those effective for decapacitation of spermatozoa. Therefore, this study tested the hypothesis that desalted and lyophilized SP could prevent premature capacitation (cryocapacitation) of Japanese Black bull spermatozoa. Seminal plasma was desalted by using Sephadex G-25 desalting column and lyophilized before added to semen extenders. Protein and lipid compositions in SP were analyzed by SDS-PAGE and thin-layer chromatography, respectively. The results revealed that progressive motility, intact acrosome, and abnormal morphology were not substantially modified by addition of SP. Stimulation of spermatozoa with calcium ionophore A23187 resulted in a time-dependent induction of the acrosome reaction, which was delayed by the desalted and lyophilized SP. There was no difference in the protein profile of SP before and after gel filtration. In total, 19 protein bands with molecular masses ranging from 5.2 to 185.8 kDa were detected and those of 185.8, 80, 34, 208, 18.8, 17.5, and 10 kDa were considered as novel proteins. Neutral lipids and phospholipids before and after gel filtration were the same, and the detected neutral lipid spots were monoacylglycerol, cholesterol, 1,2- and 1,3-diacetylglycerol, 1,2- and 1,3-saturated diacetylglycerol, whereas the detected phospholipid spots were sphingomyelin, phosphatidylcholine, phosphatidylserine, and three species of phosphatidylinositol, phosphatidylethanolamine, cerebroside, and poly-glycerol phosphatide. The results suggest that premature capacitation during freeze-thaw processes could be reduced by adding desalted and lyophilized SP.
ABSTRACT

Campylobacteriosis is a zoonotic disease which has a worldwide public health impact. The disease is endemic in Egypt; however, the epidemiology in animals and humans has not been fully characterized. The objective of this study was to compare the risk of Campylobacter faecal carriage in children exposed to Campylobacter-infected vs. non-infected backyard poultry and to identify risk factors for a backyard being classified as infected. A total of 103 households which owned backyard poultry were sampled from a rural community in Egypt. Within these households 379 poultry and 106 children were tested for C. jejuni and C. coli; 23.5% and 5.5% of poultry were positive for C. jejuni and C. coli, respectively. In the studied households; 12.3% of children were positive for C. jejuni, and 2.8% were positive for C. coli. Using logistic regression, households with poultry positive for C. jejuni had 3.86 (95% confidence interval 1.0 – 15.0) times the odds of having children positive for C. jejuni compared to those housed with poultry which all tested negative. Backyard poultry may present a transmission route of C. jejuni to children. Backyards with poor cleaning and disinfection, wet litter and manure disposed of within the backyard had increased odds of being positive for C. jejuni. Enhancing biosecurity and management in poultry backyards may reduce the risk of the disease.

PRODUCTION OF ANTICANDIDAL COTTON TEXTILES TREATED WITH OAK GALL EXTRACT

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ABSTRACT

Candida albicans, one of the most dreadful fungal pathogens threatening humans, could not be easily prevented. The anticandidal activity of oak gall extract, Quercus infectoria (QIE), was investigated as a potential natural alternative to synthetic and chemical fungicides. QIE anticandidal potentiality was confirmed using both qualitative and quantitative assays. Cotton textiles were treated with QIE and then evaluated as anticandidal fabrics. QIE-treated textiles had a potent anticandidal activity, which could completely inhibit the inoculated C.
albicans cells. The durability of anticandidal activity in QIE-treated textiles almost completely disappeared after the fourth laundering cycle. QIE could be recommended, however, as a potent anticandidal agent for preparing antiseptic solutions and emulsions and as a finishing agent for manufacturing anticandidal disposable diapers and hygienic clothes.
This study aimed to clarify the timing and infectivity of equine herpesvirus 9 (EHV-9) infection in BALB/c-nu/nu mice and their immunocompetent counterpart (BALB/c). Following intranasal inoculation with 10^5 PFU of EHV-9, specimens from 8 mice per group were collected at different times postinoculation (PI) and assessed using histopathology, immunohistochemistry for viral antigen, and quantitative real-time polymerase chain reaction for ORF30 gene expression. In BALB/c-nu/nu mice, EHV-9 antigen was abundant in olfactory epithelia of all inoculated animals, and in the olfactory bulb of 1 animal. In contrast, only 1 BALB/c mouse per time point had rhinitis, with mild to moderate immunopositivity starting from 12 to 48 h PI, followed by a gradual virus clearance at 72 h PI. Statistically, significant differences were noted in the immunohistochemistry reactions between the 2 mouse strains, indicating that BALB/c-nu/nu is more susceptible to infection. Relative expression levels of ORF30 gene in olfactory epithelia were significantly different between the 2 groups, with the exception of 12 h PI, when BALB/c-nu/nu animals showed dramatic increases in ORF30 gene expression level until 48 h PI, followed by a decline in expression level until the end of experiment. In contrast, the expression level in brains showed no differences between mouse strain except at 96 h PI. In both strains, the highest messenger RNA expression was detected at 48 h PI, followed by a decline in BALB/c mice, proving a rapid clearance of virus in BALB/c and a gradual slowing down of the increased expression levels in BALB/c-nu/nu.
immunohistochemistry in the brain and the trophoblastic cells of labyrinth, the spongiotrophoblasts and giant-cells layers of the placenta in rats inoculated in the first trimester. Virus antigen was detected in feti obtained from rats inoculated in the first and last trimesters. Virus DNA was successfully amplified by PCR in the placenta and feti of inoculated rats. EHV-9 may induce a serious impact including fetal death and abortion in the pregnant dams possibly caused by direct EHV-9 infection to the placenta and/or fetus as well as secondary effect of vascular injury.

TOXOPLASMOSIS IN THE EASTERN GREY KANGAROO, MACROPUS GIGANTEUS AND THE CAPE HYRAX, PROCAVIS CAPENSIS IN JAPAN

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1Department of Veterinary Parasitology, Faculty of Veterinary Medicine, Beni-Suef University, Beni-Suef 62511, Egypt; 2Department of Veterinary Pathology, Faculty of Veterinary Medicine, Kafr-El-Sheikh University, Egypt; 3Department of Veterinary Pathology, Faculty of Veterinary Medicine, Beni-Suef University, Beni-Suef 62511, Egypt; 4Laboratory of Veterinary Pathology, Faculty of Applied Biological Sciences, Gifu University, 1-1 Yanagido, Gifu 501-1193 Japan

ABSTRACT

Toxoplasmosis was investigated in an eastern grey kangaroo, Macropus giganteus, and four cape hyraxes, Procavia capensis, in a Japanese zoo. Clinically, the kangaroo showed neurological signs, emaciation, diarrhea, elevated AST and CK, and subjected to coma before death. One young cape hyrax had severe anorexia, while the other three died without exhibiting clinical signs. Grossly, lungs of the kangaroo were dark red in color, while hyraxes, besides, showed hepatic multifocal white foci, and intestinal multifocal hemorrhages. Histologically, the kangaroo had frequent Toxoplasma gondii pseudocysts in brain, heart and skeletal muscles. All hyraxes had multifocal necrosis with cysts containing numerous bradyzoites in liver and spleen, along with necrotic gastroenteritis and intestinal hemorrhages. Immunohistochemically, cysts showed positive reaction to anti-T. gondii antibodies. These findings indicate possible outbreaks of toxoplasmosis in eastern grey kangaroos and cape hyraxes, zoo habitants; therefore, they could be susceptible intermediate hosts for T. gondii in terms of zoonosis. This is the first report of toxoplasmosis in eastern grey kangaroos and cape hyraxes in Japanese zoos.

PROTECTIVE EFFECT OF S-METHYL CYSTEINE AGAINST TILMICOSIN-INDUCED CARDIOTOXICITY IN RATS
Mohamed Fahmy Abou Elazab\textsuperscript{1}, Ghada M. Gomaa\textsuperscript{2} and Walied Abdo\textsuperscript{3}

\textsuperscript{1}Department of Clinical Pathology; \textsuperscript{2}Department of Forensic Medicine and Toxicology; \textsuperscript{3}Department of Pathology, Faculty of Veterinary Medicine, Kafrelsheikh University, 33516, Kafr Elsheikh, Egypt

\textbf{ABSTRACT}

The present study was carried out to investigate whether S-methyl cysteine (SMC) would ameliorate the acute cardiotoxic effect of tilmicosin antibiotic in treated Wister rats. Thirty-two male rats were equally divided into four groups: control, SMC (100 mg/kg orally for five consecutive days), tilmicosin (a single dose, 75 mg/kg BW, S/C on the sixth day) and SMC+Tilmicosin (pretreated with SMC and co-injected with 75 mg/kg of tilmicosin at the sixth day). The biochemical results demonstrated marked increase in serum aspartate transaminase (AST), lactate dehydrogenase (LDH), creatine kinase (CK) activities and cardiac troponin T (cTnT) concentrations in tilmicosin-treated rats indicating severe cardiotoxicity. On the other hand, pretreatment of rats with SMC revealed marked decrease in cardiac biochemical parameters toward the normal limits. Histopathological findings of the heart sections revealed multifocal myocarditis in tilmicosin-treated rats meanwhile, (SMC+Tilmicosin) treated group showed slight vacuolation of myocardial fiber. Furthermore, the ultrastructure findings revealed myolysis and necrosis in tilmicosin-treated rats compared with intact myocardial fiber in (SMC+Tilmicosin) group.

ENHANCEMENT OF METHANE PRODUCTION FROM CO-DIGESTION OF CHICKEN MANURE WITH AGRICULTURAL WASTES

Fatma Abouelenien\textsuperscript{a}, Yuzaburo Namba\textsuperscript{b}, Maria R. Kosseva\textsuperscript{c}, Naomichi Nishio\textsuperscript{b}, Yutaka Nakashimada\textsuperscript{b}

\textsuperscript{a} Department of Hygiene and Preventive medicine, Faculty of Vet Med, Kafer Elshikh University, Egypt
\textsuperscript{b} Department of Molecular Biotechnology, Graduate School of Advanced Sciences of Matter, Hiroshima University, Kagamiyama 1-3-1, Higashi-Hiroshima 739-8530, Japan
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\textbf{ABSTRACT}

The potential for methane production from semi-solid chicken manure (CM) and mixture of agricultural wastes (AWS) in a co-digestion process has been experimentally evaluated at thermophilic and mesophilic temperatures. To the best of author’s knowledge, it is the first time that CM is co-digested with mixture of AWS consisting of coconut waste, cassava waste, and coffee grounds. Two types of anaerobic digestion processes (AD process) were used, process 1 (P1) using fresh CM (FCM) and process 2 (P2) using treated CM (TCM), ammonia stripped CM, were conducted. Methane production in P1 was increased by 93% and 50%
compared to control (no AWS added) with maximum methane production of 502 and 506 mL g\_1 VS obtained at 55 \_C and 35 \_C, respectively. Additionally, 42\% increase in methane production was observed with maximum volume of 695 mL g\_1 VS comparing P2 test with P2 control under 55 \_C. Ammonia accumulation was reduced by 39\% and 32\% in P1 and P2 tests.

REGULATION OF GLUCOSE LEVEL DURING LATE PREGNANCY AND ONSET OF LACTATION IN EGYPTIAN FEMALE BALADI GOATS

Shawky Mahmoud\textsuperscript{a}, Mohamed Azab\textsuperscript{b}

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\textbf{ABSTRACT}

The present study aimed to evaluate the hormonal regulation of blood glucose level during late pregnancy and onset of lactation in Egyptian female Baladi does. Seven healthy female Baladi goats were used to study glucose levels and its hormonal regulation during late pregnancy and early lactation. Blood Samples were collected at late pregnancy (6, 5, 4, 3, 2, 1, weeks, and one day before parturition); day of parturition and early lactation (1, 2, 3 and 4 weeks after parturition). Plasma cortisol, insulin and glucose were determined. The obtained results revealed that plasma cortisol remained low during late pregnancy and then increased significantly (P < 0.05) one day before parturition then decreased on the day of parturition and remained low for one week after parturition. Cortisol level increased markedly at 2, 3 and 4 weeks after parturition. Plasma insulin remained low at 6, 5, 4 and 3 weeks prepartum.

A significant increase was noticed at 2 weeks, 1 week and one day before parturition. Insulin concentrations decreased markedly on the day of parturition, then increased (P < 0.05) during the postpartum period. Plasma glucose concentrations remained low during late pregnancy then increased at one day before parturition, on the day of parturition and remained elevated during postpartum period. It could be concluded that late pregnancy and early lactation in does were accompanied by significant changes in plasma cortisol, insulin and glucose concentrations. Glucose levels during late pregnancy and early lactation are highly correlated with cortisol and less correlated with insulin. The results obtained point out justification of administration of cortisol. This will help in treatment of pregnancy toxaeemia in does and ensure good health during the very demanding physiological states of late pregnancy and early lactation.
INTRAOCULAR PRESSURE IN CLINICALLY NORMAL DROMEDARY CAMELS
(CAMELUS DROMEDARIUS)

Mohamed A. Marzok, Sabry A. El-khodery

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ABSTRACT

Dromedary camels (Camelus dromedaries), also known as Arabian camels, are single-humped camels that are an important livestock species for people in harsh and difficult environments.1 Camels are maintained for the production of meat, milk, leather, and wool and are also used as pack animals and for sport, transport, riding, and tourism purposes.2 Despite the dromedary camel’s popularity, information regarding various ophthalmologic conditions in this species, including reference limits for various ophthalmic variables and diagnostic tests for ocular diseases, is limited.3–5 Measurement of IOP, or tonometry, is an important part of the routine ophthalmic examination in animals,6 and knowledge of IOP values in clinically normal animals is important for the diagnosis and monitoring of ocular disorders such as focal or diffuse corneal edema, red or painful eyes, orbital trauma, lens luxation, glaucoma, and uveitis.6–9 Indentation, applanation, and rebound tonometry have traditionally been used to measure IOP indirectly in veterinary ophthalmology.10,11 In recent years, measurement of IOP in animals has evolved tremendously with the development of portable handheld digital tonometers.8 Applanation tonometry has been used to measure IOP in numerous clinically normal domestic and nondomestic animals, including dogs,12–14 cats,15,16 horses,17,18 ponies,19,20 dairy cattle,19 sheep,20 goats,21,22 llamas,23,24 alpacas,23,24 rabbits,25,26 rats,27 ferrets,28,29 chinchillas,30 capybaras,31 hedgehogs,32 beavers,33 Nubian ibex (Capra nubiana),34 Grant zebras (Equus quagga boehmi),34 oryxes,34 Arabian oryxes (Oryx leucoryx),34 Thomson gazelles (Eudorcas thomsonii),35 elands,36 fallow deer,36 addax antelope,34 wildebeests,34 rhinoceroses,34 capuchin monkeys,37 koalas,38 and lions.39 However, to our knowledge, the IOP for clinically normal dromedary camels has not been reported. The purpose of the study reported here was to use applanation tonometry to determine the IOP in clinically normal dromedary camels.
respectively. A significant decrease in IOP values was observed in both right and left eyes of the horses in treatment group at T5, T15, T30, T45, T60, and T90 in comparison with the baseline values (P < 0.05). The lowest level of IOP in romifidine-treated groups was recorded at T45 for the right and left eyes (10.25 ± 2.3 and 11.25 ± 3.5 mmHg, respectively). Conclusion Romifidine significantly decreased IOP in clinically normal horses and may be used safely for surgery or diagnostic ocular procedures in horses when specific control of IOP is required.

COMPARATIVE ANALGESIC AND SEDATIVE EFFECTS OF TRAMADOL, TRAMADOL-LIDOCAINE AND LIDOCAINE FOR CAUDAL EPIDURAL ANALGESIA IN DONKEYS (EQUUS ASINUS)

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ABSTRACT

Objective To compare anti-nociceptive and sedative effects of tramadol, a combination of tramadol-lidocaine, and lidocaine alone for perineal analgesia in donkeys. Study design Experimental 'blinded' randomized cross-over study. Animals Six healthy adult donkeys. Methods Treatments were tramadol (TR) (1.0 mg kg^-1), tramadol-lidocaine (TRLD) (0.5 and 0.2 mg kg^-1 respectively) and lidocaine (LD) (0.4 mg kg^-1) given into the epidural space. The volume of all treatments was 0.02 mL kg^-1. Nociception was tested at the perineal region by pin prick, followed, if no reaction, by pressure from a haemostat clamp. Times to onset, degree and duration of antinociception of the perineal region were recorded. Response was tested immediately after drug administration and at: 2, 5, 10, 15, 30, 45, and 60 minutes post-administration and then at 30 minute intervals thereafter until a response re-occurred. Physiologic data and degree of sedation and ataxia were recorded pre-administration and at intervals for 240 minutes post-administration. Results were analyzed using ANOVA, Kruskal–Wallis tests, and Wilks’ Lambda test as relevant. Significance was taken as p < 0.05. Results Times (minutes, mean _ SD) to onset and duration of anti-nociception, respectively were: TR 13 _ 1.6 and 220 ± 4.6; TRLD 6 + 0.8 and 180 ± 8.5; LD 4 ± 1.4 and 75 ± 4. Onset and duration times were significantly longer with TR than the other two treatments. TR never produced complete anti-nociception, whereas the TRLD and LD induced complete anti-nociceptive effects. Duration was significantly longer with TRLD than with LD alone. Epidural injections of TR and TRLD induced mild sedation. Conclusions and clinical relevance Epidural combination of TRLD produced an anti-nociceptive effect in the perineum, which was rapid in onset and had a longer duration of action than LD alone. An epidural single dose of TRLD combination would appear to provide an acceptable analgesic effect in the perineal region of donkeys.
ASSESSMENT OF PROLIFERATIVE ACTIVITY BY PROLIFERATIVE CELL NUCLEAR ANTIGEN (PCNA) AND ANTI-BROMODEOXYURIDINE (BRDU) IMMUNOLABELING IN THE TISSUES OF JAPANESE EELS (ANGUILLA JAPONICA)

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ABSTRACT

Five Japanese eels (Anguilla japonica) were examined by immunolabeling with proliferating cell nuclear antigen (PCNA) and bromodeoxyuridine (BrdU) incorporation for assessment of proliferative activities in various tissues of Japanese eels. PCNA protein was expressed in all tissues of eels, mainly in the haematopoietic tissues, especially in the anterior kidneys, an indication for the role of PCNA in haematopoiesis. Also, positive PCNA immunolabeling was frequently seen in the spleen. PCNA labeling index in kidney and spleen of Japanese eels was correlated well with BrdU incorporation which could be indicating higher proliferative activity of these organs. Absence of correlation between PCNA and BrdU in the testes may might refer to the expression of PCNA in germ and other somatic cells, while BrdU immunostaining was only noticed in phase dividing spermatogenic cells. Therefore, our results demonstrated over expression of PCNA in haematopoietic tissues and testes suggest the role of PCNA in haematopoiesis and spermatogenesis in Japanese eels. Moreover, PCNA and BrdU labeling indices could be a valuable approach for analyzing cell proliferation activity in the kidney and spleen of eel tissues.

PINEAL GLAND PLAYS A ROLE IN GONADAL DEVELOPMENT AFTER EYELIDS SEPARATION IN PUPPIES

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ABSTRACT

Several functional and morphological studies have been conducted on the pineal gland in many mammalian species; however, no published reports are available on the role of pineal gland on
the gonadal development before and after eyelids separation in puppies. Therefore, this study aimed to trace the postnatal histo-morphological changes in the pineal gland and gonads of puppies before (2, 10 and 11 days old) and after (25, 35 and 40 days old) eyelids separation in an attempt to investigate the possible role of pineal gland on the gonadal development. In general, the differentiation of pineal cells, interstitial endocrine cells of testes and stromal ovarian cells coincides with the start of eyelids separation in puppies. Histological examination of stained pineal and gonadal slices of puppies after eyelids separation revealed a remarkable differentiation of pinealocytes and testicular interstitial endocrine cells, as well as presence of some evidence of folliculogenesis in ovary. Surprisingly, melatonin receptor (MT1) protein expression levels were significantly increased in the ovaries and testes of puppies after eyelids separation. Moreover, the mRNA and protein expression of AANAT, a rate-limiting enzyme in melatonin biosynthesis, was notably increased in the pineal gland of opened eyes puppies. Our results suggest an increase of melatonin production from the pineal gland of opened eyes puppies and this could play a vital role in the developmental changes observed in the gonads of these puppies.

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**CHARACTERIZATION OF INTEGRONS AND RESISTANCE GENES IN MULTIDRUG-RESISTANT SALMONELLA ENTERICA ISOLATED FROM MEAT AND DAIRY PRODUCTS IN EGYPT**

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**ABSTRACT**

Foodborne pathogens are a leading cause of illness and death, especially in developing countries. The problem is exacerbated if bacteria attain multidrug resistance. Little is currently known about the extent of antibiotic resistance in foodborne pathogens and the molecular mechanisms underlying this resistance in Africa. Therefore, the current study was carried out to characterize, at the molecular level, the mechanism of multidrug resistance in Salmonella enterica isolated from 1600 food samples (800 meat products and 800 dairy products) collected from different street vendors, butchers, retail markets and slaughterhouses in Egypt. Forty-seven out of 69 isolates (68.1%) showed multidrug resistance phenotypes to at least three classes of antimicrobials. The incidence of multidrug-resistant isolates was higher in meat products (37, 69.8%) than in dairy products (10, 62.5%). The multidrug-resistant serovars included, S. enterica serovar Typhimurium (24 isolates, 34.8%), S. enterica serovar Enteritidis, (15 isolates, 21.8%), S. enterica serovar Infantis (7 isolates, 10.1%) and S. enterica non-typeable serovar (1 isolate, 1.4%). The highest resistance was to ampicillin (95.7%), then to kanamycin (93.6%), spectinomycin (93.6%), streptomycin (91.5%) and sulfamethoxazole/trimethoprim (91.5%). PCR and DNA sequencing were used to screen and characterize integrons and antibiotic resistance genes and 39.1% and 8.7% of isolates were positive for class 1 and class 2 integrons, respectively. β-lactamase-encoding genes were identified in 75.4% of isolates and plasmid-mediated quinolone resistance genes were identified in 27.5% of isolates. Finally, the florfenicol resistance gene, floR, was identified in 18.8% of isolates. PCR screening identified S. enterica serovar Typhimurium DT104 in both meat and dairy products. This is the first study to report many of these resistance genes in dairy products. This study highlights the high incidence of multidrug-resistant S. enterica in meat and dairy products in Egypt, with the possibility of their transfer to humans leading to therapeutic failure. Therefore, the overuse of antibiotics in animals should be drastically reduced in developing countries.
MOLECULAR ANALYSIS OF MULTIDRUG RESISTANCE IN SHIGA TOXIN-PRODUCING ESCHERICHIA COLI O157:H7 ISOLATED FROM MEAT AND DAIRY PRODUCTS

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ABSTRACT

Shiga toxin-producing Escherichia coli (STEC) O157:H7 is an important food-borne pathogen that has been implicated in numerous disease outbreaks worldwide. Little is known about the extent and molecular basis of antimicrobial resistance in STEC O157:H7 of food origin. Therefore, the current study aimed to characterize the genetic basis of multidrug resistance in 54 STEC O157:H7 strains isolated from 1600 food samples (800 meat products and 800 dairy products) collected from different street vendors, butchers, retail markets, and slaughterhouses in Egypt. Thirty-one of 54 (57.4%) isolates showed multidrug resistance phenotypes to at least three classes of antimicrobials. The highest incidence of antimicrobial resistance was to kanamycin (96.8%), followed by spectinomycin (93.6%), ampicillin (90.3%), streptomycin (87.1%), and tetracycline (80.6%). PCR and DNA sequencing were used to screen and characterize integrons and antibiotic resistance genes, and 29.6% and 5.6% of isolates were positive for class 1 and class 2 integrons, respectively. β-Lactamase-encoding genes were identified in 63.0% of isolates as follows: blaTEM-1 and blaTEM-52 in 35.2% and 1.9% isolates respectively; blaCMY-2 in 13.0% isolates; blaCTX-M in 5.6% isolates; blaSHV-12 in 5.6% isolates; and blaOXA-1 in 1.9% isolate. The plasmid-mediated quinolone resistance genes were identified in 13.0% of isolates as follows: qnrB, qnrS, and aac(6’)-Ib-cr in 5.6%, 3.7%, and 3.7% isolates, respectively. Finally, the florfenicol resistance gene floR was identified in 7.4% of isolates.

This study demonstrated that meat and dairy products are potential sources of multidrug resistant STEC O157:H7. To our knowledge, this is the first report of the occurrence of class 2 integrons, qnrB, qnrS, and aac(6’)-Ib-cr in STEC O157:H7.

MOLECULAR CHARACTERIZATION OF MULTIDRUG-RESISTANT SHIGELLA SPP. OF FOOD ORIGIN

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ABSTRACT

Shigella spp. are the causative agents of food-borne shigellosis, an acute enteric infection. The emergence of multidrug-resistant clinical isolates of Shigella presents an increasing challenge for clinicians in the treatment of shigellosis. Several studies worldwide have characterized the molecular basis of antibiotic resistance in clinical Shigella isolates of human origin, however, to date, no such
characterization has been reported for Shigella spp. of food origin. In this study, we characterized the genetic basis of multidrug resistance in Shigella spp. isolated from 1600 food samples (800 meat products and 800 dairy products) collected from different street vendors, butchers, retail markets, and slaughterhouses in Egypt. Twenty-four out of 27 Shigella isolates (88.9%) showed multidrug resistance phenotypes to at least three classes of antimicrobials. The multidrug-resistant Shigella spp. were as follows: Shigella flexneri (66.7%), Shigella sonnei (18.5%), and Shigella dysenteriae (3.7%). The highest resistance was to streptomycin (100.0%), then to kanamycin (95.8%), nalidixic acid (95.8%), tetracycline (95.8%), spectinomycin (93.6%), ampicillin (87.5%), and sulfamethoxazole/trimethoprim (87.5%). PCR and DNA sequencing were used to screen and characterize integrons and antibiotic resistance genes. Our results indicated that 11.1% and 74.1% of isolates were positive for class 1 and class 2 integrons, respectively. Beta-lactamase-encoding genes were identified in 77.8% of isolates, and plasmid-mediated quinolone resistance genes were identified in 44.4% of isolates. These data provide useful information to better understand the molecular basis of antimicrobial resistance in Shigella spp. To the best of our knowledge, this is the first report of the molecular characterization of antibiotic resistance in Shigella spp. isolated from food.

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MERS CORONAVIRUS IN DROMEDARY CAMEL HERD
SAUDI ARABIA

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ABSTRACT

A prospective study of a dromedary camel herd during the 2013–14 calving season showed Middle East respiratory syndrome coronavirus infection of calves and adults. Virus was isolated from the nose and feces but more frequently from the nose. Preexisting neutralizing antibody did not appear to protect against infection. Ongoing transmission of Middle East respiratory syndrome coronavirus (MERS-CoV) to humans underscores the need to understand the animal sources of zoonotic infection (1,2). MERS-CoV RNA has been detected in dromedary camels (3,4), and dromedary infection precedes human infection (5). We conducted a prospective study in dromedary herds in Al-Hasa, Saudi Arabia, through the peak calving season (December 2013–February 2014) to document virologic features of MERS-CoV infection in these animals.

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ABSTRACT

The pseudoparticle virus neutralisation test (ppNT) and a conventional microneutralisation (MN) assay are specific for detecting antibodies to Middle East respiratory syndrome coronavirus (MERS-CoV) when used in seroepidemiological studies in animals. Genetically diverse MERS-CoV appear antigenically similar in MN tests. We confirm that MERS-CoV was circulating in dromedaries in Saudi Arabia in 1993. Preliminary data suggest that feral Australian dromedaries may be free of MERS-CoV but larger confirmatory studies are needed.

REGULATION OF CHICK EARLY B-CELL FACTOR-1 GENE EXPRESSION IN FEATHER DEVELOPMENT

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ABSTRACT

The chick Ebf1 (early B-cell factor-1) gene is a member of a novel family of helix loop helix
transcription factors. The expression profile, regulation and significance of this gene have been extensively studied in lymphatic, nervous, adipose and muscular tissues. However, cEbf1 expression, regulation and function in the feather of chick embryo have not yet been investigated. cEbf1 expression was first detected throughout the mesenchymal core of some few feather placodes (D7–D7.5). After feathers became mature and grew distally (D9 and D10), the mesenchymal expression of cEbf1 became confined to the caudal margin of the proximal half of all formed feather buds. Because this dynamic pattern of expression resembles that of Sonic Hedgehog (Shh) protein and bone morphogenetic protein (Bmp4) plus the crucial role of these two major signals in feather development, we hypothesized that cEbf1 expression in the feather may be regulated by Shh and Bmp4. In a feather explant culture system, Shh signals are necessary to initiate and maintain cEbf1 expression in the posterior half of the feather bud, while Bmp4 is crucial for the initial cEbf1 expression in the anterior half of the feather bud. Inhibition of Shh, not only down-regulates cEbf1, but also changes the morphology of feather buds, which become irregular and fused. This is the first study to demonstrate that cEbf1 expression in the feather bud is under the control of Shh and Bmp4 signals and that expression may play a role in the normal development of feathers.

ASSOCIATION OF A NOVEL SNP IN EXON 10 OF THE IGF2 GENE WITH GROWTH TRAITS IN EGYPTIAN WATER BUFFALO (BUBALUS BUBALIS)


ABSTRACT

Insulin-like growth factor 2 (IGF2) plays an important role in muscle growth and it might be used as a marker for the growth traits selection strategies in farm animals. The objectives of this study were to detect polymorphisms in exon 10 of IGF2 and to determine associations between these polymorphisms and growth traits in Egyptian water buffalo. PCR single-strand conformation polymorphism (SSCP) and DNA sequencing methods were used to detect any prospective polymorphism. A novel single nucleotide polymorphism (SNP), C287A, was detected. It was a non-synonymous mutation and led to replacement of glutamine (Q) amino acid (aa) by histidine (H) aa. Three different SSCP patterns were observed: AA, AC, and CC, with frequencies of 0.540, 0.325, and 0.135, respectively. Association analyses revealed that the AA individuals had a higher average daily gain (ADG) than other individuals (CC and AC) from birth to 9 months of age. We conclude that the AA genotype in C287A SNP in the exon 10 of the IGF2 gene is associated with the ADG during the age from birth to 9 months and could be used as a potential genetic marker for selection of growth traits in Egyptian buffalo.
EFFECTS OF A NOVEL SNP OF IGF2R GENE ON GROWTH TRAITS AND EXPRESSION RATE OF IGF2R AND IGF2 GENES IN GLUTEUS MEDIUS MUSCLE OF EGYPTIAN BUFFALO


ABSTRACT

Insulin-like growth factor 2 receptor (IGF2R) is responsible for degradation of the muscle development initiator, IGF2, and thus it can be used as a marker for selection strategies in the farm animals. The aim of this study was to search for polymorphisms in three coding loci of IGF2R, and to analyze their effect on the growth traits and on the expression levels of IGF2R and IGF2 genes in the gluteus medius muscle of Egyptian buffaloes. A novel A266C SNP was detected in the coding sequences of the third IGF2R locus (at nucleotide number 51 of exon 23) among Egyptian water buffaloes. This SNP was non-synonymous mutation and led to replacement of Y (tyrosine) amino acid (aa) by D (aspartic acid) aa. Three different single-strand conformation polymorphism patterns were observed in the third IGF2R locus: AA, AC, and CC with frequencies of 0.555, 0.195, and 0.250, respectively. Statistical analysis showed that the homozygous AA genotype significantly associated with the average daily gain than AC and CC genotypes from birth to 9 mo of age. Expression analysis showed that the A266C SNP was correlated with IGF2, but not with IGF2R, mRNA levels in the gluteus medius muscle of Egyptian buffaloes. The highest IGF2 mRNA level was estimated in the muscle of animals with the AA homozygous genotype as compared to the AC heterozygotes and CC homozygotes. We conclude that A266C SNP at nucleotide number 51 of exon 23 of the IGF2R gene is associated with the ADG during the early stages of life (from birth to 9 mo of age) and this effect is accompanied by, and may be caused by, increased expression levels of the IGF2 gene.

EFFECTS OF A NOVEL SNP OF IGF2R GENE ON GROWTH TRAITS AND EXPRESSION RATE OF IGF2R AND IGF2 GENES IN GLUTEUS MEDIUS MUSCLE OF EGYPTIAN BUFFALO

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ABSTRACT

Expression of chick early B cell factor 1-3 (cEbf1-3) genes in regions of high retinoic acid (RA) activity, such as somites and pharyngeal arches (PAs), and regulation of other EBF
members by RA raise the possibility that the internal cue RA may regulate cEbf1-3 expression in these tissues. To check this possibility, RA gain and loss of function experiments were conducted. Ectopic expression of RA led to up-regulation of cEbf2, 3 but did not change cEbf1 expression in somites. Expectedly, inhibition of RA by disulfiram resulted in downregulation of cEbf2, 3, but did not change cEbf1 expression in somites. The same RA gain and loss of function experiments did not change cEbf1-3 expression in PAs. However, ectopic expression of RA in the cranial neural tube before migration of neural crest cells downregulated cEbf1, 3 and up-regulated cEbf2 expression in the PAs. The same experiment, but with application of disulfiram, resulted in downregulation of cEbf2, but did not alter the expression of the other two genes. We conclude that the three cEbf genes act differently in response to RA signals in somitic mesoderm. cEbf1 may be not RA dependant in somites; however, the other two cEbf genes positively respond to RA signalling in somites. Additionally, only the migratory cEbf-expressing cells into the PAs are affected by RA signals.

EFFECTS SHH REGULATES CHICK EBF1 GENE EXPRESSION IN SOMITE DEVELOPMENT


ABSTRACT

The chick early B-cell factor 1 (cEbf1) is a member of EBF family of helix loop helix transcription factors. Recently, we have proved that cEbf1 expression in feather is regulated by Shh. It is therefore possible that the somitic expression of cEbf1 is controlled by Shh signals from the notochord. To assess this hypothesis, the expression profile of cEbf1 was first detailed in somites of chick embryos (from HH8 to HH28). cEbf1 expression was mainly localized in the medial sclerotome and later around the vertebral cartilage anlagen of body and pedicles. Tissue manipulations (notochord ablation) and Shh gain and loss of function experiments were then performed to analyse whether the notochord and/or Shh regulate cEbf1 expression. Results from these experiments confirmed our hypothesis that the medial somitic expression of cEbf1 is regulated by Shh from the notochord. In conclusion, cEbf1 gene is considered as a medial sclerotome marker, downstream to and regulated by the
REGULATION OF CHICK EBF1-3 GENE EXPRESSION IN THE PHARYNGEAL ARCHES, CRANIAL SENSORY GANGLIA AND PLACODES

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\textbf{ABSTRACT}

This study was conducted to identify the regulation of the expression of the cEbf1–3 (chick early B-cell factor 1–3) genes in the pharyngeal arches (PAs), cranial sensory ganglia and placodes. cEbf1 and cEbf3 were mainly expressed in the cranial neural crest cells (NCCs) occupying the PAs, but cEbf2 was expressed in the mesenchymal core. cEbf1–3 were prominently expressed in the olfactory placodes, but cEbf1 and cEbf3 were only expressed in the otic vesicle. cEbf1 was expressed in all cranial sensory ganglia, cEbf2 (only) in the dorsolateral ganglia and cEbf3 in the trigeminal and vestibular ganglia. The removal of the source (the cranial neural tube) of the cranial NCCs before their migration to the PAs led to downregulation of cEbf1 and cEbf3 and upregulation of cEbf2 expression. Gain- and loss-of-function experiments showed that sonic hedgehog did not regulate cEbf1–3 expression in the PAs or associated ganglia. Bone morphogenetic protein 2 (Bmp2) can, however, directly and indirectly regulate cEbf1 and cEbf3 expression in the PAs and the proximal (NCC-derived) portion, but not the distal (placodal-derived) portion of the cranial sensory ganglia. Conversely, cEbf2 expression was upregulated following injection of Noggin before the migration of NCCs, but did not change after the overexpression of either Noggin or Bmp2 in the arch after NCC migration. In conclusion, Bmp2 regulates cEbf1 and cEbf3 expression in PAs and cranial sensory ganglia both directly and indirectly, via the migration of cranial NCCs. However, cEbf2 expression in the mesenchymal core of PAs is controlled by other undetermined signals.
We examined whether mutation of the platelet-derived growth factor receptor protein tyrosine kinase (PDGFR)-α and PDGFR-β genes contributes to their overexpression in canine vascular tumors. Genomic sequences of trans- or juxtamembrane regions of PDGFR-α and PDGFR-β were analysed with immunohistochemical staining and polymerase chain reaction-direct sequencing using DNA from paraffin-embedded neoplastic tissues of 27 hemangiosarcomas (HSAs) and 20 hemangiomas (HAs). Immunohistochemically, 75% of the HA cases were positive for PDGFR-α and almost most of the HA cases were negative for PDGFR-β. Of the HSA cases, 55.6% were negative for PDGFR-α and 63% were strongly positive for PDGFR-β. Among the HA cases, 1 missense mutation was detected in PDGFR-α exon 18 and 1 in PDGFR-β exon 17. Two HSA cases had missense mutations in exon 14 and 1 in exon 17 of PDGFR-β. Thus, genomic mutation of trans- or juxtamembrane regions of PDGFRs was not the main mechanism driving the activation of receptors in HSA and HA.
frequency, 2.97% of population sample. High mtDNA diversity was observed with genetic diversity and power of discrimination, 0.9982 and 0.9883, respectively. In this dataset the west Eurasian haplogroups predominated over the African haplo- groups. The results would be useful for forensic examinations and human genetic studies.