Genetic Bottleneck Analyses of Kodi Adu Goat Breed Based on Microsatellite Markers

Thiruvenkadan, A.K., Jayakumar, V., R. Saravanan, R., and ***Periasamy, K.***

Indian Veterinary Journal, 2015, 92 (3) : 24 - 27

The genetic characterization and bottleneck analysis in Kodi Adu goat was done using 25 FAO recommended microsatellite markers. The mean observed number of alleles and polymorphism information content (PIC) were estimated to be 11.52±0.95 and 0.817±0.023 respectively. The mean observed and expected heterozygosities were 0.660 ± 0.045 and 0.846 ± 0.018 respectively. The mean expected equilibrium gene diversity across 21 microsatellite loci under TAM, SMM and TPM were 0.793±0.028, 0.854±0.023 and 0.827±0.026 respectively. All the three statistical tests revealed significant deviation of Kodi Adu goats from mutation-drift equilibrium under the IAM and TPM models, however, non-significant deviation under SMM model. The mode shift analysis supported the results under SMM indicating the absence of genetic bottleneck in the recent past in Kodi Adu goats.

Specific detection of peste des petits ruminants virus antibodies in sheep and goat sera by the luciferase

Berguido, F.J., *Bodjo, S.C., Loitsch, A., Diallo, A.*

Journal of Virological Methods, 2016, 227, 40–46

Peste des petits ruminants (PPR) is a contagious and often fatal transboundary animal disease affecting mostly sheep, goats and wild small ruminants. This disease is endemic in most of Africa, the Middle, Near East, and large parts of Asia. The causal agent is peste des petits ruminants virus (PPRV), which belongs to the genus Morbillivirus in the family Paramyxoviridae. This genus also includes measles virus (MV), canine distemper virus (CDV) and rinderpest virus (RPV). All are closely related viruses with serological cross reactivity. In this study, we have developed a Luciferase Immunoprecipitation System (LIPS) for the rapid detection of antibodies against PPRV in serum samples and for specific differentiation from antibodies against RPV. PPR and rinderpest (RP) serum samples were assayed by PPR-LIPS and two commercially available PPR cELISA tests. The PPR-LIPS showed high sensitivity and specificity for the samples tested and showed no cross reactivity with RPV unlike the commercial PPR cELISA tests which did cross react with RPV. Based on the results shown in this study, PPR-LIPS is presented as a good candidate for the specific serosurveillance of PPR.

Sample preparation for avian and porcine influenza virus cDNA amplification simplified: Boiling vs. conventional RNA extraction

Fereidouni, S.R., Starick, E., Ziller, M., Harder, T. C., ***Unger, H.,*** *Hamilton, K., Globig, A.*

Journal of Virological Methods (2015) 221: 62-67. doi: 10.1016/j.jviromet.2015.04.021

RNA extraction and purification is a fundamental step that allows for highly sensitive amplification of specific RNA targets in PCR applications. However, commercial extraction kits that are broadly used because of their robustness and high yield of purified RNA are expensive and labor-intensive. In this study, boiling in distilled water or a commercial lysis buffer of different sample matrices containing avian or porcine influenza viruses was tested as an alternative. Real-time PCR (RTqPCR) for nucleoprotein gene fragment was used as read out. Results were compared with freshly extracted RNA by use of a commercial extraction kit. Different batches of virus containing materials, including diluted virus positive allantoic fluid or cell culture supernatant, and avian faecal, cloacal or oropharyngeal swab samples were used in this study. Simple boiling of samples without any additional purification steps can be used as an alternative RNA preparation method to detect influenza A virus nucleoprotein RNA in oropharyngeal swab samples, allantoic fluid or cell-culture supernatant. The boiling method is not applicable for sample matrices containing faecal material.

Detection and genome analysis of a lineage III peste des petits ruminants virus in Kenya in 2011

Dundon, W.G., *Kihu, S. M., Gitao, G.C., Bebora, L.C., John, N.M., Oyugi, J.O., Loitsch, A., Diallo, A.*

Transboundary and Emerging Diseases (2015). doi: 10.1111/tbed.12374 [Epub ahead of print]

In May 2011 in Turkana County, north-western Kenya, tissue samples were collected from goats suspected of having died of peste des petits ruminant (PPR) disease, an acute viral disease of small ruminants. The samples were processed and tested by reverse transcriptase PCR for the presence of PPR viral RNA. The positive samples were sequenced and identified as belonging to peste des petits ruminants virus (PPRV) lineage III. Full-genome analysis of one of the positive samples revealed that the virus causing disease in Kenya in 2011 was 95.7% identical to the full genome of a virus isolated in Uganda in 2012 and that a segment of the viral fusion gene was 100% identical

to that of a virus circulating in Tanzania in 2013. These data strongly indicate transboundary movement of lineage III viruses between Eastern Africa countries and have significant implications for surveillance and control of this important disease as it moves southwards in Africa.

Current status and phenotypic characteristics of Bulgarian poultry genetic resources

Teneva, A., Gerzilov, V., Lalev, M., Lukanov, H., Mincheva, N., Oblakova, M., Petrov, P., Hristakieva, P., Dimitrova, I., ***Periasamy, K.***

Animal Genetic Resources (2015) 56 : 19-27

Poultry biodiversity conservation is a great challenge for many countries. Within the last several years, the number of endangered local breeds has increased, leading to a considerable loss of genetic resources. A similar trend was observed among the poultry breeds, including chicken, local turkey and goose breeds/lines established in Bulgaria, part of which is definitely lost. Currently these breeds/lines are at risk and/or threatened with extinction. The information obtained by phenotypic characterization of these breeds is the first step for planning the management of poultry genetic resources through setting up improved selection schemes and conservation strategies. In this paper, we reviewed the current state of knowledge regarding the morphological and phenotypic diversity of local poultry breeds and some old productive poultry lines in Bulgaria.

Environmental factors and dam characteristics associated with insulin sensitivity and insulin secretion in newborn Holstein calves

Kamal, M.M., Van Eetvelde, M., Bogaert, H., Hostens, M., Vandaele, L., ***Shamsuddin, M.****, Opsomer, G.*

Animal (2015) 9: 1490-1499. doi: 10.1017/S1751731115000701

The objective of the present retrospective cohort study was to evaluate potential associations between environmental factors and dam characteristics, including level of milk production during gestation, and insulin traits in newborn Holstein calves. Birth weight and gestational age of the calves at delivery were determined. On the next day, heart girth, wither height and diagonal length of both the calves and their dams were measured. Parity, body condition score and age at calving were recorded for all dams. For the cows, days open before last gestation, lactation length (LL), length of dry period (DP) and calving interval were also calculated. The magnitude and shape of the lactation curve both quantified using the MilkBot model based on monthly milk weights, were used to calculate the amount of milk produced during gestation. Using the same procedure, cumulative milk production from conception to drying off (MGEST) was calculated. A blood sample was collected from all calves (n=481; 169 born to heifers and 312 born to cows) at least 5 h after a milk meal on day 3 of life to measure basal glucose and insulin levels. In addition, an intravenous glucose-stimulated insulin secretion test was performed in a subset of the calves (n=316). After descriptive analysis, generalized linear mixed models were used to identify factors that were significantly associated with the major insulin traits (Insb, basal insulin level; QUICKI, quantitative insulin sensitivity check index; AIR, acute insulin response; DI, disposition index) of the newborn calves. The overall average birth weight of the calves was 42.7 ± 5.92 kg. The insulin traits were significantly associated with gender and season of birth when data of all calves were analyzed. In addition, the insulin traits in calves born to cows were significantly associated with MGEST, DP and LL. The Insb was estimated to be higher in calves born to the cows having passed a higher MGEST (P=0.076) and longer DP (P=0.034). The QUICKI was estimated to be lower in calves born to the cows having passed a higher MGEST (P=0.030) and longer DP (P=0.058). Moreover, the AIR (P=0.009) and DI (P=0.049) were estimated to be lower in male compared with female calves. Furthermore, the AIR (P=0.036) and DI (P=0.039) were estimated to be lower in calves born to cows having passed a longer LL. The decisive effects of MGEST, DP and LL in cows on the insulin traits of their calves may provide a basis for developing managerial interventions to improve metabolic health of the offspring.

Evaluation of ovsynch protocols for timed artificial insemination in water buffaloes in Bangladesh

Hoque, M. N., Talukder, A. K., Akter, M., ***Shamsuddin, M.***

Turk J Vet Anim Sci (2014) 38: 418-424. doi: 10.3906/vet-1302-35

A total of 65 water buffaloes (groups A, B, and C) at =>60 days postpartum with a body condition score (BCS) of =>2.5 were selected to evaluate ovsynch protocols for timed artificial insemination (TAI). The group A buffaloes (n = 25) were treated with a simple ovsynch protocol (GnRH - Day 7 - PGF2 alpha - Day 2 - GnRH -16 h - TAI). The group B buffaloes (n = 22) received PGF2 alpha treatment 12 days before the initiation of simple ovsynch (PGF2 alpha at Day -12 + simple ovsynch; modified ovsynch). The group C buffaloes (n = 18) were treated with