ONLINE JOURNAL OF ANIMAL AND FEED RESEARCH

An International Peer-Reviewed Journal which Publishes in Electronic Format

Volume 6, Issue 6, November 2016

Online J. Anim. Feed Res., 6 (6): November 25, 2016

Behzad Shokati
PhD student, Department of Agronomy and Plant Breeding, Faculty of Agriculture, University of Maragheh, IRAN (Email: behzad_sh1987@yahoo.com)
Agriculture: Environment, Nutritive value and utilization of feeds
Ekrem LAÇİN
PhD, Professor, Dept. Animal Science and Production, Facult. Vet. Med., Atatürk University, TURKEY (Email: ekremlacin@hotmail.com)
Nutrition - Non-Ruminants
Fazul Nabi Shar
PhD, Lecturer, Faculty of Veterinary & Animal Sciences, Lasbela University of Agriculture Water & Marine Sciences, Uthal Balochistan, Pakistan (Email: fazulnabishar@yahoo.com)
Clinical Veterinary Medicine, Poultry & Animal Husbandry
Fikret Çelebi
PhD, Prof., Dep. Physiology, Facult. Vet. Med., Atatürk University, Erzurum, TURKEY (Website; Email: fncelebi@atauni.edu.tr)
Physiology and Functional Biology of Systems
Firew Tegegn
Bahir Dar University, ETHIOPIA (Email: firewtegegne@yahoo.co.uk)
Animal Nutritionist
Ferdaus Mohd. Altaf Hossain
DVM, Sylhet Agricultural University, Bangladesh; not shah Jalal University of Science & Technology, BANGLADESH (Email: ferdaus.dps@sau.ac.bd)
Microbiology, Immunology, Poultry Science, and Public Health
Hamid Mohammadzadeh
PhD, Assistant Prof., Department of Animal Science, Faculty of Agriculture, University of Tabriz, IRAN (Email: hamidmhz@ag.iut.ac.ir)
Nutrition - Ruminants
Hazim Jabbar Al-Daraji
PhD, Professor, University of Baghdad, College of Agriculture, Abu-Ghraib, Baghdad, IRAQ (Email: prof.hazimaldaraji@yahoo.com)
Avian Reproduction and Physiology
John Cassius Moreki
PhD, Department of Animal Science and Production, Botswana College of Agriculture, Gaborone, BOTSWANA (Email: jcmoreki@gmail.com)
Nutrition - Non-Ruminants, Breeders, Livestock management
Manish Kumar
Prof. Dr., Society of Education (SOE), INDIA (Email: manishzoology06@gmail.com)
Pharmacology, Ethnomedicine
Megiste Taye
PhD, Seoul National University, SOUTH KOREA (Email: mengistietaye@yahoo.com)
Comparative genomics and bioinformatics
Mohammed Yousuf Kurtu
Associate Prof., Animal Sciences Department, Haramaya University, Dire-Dawa, ETHIOPIA (Email: mkurtu2002@yahoo.com)
Animal Science, Nutrition
Muhammad Saeed
PhD candidate, Northwest A&F University, Yangling, 712100, CHINA (Email: muhammad.saeed@nwsuaf.edu.cn)
Nutrition - Ruminants
Naser Maheri Sis
PhD, Assistant Prof., Dept. Anim. Sci., I.A.U.-Shabestar, IRAN (Website; Emails: maherisis@iaushab.ac.ir; nama1349@gmail.com)
Nutrition - Ruminants, Nutritive Value, Utilization of Feeds
Nilüfer SABUNCUOĞLU ÇOBAN
PhD, Professor, Department of Animal Science and Production, Faculty of Veterinary Medicine, Atatürk University, TURKEY (Website; Email: ncoban@atauni.edu.tr)
Animal Hygiene, Physiology, Animal Welfare
Ömer ÇOBAN
PhD, Professor, Department of Animal Science and Production, Atatürk University, TURKEY (Website; ocoban@atauni.edu.tr)
Nutrition - Ruminants
Paola Roncada
PhD, Associate Professor, Veterinary Pharmacology and Toxicology, University of Bologna, ITALY (Email: paola.roncada@unibo.it)
Pharmacokinetics
Raga Mohamed Elzaki Ali
PhD, Assistant Prof., Department of Rural Economics and Development,University of Gezira, SUDAN (Email: ragaelzaki@yahoo.co.uk)
Animal-feed interactions, Nutritive value
Saeid Chekani Azar
PhD, Dept. Anim. Sci., Facult. Vet. Med., Atatürk University, TURKEY (Emails: saeid.azar@atauni.edu.tr; schekani@gmail.com)
Physiology, Product Quality, Human Health and Well-Being,
Shahin Eghbal-Saeid
PhD, Assiociate Prof., Dep. Anim. Sci., I.A.U., Khorasgan (Isfahan), IRAN (Email: shahin.eghbal@khuisf.ac.ir)
Animal Genetics and Breeding
Shahin Hassanpour
Dept. Physiology, Facult. Vet. Med., I.A.U., Shabestar, IRAN (Email: shahin.hassanpour@yahoo.com)
Physiology and Functional Biology of Systems

Join OJAFR Team

As an international journal we are always striving to add diversity to our editorial board and operations staff. Applicants who have previous experience relevant to the position may be considered for more senior positions (Section Editor, SE) within OJAFR. All other members must begin as Deputy Section Editors (DSE) before progressing on to more senior roles. Editor and editorial board members do not receive any remuneration. These positions are voluntary.

If you are currently an undergraduate, M.Sc. or Ph.D. student at university and interested in working for OJAFR, please fill out the application form below. Once your filled application form is submitted, the board will review your credentials and notify you within a week of an opportunity to membership in editorial board.

If you are Ph.D., assistant, associate editors, distinguished professor, scholars or publisher of a reputed university, please rank the mentioned positions in order of your preference. Please send us a copy of your resume (CV) or your Live DNA or briefly discuss any leadership positions and other experiences you have had that are relevant to applied Animal and Feed Researches or publications. This includes courses you have taken, editing, publishing, web design, layout design, and event planning.

If you would like to represent the OJAFR at your university, join our volunteer staff today! OJAFR representatives assist students at their university to submit their work to the OJAFR. You can also, registered as a member of OJAFR for subsequent contacts by email and or invitation for a honorary reviewing articles.

Download OJAFR Application Form

Archive

Volume 6 (6); November 25, 2016

Review

Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review.

Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K.

Online J. Anim. Feed Res., 6(6): 113-124, 2016; pii: S222877011600016-6

Abstract

Domestic goat is the first ruminant animal domesticated in the South-west Asia about 10,500 years ago from its *Capra aegagrus* and *Capra falconeri* ancestors. The archaeological evidence links its origin to the region from the Taurus Mountains of Turkey to Pakistan. Molecular data extends the origin upto the Balkans and Carpathian Mountain regions of Romania, and China. Domestic goat followed both the Mediterranean and Danubian routes to disperse into Europe, and the Silk Road and the Khyber Pass to disperse across Asia. From the six haplogroups (A, B, C, D, F and G) of domestic goat globally identified, haplogroup A has a global coverage of 89% in Asia, 98% in Europe, and absolute predominance (100%) in South and Central America; however, the African region is still poorly characterized. The predominance of haplogroups A could be as a result of its earliest domestication. Haplogroup B, C, D, F and G are very rare or even absent (e.g. haplogroups D) in Europe. Haplogroup C is present with very low frequencies in Europe (2%), Asia (1%) and in Mongolia. MtDNA lineage B was detected in few African countries and few countries in Europe, Middle East and Asia. Overall, population expansion events of the wild progenitors of domestic goats were occurred much earlier than the events of domestication.

Keywords: *Capra aegagrus, Capra falconeri,* domestic goat, genetic variation, haplogroup.

PDF XML DOAJ

Research Paper

Impact of gender determination through vent sexing on Cobb-500 broiler performance and carcass yield.

Adnan Yousaf.

Online J. Anim. Feed Res., 6(6): 125-129, 2016; pii: S222877011600017-6

Abstract

The study was conducted order to explore the effect of separated sex rearing of broiler production performance. Total no of 24,000 Cobb-500 birds was reared for 42 days and divided in two group's A =12000 male and B= 12,000 females, according to their sex with 4 replication in each treatment where each replication had 3000 birds. They were provided the same feed and water adlibitum for the whole study. Initial body weight, temperature, humidity, feed intake, weekly body weight, mortality and final live weight of broiler were recorded. The study clearly shows significant differences (P< 0.05) in term of body weight gain and FCR of males chicks as compare to females. Male birds and also showed significantly (P< 0.05) better dressing percentage than female group. Male chicks had significantly (P< 0.05) larger chest circumference females birds. The cross with the fastest growth rate also had the highest mortality. Mortality percentage was high in male chicks 4% then female's chicks 2%. The most profitable choice will be dependent on whether whole birds or parts are marketed and the relative values of the parts. All these findings together revealed that in separate sex growing male chicken showed better performance in terms of more production.

Keywords: Cobb-500 broiler, Vent Sexing, Growth Performance, FCR, Carcass

PDF XML DOAJ

Research Paper

Impact of semen quality of Aseel chicken on induced molting.

Yousaf A, Rubab F, Shahnawaz R, Jamil T, Iqbal T, BiBi N, Haider I.

Online J. Anim. Feed Res., 6(6): 130-132, 2016; pii: S222877011600018-6

Abstract

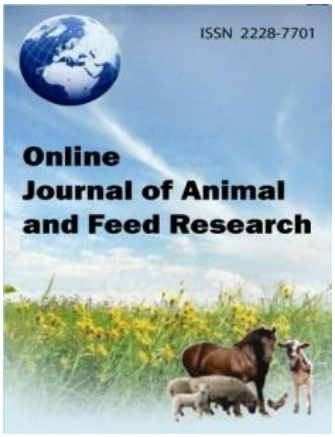
Indigenous chickens are an important source of animal proteins. Aseel is the very famous chicken breed of Pakistan which is facing the reproductive issues. Molting is economically used for the improvement of reproductive performance of male rosters. So the current experiment was designed to investigate the effect of molting on semen quality of indigenous Aseel chicken. Roosters (n=20) were divided into two groups, Group A molted (n=10) and group B non-molted (control) (n=10). Molting was performed through the method of feed restrictions. After the molting phase, semen was analyzed for six weeks. The semen quality was significantly (P< 0.05) improved in terms of volume (0.34±0.8 & 0.16±0.4 ml), mortality (73.7±2.5 & 63.5±2.2%), semen concentration (3.36±1.2 & 1.63±0.2 x 115/ml), morphological defect of sperm, (6.5±0.5 & 8.7±0.6 %) and livability of sperm (75±2.3 & 64±2.5%) were significant (P< 0.05) better for group A as group B. It was concluded that molting could be used for improvement of semen quality of indigenous Aseel chicken to cover the reproductive problems.

Key Words: Aseel chicks, Semen quality, Molting & NonMolting

PDF XML DOAJ

Archive

Online Journal of Animal and Feed Research



ISSN: 2228-7701

Frequency: Bimonthly

Current Issue: 2016, Vol: 6, Issue: 6 (November)

Publisher: SCIENCELINE

Online Journal of Animal and Feed Research is an international peer-reviewed journal, publishes the full text of original scientific researches, reviews, and case reports in all fields of animal and feed sciences, bimonthly and freely on the ınternet ...view full aims and scope

www.jwpr.science-line.com

» OJAFR indexed/covered by NLM/PubMed, CABI, CAS, AGRICOLA, DOAJ, Ulrich's™, GALE, ICV 2015 = 71.65), Worldcat, EZB, TOCs ...details

» Open access full-text articles is available beginning with Volume 1, Issue 1.

» Full texts and XML articles are available in ISC-RICeST and DOAJ.

» This journal is in compliance with Budapest Open Access Initiative and International Committee of Medical Journal Editors' Recommendations.

» We are member of WAME

» High visibility of articles over the internet.

Editorial Offices:
Atatürk University, Erzurum 25100, Turkey
University of Manitoba, Winnipeg, Manitoba R3T 2N2, Canada
University of Maragheh, East Azerbaijan, Maragheh 55136, Iran
Homepage: www.science-line.com
Phone: +98 914 420 7713 (Iran); +90 538 770 8824 (Turkey); +1 204 8982464 (Canada)
Emails:
administrator@science-line.com
saeid.azar@atauni.edu.tr

Online Journal of Animal and Feed Research

Volume 6, Issue 6: 113-124; Sep 25, 2016 ISSN 2228-7701

DOCUMENTING RADIOCARBON EVIDENCES, Y-CHROMOSOME, MITOCHONDRIAL DNA AND AUTOSOMAL MARKERS ON ORIGIN OF DOMESTICATION AND ROUTES OF GOAT GLOBAL DIVERGENCE: A Review

Getinet Mekuriaw TAREKEGN[1,4,5]✉, Wenguang ZHANG[2], Okeyo MWAI[3], Tadelle DESSIE[4], Appolinaire DJIKENG[3,5] and Kassahun TESFAYE[1]

[1]*Addis Ababa University, department of Microbial, Cellular and Molecular Biology, Addis Ababa, Ethiopia*
[2]*Inner Mongolia Agricultural University, Hohhot, China*
[3]*International Livestock Research Institute (ILRI), Nairobi, Kenya*
[4]*International Livestock Research Institute (ILRI), Addis Ababa, Ethiopia*
[5]*Biosciences eastern and central Africa (BecA), Nairobi, Kenya*
✉E-mail: yafetgetinet@gmail.com

ABSTRACT: Domestic goat is the first ruminant animal domesticated in the South-west Asia about 10,500 years ago from its *Capra aegagrus* and *Capra falconeri* ancestors. The archaeological evidence links its origin to the region from the Taurus Mountains of Turkey to Pakistan. Molecular data extends the origin upto the Balkans and Carpathian Mountain regions of Romania, and China. Domestic goat followed both the Mediterranean and Danubian routes to disperse into Europe, and the Silk Road and the Khyber Pass to disperse across Asia. From the six haplogroups (A, B, C, D, F and G) of domestic goat globally identified, haplogroup A has a global coverage of 89% in Asia, 98% in Europe, and absolute predominance (100%) in South and Central America; however, the African region is still poorly characterized. The predominance of haplogroups A could be as a result of its earliest domestication. Haplogroup B, C, D, F and G are very rare or even absent (e.g. haplogroups D) in Europe. Haplogroup C is present with very low frequencies in Europe (2%), Asia (1%) and in Mongolia. MtDNA lineage B was detected in few African countries and few countries in Europe, Middle East and Asia. Overall, population expansion events of the wild progenitors of domestic goats were occurred much earlier than the events of domestication.

Keywords: *Capra aegagrus, Capra falconeri,* domestic goat, genetic variation, haplogroup.

REVIEW ARTICLE
pii: S222877011600016-6
Received 22 Oct. 2016
Accepted 15 Nov. 2016

INTRODUCTION

Genetic studies of livestock populations focus on questions of domestication, within and among-breed diversity, breed history and adaptive variation (Lenstra et al., 2012). Goats are widely distributed throughout the world (Abdel-Aziz, 2010), and Asia and Africa account for about 81% of the total world goat populations (Garrine, 2007). Recent reports indicated that there are >1,000 goat breeds (Dong et al., 2012; FAO) comprising >868 million goats which are kept around the world (Nomura et al., 2012). The global distribution of goats have been influenced by various factors, which include; commercial trade, wars, or migration of people with their livestock (Clutton-Brock, 2000), exploratory movements of humans throughout the world (Porter, 1996). This was followed by a more rapid global spread as a result of inter continentals trade in livestock across the Mediterranean basin during the Phoenician, Greek and Roman periods (Pariset et al., 2009).

Given the on-going climate change phenomena many developing countries will have to exploit more marginal agricultural areas to goats are better suited (FAO, 2007; Pariset et al., 2009; Castel et al., 2010). To do this, well designed and appropriately implemented goat breeding programs are needed. Such breeding programs and schemes however do not exist in developing countries (Pariset et al., 2009). This might be because that information related to evolution, genetic diversity and utility of goats is very limited or poorly documented.

In order to design good breeding programs, better understanding of the genetic diversity and structures of the existing goat populations need to be understood. Various genetic and radiocarbon dating tools exist and can be used to investigate the origins, domestication and dispersion patterns of goats and other small ruminants (Luikart et al., 2006; Feng-Hua et al., 2015). With this respect, *Capra hircus* is to the growing list of domestic animals that

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

have been widely surveyed for mtDNA sequence variation (Luikart et al., 2001). Molecular tools provide stronger and increasingly cheaper and quicker means for characterization (Manceau et al., 1999). Hither to development of molecular tools and procedures phylogenetic relationships and the evolutionary history of *Capra* species were poorly distilled and understood (Pidancier et al., 2006). In addition, available reports so far have some discordance to each other.

This review therefore aims at assessing various reports and past studies on the origin and domestication of indigenous goats globally in order to lay a better understanding of indigenous goat genetic diversity.

ORIGIN AND SOURCE OF GOAT DOMESTICATION

Origin of goat domestication

Goat domestication was an integral part of the rise of agriculture (Fernández et al., 2006) and the adoption of agricultural practices throughout much of the world (Luikart et al., 2006). Goat, the *''poor man's cow''* (MacHugh et al., 2001), was certainly the first ruminants to be domesticated along with their close relative, sheep (Devendra and Mcleroy, 1982; Melinda et al., 2006). It is believed that the goats might have been domesticated in high, rocky mountain regions extending from the Taurus Mountains of Turkey into Pakistan (Epstein, 1971) about 10,500 years ago (Zeder and Hesse, 2000), and then spread quickly following patterns of human migration and trade (Luikart et al., 2001; Fernández et al., 2006). However, the exact location still remains uncertain (Sardina et al., 2006). Payne and Wilson (1999) reported south-west Asia (Iran and Iraq) (the most likely origin of the domestication of goats), south of Levant (Horwitz et al., 1999) (Figure 1) and Mehrgarh (Sultana et al., 2003) to be the ancient centers of goat domestication. The analysis of ancient goat DNA from Inner Mongolia region was closely genetically related to Chinese modern goats suggesting China is also considered the possible center of domestication particularly for sub-haplogroups B1 and B2 (Han et al., 2009). A recent study conducted on mtDNA hypervariable (HVI) region of ancient DNA indicated that Central Zagros has possibly played a key role for domestication of *C. hircus* (Mazdarani et al., 2014).

In contrast to this, the Balkans or Carpathian Mountain regions of Romania and Southern France were also suggested to be the origin of goats following a divergent lineage C and distinct lineage 3 found in Switzerland and Slovenia (Fernandez et al., 2006; Luikart et al., 2006; Pereira et al., 2009). However, the limited sample size casts doubts on these suggested regions to be the other centre of domestications of *C. hircus*. In addition, this is contrary to the hypothesis of domestication stated by Luikart et al. (2001) for lineage C, which is far from putative domestication, centers (Naderi et al., 2008) and questions the previous premises of domestication in general. Moreover, the presence of lineage A and C in South-east and Central Europe could be accompanied by the first Neolithic migration waves (Colli et al., 2015).

Sources of wild gene pool of goat domestication

Historical as well as archeological evidences indicate that the domestic goats might have been domesticated from two wild *Capris* (*C. aegagrus* and *C. falconeri*) species (Epstein, 1971), and from markhor (*C. falconeri*) in West Asia and the ibex in East Asia (Harris, 1962). However, it was earlier proposed that bezoar (*C. aegagrus*) is the most likely ancestor of domestic goats (Harris, 1962; and Zeuner, 1963). The MtDNA analysis strengthened this idea, hence a least four different strains of wild *Capra* might have been the source of the modern domestic goats (Sultana et al., 2003). The three species of the wild goat, bezoars (*C. aegagrus*), markhors (*C. falconeri*) and ibex (*C. ibex*), are closely related to the modern domestic goat (*C. hircus*). According to the studies of Mannen et al. (2001) and Sultana et al. (2003), the bezoar goat is the closest and likely be matriarchal ancestor of domestic goats. A recent extensive whole mitochondrial genome analysis confirmed the bezoar (*C. aegagrus*) is the most contributor for formation of the identified haplogroups of *C. hircus* (Colli et al., 2015). Sindh Ibex (*C. aegagrus blythi*) was also indicated as a possible contributor to the genetics of domestic goats (Sultana et al., 2003). Luikart et al. (2001) also concluded the presence of multiple maternal origins of goats, however, the monophyletic and paraphyletic trees (Naderi et al., 2008) obtained do not support multiple origins.

Luikart et al. (2001) indicated that three goat lineages arose from genetically discrete populations rather than from a single wild population and the possible multiple maternal lineages could have been originated via introgression rather than separate domestication events. This idea strengthens the paraphyletic tree nature rather than monophyletic tree. The three distinct lineages could be related to either (*i*) three separate maternal origins from genetically distinct populations, or (*ii*) one origin from an extremely large population containing three highly divergent lineages. However, all the domestic goat lineages (A, B, C and D) examined in Indian goat populations fall into a single monophyletic group that is distinct from all available wild goat sequences (Joshi et al., 2004), and the authors hypothesized that the contributing lineages found in India goats were derived from an unknown population that might have become rare or extinct.

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

There are still discordances between mtDNA and Y-chromosome phylogenies at which the intimations can be explained. According to Pidancier et al. (2006) the following remain unresolved: i) Amplification of nuclear-mtDNA copies; that is, laboratory artifacts and in most cases authors use many bone samples, for which nuclear amplification is less probable than mitochondrial amplification because of DNA quantity and quality ii) selection, iii) lineage sorting of ancestral polymorphisms or iv) horizontal transfer of genes which may result from hybridization and introgression in mammals. In relation with the latter hypothesis, the mtDNA control region and Y-chromosome analyses indicated the possible case of recent introgressive hybridization in *Capra* between *C. cylindricornis* individuals from Daghestan groups and Daghestan *C. aegagrus* rather than with its conspecifics (Pidancier et al., 2006).

However, in spite of some contradiction, the closest possible wild source of the present domestic goat is the bezoars (*C. aegagrus*). This is also supported by the following evidences: the branch length between the *cyt b* and mtDNA control region is shortest from domestic goats to the wild goat *C. aegagrus* (Manceau et al., 1999; Luikart et al., 2006). The mtDNA analysis revealed that the domestic goat originated from Bezoar goat (*C. aegagrus*) (Takada et al., 1997; Manceau et al., 1999; MacHugh and Bradley, 2001; Colli et al., 2015). These are consistent with the Y-chromosome and autosomal (microsatellite) marker based findings of Luikart et al. (2006) and Pidancier et al. (2006), as with those of morphological studies, archaeological data, and inferred geographical distribution of wild *Capra spp* (Smith, 1998). In addition to the above maternal and paternal origin evidences, the paleontological evidence also supports the *C. aegagrus* to be the closest ancestor of domestic goats (Porter, 1996). The second-closest taxon to domestic goats, based on the Y chromosome, is *C. falconeri,* which is a species separated from both domestic goats and *C. aegagrus* by two to three mutations (Luikart et al., 2006).

IDENTIFICATION OF LINEAGE, DISPERSION ROUTES AND GLOBAL COVERAGE OF DOMESTIC GOATS

Identification of lineages

There is no clear definition between lineage and haplogroup. While Luikart et al. (2001) and Sultana et al. (2003) put both alternatively. Nomura et al. (2013) indicated lineage is source of wild ancestor whereas haplogroup is common ancestor. For this paper, both terminologies have been used interchangeably. Bearing this in mind, various scholars have identified six lineages of domestic goat which dispersed throughout the world following various routes of dispersion at different times. Luikart et al. (2001) identified three lineages (A, B, C) by sequencing HVI. Sultana et al. (2003) revealed four lineages (A, B, C and D) by sequencing both *d*-loop and *cyt b* regions in Pakistan's goats. Joshi et al. (2004) revealed five lineages (A, B, C, D and E) in Indian goats. Naderi et al. (2007) identified six lineages (A, B, C, D, F, G) from sequencing of HVI and disproved existence of haplogroup E rather those haplotypes which were named by this haplogroup created sub-haplogroup B1 and B2 which were moved to North, East and South East Asia. Studies have also reported the presence of sub-haplogroups (Han et al., 2010, Nomural et al., 2013; Akis et al., 2014; Colli et al., 2015). The ancient DNA analysis indicated that goats from haplogroup B were detected in the Swiss Alps which were later replaced by haplogroup A and C (Schlumbaum et al., 2010). Chen et al. (2005) had also found four mitochondrial lineages (A, B, C and D) in Chinese goat breeds. Similarly, by amplifying HVI, Nomura et al. (2013) confirmed the presence of all previously identified lineages/haplogroups except lineage G. This could be because of the divergence regions of the later lineage only towards to South-west Asia and Europe, and it could be also because of their limited focus to South, East and South-east Asia. A recent and extensive study conducted on whole mitochondrial genome revealed various clades of haplogroups (A1-A7, B1, C1a, D1 and G) (Colli et al., 2015).

However, based on the microsatellite markers, the three lineages identified by Nomura et al. (2012) differ slightly from those reported by Luikart et al. (2001) particularly for the Asian goat populations. Nomura et al. (2012) investigated two different lineages, which dispersed to South and South-East Asian countries. However, these haplogroups were considered earlier as a lineage (Luikart et al., 2001). On the other hand, the two different lineages identified by Luikart et al. (2001) which spread to North (Mongolia) and East Asia regions were merged and reported as a lineage (Nomura et al., 2012). Besides, an additional lineage which was moved to South-East Asia (including Taiwan, Japan and Korea) was also identified. In general, wider wild origins/lines are found in Asia than other parts of the world, as a result the regional genetic diversity is also comparatively higher.

Dispersion routes and global coverage of domestic goat

Domestic goats had been diverged following various routes of divergence globally from its initial domestication areas. It had followed Mediterranean and Danubian routes to arrive in Europe and was aligned with the routes of Neolithic culture diffusion in the region (Fernández et al., 2006). Civilizations like Phoenicians, Greeks, Romans and Berbers probably introduced new species of animals and new breeds of livestock in South-west Europe

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

following the sea route (Pariset et al., 2009). The archaeological data and radio carbon dates on bones indicated, in Western Europe, goats had arrived earlier through Mediterranean route compared with the Danubian route (Zilháo, 2001; Voruz, 1999; Guilaine, 2003). In Asia, dispersion of the three types of lineages from the domestication centre followed two main routes (the Silk Road and the Khyber Pass) (Devendra and Nozawa, 1976). The latter route was one of the known Silk Roads in the world found between Afghanistan and Pakistan and served for the migration of the Nubian goat type, which had descended from the Savannah type, to Indian subcontinent. Similarly, the former route to Asia served for expansion of both Bezoar-type and Savannah-type goat (Devendra and Nozawa, 1976).

Based on the microsatellite evidence, the East Asian cluster corresponded morphologically to the Bezoar type and the Mongolian cluster corresponded to the Savannah type (Nomura et al., 2012). Taiwan goats are direct descendants of Chinese indigenous goats during the seventeen century by immigrants, and the Savannah type reached back to Mongolia from the Indian subcontinent and China (Nomura et al., 2012). The genetic subdivisions of East Asian goats were consistent with the migration history of goats and also with morphological and geographical classifications (Nomura et al., 2012). Amills et al. (2008) tried to fairly address wide geographical distribution of the populations and reported the existence of genetic variation at continental level despite smaller sample sizes used in many of the study populations. The haplogroups of the wild bezoar did not decline in population size since the Early Holocene suggesting the bezoar populations were not modified so much by humans (Naderi et al., 2008).

Despite the inherent and unavoidable bias of sampling, haplogroup A is the earliest (~10,000 YA) expanded lineage and is known to occur throughout the world including Africa and parts of Asia, haplogroup F is linked to Europe (particularly in Sicily) and haplogroup D limited to Asia (Luikart et al., 2001; Naderi et al., 2007, 2008; Pereira et al., 2005, 2009; Han et al., 2010; Hughes et al., 2012). The global coverage of haplogroup A is 89% in Asia, and 98% in Europe (Pereira et al., 2005). However, though Pereira (*ibid*) reported 100% pre-dominance of haplogroup A in Middle East and Africa, Naderi et al. (2007) detected Haplogroup G (in Egypt, Saudi Arabia Turkey and Iran), haplogroup B in Namibia and South Africa together with haplogroup A. This haplogroup was also detected in Canary Islands and southern and eastern Asian countries: Pakistan, India, Malaysia, China and Mongolia (Amills et al., 2004; Pereira et al., 2005; Luikart et al., 2006; Han et al., 2010; Nomura et al., 2013). The ancient DNA showed that goats from sub-haplogroup B1 were present in alpine areas of Switzerland in 4500 YA (Schlumbaum et al., 2010); and this haplogroup is the result of a second domestication event (Luikart et al., 2001) and represents a relatively recent expansion (Pereira et al., 2005). Haplogroups A and C show conspicuous rapid expansion and haplogroups B and G show slow expansions; population size of haplogroup F has been slowly declined (Nomura et al., 2013).

Recent studies have also indicated the presence of haplogroup A and G in Kenya (Kibegwa et al., 2015) and Ethiopia in which 89% of the haplotpyes from the total 231 haplotypes detected belongs to haplogroup A (Getinet, 2016). Akis et al. (2014, 2016) also reported the presence of haplogroups A, B1, C, D and G in Anatolia region. There is an absolute predominance of lineage A in the Atlantic archipelagos and SCA (Amills et al., 2008). Lineages B, C, D, F and G are absent in SCA goats (Amills et al., 2008), and are also very rare or even absent in Europe (haplogroup D) (Luikart et al., 2001; Joshi et al., 2004; Amills et al., 2004; Azor et al., 2005; Pereira et al. 2005; Naderi et al. 2007). The ancient DNA showed existence of Haplogroup B in Swiss Alps in former times (Schlumbaum et al., 2010). In general, the contribution of haplogroup B, D, F and G in domestic goats is very low (7.69%) (Naderi et al., 2008).

Though the origin and evolution of haplogroup C still remains controversial, it is present with very low frequencies in Europe (<5%) (for example, Iberian Peninsula, Slovenia and Switzerland), Asia (1%) and in Mongolia which represent recent secondary expansion (Luikart et al., 2001; Pereira et al., 2005). It is also found in Near Eastern populations except in Pakistan (Luikart et al., 2001; Sultana et al., 2003), and recently in Corsica (Hughes et al., 2012) and Anatolia (Akis et al., 2014). This dispersion may suggest older origin (Pereira et al., 2005); however, the sampling employed was less comprehensive. Fernández et al. (2006) also explained both lineages A and C coexist in Europe, and were represented among the first populations of domestic goats that entered into Western Europe. This coexistence of lineages A and C in southwestern Europe, since as early as the beginning of the Neolithic, may have resulted from either the succession of different waves of goats bearing different haplotypes between the first Impressa (7,700–7,500 B.P.) and Cardial (7,500–7,000 B.P.) time periods, or from one wave bearing all of the diversity as early as the first Impressa steps (Fernández et al., 2006), which is the first arrival of goats to this region. This finding is consistent with the first waves of arrival of Neolithic farmers (7,500YA) through the Mediterranean route.

Unlike the absence of a strong phylogeographic structure in the Spanish peninsula, European, African and Asian populations, the ancestral Canarias goat mitochondrial haplotypes are still highly ubiquitous in some of the breeds providing a recognizable population structure (Amills et al., 2004). On the other hand, from the historical perspective Iberian livestock were extensively transported from South of Spain and Portugal to America, and

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

similarly from Portugal, Africa and Canary Islands to Cape Verde by Portuguese sailors during the 15th century (Rodero et al., 1992). The similar haplotypes obtained in Cape Verde with Canary Islands (Amills et al., 2008) can be a very good witness despite the limited contribution of the Atlantic archipelagos to the large-scale population process (Rodero et al., 1992).

However, the mtDNA analysis indicated that the initial goats (that is, variant B) arrived in the Canary Islands by the first settlers 3000YA (Amills et al., 2004). Capote et al. (2004) had also reported the first inhabitants of the Canary Islands settled at the archipelago carrying a small number of domestic animals in 2200YA. Despite the time variation seen in these reports, the first settlers of the Islands are believed to be the Berber people of Morocco though there is no clear evidence till now. Especially the *caprine* breeds of Canary Islands are likely to have North African origin, and were isolated for 1700 years until Spanish colonization but had an important influence in the constitution of the American mosaic of breeds and breed types (Capote et al., 2004). It is also reported that the majority of the Canarian domestic animals prior to the colonization are of virtually unknown origin but assumed to most probably be from the African continent, for instance, the three types of Canarian Caprines (Fresno et al., 1992) look like the African relatives. However, mtDNA analysis of Pereira et al. (2009) could not substantiate this assumption of gene flow into the Canary Islands from the Maghreb (North West African countries except Egypt) rather the Y-chromosome analysis. The latter analysis revealed presence of three main haplotypes (Pereira et al., 2009) with the most frequent haplotype Y2 reaching 76.09% frequency in Morocco. Haplotypes Y1A and Y1B occur at 19.57% and 4.35%, respectively, which is consistent with findings of Amills et al. (2004) though it contradicts the mtDNA analysis of Pereira et al. (2009). In support of the mtDNA analysis, the plot of pair wise F_{ST} genetic distances indicates that the Canary goats are closer to Middle East goat than North Africa goat (Pereira et al., 2009) suggesting the Canary goats diverged from the centre of origin via Mediterranean Sea instead of terrestrial routes. This idea can be strengthened by the presence of strong phylogeographic relationships among Canary island populations compared with other regions (Amills et al., 2004).

In general, despite this discordance of inference between the mtDNA and Y-chromosome, male flocks from Asia might have moved via Morocco to Canary Islands. But, still it does not necessary mean the origin of Canarian goat population is only from Africa. The maternal origin has also strong implication about the other origin of Canarian goats to be directly from the center of origin via Mediterranean Sea.

The presence of variant A found in some of the breeds in the Canary Islands (Amills et a., 2004) might be because of the introgression between the native goats (variant B) with other European and African breeds around 500-600YA following the Spanish colonization (Capote et al., 1999). Y-chromosome analysis also supported the presence of bidirectional gene flow between Africa and southern Iberia (Pereira et al., 2009). However, there is no genetic footprint of Iberian goats rather that of Canarias's in South and Central American (SCA). It is argued that the Iberian populations had a poor phylogeographic structure at the time of the American colonization, and the Canarian goats contributed to the foundation of the current genetic pool of SCA goat breeds (two Andean populations of Chile and Argentina have descended from Canarian goats) (Amills et al., 2008). Morphological similarity between Canarian and American goats is the other supporting evidence about the contribution of the Canarian goats to their American counterparts (Capote et al., 2004). In connection with this, there is a high diversity of mtDNA lineages in Moroccan populations with 54 different (all belong to haplogroup A) haplotypes (Pereira et al., 2009) which are similar in number and type of South and Central American goat haplotypes (Amills et al., 2008). Besides, Pereira et al. (2009) did not report the existence of this variant B in Morocco. However, there is no concrete evidence about either the transportation of goats from the Canary Islands to SCA at a considerable scale or rapidly disseminated in SCA with one or few introduction events (Amills et al., 2008).

Still the point which needs to be clear is that if variant B is found in Canary Islands and Morocco, and all haplotypes found in SCA that belong to lineage A are descendants of the Canary Islands, why variant B is not found in SCA? This could possibly be due to the limited coverage of the study populations in SCA and small sample size used and/or might be because of the absence of examining the divergence from paternal perspective that could probably indicate the connection it would have had with Africa. The other possible reasons might be variant B could have been extinct in SCA or it could have been only lineages A which was transported to SCA. On the other hand, the regional analysis of genetic diversity suggests nucleotide and haplotype diversities are particularly reduced into two Andean populations located in Chile and Argentina compared to Cape Verdean goats implying these two populations descended from Canarian goats (Amills et al., 2008).

Despite the limited molecular data report, the archaeological data indicate that domestic goats were first introduced into the African continent through the i) Mediterranean coast ii) Red Sea Hills iii) overland via the Sinai Peninsula and Nile Delta in 7,000YA (Hassan, 2000; Gifford-Gonzalez and Hanotte, 2011) (Figure1). Similarly, the archaeological data suggested that goats and sheep spread rapidly from the Near East into the Central Sahara and Ethiopian highlands between 6,500 BP and 5,000 BP (Clutton-Brock, 2000) and later expanded to south because of, besides the tsetse barrier, the increasing aridity of North Africa (Smith, 1992). Radiocarbon dates of goat and

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

sheep bones from various archaeological sites along the North African coast (dated 6,000 BP at Grotte Capeletti in Algeria or 6,800 BP at Haua Fteah in Cyrenaica, Libya) are similar to those excavated in the eastern Sahara, suggesting a very rapid dispersal of small ruminants from Southwest Asia into North Africa between 7,000 BP and 6,000 BP (Hassan, 2000). In contrast to this, mtDNA diversity (lineage A) suggested recent time of expansion (<3,000YA) in the African continent via south of Saharan desert (Luikart et al., 2006). The route of introduction into the African region is believed either through the present-day Sahara desert by overland diffusion or along the Mediterranean coast (Hassan, 2000) (Figure 2). The mtDNA and Y-chromosome analyses strengthened the use of both Mediterranean route in the east-to-west movement of domestic goats and the terrestrial transport along the North African continent (Pereira et al., 2009).

However, there is no indication of Median joining network on the movement of domestic goat from Egypt to North Africa towards Morocco, rather this route might be extended from Egypt directly to Ethiopia following the Nile Valley. The absence of Egypt route to North-west Africa seems contradictory with the archeological findings. In general, Figure 2 summarizes the global dispersion routes of *C.hircus* from center of domestication areas.

Figure 1 - Origin and divergence of goat into Africa:based on archaeological information (Gifford-Gonzalez and Hanotte, 2011).

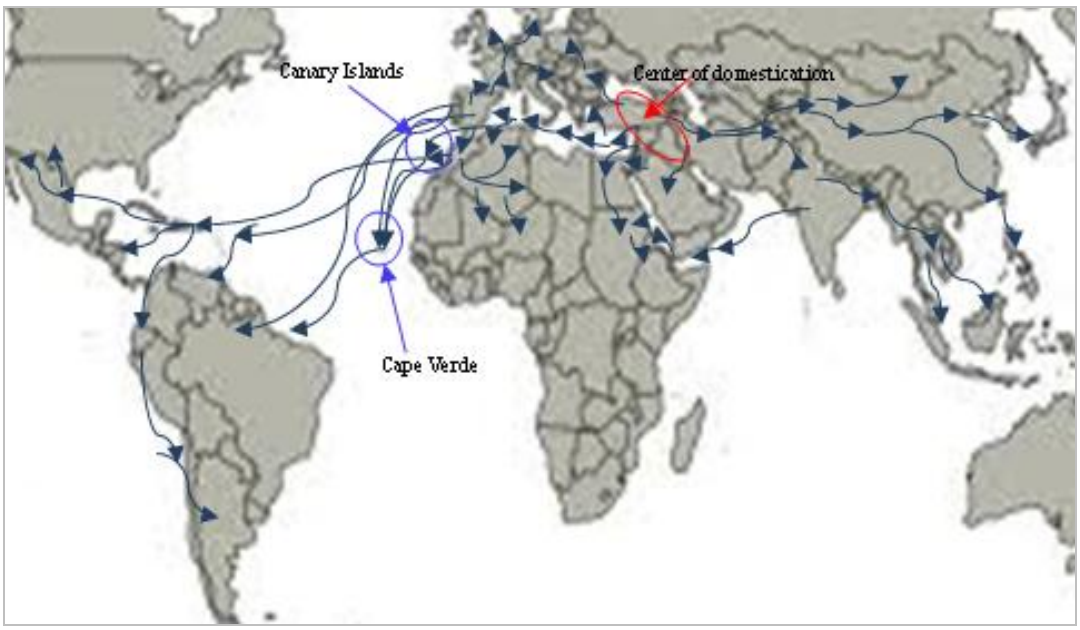


Figure 2 - Summary of global dispersion routes of domestic goat: inferred from various reported discussed in the text.

Divergence of *Capra hircus* haplogroups: the time and expansion

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

More fossils being exposed in regions of geological activity (Pagani et al., 2012) and as a consequence, do not always point to the real divergence time. It is because of the fact that the first stratigraphic appearance of taxa in the fossil record may be subject to sporadic sedimentary disruptions due to erosion or lack of sedimentation during regression and/or irregular sedimentary processes (Nomura et al., 2013). In addition, only very few paleontological data are available for species of the genus *Capra* because their preferred mountainous habitats are not favorable for fossil preservation (Simpson, 1945). Instead, scholars have employed various molecular techniques to be able to know time of divergence of organisms since last decade.

Molecular techniques have been used to date divergence of the wild progenitors (Nomura et al., 2013). Sequence divergence (SD), the estimated divergence times between the mtDNA lineages A and D for goats have been estimated to be from 260,483-371,052YA (Sultana et al., 2003). Given the time variation, the estimated times for most recent common ancestors (MRCAs) of each haplogroup (32,300 to 90,950 YA) and the times of nodes with star-like branching pattern (17,210 and 90,950YA) can be indicative for prior expansion of goats before domestication (10,000YA) (Zeder and Hesse, 2000; Nomura et al., 2013). Lineage A is believed to have been expanded initially about 10,000YA, and then the less abundant lineages may have expanded about 6,000 to 6,110YA (lineage C), and 2,130 -2,600YA (Asian lineage B) (Luikart et al., 2001 and 2006). However, Fernández et al. (2006) indicated the third event of domestication (haplogroup C) dated 7,500YA in Southern France. The latter is however inconsistent with the previous premises in both place of origin and time of domestication.

For Indian goat populations, the MRCA calibrated against the fossil record was 103,000-143,000 or 201,000-280,000YA (Joshi et al., 2004) which agrees with the study of Luikart et al. (2001) particularly for lineage A. For the goat populations in Pakistan, the new lineage D revealed high sequence diversity (SD) from lineage A and may be the oldest branch under domestication, while lineages B and C showed lower SD and might have been domesticated during an advanced stage of the domestication process (Sultana et al., 2003). Apart from this, the four lineages (A, B, C, and D) of *Cyt b* indicated that the estimated MRCA of the domestic goat lineages was 427,006 to 597,806YA (Sultana et al., 2003); however, lineage D diverged from lineage A more recently (265,038-371,052YA). This finding is strengthened by the *d*-loop average SD value estimation (4.59%) of the four lineages (A, B, C and D) and 2.8% of lineages A and D, which is the most recent divergence (Sultana et al., 2003). However, this seems too early compared to the mtDNA HVI analysis of Joshi et al. (2004) that showed the three lineages (A, B and C) had diverged over 200,000YA. The mt-lineages exhibiting lower (higher) SD could have been captured and adopted at later (earlier) periods of domestication (Sultana et al., 2003). The ancient divergence time and the different geographical localizations of the lineages suggest the likelihood of either multiple domestication events or introgression of additional lineages after the original domestication (Joshi et al., 2004).

GOAT POPULATION DIFFERENTIATION AND GENE FLOW

Despite the huge global goat population size, the genetic diversity of goats as revealed by maternal mitochondrial and nuclear (microsatellite) DNA marker studies contemporary domestic goats (*C. hircus*) show far weaker intercontinental population structuring than other livestock species (Luikart et al., 2001). The highest proportion (90%) of the current domestic goat mtDNA haplotypes belongs to haplogroup A which could not have been changed dramatically in the expanding goat population since domestication (Naderi et al., 2008). This suggests that haplogroup A goats, may have been dispersed more often, more successfully and more extensively than other livestock (Luikart et al., 2001; Fernández et al., 2006; Nomura et al., 2012). The genetic distance between the Portuguese goat breeds is not positively correlated with the geographical distribution of these breeds (Pereira et al., 2005). This therefore is a very good example for the above argument from a micro-geography perspective. Geographically most distant breeds (Algarvia and Bravia) show the lowest genetic distance (F_{ST}=0.020), while the most divergent breeds are Serpentina and Charnequeira (F_{ST}=0.083) with a closer geographical distribution. In addition, the genetic variation estimated by MNA and AR (allelic richness) within-country populations of Asian goats was lower than that of European breeds (Nomura et al., 2012). The average F_{ST} (0.13, 0.07) estimates of Asia (Nomura et al., 2012) and European goat breeds (Cañón et al., 2006) strengthened this notion. This lack of relationship between genetic distances and microgeography can be interpreted to mean and to have resulted from complex and diverse female stocks in the origins of Portuguese breeds and/or extensive successive introduction of extraneous female individuals (Pereira et al., 2005).

From the macrogeography perspective, like horse (Equus caballus) (Kim et al., 1999), there is low mtDNA population structure in domestic goats compared to cattle (Luikart et al., 2001; MacHugh and Bradley, 2001). Only about 10% of the total mtDNA variation in domestic goats (*C. hircus*) was due to differences among continents (Luikart et al., 2006). It is far lower than estimates of 54–80% intercontinental variation in cattle for the same mtDNA region (HVI). Investigation of negative values, the converse is also true for the positive values, in all bezoars

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

made in Tajima's D (Tajima, 1989) estimates indicate the presence of population expansion events of bezoars that are closer to domestic goat since recently (Nomura et al., 2013). These all finding imply that geographical location has little relevance to the mtDNA type that a particular animal possesses or the absence of clear tie between the genetic make-up of goats and geography rather at within-population level (MacHugh and Bradley, 2001; Amills et al., 2008). This might also be due to the extensive intercontinental dispersion and high gene flow of goats compared with cattle (Luikart et al., 2006). A relative lack of breed standardization, herdbook breeding, parentage control and rigorous management might have facilitated gene flow between geographically nearby breeds (Cañón et al., 2006).

Moreover, the founder effect has also contributed to the decreased genetic diversity. For instance, upon the conquest and colonization of the New World by the Spanish and Portuguese, goats and other livestock species were massively transported through the Atlantic Ocean for food in exploratory and military expeditions (Rodero et al., 1992). In Brazil, goats were first introduced by Portuguese settlers during the beginning of 16th century (Machado et al., 2000). This depicts the current gene pool of South and Central America goats was founded in the last five centuries (Amills et al., 2008).Similarly, Mongolian goat populations have the lowest genetic distance in contrary to the geographical distances (Takahashi et al., 2008; Nomura et al., 2012). However, Pariset et al. (2009) revealed significant and positively correlated genetic and geographic distances.

On the other side, the within population variation estimated values are the other indications of the weak structuring of goat breeds that support the utilization of domestic goats as a portable food resource accompanying human migratory movements (Amills et al., 2008). Hence, around 69% of the genetic variation corresponds to the within-population component for South and Central American goats and almost similar to Iberian and European breeds, but haplotype diversities were somewhat lower (Amills et al., 2008). Apparently, almost similar estimates (78.7% and 77%) of within breed genetic variations were reported in European, African and Asian goat mitochondrial sequences (Luikart et al., 2001; and Naderi et al., 2007). Still this estimation is higher (83%) for Indian goats (Joshi et al., 2004). From the AMOVA analysis 96.65% of variation occurs within breeds, the remaining 3.35% from among breed variation, for Portuguese goat populations (Pereira et al., 2005). However, for the latter report, comparatively high within breed diversity found in all breeds and the sharing of some haplotypes with other foreign breeds is consistent with the repeated introduction of exotic animals into the Portuguese gene pool in last centuries (Pereira et al., 2005). All the above estimates are very high compared with the within breed (45%) and amongst-group components of the total variation of cattle (Luikart et al., 2001).

Despite the above reports which revealed the weak phylogeographic structure in goat compared to other domestic animals, there is significant mtDNA variation among Indian goat breeds (Joshi et al., 2004). However, this study was limited only to mtDNA and did not include autosomal and/or Y-chromosomal markers, and hence was unable to show the overall gene flow from paternal perspective.

CONCLUSION

With respect to the global coverage of the study of origin of goat, Africa has been poorly addressed compared to other parts of the world. Maternal origins of domestic goats have been checked in African countries that include Algeria, Egypt, Libya, Morocco, Nigeria, Senegal, Tunisia, Mozambique, Namibia, South Africa, Zimbabwe, Kenya and Ethiopia (Luikart et al., 2001; Naderi et al., 2007; Awotunde et al., 2015; Kibegwa et al., 2015; Getinet, 2016). With the exception of Ethiopia, the number of animals included the studies ranges from one to 60 in those countries listed. Recently, large number of animals (N=309) from 13 goat populations were employed to check maternal origin and populations dynamics of Ethiopian indigenous goat populations by the first author of this paper (Getinet, 2016). This calls for more detailed investigation in Africa with the view to elaborate genetic lineages and patterns of dispersions. Population size, sample size and sampling in general highly determine the strength of evidence generated about source of origin of domestication and divergence of species. The report by Nomura et al. (2013) can be a very good indication of how sampling matters in this regard. Sampling of haplogroups focused on haplogroups A and B1 while apparently overlooking others. As a consequence, contribution of haplogroups other than haplogroup A might have been underestimated (MacHugh and Bradley, 2001). Haplogroup A takes the lion share of the present global goat genetic divergence studies. Similarly, some works conducted earlier, like Luikart et al. (2001, 2006), had limitation of small sample size and the wild samples were from zoo where hybridization is likely and attribution can be dubious. With respect to sample size, Luikart et al. (2006) confirmed that samples from additional wild populations of *C. falconeri,* the second closest specie next to *C .aegagrus* to domestic goat, are needed to clarify the possibility that *C. falconeri* gave rise to Cashmere breeds or to other domestic goats from eastern Asia. Despite the wide area coverage, Amills et al. (2008) had also used small sample size.

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

On the other hand, inferences about the location of origin from a single type of molecular data (diversity levels) can be made with caution because they can either be unsatisfactory or even potentially misleading. It is therefore imperative to triangulate information against other analyses, such as the geographic distribution of lineages and historical or temporal distributions (for example, using ancient DNA) (Luikart et al., 2006). There are good starts, but they are few in number, on the inclusion of ancient DNA for the study of maternal origins of domestic goats (Luikart et al., 2006; Han et al., 2010; Schlumbaum et al., 2010; Hughes et al., 2012, Mazdarani et al., 2014; Akis et al., 2016). In addition, despite the highly informative nature of mtDNA data for the study of origin and divergence of species, it is essential to complement it with inferences made from Y-chromosome since the latter is free of recombination (MacHugh and Bradley, 2001). The effort made in combining mtDNA with Y-chromosome in the study of origin and divergence of goat populations is very much limited.

Luikart et al. (2006) had also suggested that ancient DNA sequencing in combination with extensive sampling of contemporary local breeds provides exciting potential as a method of inferring the origins and diffusion of domestic taxa, especially to combine archaeozoological and ancient DNA studies to assess the pattern of diffusion of DNA lineages through time and space. Because of the variation in fruition of vitality of the two DNA types it is highly recommended to combine the nuclear DNA with mtDNA for the study of population structure.

Acknowledgement

We would like to acknowledge Workneh Ayalew for his support in reviewing the paper before submission.

Competing interest

The authors declared that there is no competing interest.

REFERENCES

Abdel Aziz M (2010). Present status of the world goat populations and their productivity. Lohmann information. 45(2): 42-52.

Akis I, Oztabak K, Mengi A, Un C (2014). Mitochondrial DNA diversity of Anatolian indigenous domestic goats. J. Anim. Breed. Genet. 131: 487–495.

Akis I, Onar V, Toker N, Belli O, Pazvant G and Oztabak K (2016). Ancient DNA analysis of Anatolian goat remains excavated from a Urartian Castle in eastern Turkey. Int. J. Osteoarchaeol. 26: 246–254

Amills M, Capote J, Toma`s A, Kelly L, Obexer-Ruff G, Angiolillo A, Sanchez A (2004). Strong phylogeographic relationships among three goat breeds from the Canary Islands. J. Dairy Res. 71:257–262.

Amills M, Ramı´rez O, Toma`s A, Badaoui B, Marmi J, Acosta J, Sa`nchez A, Capote J (2008). Mitochondrial DNA diversity and origins of South and Central American goats Animal Genetics. 40:315–322.

Awotunde EO, Bemji MN, Olowofeso O, James IJ, Ajayi OO, Adebambo AO (2015). Mitochondrial DNA sequence analyses and phylogenetic relationships among two Nigerian goat breeds and the South African Kalahari Red. Anim. Biotechnol. 26:180-187.

Azor PJ, Monteagudo LV, Luque M, Tejedor MT, Rodero E, Sierra I, Herrera M, Rodero A, Arruga MV (2005). Phylogenetic relationships among Spanish goats breed. Anim. Genet. 36:423–425.

Cañón J, García D, García-Atance MA, Obexer-Ruff G, Lenstra JA, Ajmone-Marsan P, Dunner S (2006). Geographical partitioning of goat diversity in Europe and the Middle East. Anim. Genet. 37(4):327-334.

Capote J, Fresno MR, Álvarez S (1999). The Canarian goat breeds: characterization and present situation. Ovis. 62:11–22.

Capote J, Tejera A, Amills M, Argüello A, Fresno M, López JL (2004). Influencia histórica y actual de los genotipos canarios en la población caprina Americana. Agri. 35: 49-60.

Castel JM, Ruiz FA, Mena Y, Sánchez-Rodríguez M (2010). Present situation and future perspectives for goat production systems in Spain. J. Small Ruminant Res. 89:207–210.

Chen SY, Su YH, Wu SF, Sha T, Zhang YP (2005). Mitochondrial diversity and phylogeographic structure of Chinese domestic goats. Molecular Phylogenetics and Evolution. 37:804–814.

Clutton-Brock J (2000). Cattle, sheep, and goats south of the Sahara: an archaezoological perspective. In: Blench RM, MacDonald KC, editors. The origins and development of African livestock: archaeology, genetics, linguistics and ethnography. London: UCL Press. Pp. 30-37.

Colli L, Lancioni H, Cardinali I, Olivieri A, Capodiferro MR, Pellecchia M, RzepusM, Zamani W, Naderi S, Gandini F, Vahidi SMF, AghaS, Randi E, Battaglia V, Sardina MT, Portolano B, Rezaei HR, Lymberakis P, Boyer F, Coissac E, Pompanon F, Taberlet P, Marsan PA and Achilli A, 2015. Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. BMC Genomics. 16:1115.

Devendra C, McLeroy GB (1982). Goat and sheep production in the tropics. Intermediate tropical agriculture series. Longman Group, U.K. Pp. 271.

Devendra C, Nozawa K (1976). Goat in South East Asia – their status and production. Zeitschrift fu¨r Tierzu¨chtung und Zu¨chtungsbiologie: Organ der Reichsarbeitsgemeinschaft Tierzucht im Forschungsdienst. 93:101–20.

Dong Y, Xie M, Jiang Y, Xiao N, Du X, Zhang W, Tosser-Klopp G, et al (2012). Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (Capra hircus). Nature Biotechnol. 31:135–141.

Epstein H (1971). The Origins of the Domestic Animals of Africa. Africana Publishing Corporation, London. 143: 1–30.

FAO (Food and Agriculture Organization of the United Nations) (2007). The State of the World's Animal Genetic Resources for Food and Agriculture, edited by Barbara Rischkowsky and Dafydd Pilling. Rome, Italy.

Feng-Hua L, Wei-Feng P, Ji Y, Yong-Xin Z, Wen-Rong L, Ming-Jun L (2015). Mitogenomic meta-analysis identifies two phases of migration in the history of eastern Eurasian sheep. Mol. Biol. Evol. doi: 10.1093/molbev/msv139

Ferná ndez H, Hughes S, Vigne JD, Helmer D, Hodgins G, Miquel C, Hänni C, Luikart G, Taberlet P (2006). Divergent mtDNA lineages of goats in an Early Neolithic site, far from the initial domestication areas. PNAS. 103:42:15375–15379.

Fresno M, Capote JF, Camacho ME, Darmanin N, Delgado JV (1992). The Canary Islands breeds: Past, present and future. Arch. Zootec. 41:513-518.

Garrine CMLP (2007). Genetic characterization of indigenous goat populations of Mozambique. MSc thesis. Department of Production Animal studies in Faculty of Veterinary Science, University of Pretoria.

Getinet MT (2016). Molecular characterization of Ethiopian indigenous goat populations: genetic diversity and structure, demographic dynamics and assessment of the kisspeptin gene polymorphism. Doctoral dissertation, Addis Ababa University, Ethiopia.

Gifford-Gonzalez D, Hanotte O (2011). Domesticating animals in Africa: Implications of genetic and archaeological findings. J. World Prehist. 24:1–23

Guilaine J (2003). De la Vague á la Tombe. La Conquéte Néolithique de la Méditerranée Le Seuil, Paris. ISBN: 2-02-055388-0; 375PHan L, Yu HX, Cai DW, Shi HL, Zhu H, Zhou H, 2010. Mitochondrial DNA analysis provides new insights into the origin of the Chinese domestic goat. J. Small Ruminant Res. 90: 41-46.

Harris DR (1962). The distribution and ancestry of the domestic goat. Proc. Linn. Soc. London. 173:79.

Hassan FA (2000). Climate and cattle in North Africa: a first approximation. In: Blench RM, MacDonald KC, editors. The origins and development of African livestock: archaeology, genetics, linguistics and ethnography. London: UCL Press. Pp. 61–86.

Horwitz LK, Tchernov E, Ducos P, Becker C, Von den Driesch A, Martin L, Garrard A (2000). Animal domestication in the Southern Levant. Pale´ orient. 25(2):63– 80.

Hughes S, Ferna´ndez H, Cucchi T, Duffraisse M, Casabianca F, Istria D, Pompanon F, Vigne JD, Hänni C, Taberlet P (2012). A Dig into the past mitochondrial diversity of Corsican goats reveals the influence of secular herding practices. PLoS ONE 7(1): e30272. doi:10.1371/journal.pone.0030272.

Joshi MB, Rout PK, Mandal AK, Tyler-Smith C, Singh L, Thangaraj K (2004). Phylogeography and Origin of Indian Domestic Goats. Mol. Biol. Evol. 21(3):454–462.

Kibegwa FM, Githui KE, Jung'a JO, Badamana MS, Nyamu MN (2015). Mitochondrial DNA variation of indigenous goats in Narok and Isiolo counties of Kenya. J. Anim. Breed. Genet. 133: 238-247.

Kim KI, Yang YH, Lee SS, Park C, Ma R, Bouzat JL, Lewin HA (1999). Phylogenetic relationships of Cheju horses to other horse breeds as determined by mtDNA D-loop sequence polymorphism. Anim. Genet. 30:102–108.

Lenstra JA, Groeneveld LF, Eding H, Kantanen J, Williams JL, Taberlet P, Nicolazzi EL, Sölkner J, Simianer H, Ciani E, Garcia JF, Bruford MW, Ajmone-Marsan P, Weigend S (2012). Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. J. Anim. Genet. 43(5):483–502.

Luikart G, Gielly L, Excoffier L, Vigne JD, Bouvet J, Taberlet P (2001). Multiple maternal origins and weak phylogeographic structure in domestic goats. PNAS. 98(10):5927–5932.

Luikart G, Fernández H, Mashkour M, England, P.R. and Taberlet, P., 2006. Origins and Diffusion of Domestic Goats Inferred from DNA Markers Example Analyses of mtDNA, Y Chromosome, and Microsatellites. Documenting documentations: New genetic and archaeological paradigms. University of California press. Berkeley Los Angeles London.

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

Machado TMM, Chakir M, Lauvergne JJ (2000). Genetic distances and taxonomic trees between goats of Ceará State (Brazil) and goats of the Mediterranean region (Europe and Africa). Genet. Mol. Biol. 23(1):121-125.

MacHugh, D.E. and Bradley, D.G., 2001. Livestock genetic origins: Goats buck the trend. PNAS Vol. 98, no. 10, Pp 5382–5384

Manceau V, Després L, Bouvet J, Taberlet P (1999). Systematics of the genus Capra inferred from mitochondrial DNA sequence data. Mol. Phylogenet. Evol. 13:504–510.

Mannen H, Nagata Y, Soichi TS (2001). Mitochondrial DNA Reveal That Domestic Goat (Capra hircus) Are Genetically Affected by Two Subspecies of Bezoar (Capra aegagurus). Biochem. Genet. 39(5/6).

Mazdarani FH, Akbari MT, Fard RMN, Hessari M, Pour KC, 2014. Molecular identification of *Capra hircus* in East Chia Sabz, an Iranian pre-pottery Neolithic site, Central Zagros, based on mtDNA. The Journal of Animal & Plant Sciences, 24(3): 945-950.

Melinda ZA, Emshwiller E, Smith BD, Bradley DG (2006). Documenting domestication: the intersection of genetics and archaeology. Trends Genet. 22:139–155.

Naderi S, Rezaei HR, Taberlet P, Zundel S, Rafat SA, Naghash HR, El-Barody MAA, Ertugrul OF, Econogene Consortium (2007). Large-scale mitochondrial DNA analysis of the domestic goat reveals six maternal lineages with high haplotype diversity. PLoS ONE 10:e1012.

Naderi, S., Rezaei, H.R., Pompanon, F.O., Blum, M.G.B., Negrini, R., Naghash, H.R., Balkız, O., Mashkour, M., Gaggiotti, O.E., Ajmone-Marsan, P., Kence, A., Vigne, J.D. and Taberet, P., 2008. The goat domestication process inferred from large-scale mitochondrial DNA analysis of wild and domestic individuals. PNAS 105(46): 17659–17664.

Nomura K, Ishii K, Dadi H, Takahashi Y, Minezawa M, Cho CY, Sutopo, Faruque MO, Nyamsamba D, Amano T (2012). Microsatellite DNA markers indicate three genetic lineages in East Asian indigenous goat populations. Anim. Genet. 43:760–767.

Nomura K, Yonezawa T, Mano S, Kawakami S, Shedlock AM (2013). Domestication Process of the Goat Revealed by an Analysis of the Nearly Complete Mitochondrial Protein-Encoding Genes. PLoS ONE 8(8): e67775.

Pariset L, Cuteri A, Ligda C, Ajmone-Marsan P, Valentini A, ECONOGENE Consortium (2009). Geographical patterning of sixteen goat breeds from Italy, Albania and Greece assessed by Single Nucleotide Polymorphisms. BMC Ecology 2009, 9:20 doi:10.1186/1472-6785-9-20

Pagani L, Kivisild T, Tarekegn A, Ekong R, Plaster C, Romero IG, Ayub Q, Mehdi SQ, Thomas MG, Luiselli D, Bekele E, Bradman N, Balding DJ, Tyler-Smith C (2012). Ethiopian Genetic Diversity Reveals Linguistic Stratification and Complex Influences on the Ethiopian Gene Pool. Am. J. Human Genet. 91:83–96.

Payne WJA, Wilson RT (1999). An introduction to Animal Husbandry in the tropics. Fifth edition. Blackwell Science Ltd: London.

Pereria F, Pereira L, Van Asch B, Bradley DG, Amorim A (2005). The mtDNA catalogue of all Portuguese autochthonous goat (Capra hircus) breeds: high diversity of female lineages at the western fringe of European distribution. Mol. Ecol. 14, 2313–2318.

Pereira F, Queirós S, Gusmão L, Nijman IJ, Cuppen E, Lenstra JA, Econogene Consortium, Davis SJM, Nejmeddine F, Amorim A (2009). Tracing the History of Goat Pastoralism: New Clues from Mitochondrial and Y Chromosome DNA in North Africa. Mol. Biol. Evol. 26(12):2765–2773.

Pidancier N, Jordan S, Luikart G, Taberlet P (2006). Evolutionary history of the genus Capra (Mammalia, Artiodactyla): Discordance between mitochondrial DNA and Y-chromosome phylogenies. Mol. Phylogenet. Evol. 40:739–749.

Porter V (1996). Goats of the World. Farming Press, Ipswich, U.K.

Rodero A, Delgado JV, Rodero E (1992). Primitive andalusian livestock, their implications in the discovery of America. Archivos de Zootecnia. 41, 383–400.

Sardina MT, Ballester M, Marmi J, Finocchiaro R, van Kaam JBCHM, Portolano B, Folch JM (2006). Phylogenetic analysis of Sicilian goats reveals a new mtDNA lineage. Anim. Genet. 37:376–378.

Schlumbaum A, Campos PF, Volken S, Volken M, Hafner A, Schibler J (2010). Ancient DNA, a Neolithic legging from the Swiss Alps and the early history of goat, J. Archaeol. Sci. doi:10.1016/j.jas.2009.12.025.

Simpson GG (1945). The principles of classification of mammals. Bull. Am. Mus. Nat. Hist. 85:1–350.

Smith AB (1992). Origins and spread of pastoralism in Africa. Ann Rev Anthropol. 21:125–141.

Smith BD (1998). The emergence of agriculture. New York: Scientific American Library.

Sultana S, Mannen H, Tsuji S (2003). Mitochondrial DNA diversity of Pakistani goats. Anim. Genet. 34:417–421

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

Tajima F (1989). Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. Genet. 123: 585–595.

Takada T, Kikkawa Y, Yonekawa H, Kawakami S, Amano T (1997). Bezoar (Capra aegagrus) is a matriarchal candidate for ancestor of domestic goat (Capra hircus): evidence from the mitochondrial DNA diversity. Biochem. Genet. 35:315–326.

Takahashi MK, Frost C, Oyadomari K, Pinho M, Sao D, Chima-Okereke O, Gharakhanian E (2008). A novel immunodetection screen for vacuolar defects identifies a unique allele of VPS35 in S. cerevisiae. Mol. Cell Biochem. 311(1-2):121-36

Voruz JL (1999). Chronologies Néolithiques. De 6000 á 2000 avant nótre ére dans le Bassin Rhodanien. Revue archéologique du Centre de la France, Année. 38(1):236-237.

Zeder M, Hesse B (2000). The initial domestication of goats (Capra hircus) in the Zagros Mountains 10,000 years ago. Sci. 287: 2254–2257.

Zeuner FE (1963). A history of domestic animals. Hutchinson and Co. Ltd: London.

Zilháo J (2001). Radiocarbon evidence for maritime pioneer colonization at the origin of farming in west Mediterranean Europe. Proc. Natl. Acad. Sci. 98:14180-14185.

To cite this paper: Tarekegn GM, Zhang W, Mwai O, Dessie T, Djikeng A, Tesfaye K. 2016. Documenting radiocarbon evidences, Y-chromosome, mitochondrial DNA and autosomal markers on origin of domestication and routes of goat global divergence: a review. *Online J. Anim. Feed Res*., 6(6): 113-124.
Scienceline/Journal homepages: www.science-line.com; www.ojafr.ir

Online Journal of Animal and Feed Research

Volume 6, Issue 6: 125-129; Sep 25, 2016 ISSN 2228-7701

IMPACT OF GENDER DETERMINATION THROUGH VENT SEXING ON COBB-500 BROILER PERFORMANCE AND CARCASS YIELD

Adnan YOUSAF✉

Sadiq Poultry (Pvt) Limited, Rawalpindi, Pakistan

✉Email: dr.adnan011@gmail.com

ABSTRACT: The study was conducted in order to explore the effect of separated sex rearing of broiler production performance. Total no of (n=24,000) Cobb-500 birds were reared for 42 days and divided in two group's A =12000 male and B= 12,000 females, according to their sex with 4 replication in each treatment where each replication had 3000 birds. They were provided the same feed and water *ad libitum* for the whole study. Initial body weight, temperature, humidity, feed intake, weekly body weight, mortality and final live weight of broiler were recorded. The study clearly shows significant differences (P<0.05) in term of body weight gain and FCR for males chicks compare to females. Male birds also showed significantly (P<0.05) better dressing percentage than female group. Male chicks had significantly (P<0.05) larger chest circumference females birds. The cross with the fastest growth rate also had the highest mortality. Mortality percentage was high in male chicks 4% then female's chicks 2%. The most profitable choice will be dependent on whether whole birds or parts are marketed and the relative values of the parts. All these findings together revealed that in separate sex growing male chicken showed better performance in terms of more production.

Keywords: Cobb-500 broiler, Vent Sexing, Growth Performance, FCR, Carcass

ORIGINAL ARTICLE
pii: S222877011600017-6
Received 28 Oct. 2016
Accepted 20 Nov. 2016

INTRODUCTION

Poultry industry plays a key role in GDP of countries (FAO, 2011), which provided fresh meat and full fill from the protein (Hussain, 2015). To enhance the daily production of poultry scientific and technological development of poultry is crucial now a day (Hussain, 2015). In order to worldwide scale, there is great tendency to provide chicken meat especially boneless and skinless broiler breast meat as increase consumption (Abdullah et al., 2010). This change put in the poultry industry is prominence to improve the breast meat yield and mass muscles development in young chicks (Abdullah et al., 2010). Improving the performance of growth and meat production breeder industry are continues strives on this (Mehaffey et al., 2006).

The main conditions which influence the meat yield in broiler are feed, sex, age, body weight and environmental condition at poultry house (Lopez et al., 2011). However, to achieve targeted goals it is strongly related to getting high carcass yield and growth performance at poultry house in less FCR. In poultry broiler strain are generally raise to fulfill the nutrition requirements in short period and also a very short source of income, for maximizes their profitability selection of bird on basis of sexing are reared. It was noted that local farmer buys sexed chicks and raised it separately sheds male & females in their poultry house, male's growing fast as compared to female chicken (Musa et al., 2006). So, the present study was undertaken to know the effect of separate sex growing on the incidence of metabolic disorders and the production performances of broilers reared under separate sex growing.

MATERIALS AND METHODS

All procedures in this study were approved by the Animal Care and Pakistan Poultry Association as international standers.

Site Selection

The study was carried out at Sadiq Poultry (Pvt) Limited, Chakri Hatchery Rawalpindi. Which is full fill from the latest hatchery automation ISO 1900-2000 certified hatchery. This is the largest eggs capacity hatchery of south Asia, which is producing the best quality of chicks through single stage incubation system.

To cite this paper: Yousaf A. 2016. Impact of gender determination through vent sexing on Cobb-500 broiler performance and carcass yield. *Online J. Anim. Feed Res.*, 6(6): 125-129.
Scienceline/Journal homepages: www.science-line.com ; www.ojafr.ir

Eggs Classification

Eggs (wt. 53-60 g) from broiler breeders (Cobb-500, 42-46 weeks of age) were selected. Hatchable eggs were selected on the basis of shell quality, weight and color. Only oval shape good quality intact eggs were selected for hatching. The substandard eggs such as cracked, misshapen, blood-stained, dirty, toe-punched and elongated were rejected. These eggs were collected at farm and stored at 20°C and 75% relative humidity until used in hatching trail. Before, trail eggs were fumigated with 20 g $KMnO_4$and 40ml formalin (40%) and 40 ml of water for 100ft 3 areas for 15 minutes. All the hatchable eggs were pre-heated at 82 °F for 5 hours in the incubator. Completion of pre-heating stage the incubation stage started automatically (Ross prime age). It prevents condensation and reduced variation in eggs internal temperatures.

Incubation stage Program

Stander single stage incubation stage program was used in the setter, with gradually decreasing machine temperature on every stage, starting from 100.3°F. Both of groups were treated with same incubation program (Ross Prime age Recommended by Chicks Master USA). After 449 hours (18.07 days) fertility was checked through the candling process, only fertile eggs were shifted to hatcher for next 56 hours. Water loss was recorded for all flocks' eggs. The normally average water loss is about 11-13%. While in the single stage incubation system water loss were recorded between 10.5-11.5%. Fertility of eggs was checked through the candling process; only fertile eggs were transferred to the hatcher. A standard hatching program (Ross Prime age recommended by chicks master USA) was used in the hatcher, where the stage beginning at a set point temperature of 98.5°F at day18.7, which was gradually decreased to 96.6°F at day 21. Normally approximately 21.08 days (after 506 h of incubation including drying), the hatching process was ended.

Chicks Grading/Yield Measure

Chick yield was measured with the average weight of fresh eggs at the setting time, with the average weight of day-old chicks. Chicks were treated for full-time incubation period 21 days (506 hours). Body weights of chick were determined immediately after chick collection. Female chicks hatched earlier than male chicks. Hatch out chicks was graded through conveyor. Only stranded chicks were shifted to box after counting, while dead, week, and unhealed naval chicks were removed as the international standard recommended by International Poultry Association.

Vent Sexing of Chicks

Chicks (male 12000 and female's 12000) were isolated through vent sexing. The qualified team identified male and females chicks.

Chick's group classification

Total 24000day-old Cobb 500 chicks (Male 12000, Females 12,000) were taken for entire study from SP Hatchery Chakri. The study was conducted at the Sadiq Broiler Farm, Khilari (Chakri, Rawalpindi) for a period of 42 days. The broiler chicks were separated by vent sex. Males and females can be separated through vent sexing (Austic and Nesheim, 1990). The chicks were sexed at day-1 at Sadiq Poultry (Pvt) Limited, Chakri Hatchery to establish separate male and female flocks. There were two treatments i.e male chicks and female chicks 4 replications in each treatment. Three thousand chicks were allocated for each replication. Fresh, clean and sun-dried rice husk was used as shallow litter (5-inch depth) on the floor.

Poultry House Conditions/Feed

The chicks were delivered to poultry houses through environmentally controlled vehicles (24^0C temperature and 65% humidity). At the farm, chicks were offered water and feed immediately. All the chicks were fed and watered *ad libitum* on proprietary broiler starter and finisher diets. Round plastic feeders and drinkers were used. SB feed was offered to chicks during the whole period of study. The continuous light was applied during the whole study. For the first 2 weeks, four 40-watt tube lights were used at night to facilitate eating and drinking of the birds. Rest of the week's 1-hour dark was allowed at night in two times. The chicks were brooding for 7 days; brooding temperature was adjusted (95 ^{0}F) with house temperature (Table 1). The chickens were fed with starter diets from 1 to 13 d (3010 Kcal ME/kg, 22% crude protein), grower diets from 14 to 30 d (3175 Kcal ME/kg, 20% crude protein) and finisher diets from 31 to 42 d of age (3227 Kcal ME/kg, 18% crude protein). Water and feed were supplied *ad libitum*. The diet was formulated according to the recommendations of the NRC (1994) using WUFFDA formulation software program. Intake of feed and water was taken daily, while body weight and total feed consumed was recorded on weekly basis. Organ weight and carcass measurements were also taken at the end of

To cite this paper: Yousaf A. 2016. Impact of gender determination through vent sexing on Cobb-500 broiler performance and carcass yield. *Online J. Anim. Feed Res.*, 6(6): 125-129.
Scienceline/Journal homepages: www.science-line.com ; www.ojafr.ir

the study. Poultry house conditions were same for all group's temperature. For Ventilation Viper Touch (Big Dutchman) system was installed.

Table 1 - Environmental condition of Poultry House

Parameters	1st Week	2nd Week	3rd Week	4th Week	5th Week
Temperature (^{0}F)	95-86	86-83	83-77	77-75	75
Humidity (%)	65	65	65	65	65
Ventilation (m^3/hour/bird)	0.07	0.25	0.40	0.59	0.87

Statistical analyses

Statistical analysis of data collected in this completely randomized design was performed using the SAS® statistical program. The descriptive analyses of data were conducted to verify the assumptions of analysis of variance (T-test), which demonstrated the need to transform the feed conversion, livability and yield variables. This transformation was done by the base 10 log scales.

RESULTS AND DISCUSSION

Results from this study clearly show significant differences in body weight gain between broilers (Male & Females) at various ages. These results are similar to those reported by (Mehaffey et al., 2006). Isolation of sex difference the effect on the weight of the birds is usually observed in broilers as such it was documented by (Fanatico et al., 2005). There was the significant effect ($P<0.05$) of interaction between sex male and females chicks. The detail sex difference on growth characteristics among male and females cobb-500 broiler chicks is presented in Table No2. Male broilers are often heavier carcass and body weight than females (Young et al., 2001). In their entire study, it was documented that the male's chicks remain heavier than the females. Group **A** Males show better result in term of weight gain and FCR as compare to group **B** Females as showed in Table 2.

Table 2 - Average chicks weight, FCR, livability and yield by sex

Feature	Male	Females	Means
Weight gain (kg) from 0 to 21 days	0.395^a	0.370^b	0.387
Weight gain (kg) from 22 to 42 days	2.256^a	2.110^b	2.133
Feed conversion (g:g) at 21 days	1.487^a	1.677^b	1.578
Feed conversion (g:g) at 42 days	2.287^a	2.367^b	2.327
Livability (%) at 21 days	98.38^a	99.58^a	98.98
Livability (%) at 42 days	98.48^a	99.51^a	99.01
Carcass yield (%)	75.95^a	74.35^b	75.15
Breast yield (%)	23.25^b	25.31^a	24.35
Leg yield (%)	28.03^a	26.65^b	27.45

^{a,b} means in the same row with different superscripts differ significantly ($P<0.05$)

Regarding FCR, the sex effect was not observed at the age of 20 days. In all other ages, males had better feed conversion than females, indicating their greater feed efficiency. Feed intake and FCR their existence significant effect ($P<0.05$) difference in the parameters. With the numerical females consumed more feed and gain less weight which presented poor FCR, which is the economically poor result as compared to males. (Malone et al., 1979) reported male is significantly better in term of live weight than females. Males can get prepared before then females chicks which are as result of less FCR (Lana et al., 2000, Viana et al., 2000). Differences in growth performance between female and male broilers were in agreement with those previously reported (Lopez et al., 2011). Although there was no incidence of diseases during the whole study periods, mortalities of 2% for group B (females), whereas as 4% for group A (males) were recorded. The result of sex isolation rearing on carcass measure of cobb-500 broiler shows significant ($P<0.05$) expect in the neck length Table no 3. Males show higher neck length then female's chicks as documented by (Al-Qamashoui et al., 2014) generally males are superior to females (Guni and Katule, 2013). Shanks of female's chicks were recorded smaller than males (Munira et al., 2006). The results in tables were collected for strains under the same environmental conditions. There was no effect of sex on bird's

To cite this paper: Yousaf A. 2016. Impact of gender determination through vent sexing on Cobb-500 broiler performance and carcass yield. *Online J. Anim. Feed Res.*, 6(6): 125-129.
Scienceline/Journal homepages: www.science-line.com ; www.ojafr.ir

livability, a result also observed by (Hellmeister Filho, 2002). Fast-growth resulted in increased appetite, lower feed conversion, higher BW, and greater meat yield (Joseph and Moran, 2005). The findings of this work tended to show that male Cobb-500 broilers had better performance significant ($P<0.05$) in terms of weight gain and carcass parameters measured, when compared to their female as documented by (Kidd et al., 2005). The male showed considerably improved growth rate; this rapid growth was accompanied by an increase in fat deposition (Griffin, 1996). However, this work did not go into measuring the fat deposits.

Table 3 - Effect of sex difference on carcass characteristics of broiler chicken

Parameters	Male	Females
Average carcass weight (kg)	0.85 ±0.95	0.65 ± 0.36
Body girth (cm)	38.08 ± 0.22	37.06 ± 0.41
Body length (cm)	39.65 ± 0.25	36.87 ± 0.42
Breast (cm)	11.12 ± 0.12	10.45 ± 0.12
Shank length (cm)	16.96 ± 0.23	15.24 ± 0.23
Thigh (cm)	14.15 ± 0.23	13.45 ± 0.25
Neck (cm)	3.25 ± 1.23	2.75 ± 1.00

CONCLUSION

For the purpose of increased maximization of profit in broiler industry, broiler production can be carried out based on sex separation. Males can be raised separately from females and fattened for market or as cut-up carcass parts and sold as such.

Acknowledgments

The author is thankful to respectable Director of Sadiq Poultry (Pvt) limited Mr. Salman Sadiq and Project Coordinator Engr. Jawad Kiwan Qazi for their full support, motivation, fruitful suggestions and encouragement during the whole period of research work. The author is also grateful to Dr. Kashif for their cooperation.

Conflict of interests

The authors declare that they have no conflict of interest with respect to the research, authorship, and/or publications of this article.

REFERENCE

Abdullah AY and Matarneh SK (2010). Broiler performance and the effects of carcass weight, broiler sex, and post chill carcass aging duration on breast fillet quality characteristics. J. Appl. Poult. Res., 19:46–58.

Al-Qamashoui B, Mahgoub O, Kadim I and Schlecht E (2014). Towards Conservation of Omani local chicken: Phenotypic characteristics, Management Practices, and Performance traits. Asian-Australian Journal of Animal Sciences, 6: 174-182.

Austic Richard E and Nesheim MC (1990). Poultry Production, Lea & Febiger, Chicago, USA FAO (2011). Per capita meat consumption declined by 1.7pc. Food and Agriculture Organization Results. Brazilian J. Poult. Sci., 10: 17–22

Fanatico AC, Pillai, PB and Cavitt LC et al. (2005) Evaluation of Slower-Growing Broiler Genotypes Grown with and Without Outdoor Access: Growth Performance and Carcass Yield. Poult. Sci., 84: 1321-1327.

Guni FS and Katule AM (2013). Characterization of local chickens in selected districts of the Southern Highlands of Tanzania: I. Qualitative characters. Livestock Research for Rural Development, 25(9). http://www.lrrd.org/lrrd25/9/guni25153.htm; accessed 15 Oct. 2015.

Hellmeister Filho, P. Efeitos de Fatores Genéticos e do Sistema de Criação sobre o Desempenhoe o Rendimento de Carcaça de Frangos Tipo Caipira. (2002). 77f. Tese (Doutorado em Agronomia). Universidade de São Paulo, Piracicaba.

Hussain J, Rabbani I, Aslam S and Ahmad HA (2015). An overview of poultry industry in Pakistan" worlds Poultry Sci J., 71(4): 689-700

Joseph NS and Moran ET Jr. (2005). Characteristics of eggs, embryos, and chicks from broiler breeder hens selected for growth or meat yield. J. Appl. Poult. Res., 14: 275–280.

Kidd MT, Corzo A, Hoehler D, Miller ER and Dozier III WA (2005). Broiler responsiveness (Ross×708) to diets varying in amino acid density. Poult. Sci., 84: 1389– 1396.

Lana GRQ, Rostagno HS, Albino LFT and Lana AMQ (2000). Efeito da Temperatura Ambiente e da Restrição Alimentar sobre o Desempenho e a Composição da Carcaça de Frangos de Corte. Rev. Bras. Cienc. Avic., 29: 1117-1123.

Lopez KP, Schilling MW and Corzo A (2011). Broiler genetic strain and sex effects on meat characteristics. Poult. Sci., 90: 1105–1111.

Marlone GW, Chaloupka GW, Merkley JW and Littlefield LH (1979). Evaluation of five commercial broiler crosses I. Grow-out performance. Poult Sci., 58: 509-515

Mehaffey JM, Pradhan SP, Meullent JF, Emmert JL, Mckee SR and Owens CM (2006). Meat quality evaluation of minimally aged broiler breast fillets from five commercial genetic strains. Poult. Sci., 85:902–908.

Munira KN, Uddin MJ, Faruque S, Parvez MS, Miah MY and Siddiqui MSI (2006). Comparative study on carcass characteristics of different genetic groups of spent hens in Bangladesh. Int J. Poult. Sci., 5 (2): 178-180.

Musa HH, Chem GH, Cheng, JH, Li BC and Mekki DM (2006). Study on carcass characteristics of chicken breeds raised under the intensive condition. Int. J. Poult Sci. 5 (6): 530-533

Viana CFA, Silva MA, Pires AV et al. (2000). Influência de Grupos Genéticos e de Níveis de Energia sobre Características de Carcaça de Frangos de Corte. Rev. Bras. Zootec., 29: 1067-1073.

Young, LL, Northcutt JK, Buhr RJ, Lyon CE and Ware GO (2001). Effects of age, sex, and duration of post-mortem aging on percentage yield of parts from broiler chicken carcasses. Poult. Sci., 80: 376–379.

To cite this paper: Yousaf A. 2016. Impact of gender determination through vent sexing on Cobb-500 broiler performance and carcass yield. *Online J. Anim. Feed Res.*, 6(6): 125-129.
Scienceline/Journal homepages: www.science-line.com ; www.ojafr.ir

Online Journal of Animal and Feed Research

Volume 6, Issue 6: 130-132; Sep 25, 2016 ISSN 2228-7701

IMPACT OF SEMEN QUALITY OF ASEEL CHICKEN ON INDUCED MOLTING

Adnan YOUSAF[1], Faiza RUBAB[2], Rehana SHAHNAWAZ[3], Tahseen JAMIL[4], Tahir IQBAL[4], Naila BIBI[4], Irfan HAIDER[4]

[1]*Sadiq Poultry (Pvt) Limited, Rawalpindi, Pakistan*
[2]*Department of Animal Reproduction, Sindh Agriculture University Tandojam, Pakistan*
[3]*Department of Veterinary Pharmacology, Sindh Agriculture University Tandojam, Pakistan*
[4]*Faculty of Animal Husbandry and Veterinary Sciences, Sindh Agriculture University Tandoajm, Pakistan*
Email: dr.adnan011@gmail.com

ABSTRACT: Indigenous chickens are an important source of animal proteins. Aseel is the very famous chicken breed of Pakistan which is facing the reproductive issues. Molting is economically used for the improvement of reproductive performance of male rosters. So the current experiment was designed to investigate the effect of molting on semen quality of indigenous Aseel chicken. Roosters (n=20) were divided into two groups, Group A molted (n=10) and group B non-molted (control) (n=10). Molting was performed through the method of feed restrictions. After the molting phase, semen was analyzed for six weeks. The semen quality was significantly (P<0.05) improved in terms of volume (0.34±0.8 & 0.16±0.4 ml), mortality (73.7±2.5 & 63.5±2.2%), semen concentration (3.36±1.2 & 1.63±0.2 x 115/ml), morphological defect of sperm, (6.5±0.5 & 8.7±0.6 %) and livability of sperm (75±2.3 & 64±2.5%) were significant (P< 0.05) better for group A as group B. It was concluded that molting could be used for improvement of semen quality of indigenous Aseel chicken to cover the reproductive problems.

Key Words: Aseel chicks, Semen quality, Molting & Non-Molting

ORIGINAL ARTICLE
pii: S222877011600018-6
Received 30 Oct. 2016
Accepted 20 Nov. 2016

INTRODUCTION

Poultry is the 2nd largest industry of Pakistan whose play a dynamic role in the GDP of the country (Hussain , 2015, FAO, 2011). Poultry production is mainly dependent upon traditional extensive production system using native breeds (Ani, 1990). Indigenous chickens are an important source of animal proteins (Roberts et al., 1999). The word Aseel is derived from Arabic which means "pure" or "thoroughbred". The Aseel chicks breed has some advantages as compared to another indigenous breed. In Pakistan, Aseel, Naked-neck, Desi, and Fayoumi are reared as backyard chickens mainly for the source of protein and income (Usman et al., 2014). It is very famous among all of them which are mostly reared in the rural area of Pakistan. Due to their poor fertility and hatchability percentage, there is no commercial farming of it. It is also reared as the game bird for fighting purpose (Jabbar et al., 2015). Aseel is famous for its majestic gait, pugnacity, its stamina and dogged properties (Jabbar et al., 2015). It is immune system is much enhanced against diseases as compared to other native breeds (Jatoi et al., 2014). Its eggs and meats contain rich protein, iron and amino acids (Mohan et al., 2008).

However, Aseel breed is facing the problems of poor growth rate, late maturity, less persistence and number of egg production, broodiness and low fertility and hatchability rates (Amjad et al., 2012). The low fertility may be due to the poor semen quality and there is no baseline data available about semen quality of Aseel. The reproductive capacity of chicken male's starts to decline after 50 weeks of age so molting could be used to regain their reproductive capacity. The current experiment was designed to evaluate the effects of molting on semen quality of native Aseel chicken.

MATERIALS AND METHODS

Selection of site/Roosters

The current experiment was designed at Sadiq R & D farm Mandra District Rawalpindi. For this purpose Aseel roosters (n=20) having 2-2.5 kg body weight and 1-1.5 years of age were selected on the basis of early semen quality and caged individually. Male Aseel were divided into two groups group A molted (n=10) and group B non-molted (control) (n=10).

To cite this paper: Yousaf A, Rubab F, Shahnawaz R, Jamil T, Iqbal T, BiBi N, Haider I. 2016. Impact of semen quality of Aseel chicken on induced molting. *Online J. Anim. Feed Res.*, 6(6): 130-132.
Scienceline/Journal homepages: www.science-line.com ; www.ojafr.ir

Feeding Procedure

For the group A, molting was performed by withdrawal daily feed intake of maize up to 60gram. Water was proved *ad libitum* through automatic nipple system. During the entire study, artificial light was avoided for whole molting period of 6 weeks. While group B non-molted was provided 16 hours artificial full light as such water was proved *ad libitum* through automatic nipple system. Feed with 110 grams/ rooster were provided daily once a day.

Collection of Semen

A collection of semen was performed once (Thursday) in a week by performing the abdominal massage as documented (Riaz et al*.,* 2004) for six weeks. Semen was collected very carefully to avoided stress. Only without blood, urine and feces semen were recommended for further analysis. Insulin syringe was used to measure of semen.

Analyzing of Semen Quality

After collection of semen to ensure and check the quality and mortality semen were sent to the laboratory for evaluation. Placed drop of fresh semen on sterilized glass slide having a temperature of 38 ^{0}C and covered with glass cover slip. Mortality was observed through the light microscope under 100X. Five trials were performed before taking final decision. Dilution rate was remaining 1:500 as documented (Riaz et al., 2006). To identify the spermatozoa stander staining technique were used using eosin-nigrosin.

Statistically Analysis

Statistical analysis of data collected in this student's T-Test was performed using the statistical software SAS (version 9.2).

RESULTS AND DISCUSSION

The significant difference ($P<0.05$), was observed for volume, concentration, mortality, livability and morphological defects in molted and non-molted. Volume of semen (0.34±0.8 & 0.16±0.4 ml), mortality (73.7±2.5 & 63.5±2.2%), semen concentration (3.36±1.2 & 1.63±0.2 x 115/ml) and livability of sperm (75±2.3 & 64±2.5%) were significant ($P<0.05$) better for group A (molted males) as group B (Non-molted males). Significantly ($P<0.05$) (6.5±0.5 & 8.7±0.6 %) better results were recorded for group A as compare to group B in term of morphological defect of sperm showed in Table 1.

Table 1 - Impact of semen quality of Aseel chicken on induced molting

Parameters	Group A (Molted Males)	Group B (Non-Molted Males)
Volume (ml)	0.34±0.8 ^{a}	0.16±0.4 ^{b}
Concentration (x115/ml)	3.36±1.2 ^{a}	1.63±0.2 ^{b}
Mortality %	73.7±2.5 ^{a}	63.5±2.2 ^{b}
Livability (%)	75±2.3 ^{a}	64±2.5 ^{b}
Morphological defects (%)	6.5±0.5 ^{a}	8.7±0.6 ^{b}

^{a,b} denote the difference between semen quality of molted and non-molted groups ($P<0.05$)

Molting is the complex physiological procured which directly enhanced the reproductive and endocrine system of males (Khan, 2011). Molting in males is economical better and commonly practiced in broiler breeders. The current experiment shows that semen quality in terms of volume, concentration, motility, live sperms and morphological defects was improved ($P<0.05$) by the molting in Aseel chicks. Similar results were documented by (Khan et al., 2012) where in broiler breeder, molting enhances the semen quality and fertility.

CONCLUSION

On the basis of available literature, it can be concluded that Aseel chicken has the great potential to be improved for growth-related traits. It was concluded that semen quality is improved by the process of inducing molting in Aseel chicks.

To cite this paper: Yousaf A, Rubab F, Shahnawaz R, Jamil T, Iqbal T, BiBi N, Haider I. 2016. Impact of semen quality of Aseel chicken on induced molting. *Online J. Anim. Feed Res*., 6(6): 130-132.
Scienceline/Journal homepages: www.science-line.com ; www.ojafr.ir

Acknowledgments

The author is thankful to Director of Sadiq Poultry (Pvt) limited Mr. Salman Sadiq and professor Dr. Rehana Shahnawaz and Engr. Shahzad Yousaf for their full support, motivation, fruitful suggestions and encouragement during the whole period of research work.

Competing interests

The authors declare that they have no conflict of interest with respect to the research, authorship, and/or publications of this article.

REFERENCES

Amjad I, Akram M, Sahota AW, Javed K, Hussain J, Sarfraz Z and Mehmood S (2012). Laying characteristics and egg geometry of four varieties of indigenous aseel chicken in Pakistan J. Anim. Pl. Sci., 22: 848-852.

Ani I (1990). Indigenous chicken production in South-east Asia. World's Poultry Congress; 46: 5-7.

FAO (2011). Per capita meat consumption declines by 1.7pc. Food and Agriculture Organization Results. Brazilian J. Poult. Sci., 10: 17–22

Hussain J, Rabbani I, Aslam S and Ahmad HA (2015). An overview of poultry industry in Pakistan. World Poult. Sci J., 71(4): 689-&700

Khan RU, Rahman ZU, Javed I and Muhammad F (2012). Effect of vitamins, probiotics and protein on semen traits in post-molt male broiler breeders. Anim. Reprod. Sci., 135: 85-90.

Khan RU, (2011). Antioxidants and poultry semen quality. World Poult. Sci. J., 67: 297–308.

Jabbar A, Abbass W, Riaz A, Ahmad M, Sattar A and Akram M (2015). Effects of Induced Molting on Semen Quality of Indigenous Chicken Aseel. Pakistan J. Zool., 47(4): 1199-1200.

Riaz A, Aleem M and Ijaz A (2006). Relationship of body weight, testes biometry and sperm production in broiler breeder. Korean J. Poult. Sci., 33: 165-169.

Riaz A, Aleem M, Ijaz, A, Saeed MA and Latif A (2004). Effect of collection frequency on the semen quality of broiler breeder. Br. Poult. Sci., 45: 823-827.

Roberts JR, Choct M and Ball W (1999). Effect of different commercial enzymes on egg and egg shell quality in four strains of laying hen. Proc. Aust. Poult. Sci. Sym, vol. 11, pp. 139-142.

Usman M, Basheer A, Akram M and Zahoor I (2014). Comparative Study of Production Performance and Egg Quality Parameters of Naked-Neck and Indigenous Aseel Chicken of Pakistan. J. Basic Appl. Sci., 10: 160-163

To cite this paper: Yousaf A, Rubab F, Shahnawaz R, Jamil T, Iqbal T, BiBi N, Haider I. 2016. Impact of semen quality of Aseel chicken on induced molting. *Online J. Anim. Feed Res.*, 6(6): 130-132.
Scienceline/Journal homepages: www.science-line.com ; www.ojafr.ir

Instructions for Authors

OJAFR EndNote Style Manuscript Template Sample Articles Declaration form

Manuscript as Original Research Paper, Short Communication, Case Reports and Review or Mini-Review are invited for rapid peer-review publishing in the *Online Journal of Animal and Feed Research (ISSN 2228-7701)*.

Papers can be in any relevant fields of Animal Sciences (Animal Nutrition, Physiology, Reproduction, Genetics and Breeding, Behavior, Health, Husbandry and its economic, Animal products and Veterinary medicines of domestic animals) and relative topics. The journal does encourage papers with emphasis on the nutritive value and utilization of feeds that is depended to methods of Improvement, Assessment, Conserving and Processing feeds, Agronomic and climatic factors, Metabolic, Production, Reproduction and Health responses to dietary inputs (e.g., Feeds, Feed Additives, Specific Feed Components, Mycotoxins). Also, Mathematical models relating directly to animal-feed interactions, Analytical and experimental methods for Feed Evaluation as well as Animal Production studies with a focus on Animal Nutrition that do have link to a feed (Food Science and Technology) are acceptable relative topics for OJAFR**.**

Submission

The manuscript should preferentially be submit online. For facile submission, please embed all figures and tables at the end of the manuscript to become one single file for submission. Once submission is complete, the system will generate a manuscript ID and password sent to author's contact email. If you have any difficulty in submitting the manuscript, kindly send via email: editors@ojafr.ir. All manuscripts must be checked (by English native speaker) and submitted in English for evaluation in totally confidential and impartial way.

Supplementary information:

Author guidelines are specific for each journal. Our MS Word template can assist you by modifying your page layout, text formatting, headings, title page, image placement, and citations/references such that they agree with the guidelines of journal. If you believe your article is fully edited per journal style, please use our Word template before submission.
Supplementary materials may include figures, tables, methods, videos, and other materials. They are available online linked to the original published article. Supplementary tables and figures should be labeled with a "S", e.g. "Table S1" and "Figure S1". The maximum file size for supplementary materials is 10MB each. Please keep the files as small as possible to avoid the frustrations experienced by readers with downloading large files.

Submission to the Journal is on the understanding that:

1.The article has not been previously published in any other form and is not under consideration for publication elsewhere;
2.All authors have approved the submission and have obtained permission for publish work.
3.Researchers have proper regard for conservation and animal welfare considerations. Attention is drawn to the *'Guidelines for the Treatment of Animals in Research and Teaching'*. Any possible adverse consequences of the work for populations or individual organisms must be weighed against the possible gains in knowledge and its practical applications. If the approval of an ethics committee is required, please provide the name of the committee and the approval number obtained.

Ethics Committee Approval

Experimental research involving human or animals should have been approved by author's institutional review board or ethics committee. This information can be mentioned in the manuscript including the name of the board/committee that gave the approval. Investigations involving humans will have been performed in accordance with the principles of *Declaration of Helsinki*.
And the use of animals in experiments will have observed the *Interdisciplinary Principles and Guidelines for the Use of Animals in Research, Testing, and Education* by the New York Academy of Sciences, Ad Hoc Animal Research Committee.
If the manuscript contains photos or parts of photos of patients, informed consent from each patient should be obtained. Patient's identities and privacy should be carefully protected in the manuscript.

Presentation of the article

Main Format:

First page of the manuscripts must be properly identified by the title and the name(s) of the author(s). It should be typed in Times New Roman (font sizes: 12pt in capitalization for the title and the main text, double spaced, in A4 format with 2cm margins. All pages and lines of the main text should be numbered consecutively throughout the manuscript. The manuscript must be saved in a .doc format, (not .docx files). Abbreviations in the article title are not allowed except the well-known ones.

Manuscripts should be arranged in the following order:

a. TITLE (brief, attractive and targeted);

b. Name(s) and Affiliation(s) of author(s) (including post code) and corresponding E-mail;

c. ABSTRACT;

d. Key words (separate by semicolons; or comma,);

e. Abbreviations (used in the manuscript);

f. INTRODUCTION;

g. MATERIALS AND METHODS;

h. RESULTS;

i. DISCUSSION;

j. CONCLUSION;

k. Acknowledgements (if there are any);

1. REFERENCES;

m. Tables;

n. Figure captions;

o. Figures;

The sections "RESULTS AND DISCUSSION" can be presented jointly.

The sections "DISCUSSION AND DISCUSSION" can be presented jointly.

Article Sections Format:

Title should be a brief phrase describing the contents of the paper. Title Page should include the author(s)'s full names and affiliations, the name of the corresponding author along with phone and e-mail information. Present address(es) of author(s) should appear as a footnote.

Abstract should be informative and completely self-explanatory, briefly present the topic, state the scope of the experiments, indicate significant data, and point out major findings and conclusions. The abstract should be 150 to 300 words in length. Complete sentences, active verbs, and the third person should be used, and the abstract should be written in the past tense. Standard nomenclature should be used and abbreviations should be avoided. No literature should be cited.

Following the abstract, about 3 to 7 **key words** should be listed.

Introduction should provide a clear statement of the problem, the relevant literature on the subject, and the proposed approach or solution. It should be understandable to colleagues from a broad range of scientific disciplines.

Materials and Methods should be complete enough to allow experiments to be reproduced. However, only truly new procedures should be described in detail; previously published procedures should be cited, and important modifications of published procedures should be mentioned briefly. Capitalize trade names and include the manufacturer's name and address. Subheadings should be used. Methods in general use need not be described in detail.

Results should be presented with clarity and precision. The results should be written in the past tense when describing findings in the author(s)'s experiments. Previously published findings should be written in the present tense. Results should be explained, but largely without referring to the literature. Discussion, speculation and detailed interpretation of data should not be included in the results but should be put into the discussion section.

Discussion should interpret the findings in view of the results obtained in this and in past studies on this topic. State the conclusions in a few sentences at the end of the paper. The Results and Discussion sections can include subheadings, and when appropriate, both sections can be combined.

Conclusion should be brief and tight, providing a few specific tasks to accomplish: 1-Re-assert/Reinforce the Thesis; 2-Review the Main Points; 3- Close Effectively. The Conclusion section should not be similar to the Abstract content.

Declarations including Ethics, Consent to publish, Competing interests, Authors' contributions, and Availability of data and materials are necessary.

Acknowledgments of persons, grants, funds, etc should be brief.

Tables should be kept to a minimum and be designed to be as simple as possible. Tables are to be typed double-spaced throughout, including headings and footnotes. Each table should be on a separate page, numbered consecutively in Arabic numerals and supplied with a heading and a legend. Tables should be self-explanatory without reference to the text. The details of the methods used in the experiments should preferably be described in the legend instead of in the text. The same data should not be presented in both table and graph forms or repeated in the text.

The Figure legends should be typed in numerical order on a separate sheet. Graphics should be prepared using applications capable of generating high resolution GIF, TIFF, JPEG or PowerPoint before pasting in the Microsoft Word manuscript file. Use Arabic numerals to designate figures and upper case letters for their parts (Figure 1). Begin each legend with a title and include sufficient description so that the figure is understandable without reading the text of the manuscript. Information given in legends should not be repeated in the text.

Declarations section - Please include declarations heading

Please ensure that the sections:
-Ethics (and consent to participate)
-Consent to publish
-Competing interests
-Authors' contributions
-Availability of data and materials
are included at the end of your manuscript in a Declarations section.

Consent to Publish

Please include a 'Consent for publication' section in your manuscript. If your manuscript contains any individual person's data in any form (including individual details, images or videos), consent to publish must be obtained from that person, or in the case of children, their parent or legal guardian. All presentations of case reports must have consent to publish. You can use your institutional consent form or our consent form if you prefer. You should not send the form to us on submission, but we may request to see a copy at any stage (including after publication). If your manuscript does not contain any individual person's data, please state "Not applicable" in this section.

Authors' Contributions

For manuscripts with more than one author, OJAFR require an Authors' Contributions section to be placed after the Competing Interests section. An 'author' is generally considered to be someone who has made substantive intellectual contributions to a published study. To qualify as an author one should 1) have made substantial contributions to conception and design, or acquisition of data, or analysis and interpretation of data; 2) have been involved in drafting the manuscript or revising it critically for important intellectual content; and 3) have given final approval of the version to be published. Each author should have participated sufficiently in the work to take public responsibility for appropriate portions of the content. Acquisition of funding, collection of data, or general supervision of the research group, alone, does not justify authorship.
We suggest the following format (please use initials to refer to each author's contribution): AB carried out the molecular genetic studies, participated in the sequence alignment and drafted the manuscript. JY carried out the immunoassays. MT participated in the sequence alignment. ES participated in the design of the study and performed the statistical analysis. FG conceived of the study, and participated in its design and coordination and helped to draft the manuscript. All authors read and approved the final manuscript.
For authors that equally participated in a study please write '**All/Both authors contributed equally to this work**.' Contributors who do not meet the criteria for authorship should be listed in an acknowledgements section.

Competing Interests

Competing interests that might interfere with the objective presentation of the research findings contained in the manuscript should be declared in a paragraph heading "Competing interests" (after Acknowledgment section and before References). Examples of competing interests are ownership of stock in a company, commercial grants, board membership, etc. If there is no competing interest, please use the statement "The authors declare that they have no competing interests.".
Online Journal of Animal and Feed Research adheres to the definition of authorship set up by the International Committee of Medical Journal Editors (ICMJE). According to the ICMJE authorship criteria should be based on 1) substantial contributions to conception and design of, or acquisition of data or analysis and interpretation of data, 2) drafting the article or revising it critically for important intellectual content and 3) final approval of the version to be published. Authors should meet conditions 1, 2 and 3. It is a requirement that all authors have been accredited as appropriate upon submission of the manuscript. Contributors who do not qualify as authors should be mentioned under Acknowledgements.

Change in authorship

We do not allow any change in authorship after provisional acceptance. We cannot allow any addition, deletion or change in sequence of author name. We have this policy to prevent the fraud.

Acknowledgements

We strongly encourage you to include an Acknowledgements section between the Authors' contributions section and Reference list. Please acknowledge anyone who contributed towards the study by making substantial contributions to conception, design, acquisition of data, or analysis and interpretation of data, or who was involved in drafting the manuscript or revising it critically for important intellectual content, but who does not meet the criteria for authorship. Please also include their source(s) of funding. Please also acknowledge anyone who contributed materials essential for the study.
Authors should obtain permission to acknowledge from all those mentioned in the Acknowledgements. Please list the source(s) of funding for the study, for each author, and for the manuscript preparation in the acknowledgements section. Authors must describe the role of the funding body, if any, in study design; in the collection, analysis, and interpretation of data; in the writing of the manuscript; and in the decision to submit the manuscript for publication.

Data Deposition

Nucleic acid sequences, protein sequences, and atomic coordinates should be deposited in an appropriate database in time for the accession number to be included in the published article. In computational studies where the sequence information is unacceptable for inclusion in databases because of lack of experimental validation, the sequences must be published as an additional file with the article.

References

An OJAFR reference style for **EndNote** may be found **here**.

1. All references to publications made in the text should be presented in a list with their full bibliographical description.

2. In the text, a reference identified by means of an author‘s name should be followed by the date of the reference in parentheses. When there are more than two authors, only the first author‘s surename should be mentioned, followed by ’et al‘. In the event that an author cited has had two or more works published during the same year, the reference, both in the text and in the reference list, should be identified by a lower case letter like ’a‘ and ’b‘ after the date to distinguish the works.
3. References in the text should be arranged chronologically (e.g. Kelebeni, 1983; Usman and Smith, 1992 and Agindotan et al., 2003). 'et al.' should not be italic. The list of references should be arranged alphabetically on author's surnames, and chronologically per author. If an author's name in the list is also mentioned with co-authors, the following order should be used: Publications of the single author, arranged according to publication dates - publications of the same author with one co-author - publications of the author with more than one co-author. Publications by the same author(s) in the same year should be listed as 1992a, l992b,etc.
4. Names of authors and title of journals, published in non-latin alphabets should be transliterated in English.
5. A sample of standard reference is "1th Author surname A, 2th Author surname B and 3th Author surname C (2013). Article title should be regular, in sentence case form, and 9 pt. Online Journal of Animal and Feed Research, Volume No. (Issue No.): 00-00." (Journal titles should be full and not italic.)
6. If available please add DOI numbers or the link of articles at the end of each reference.

Examples (at the text):
Abayomi (2000), Agindotan et al. (2003), (Kelebeni, 1983), (Usman and Smith, 1992), (Chege, 1998; Chukwura, 1987a,b; Tijani, 1993,1995), (Kumasi et al., 2001).

Examples (at References section):
a) For journal:
Lucy MC (2000). Regulation of ovarian follicular growth by somatotropin and insulin- like growth factors in cattle. Journal of Dairy Science, 83: 1635-1647.
Kareem SK (2001). Response of albino rats to dietary level of mango cake. J. Agric. Res.Dev. pp 31-38.
Chikere CB, Omoni VT and Chikere BO (2008). Distribution of potential nosocomial pathogens in a hospital environment. African Journal of Biotechnology. 7: 3535-3539.

b) For symposia reports and abstracts:
Cruz EM, Almatar S, Aludul EK and Al-Yaqout A (2000). Preliminary Studies on the Performance and Feeding Behaviour of Silver Pomfret (Pampus argentens euphrasen) Fingerlings fed with Commercial Feed and Reared in Fibreglass Tanks. Asian Fisheries Society Manila, Philippine 13: 191-199.

c) For edited symposia, special issues, etc., published in a journal:
Korevaar, H., 1992. The nitrogen balance on intensive Dutch dairy farms: a review. In: A. A. Jongebreur et al. (Editors), Effects of Cattle and Pig Production Systems on the Environment: Livestock Production Science. 31: 17-27.

d) For books:
AOAC (1990). Association of Official Analytical Chemists. Official Methods of Analysis, 15th Edition. Washington D.C. pp. 69-88.
Pelczar JR, Harley JP, Klein DA (1993). Microbiology: Concepts and Applications. McGraw-Hill Inc., New York, pp. 591-603.

e) Books, containing sections written by different authors:
Kunev, M., 1979. Pig Fattening. In: A. Alexiev (Editor), Farm Animal Feeding. Vol. III. Feeding of Different Animal Species, Zemizdat, Sofia, p. 233-243 (Bg).
In referring to a personal communication the two words are followed by the year, e.g. (Brown, J. M., personal communication, 1982). In this case initials are given in the text. Where available, URLs for the references have been provided.

Formulae, numbers and symbols

1. Typewritten formulae are preferred. Subscripts and superscripts are important. Check disparities between zero (0) and the letter 0, and between one (1) and the letter I.
2. Describe all symbols immediately after the equation in which they are first used.
3. For simple fractions, use the solidus (/), e.g. 10 /38.
4. Equations should be presented into parentheses on the right-hand side, in tandem.
5. Levels of statistical significance which can be used without further explanations are *P < 0.05, **P < 0.01, and ***P<0.001.
6. In the English articles, a decimal point should be used instead of a decimal comma.
7. Use Symbol fonts for "±"; "≤" and "≥" (avoid underline).
8. In chemical formulae, valence of ions should be given, e.g. Ca2+ and CO32-, not as Ca++ or CO3.
9. Numbers up to 10 should be written in the text by words. Numbers above 1000 are recommended to be given as 10 powered x.
10. Greek letters should be explained in the margins with their names as follows: Aα - alpha, Bβ - beta, Γγ - gamma, Δδ - delta, Eε - epsilon, Zζ - zeta, Hη - eta, Θθ - theta, Iι - iota, Kκ - kappa, Λλ - lambda, Mμ - mu, Nν - nu, Ξξ - xi, Oο - omicron, Ππ - pi, Pρ - rho, Σσ - sigma, Tτ - tau, Yυ - ipsilon, Φφ - phi, Χχ - chi, Ψψ - psi, Ωω - omega. Please avoid using math equations in Word whenever possible, as they have to be replaced by images in xml full text.

Abbreviations
Abbreviations should be presented in one paragraph, in the format: "term: definition". Please separate the items by ";".
E.g. ANN: artificial neural network; CFS: closed form solution; ....

Graphical Abstract:

Authors of accepted articles should provide a graphical abstract (a beautifully designed feature figure) to represent the paper aiming to catch the attention and interest of readers. Graphical abstract will be published online in the table of content. The graphical abstract should be colored, and kept within an area of 12 cm (width) x 6 cm (height) or with similar format. Image should have a minimum resolution of 300 dpi and line art 1200dpi.

Note: Height of the image should be no more than the width. Please avoid putting too much information into the graphical abstract as it occupies only a small space. Authors can provide the graphical abstract in the format of PDF, Word, PowerPoint, jpg, or png, after a manuscript is accepted for publication.

If you have decided to provide a Professional Graphical Abstract, please click **here**.

Review/Decisions/Processing

Firstly, all manuscripts will be checked by Docol©c, a plagiarism finding tool. The received papers with plagiarism rate of more than 40% will be rejected. Manuscripts that are judged to be of insufficient quality or unlikely to be competitive enough for publication will be returned to the authors at the initial stage. The remaining manuscripts go through a double-blind review process by two reviewers selected by section editor (SE) or deputy SE of OJAFR, who are research workers specializing in the relevant field of study. One unfavourable review means that the paper will not be published and possible decisions are: accept as is, minor revision, major revision, or reject. The corresponding authors should submit back their revisions within 14 days in the case of minor revision, or 30 days in the case of major revision. Manuscripts with significant results are typically reviewed and published at the highest priority. The editor who received the final revisions from the corresponding authors shall not be hold responsible for any mistakes shown in the final publication.

Plagiarism: There is an instant policy towards plagiarism (including self-plagiarism) in our journals. Manuscripts are screened for plagiarism by Docol©c, before or during publication, and if found they will be rejected at any stage of processing.

Date of issue

All accepted articles are published bimonthly around 25th of January, March, May, July, September and November, each year in full text on the Internet.

Publication charges

Articles of *Online Journal of Animal and Feed Research (ISSN 2228-7701)* are freely accessible. No peer-reviewing charges are required. Publication of short reports and letter are free of charge; however, a negligible editor fee (100 USD) will be applied for long research and review papers (more than 10 pages) before copyediting and publication. Instruction for payment is sent during publication process as soon as manuscript is accepted.

The Waiver policy

The submission fee will be waived for invited authors, authors of hot papers, and corresponding authors who are editorial board members of the *Online Journal of Animal and Feed Research*. The Journal will consider requests to waive the fee for cases of financial hardship (for high quality manuscripts and upon acceptance for publication). Requests for waiver of the submission fee must be submitted via individual cover letter by the corresponding author and cosigned by an appropriate institutional official to verify that no institutional or grant funds are available for the payment of the fee. Letters including the manuscript title and manuscript ID number should be sent to: editors@ojafr.ir. It is expected that waiver requests will be processed and authors will be notified within two business day.

The OA policy

Online Journal of Animal and Feed Research is an Open Access journal which means that all content is freely available without charge to the user or his/her institution. Users are allowed to read, download, copy, distribute, print, search, or link to the full texts of the articles, or use them for any other lawful purpose, without asking prior permission from the publisher or the author. This is in accordance with the *BOAI definition of Open Access*.

Submission Preparation Checklist

Authors are required to check off their submission's compliance with all of the following items, and submissions may be returned to authors that do not adhere to the following guidelines:

- -The submission has not been previously published, nor is it before another journal for consideration (or an explanation has been provided in -Comments to the Editor).
- -The submission file is in Microsoft Word, RTF, or PDF document file format.
- -Where available, URLs for the references have been provided.
- -The text is double-spaced; uses a 12-point font; and all illustrations, figures, and tables are placed within the text at the appropriate points, rather than at the end.
- -The text adheres to the stylistic and bibliographic requirements outlined in the Author Guidelines.

***

(Revised on 22 January 2015)

Editorial Offices:
Atatürk University, Erzurum 25100, Turkey
University of Manitoba, Winnipeg, Manitoba R3T 2N2, Canada
University of Maragheh, East Azerbaijan, Maragheh 55136, Iran
Homepage: www.science-line.com
Phone: +98 914 420 7713 (Iran); +90 538 770 8824 (Turkey); +1 204 8982464 (Canada)
Emails:
administrator@science-line.com
saeid.azar@atauni.edu.tr

Scienceline Publishing Corporation

Scienceline Publication, Ltd is a limited liability non-profit non-stock corporation incorporated in Turkey, and also is registered in Iran. Scienceline journals that concurrently belong to many societies, universities and research institutes, publishes internationally peer-reviewed open access articles and believe in sharing of new scientific knowledge and vital research in the fields of life and natural sciences, animal sciences, engineering, art, linguistic, management, social and economic sciences all over the world. Scienceline journals include:

Online Journal of Animal and Feed Research

ISSN 2228-7701; Bi-monthly
View Journal I Editorial Board
Email: editors@ojafr.ir
Submit Online >>

Journal of Civil Engineering and Urbanism

ISSN 2252-0430; Bi-monthly
View Journal I Editorial Board
Email: ojceu@ojceu.ir
Submit Online >>

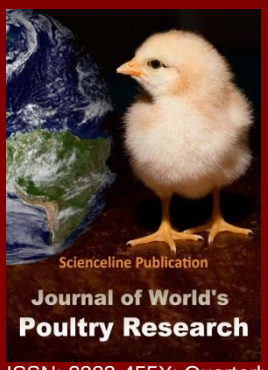
Journal of Life Sciences and Biomedicine

ISSN: 2251-9939; Bi-monthly
View Journal I Editorial Board
Email: editors@jlsb.science-line.com
Submit Online >>

Asian Journal of Medical and Pharmaceutical Researches

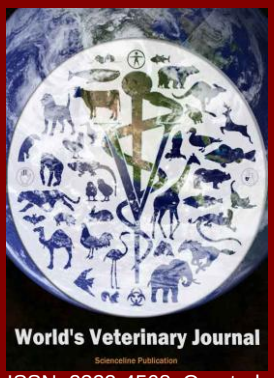
ISSN: 2322-4789; Quarterly
View Journal I Editorial Board
Email: editor@ajmpr.science-line.com
Submit Online >>

Journal of World's Poultry Research



ISSN: 2322-455X; Quarterly
View Journal I Editorial Board
Email: editor@jwpr.science-line.com
Submit Online >>

World's Veterinary Journal

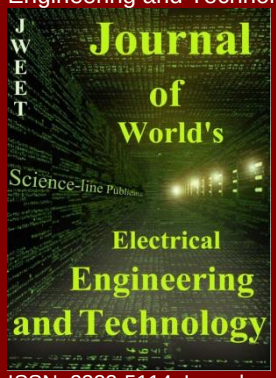


ISSN: 2322-4568; Quarterly
View Journal I Editorial Board
Email: editor@wvj.science-line.com
Submit Online >>

Journal of Educational and Management Studies

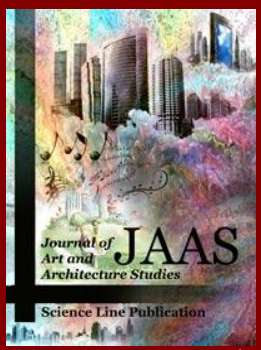
ISSN: 2322-4770; Quarterly
View Journal I Editorial Board
Email: info@jems.science-line.com
Submit Online >>

Journal of World's Electrical Engineering and Technology



ISSN: 2322-5114; Irregular
View Journal I Editorial Board
Email: editor@jweet.science-line.com
Submit Online >>

Journal of Art and Architecture Studies



ISSN: 2383-1553; Irregular
View Journal I Editorial Board
Email: jaas@science-line.com
Submit Online >>

Asian Journal of Social and Economic Sciences

ISSN: 2383-0948; Quarterly
View Journal I Editorial Board
Email: ajses@science-line.com
Submit Online >>

Journal of Applied Business and Finance Researches

ISSN: 2382-9907; Quarterly
View Journal I Editorial Board
Email: jabfr@science-line.com
Submit Online >>

Scientific Journal of Mechanical and Industrial Engineering

ISSN: 2383-0980; Quarterly
View Journal I Editorial Board
Email: sjmie@science-line.com
Submit Online >>