Perspective review article

Animal Reproduction Update

Year 2024, Volume-4, Issue-1 (January - June)

ACS Publisher
www.acspublisher.com

Buffaloes are 'Black Gold' not Black Cows

Priya, Meeti Punetha, Pradeep Kumar, P S Yadav, Dharmendra Kumar*

Animal Physiology and Reproduction Division, ICAR-Central Institute for Research on Buffaloes, Hisar-125001, Haryana, India

ARTICLE INFO

Key Words: Bovidae; *Bos*; *Bubulus*; distinct characteristics; livestock.

doi: 10.48165/aru.2023.4.1.6

ABSTRACT

Buffalo and cow, both are vital to global agricultural landscapes; possess distinct traits that shape their roles in farming. Despite belonging to the Bovidae family, buffaloes excel in resilience and adaptability to harsh environments, while cows thrive in temperate climates. Their evolutionary history reveals separate domestication events, with buffaloes originating later, around 3,000–7,000 years ago. Their chromosome numbers and breeding patterns reflect their genetic differences. Anatomically, buffaloes exhibit unique digestive, reproductive, and thermoregulatory adaptations, influencing productivity. Buffalo milk, richer in fat and solids, surpasses cow milk in nutritional value, driving its prominence in global dairy markets. FAO data indicates a notable surge in buffalo milk production, outpacing that of cows global. This perspective review discusses the diverse benefits of buffalo and highlights the importance of distinguishing between buffaloes and cows in order to comprehend their crucial contributions to agricultural livelihoods and global culinary traditions.

Introduction

The buffalo and the cow are two iconic creatures that stand out in the rich tapestry of agricultural settings. Both buffaloes and cows, esteemed for their valuable contributions to farming communities globally, contain distinct characteristics and attributes that determine their responsibilities in agriculture. Since they are both members of the Bovidae family and provide milk, meat, and draught, buffaloes and cows may initially seem to be comparable. However, a closer examination reveals distinct characteristics that set them apart. One of the most notable differences is their adaptability to various environments. Buffaloes, renowned for their resilience and ability to thrive in challenging conditions, are often found in regions with hot climates and limited resources. Their sturdy build and efficient feed conversion make them well-suited for marginal landowners where other livestock may struggle to survive. In contrast, cows are more commonly associated with temperate climates and lush pastures, although they too can adapt to a range of environments with proper management. The production of milk is another key distinction. While both buffaloes and cows produce milk rich in nutrients, there are differences in composition

---

*Corresponding author.

E-mail address: dkumarbt@gmail.com (Dharmendra Kumar)

Received 12.05.2024; Accepted 20.05.2024

Copyright @ Animal Reproduction Update (https://acspublisher.com/journals/index.php/aru)

and volume (Siddiky andFaruque, 2018; Hegde, 2019). Many culinary traditions favour buffalo milk for its rich flavour and creamy texture, praising its higher fat content and solids. Cows, on the other hand, typically produce larger quantities of milk but with lower nutritional values, making them the primary source of dairy products in many parts of the world. In brief, buffaloes and cows are both indispensable assets to farming communities worldwide, each offering unique benefits and opportunities (Bertoni et al., 2020). Whether it's the resilience of the buffalo in challenging environments or the productivity of the cow in dairy production, these animals continue to shape the agricultural landscape and nourish communities around the globe. This review aims to explore the comparative advantages of buffalo over cows, particularly focusing on their genetics, anatomy, phenotype, production, and nutritional aspects.

Origin and ancestral history

The Bovidae family, the largest within the Artiodactyla order, encompasses a diverse range of species. Within the Bovidae family, the subfamily Bovinae, also known as bovines, comprises nine genera: *Bos* (cattle), *Poephagus* (yak), *Bison* (bison), *Syncerus* (African buffalo), *Boselaphus* (nilgai), *Pseudoryx* (saola), *Tetracerus* (four-horned antelope), *Tragelaphus* (kudu and relatives), and *Bubalus* (domestic buffalo). *Bubalus*, a genus within the Bovidae family was distributed widely across Europe and Asia during the Pleistocene era. Humans have subjected both water buffalo and cattle to significant artificial selection for similar traits since their domestication, despite their divergence over 5.8 million years ago (Mintoo et al., 2019). The two distinct subspecies of water buffalo, the river (*Bubalisbubalis*) and the swamp (*Bubaliskerebau*), originated around 900,000 years ago from separate populations of the most likely ancestor, the wild Asian water buffalo. These subspecies evolved in different geographical regions. Current findings suggest that domestication began with a wild Swamp-like ancestor, which was widespread across mainland of Asia and later diverged into the present *B. arnee* population (Lei et al., 2007; Colli et al., 2018). Two independent domestication events occurred for river and swamp buffaloes. Water buffalo domestication occurred relatively recently, around 3,000–7,000 years ago, which is much later compared to that of cattle, *Bostaurus* (10,000 years ago). The domestication of the river buffalo likely started around 6,300 years ago in north-western India (Minervino et al., 2020). Domesticated river buffalo spread westward across Anatolia, Egypt, and south-western Asia, eventually reaching the Balkans and the Italian peninsula (Kumar et al., 2007). The process of river buffalo domestication was complex, involving multiple maternal lineages and the successive introgression of wild animals into domestic stocks (Nagarajan et al., 2015). The Arab invasion in the eighth century brought water buffalo to Egypt and Italy, and during the Ottoman Empire's expansion in the fifteenth century, crusaders also introduced them to the Balkans and Turkey. On the other hand, the domestication of swamp buffaloes likely occurred near the China-Indochina border around 3,000–7,000 years ago, leading to their spread across Southeast Asia. While swamp buffalo display strong phenotypic uniformity, molecular studies have revealed higher diversity in maternal and paternal lineages, significant genetic differentiation influenced by geography, and limited gene flow (Sun et al., 2020; Zhang et al., 2020). However, there is an exception, with a swamp buffalo lineage from China showing a complex diversity pattern, suggesting long-term gene flow likely due to extensive migrations alongside human movements (Yue et al., 2013).

Cattle are descendants of the aurochs, a wild species that once roamed the forests of Europe and Asia. But new genomic studies have found that the genetic patterns of cattle and buffalo breeds are similar. This suggests that both species were domesticated separately but developed similar mutations (Dutta et al., 2020). Genetic research suggests that approximately 10,500 years ago, approximately 80 female aurochs domesticated in what is now southeastern Turkey, giving rise to the global cattle population. Since then, the global bovine population has surpassed 1.4 billion, comprising two primary subspecies: *Bostaurus* (taurus cattle) and *Bosindicus* (zebu cattle). The processes of cattle domestication and selective breeding have resulted in the emergence of over 1000 distinct breeds (Felius et al., 2015). Archaeological findings from the Middle East suggest that the domestication process of *Bostaurus* followed a particular pathway. Initially, there was a transition from generalized to specialized hunting, leading to the management of herds in the natural habitats of their wild ancestors (Zeder, 2009; Zeder, 2011). The domesticated aurochs eventually evolved into humpless domestic cattle, known as *Bostaurus*. From the Fertile Crescent, a crescent-shaped region in Western Asia,they spread to Eurasia and Africa. Aurochs domestication was also significant on the Indian subcontinent, including modern-day India and Pakistan, was another significant site of Aurochs domestication. Approximately 2,000 years after the initial domestication, a secondary domestication event occurred in the Indus Valley, resulting in the development of the Aurochs subspecies that later evolved into *Bosindicus* (Patel, 2009).

Genetic differences

The most common cattle across several continents are taurine and indicine, followed by river and swamp buffalo. Domestic forms of the yak, banteng, and gaur are mostly found near the areas where their wild ancestors lived. Cattle have 60 chromosomes, while river and swamp buffalo have 50 and 48, respectively. In cattle, there are 58 acrocentric autosomes and two bi-armed sex chromosomes, whereas in buffalo, there are 38 acrocentric autosomes, five pairs of bi-armed autosomes, and two bi-armed sex chromosomes. The buffalo's chromosomes consist of five pairs of bi-armed chromosomes, which correspond to ten one-armed pairs in cattle. These five pairs of buffalo chromosomes (1–5) came from centric fusion translocations between certain cattle chromosomes: 1–25, 2-23, 8–19, 5-28, and 16–29 (Di Berardino et al., 1981; Di Berardino and Iannuzzi, 1984; Iannuzzi et al., 1987; 1990). Comparative cytogenetics and gene mapping demonstrate genetic homology via chromosome band homology and conservation (Lalley et al., 1978; O'Brien and Nash, 1982). Despite different chromosome numbers, there's significant chromosome homology between them, as evidenced by similar banding patterns. Molecular phylogenies indicate that taurine and zebu cattle can cross with other bovines, with the exception of buffaloes (Lenstraand Bradley, 1999; Buntjer et al., 2002; Verkaar et al., 2004; Nijman et al., 2008; MacEachern et al., 2009; Decker et al., 2009). Interspecific breeding occurs either spontaneously or for specific purposes, such as terminal crossing or breed improvement. Offspring from taurine-zebu hybrids are fertile, but crossing zebu or taurine cattle with other species results in fertile cows and sterile bulls. The same fertility pattern applies to swamp and river buffalo (Yindee et al., 2010; Groeneveld et al., 2010). The two subspecies interbreed, resulting in offspring with 49 chromosomes. Male hybrids may encounter fertility issues, while female hybrids tend to have longer intervals between calving. However, further backcrossing primarily observes these challenges in subsequent generations.

Phenotypic and anatomical differences

Both cattle and buffalo are members of the Bovidae family; however, their distinct karyotypes reflect differences in their anatomical, behavioral, physiological, phenotypic, and morphometric traits. Variations in digestive, reproductive, and thermoregulatory systems also contribute to their divergent production traits (Bertoni et al., 2020). Buffalo often exhibit superior body measurements compared to cattle.Skin thickness also shows a significant difference between the two species (Bertoni et al., 2020). The morphology of the two buffalo subspecies also differs significantly. River buffaloes tend to be larger, weighing between 450 and 1,000 kg, with curled horns. In contrast, swamp buffaloes are smaller and lighter, typically weighing between 325 and 450 kg (Cockrill, 1974; Borghese, 2005).

The main anatomical and physiological distinctions between buffalo and cow are evident in the digestive tract, reproductive system, thermoregulation, mammary gland, and hooves, contributing to variations in productivity and reproductive capabilities. River buffaloes, though considered large ruminants like dairy cows, exhibit differences in their digestive systems. Compared to domestic cattle, they have longer and more capacious gastrointestinal tracts, faster tract passage, improved digestion, ruminal contractions, and a distinct microbiota. These differences enable river buffaloes to efficiently use nutrients, particularly in systems dominated by low-to-medium-quality forages. Comparative studies have shown that the rumen-reticulum complex in buffaloes can store more food than that of cattle, and that buffaloes also retain more food (Angulo et al., 2005; USDA, 2018). Also, compared to cattle, dairy buffaloes have a wider range of microorganisms living in their rumen. These include cellulolytic, proteolytic, amylolytic, and lipolytic bacteria and fungi, which break down forage cell walls and proteins more efficiently (Singh et al., 1992). This leads to a higher conversion rate of low-quality forage into volatile fatty acids (VFA) and ammonia (Chanthakhoun et al., 2012). Notably, river buffaloes produce less methane, contributing to reduce greenhouse gas emissions compared to dairy cows or beef cattle (Pant and Roy, 1970; Ranjhan, 1992; Franzolin and Dehority, 1999; Malik et al., 2021).

Buffalo and dairy cows share similar reproductive organs; however, dairy cows are slightly larger and weigh less than buffalo cows and are less stiff and muscular. This could help to explain why uterine prolapses are more common in dairy buffaloes (De Rosa et al., 2015). Biometric analyses have demonstrated that bovines and Murrah buffaloes exhibit distinct reproductive parameters, underscoring the evident disparities in their anatomical characteristics (Sane et al., 1965; Carvalho et al., 2010; De Rosa et al., 2015). In addition, river buffaloes have specific benefits in regulating their body temperature in extremely hot situations, which sets them apart from dairy and feedlot cattle. They possess less abundant hair and a denser outer layer of skin with a significant amount of melanin, which absorbs heat and offers defence against UV rays. Buffaloes have a lesser number of sweat glands, but their greater size helps them regulate their body temperature. To cope with extreme temperatures, they rely on extra processes such as seeking shade, water sources, and mud to maintain a normal body temperature and stay comfortable. In general, the morpho-physiological disparities between river buffaloes and dairy cattle highlight their unique adjustments to different environmental conditions and production systems.

Milk productivity difference

Milk production in buffaloes follows a distinct lactation curve, characterized by a rapid increase, peak, plateau phase, and gradual decline until the end of lactation. The ability to maintain high milk production levels after the peak, known as lactation persistence, is economically significant (Togashi and Lin, 2004; Boselli et al., 2020). Water buffalo, among the most productive domestic animals, boasts a longer productive lifespan compared to cattle, making it economically vital, particularly for small-scale producers in developing nations (Minervino et al., 2020). Buffaloes possess a superior ability to convert low-nutrient feed into milk, making them valuable in the agricultural sector. Global farmers cultivate this docile, intelligent, and curious animal, primarily prized for its high-quality meat and rich milk. Buffalo milk is gaining recognition for its intrinsic value as a dairy product, consumed directly in many Asian countries and transformed into high-demand dairy products elsewhere (Younas et al., 2013; Borghese and Moioli, 2016). According to FAO data, buffalo milk production accounted for approximately 15.14% of global fresh milk production in 2018, with Asia leading the way (accounting for 35.30% of the total milk production), where buffaloes are major milk producers in countries like India, Pakistan, Egypt, and Nepal. Moreover, Egypt and Nepal have a higher population of dairy buffaloes than cows. The top ten buffalo milk producers, including India at the top, followed by Pakistan, China, Egypt, Nepal, Italy, Myanmar, Iran, Colombia, and Brazil, contribute to 97.59% of global production (FAO, 2019). The reported values only represent estimates of the actual production potential of the species due to the lack of production data from over 50 out of the 77 countries that raise buffaloes. Out of the 208 million buffaloes globally, countries lacking buffalo milk production data raise approximately 7.48 million of these animals. Italy, the fifth-largest global milk producer (97% of buffalo milk production in Europe), stands out as the only country with an official system that provides real-time information on milk production and the entire buffalo supply chain since 2014 (Vecchio et al., 2017).

Based on FAO data, global buffalo milk production surged by 32.57% between 2011-2018, rising from 96 to 127 million tons. In contrast, cattle milk production experienced a more modest growth of 10.67%, increasing from 617 to 683 million tons during the same period. As per the expert analysis, cow's milk production reached 757.5 million tons in 2022, marking a 0.7% increase compared to the previous year. Buffalo milk, on the other hand, exhibited notable growth dynamics, with production totaling 142.5 million tons, reflecting a 3.3% increase from 2021. Buffalo milk production has seen a significant increase, outpacing that of cattle milk, with factors such as breed, production purpose, breeding type, feeding techniques, and genetic selection influencing manufacturing (Pasha and Hayat, 2012; Ahmad et al., 2017). Compared to cow's milk, buffalo milk contains roughly double the fat content and approximately 30% more total solids, making it nutritionally richer and more energy-dense (Costa et al., 2020). Table 1 presents a comparison of the compositions of buffalo and cow milk. Buffalo milk plays a crucial role in the cheese industry, particularly in the production of mozzarella cheese. The designation "Mozzarella di BufalaCampana PDO" guarantees the cheese's exclusive production from buffalo milk in specific regions of Italy, underscoring the significance of buffalo milk in the global dairy landscape (Borghese and Moioli, 2016; Cesarani, 2021).

Table 1: Milk compositions of buffalo and cow (Salman et al., 2014; Hegde, 2019; Kausar et al., 2023)

S.No.	Components	Buffalo milk	Cow milk
1.	Fat (%)	5.25	4.04
2.	Protein (%)	4.13	3.80
3.	Carbohydrate (gm)	5.00	4.40
4.	Calcium (mg/100g)	195.00	120.00
5.	Phosphorus (mg/100 g)	268	213
6.	Magnesium(mg/100 g)	30.0	23.0
7.	Potassium (mg/100 mg)	107.0	185.0
8.	Sodium (mg/100 g)	65	73
9.	Cholesterol (mg/100g)	8.00	14.00

10.	Lactose (%)	4.82	4.28
11.	Water (g/100g)	81.10	87.80
12.	Total solids (%)	15.03	12.84
13.	Saturated Fatty Acids (g/100g)	4.20	2.40
14.	MuFAs: Monounsaturated Fatty Acids (g/100g)	1.70	1.10
15.	PuFAs: Polyunsaturated Fatty Acids (g/100g)	0.20	0.10
16.	Ash (%)	0.82	0.72
17.	Calorific values (Kcal/100g)	83.11	66.77
18.	Energy (KJ/100g milk)	463.00	275.00
19.	Somatic cell count (per mL)	135916.78	161608.70
20.	Electrical conductivity (mS/cm)	4.55	5.70
21.	pH	6.56	6.61
22.	N-acetyl-β-D-glucosaminidase (NAGase) activity (units/ml)	46.93	46.43
23.	Mineral (gm)	6.50	4.10
Physical characters			
24.	Viscosity (cP)	2.04	1.86
25.	Fat globule size (μm)	5.01	3.85
26.	Phosphatase activity (units/100)	28.00	82.00
27.	Fluorescence under UV light	Greenish Yellow	Pale Bluish

Conclusion

Both buffalo and cow belong to the Bovidae family and serve as sources of milk, meat, and draught; however, their distinct traits and qualities shape their roles in agriculture. Buffaloes, renowned for their resilience and ability to thrive in challenging conditions, excel in hot climates and marginal lands where other livestock may struggle. With their sturdy build and efficient feed conversion, buffaloes prove invaluable assets for small-scale producers in developing nations. They exhibit superior digestive efficiency, enabling them to convert low-nutrient feed into high-quality milk, making them economically vital in regions like Asia and Egypt. Notably, buffalo milk, prized for its rich flavour and creamy texture, plays a critical role in various culinary traditions and dairy products worldwide, particularly in the production of mozzarella cheese. In contrast, cows are more commonly associated with temperate climates and lush pastures, yet they too display adaptability to a range of environments with proper management. Cows typically produce larger quantities of milk, but with lower fat content and solids compared to buffalo milk. Despite this, they remain the primary source of dairy products in many parts of the world, contributing significantly to global milk production.

The ancestral histories and genetic differences between buffaloes and cows further highlight their distinct evolutionary paths and breeding characteristics. While both species underwent domestication by humans, they diverged over millions of years, resulting in differences in chromosome numbers and genetic homology. These genetic variances contribute to phenotypic and anatomical distinctions, impacting traits such as size, skin thickness, and reproductive capabilities. Moreover, buffalo and cow physiologies also exhibit adaptations to varying environmental conditions, particularly in thermoregulation and digestive efficiency. Buffaloes, with their thicker skin and lower density of sweat glands, excel in heat tolerance, while their efficient digestive systems enable them to utilize low-quality forages effectively. These adaptations underscore their suitability for challenging climates and extensive grazing systems.

In conclusion, buffalo represent a valuable asset in livestock production, often outperforming cows in terms of economic returns, ecological sustainability, and nutritional value. Their resilience, productivity, and versatility make them a compelling choice for farmers seeking to maximize profitability while minimizing environmental impact. Therefore, we can rightfully consider buffalo as the "black gold" of livestock farming.

References

Ahmad M, Bhatti J A, Abdullah M, Javed K, Din R u, Ali M, Rashid G, Ahmed N, Jehan M. Effect of different ambient management interventions on milk production and physiological performance of lactating Nili-Ravi buffaloes during hot humid summer. Livestock Res Rural Dev. 2017, 29:230.

Angulo RA, Noguera RR, Berdugo JA. The water buffalo (*Bubalus bubalis*) an efficient user of nutrients; aspects on fermentation and ruminal digestion.Livestock Res Rural Dev, 2005: 17.

Bertoni A, Napolitano F, Mota-Rojas D, Sabia E, Álvarez-Macías A, Mora-Medina P, Morales-Canela A, Berdugo-Gutiérrez J, Legarreta IG. Similarities and differences between river buffaloes and cattle: Health, physiological, behavioral and productivity aspects. J Buffalo Sci, 2020, 9: 92-109.

Borghese A, Moioli B. Buffalo: Mediterranean region. In: Reference Module in Food Science (Elsevier), 2016.

Borghese A. Buffalo Production and Research. Rome: FAO Regional Office for Europe, 2005.

Boselli C, De Marchi M, Costa A, Borghese A. Study of milkability and its relation with milk yield and somatic cell in mediterranean Italian water buffalo. Front Vet Sci. 2020 7:432. doi: 10.3389/fvets.2020.00432.

Buntjer JB, Otsen M, Nijman IJ, Kuiper MT, Lenstra JA. Phylogeny of bovine species based on AFLP fingerprinting. Heredity (Edinb).2002, 88: 46-51.

Carvalho N, Gimenes L, Reis EL, Cavalcante AK, Mello JE, Nichi M, Nicacio AC, Nasser L. FT, Rezende LFC, Wisnesck CA, Moura CEB, Benedicto HB, Bombonato PP, Baruselli PS. Biometry of genital system from buffalo (Murrah) and bovine (Nelore) females. RevistaVeterinaria, 2010, 21(1):276.

Cesarani A, Biffani S, Garcia A, Lourenco D, Bertolini G, Neglia G, M Ignacy, Macciotta N PP. Genomic investigation of milk production in Italian buffalo. Italian J AnimSci, 2021, 20(1): 539–547. doi: 10.1080/1828051X.2021.1902404

Chanthakhoun V, Wanapat M, Kongmun P, Cherdthong A. Comparison of ruminal fermentation characteristics and microbial population in swamp buffalo and cattle. Livestock Sci, 2012, 143(2-3): 172-176. doi: 10.1016/j.livsci.2011.09.009.

Cockrill WR. The husbandry and health of the domestic buffalo. Rome: Food and Agriculture Organization of the United Nations, 1974.

Colli L, Milanesi M, Vajana E, Iamartino D, Bomba L, Puglisi F, Del Corvo M, Nicolazzi EL, et al. New insights on water buffalo genomic diversity and post-domestication migration routes from medium density SNP chip data. Front Genet. 2018;9:53. doi: 10.3389/fgene.2018.00053.

Costa A, Negrini R, De Marchi M, Campanile G, Neglia G. Phenotypic characterization of milk yield and quality traits in a large population of water buffaloes. Animals (Basel). 2020;10(2):327. doi: 10.3390/ani10020327.

De Rosa G, Grasso F, Winckler C, Bilancione A, Pacelli C, Masucci F, Napolitano F. Application of the Welfare Quality protocol to dairy buffalo farms: Prevalence and reliability of selected measures. J Dairy Sci. 2015;98(10):6886-96. doi: 10.3168/jds.2015-9350.

Decker JE, Pires JC, Conant GC, McKay SD, Heaton MP, Chen K, Cooper A, Vilkki J, Seabury CM, et al. Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. ProcNatlAcadSci U S A. 2009;106(44):18644-9. doi: 10.1073/pnas.0904691106.

Di Berardino D, Iannuzzi L, Bettini TM, Matassino D. Ag-NORs variation and banding homologies in two species of Bovidae: *Bubalus bubalis* and *Bos taurus*. Can J Genet Cytol. 1981;23(1):89-99. doi: 10.1139/g81-011.

Di Berardino D, Iannuzzi L. Detailed description of RBA-banded chromosomes of river buffalo (*Bubalus bubali* L.). Genet SelEvol (1983), 1984;16(3):249-60. doi: 10.1186/1297-9686-16-3-249.

Di Meo GP, Iannuzzi L, Perucatti A, Ferrara L. Identification of nucleolus organizer chromosomes in sheep (Ovisaries L.) by sequential GBG/Ag-NOR and RBG/Ag-NOR techniques. Cytobios. 1993;75(302-303):183-90.

Dutta P, Talenti A, Young R, Jayaraman S, Callaby R, Jadhav SK, Dhanikachalam V, Manikandan M, Biswa BB, Low WY, Williams JL, Cook E, Toye P, Wall E, Djikeng A, Marshall K, Archibald AL, Gokhale S, Kumar S, Hume DA, Prendergast JGD. Whole genome analysis of water buffalo and global cattle breeds highlights convergent signatures of domestication. Nat Commun. 2020;11(1):4739. doi: 10.1038/s41467-020-18550-1.

FAO, FAOSTAT. Available online at: http://www.fao.org/faostat/en/#data/QA (accessed January 19, 2020), 2019.

Felius M, Beerling M-L, Buchanan DS, Theunissen B, Koolmees PA, Lenstra JA.On the history of cattle genetic resources. Diversity, 2014; 6(4):705-750. Doi:10.3390/d6040705

Franzolin R, Dehority BA. 1999 Comparison of protozoal populations and digestion rates between water buffalo and cattle fed an all forage diet. J Applied Anim Res, 16: 33-46.

Groeneveld LF, Lenstra JA, Eding H, Toro MA, Scherf B, Pilling D, Negrini R, Finlay EK, Jianlin H, Groeneveld E, Weigend S; GLOBALDIV Consortium. Genetic diversity in farm animals--a review.Anim Genet. 2010;41Suppl 1:6-31. doi: 10.1111/j.1365-2052.2010.02038.x.

Hegde N. Buffalo husbandry for sustainable development of small farmers in India and other developing countries. Asian J Res AnimVeSci, 2019; 2:1-20. Doi: 10.9734/ajravs/2019/v2i156.

Iannuzzi L, Di Berardino D, Gustavsson I, Ferrara L, Di Meo GP.Centromeric loss in translocation of centric fusion type in cattle and water buffalo.Hereditas. 1987;106(1):73-81. doi: 10.1111/j.1601-5223.1987.tb00238.x.

Kausar R, Hameed A, Jamil H, Iqbal Z, Bahadur SK, Jabbar J, Sabir A. Comparative analysis of buffalo and cow milk for quality characteristics and β-N-acetyl-glucosaminidase activity in non-infected animals. Emirates J Food and Agri, 2023; 35(3):203. Doi: 10.9755/ejfa.2023.v35.i3.2965.

Kumar S, Nagarajan M, Sandhu JS, Kumar N, Behl V. Phylogeography and domestication of Indian river buffalo. BMC Evol Biol. 2007;7:186. doi: 10.1186/1471-2148-7-186.

Lalley PA, Minna JD, Francke U. Conservation of autosomal gene synteny groups in mouse and man.Nature. 1978;274(5667):160-3. doi: 10.1038/274160a0.

Lei CZ, Zhang W, Chen H, Lu F, Liu RY, Yang XY, Zhang HC, Liu ZG, Yao LB, Lu ZF, Zhao ZL. Independent maternal origin of Chinese swamp buffalo (*Bubalusbubalis*). Anim Genet. 2007;38(2):97-102. doi: 10.1111/j.1365-2052.2007.01567.x.

Lenstra JA, Bradley DG. Systematics and phylogeny of cattle. In the Genetics of Cattle, Fries R and Ruvinsky A, Eds., CABI Publishing, Oxon, New York, 1999:1-14.

MacEachern S, McEwan J, Goddard M. Phylogenetic reconstruction and the identification of ancient polymorphism in the Bovini tribe (Bovidae, Bovinae).BMC Genomics. 2009;10:177. doi: 10.1186/1471-2164-10-177.

Malik PK, Trivedi S, Mohapatra A, Kolte AP, Sejian V, Bhatta R, Rahman H. Comparison of enteric methane yield and diversity of ruminal methanogens in cattle and buffaloes fed on the same diet. PLoS One. 2021;16(8):e0256048. doi: 10.1371/journal.pone.0256048.

Minervino AHH, Zava M, Vecchio D, Borghese A. Bubalusbubalis: A Short Story. Front Vet Sci. 2020;7:570413. doi: 10.3389/fvets.2020.570413.

Mintoo AA, Zhang H, Chen C, Moniruzzaman M, Deng T, Anam M, EmdadulHuque QM, Guang X, Wang P, Zhong Z, Han P, Khatun A, Awal TM, Gao Q, Liang X. Draft genome of the river water buffalo. EcolEvol. 2019;9(6):3378-3388. doi: 10.1002/ece3.4965.

Nagarajan M, Nimisha K, Kumar S. Mitochondrial DNA Variability of Domestic River Buffalo (*Bubalus bubalis*) Populations: Genetic Evidence for Domestication of River Buffalo in Indian Subcontinent. Genome BiolEvol. 2015;7(5):1252-9. doi: 10.1093/gbe/evv067.

Nijman IJ, Van Boxtel DJ, Van Cann LM, Cuppen E, Lenstra JA. Phylogeny of Y-chromosomes from interbreeding bovine species. Cladistics, 2008;24:723-726.

O'Brien SJ, Nash WG. Genetic mapping in mammals: chromosome map of domestic cat. Science. 1982;216(4543):257-65. doi: 10.1126/science.7063884.

Pant HC, Roy A. Studies on the rumen microbial activity of buffalo and zebu cattle: Concentrations of micro-organisms and total and particulate nitrogen in the rumen liquor. Indian J AnimSci, 1970: 40: 600-609.

Pasha TN, Hayat Z. Present situation and future perspective of buffalo production in Asia: history and domestication of buffalo in Asia. J Anim Plant Sci, 2012; 22:250–256.

Patel A. Occupational histories, settlements, and subsistence in Western India: what bones and genes can tell us about the origins and spread of pastoralism.Anthropozoologica, 2009; 44: 173–188.

Ranjhan S. Nutrition of river buffaloes in Southern Asia. In: Tulloh J & Holmes H. (Eds.), Buffalo Production (1st ed.), Asia, 1992:111-134.

Salman M, Khaskheli M, Haq I, Talpur AR, Khuhro AP, Rauf M, Hamid H, Aziz A. Comparative studies on nutritive quality of buffalo and cow milk. International J Res Applied, Natural Social Sci, 2014; 2(12): 69-78.

Sane CR, Kaikini AS, Deshpande BR, Koranne GS, Desai VG.Study of biometry of genitalia of Jaffri buffalo-cows (*Bos bubalis*). Indian Vet J, 1965; 42: 591.

SiddikyMd, Faruque MO. Buffaloes for dairying in South Asia: potential, challenges and way forward. SAARC J Agri. 2018; 15: 227. Doi:10.3329/sja.v15i2.35167.

Singh S, Pradhan K, Bathia SK. Relative ruminal microbial profile of cattle and buffalo fed wheat straw-concentrate diet. Indian J AnimSci, 1992: 62, 1197-1202.

Sun T, Wang S, Chanthakhoun V, Dang R, Huang Y, Chen H, Lei C. Multiple domestication of swamp buffalo in China and South East Asia.J Anim Breed Genet. 2020;137(3):331-340. doi: 10.1111/jbg.12445.

Togashi K, Lin CY. Efficiency of different selection criteria for persistency and lactation milk yield. J Dairy Sci. 2004;87(5):1528-35. doi: 10.3168/jds.S0022-0302(04)73304-4.

USDA-United States Department of Agriculture. Milk Production In: Economics, Statistics and Market Information System (ESMIS) 2018: Avaliable from: https://usda.library.cornell.edu/concern/publications/h989r321c?locale=en

Vecchio D, Bertocchi L, Galiero G, Romano F, Corrado F, Noschese R, et al. The mediterranean Italian buffalo: research for supply chain sustainability. VeterinariaItaliana, 2017;53(1): 40-43.

Verkaar EL, Nijman IJ, Beeke M, Hanekamp E, Lenstra JA. Maternal and paternal lineages in cross-breeding bovine species. Has wisent a hybrid origin? Mol Biol Evol. 2004;21(7):1165-70. doi: 10.1093/molbev/msh064.

Yindee M, Vlamings BH, Wajjwalku W, Techakumphu M, Lohachit C, Sirivaidyapong S, Thitaram C, Amarasinghe AA, Alexander PA, Colenbrander B, Lenstra JA. Y-chromosomal variation confirms independent domestications of swamp and river buffalo. Anim Genet. 2010;41(4):433-5. doi: 10.1111/j.1365-2052.2010.02020.x.

Younas M, Ishaq K, Yaqoob M, Ahmad T. Virtues of the milk from water buffalo. Buffalo Bull, 2013;32: 857–865.

Yue XP, Li R, Xie WM, Xu P, Chang TC, Liu L, Cheng F, Zhang RF, Lan XY, Chen H, Lei CZ. Phylogeography and domestication of Chinese swamp buffalo. PLoS One. 2013;8(2):e56552. doi: 10.1371/journal.pone.0056552.

Zeder MA. The Neolithic macro-(r)evolution: Macro evolutionary theory and the study of culture change. J Archaeological Res, 2009; 17(1): 1–63.

Zeder MA.The origins of agriculture in the Near East. Current Anthropology, 2011; 52(S4), 221–225.

Zhang Y, Colli L, Barker JSF. Asian water buffalo: domestication, history and genetics. Anim Genet. 2020;51(2):177-191. doi: 10.1111/age.12911.