Indian Journal of Animal Sciences **86** (12): 1366–1377, December 2016/Review Article

Genetics of domestication and world-wide introduction of *Bos indicus* (Zebu) and *Bos taurus* (Taurine) cattle

SUSHIL KUMAR[1], RENU KUMARI[2], VISHAKHA SHARMA[3] and M P YADAV[4]

National Academy of Agricultural Sciences, Pusa Campus, New Delhi 110 012 India

Received: 08 June 2016; Accepted: 07 September 2016

ABSTRACT

Neolithic people who had already domesticated crops such as barley and wheat, domesticated cattle more than 8,500 years ago. This development transitioned human populations from hunter-gatherers to sedentary complex societies. Modern cattle comprise mainly of two species (or types) *Bos taurus* (taurine) and *Bos indicus* (zebu or Indicine) which are distributed world-wide; and some minor species of cattle, including *Bos grunniens* (yak), *Bos frontalis* (gayal/mithun) and *Bos javanicus domesticus* (Bali banteng) are also important in East and Southeast Asia. Neolithic period onwards cattle have been deployed to plough land for efficient agriculture; yield milk, meat and leather and for making yoghurt, cheese and ghee from milk; transport people and goods in carts. Historical accounts of 10000 years and archaeological findings of Neolithic period have been complemented by recent mitochondrial and nuclear genetical-genomical evidences to understand the pre- and post- domesticated history of cattle. Analyses of nuclear and mitochondrial genome sequences for polymorphism at DNA markers in ancient (extinct) and modern cattle has revealed the parentage of cattle species, approximate dates and places of their domestication, approximate dates and routes of their migration to new habitats on different continents, and times and places of introgression from wild aurochs in Europe and Africa and admixture between species. Cattle have undergone natural and strong artificial selection for adaptation to varied environments, fertility, social behaviour, milk and meat yields, milk quality and aesthetic morphological features which have had pronounced effect on cattle genome, causing reduction in genetic variability. Here a brief review is presented about genetical evidence on above aspects and future research directions are also identified.

Key words: African taurine, Ancient cattle DNA, Banteng, Fertile crescent, Gaur, Indus valley, Mithun, Neolithic farmers, Yak

The interaction between domestic cattle and humans is an example of symbiotic relationship. There are five domesticated species (types) of the bovine genus *Bos* (family, Bovidae; subfamily, Bovinae; tribe, Bovini; 2n = 58+XY): Taurine and zebu are present world-wide; and banteng, gayal and yak are distributed in parts of Southeast Asia (Table 1). Domestication of cattle followed the advent of agriculture in the Neolithic period (Fuller *et al.* 2006, 2014; Fuller and Murphy 2014). Since their domestication 2,500 to 10,500 years ago (ya), cattle have served human civilizations as draught animals for ploughing of agricultural fields and wheeled transportation and as sources of milk, meat, skin, hide, leather and dung-fuel/fertilizer; and as the earliest form of capital. Cattle owners provided care and water, feed, housing and shelter from prey to the retained cattle. There are now more than 800 recognized breeds of cattle (>30 in India) in the world, in addition to non-descript hybrids between different breeds and types of cattle (Felius 1995, Felius *et al.* 2014, Hongo 2011). Modern breeds of cattle yield on average basis 20l milk/day, containing 650 g milk protein and 750 g fat (Pehrsson *et al.* 2000). The world-wide yearly milk and meat production from cattle in 2015 was, 636 million tonnes (61 million tonnes in India) and 58.4 million tonnes (4.2 million tonnes in India) respectively, yearly yield of milk from other livestock-buffaloes, goats, sheep, camels, equines and yak was~ 125 million tonnes (dairy.ahdb.org.uk/market-information/supply; beef2live.com/story-world-beef production-ranking). In 2015, a cattle population of 965 million (301 million in India; beef2live.com/story-world-cattle-inventory-ranking) was able to meet the cow dairy requirements of 7.39 billion world population of humans (1.29 billion in India; www.worldmeters.info/world-population). Clearly, domestication of cattle was one of the most important developments for the cultural, demographic and economic advancement of human society, and acquirement of health promoting alleles by humans (Reich *et al.* 2009, Curry 2014, Mathieson *et al.* 2015, Kumar and Kumari 2016).

Present address: [1]Honarary (Emeritus) Scientist (sushil2000_01@yahoo.co.in), [4]Professor (yadav_mp@hotmail.com), [2]Research Associate (renu_kum2006@yahoo.co.in), National Institute of Plant Genome Research. [3]Research Associate (vishakha59 @gmail.com), SKAIRED.

Each cell of a cattle contains mitochondria possessing 103 copies of their DNA genome and a nucleus which contains 2 copies each of 29 autosomes and XX (in females) or XY (in males) sex chromosomes (Kieffer and Cartwright 1968). DNA sequences of mitochondrial and nuclear chromosomes of taurine and zebu cattle are known (Heindler *et al.* 2008, Zimn *et al.* 2009, Canavez *et al.* 2012). The cells of both cattle types carry genetic information about evolution of the cattle, in the form of mitochondrial genome haplotypes and frequencies of nuclear autosomal and Y chromosomal sequence alterations (alleles) and selective sweeps. Whereas the mitochondrial haplotypes are inherited through females, the nuclear markers are contributed to progeny by both male and female parents. Genetic variation accumulates with time/over generations, therefore, early domesticates are expected to carry less DNA sequence variation than their modern descendants. Archaeological skeletones (bones and teeth) of ancient cattle discovered in India, China, Southeast Asia, Middle East, Africa and Europe were used for DNA sequence analyses to elicit paleogenetic information about cattle ancestry, domestication and post-domestication movement. Comparative analysis of polymorphism in many thousand nuclear genome DNA markers and several mitochondrial DNA markers among hundreds of ancient cattle and thousands of extant cattle, later of breeds common in different parts of world, has generated information about the complex evolutionary history of cattle populations, including times and geographic locations of domestication events for different types of cattle and times and routes of their initial introduction from areas of domestication to parts of different continents (Loftus *et al.* 1999,Christian 2000, Copley *et al.* 2003, Freeman *et al.* 2004, Baig *et al.* 2005, Beja-Pereira *et al.* 2006, Bollongino *et al.* 2006, 2013, Edwards *et al.* 2007, Chen *et al.* 2010, Larson and Burger 2013, McTavish *et al.* 2013, 2014, Stock and Gifford-Gonzalez 2013, Magee *et al.* 2014, Decker *et al.* 2014, Schibler *et al.* 2014, Orlando 2015, Park *et al.* 2015, Scheu *et al.* 2015). Here, we briefly reviewed the results of these archaeozoological-cum-genetic-cum-historiogeographic studies.

Origin of domestic taurine and zebu (indicine) cattle

Cattle-like fiercely wild animals of huge size belonging to the taxa *Bos primigenius* or aurochs, descendant of *Bos acutifrons*, were the progenitor of major domestic cattle species (Perkins 1969, Epstein and Nason 1984, McKenna and Bell 1997, Bradley *et al.* 1998, Lenstra and Bradley 1999,Clutton-Brock 1999, Mona *et al.* 2010, McTavish *et al.* 2013, Felius *et al.* 2014, 2015, Orlando 2015, Park *et al.* 2015). From several million years ago (mya), *Bos primigenius* was endemic to a vast geographical area, including the grass plains of Asia (India), Central Asia (Steppes = Ukraine, Russia, Kyrgystan, China, Mongolia), Middle East, North Africa and Europe (Mona *et al.* 2010). Fossilized remnants of the species dating back to two mya have been discovered in India (Van Vuure 2001). Paleogenetic evidence has further established that about 250,000 ya, aurochs had genetically diverged into sub-species, 2 of which were *Bos primigenius primigenius* that ranged in Northeast Asia and Europe (Eurasia), and *Bos primigenius namadicus* which ranged in India (Van Vuure 2001, Mona *et al.* 2010, Orlando 2015). The domesticated descendants of these species, now extinct, were the main resource of genetic variability present in the modern cattle in the world (Lenstra and Bradley 1999, Troy *et al.* 2001, Lenstra and Felius 2014).

In the Neolithic period, about 10,500 ya, hunter gatherers who had converted to sedentary pastoralism (Diamond 2002, Ellis *et al.* 2013), located in fertile crescent in the boundary region of present day Turkey and Syria, domesticated *Bos taurus* or taurine cattle from among the *Bos primigenius primigenius* aurochs of the area (Troy 2001, Peters *et al.* 2005, Ho and Shapiro 2011, Hongo 2011, Vigne 2011, Schibler *et al.* 2014). Genetic analysis of ancient and modern taurine cattle showed that there was genetic bottleneck in the domestication process since only 80 or 81 female aurochs were the founding ancestors of extant taurine cattle (Ajman-Marson *et al.* 2010, Bollingino *et al.* 2012, Lenstra *et al.* 2014, Lenstra and Felius 2014, Scheu *et al.* 2015). The taurine cattle inherited from their founding mothers at least 6 types of mitochondrial haplogroups T, T1, T2, T3, T4 and T5 (a haplogroup structure is characterized by sequence of a 240 bp hypervariable mitochondrial (mt) DNA control region, variation in which is due to insertional and point mutations, base substitutions, deletions and additions) (Troy *et al.* 2001, Achilli *et al.* 2009). Domesticated in Eurasia, the taurine cattle are well adapted to temperate climatic conditions. Their other domestication attributes included tamed docile behaviour in human presence, ability to efficiently utilize grass and leaves as feed, faster rate of growth, smaller size, shorter lifespan and reduced sexual dimorphism as compared to aurochs, and ability to breed in captivity (Turner 1980, Felius 1995, Taberlet *et al.* 2011, Lenstra and Felius 2014).

Further domestication of *Bos primigenius namadicus* aurochs resulted into *Bos indicus* or zebu (indicine) cattle by the Indus valley farmers about 8,500 ya. The zebu domesticates inherited from their female parents I1 mt DNA haplogroup (Naik 1978, Loftus *et al.* 1994, Baig *et al.* 2005, Bradley *et al.* 2006, Fuller 2006, Jarrige 2006, Zeder *et al.* 2006, Singh 2008, Hiendleder *et al.* 2008, Armone-Marson 2010, Chen *et al.* 2010, Murray *et al.* 2010, Colledge *et al.* 2013, Magee *et al.* 2014). Another independent domestication of indicine cattle is proven to have occurred in the Indo-Gangetic plains area about 4000 ya. These domesticates carried I2 mt DNA haplogroup (Chen *et al.* 2010, Murray *et al.* 2010, Magee *et al.* 2014). The domesticated zebu cattle had some of the same traits as in domestic taurine cattle. However, zebu cattle is different from taurine cattle morphologically, anatomically and physiologically. Zebu domesticated in semi-temperate conditions bore smoother coat, a hump over shoulders, flapped rather than erect ears, more pendulous dewlap and

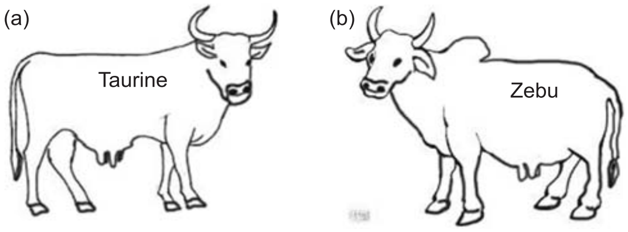

Fig. 1. Diagrammes of *Bos taurus* (Taurine) and *Bos indicus* (Zebu or Indicine) cattle. Taurine is humpless and bears erect ears. Contranstingly Zebu has a hump at shoulders and bears drooping ears.

larger sweat glands, and had predominance of intramuscular fat rather than subcutaneous fat, lower metabolic rate, late maturity and tolerance towards ticks (insects) and intestinal parasites (protozoa), water-stress, feed-stress, high humidity and high temperature (Utech *et al.* 1978, Hansen 2004, Bahbahani *et al.* 2015), European taurine and Indian zebu can both tolerate low temperatures (say –13ºC) equally well, however taurines barely tolerate 25ºC whereas zebu can tolerate temperatures beyond 42ºC (Frisch and Vercoe 1977, Turner 1980, Grigson 1991, Hall 2004, Lenstra and Felius 2014). Beta casein in the milk of taurine called A1 beta casein has histidine at 67th position in the 209 amino acid (aa) long sequence. Corresponding position in the beta casein called A2 beta casein in zebu has proline. This mutation in taurine beta casein (A1) results in production of a 7 (aa) long digestion product called beta casomorphin–7 (BCM 7), which has been intriguingly implicated as a cause of several human disease conditions resulting from consumption of the taurine's milk (Beales *et al.* 2002, Hill 2003, Woodford 2009, Sodhi *et al.* 2012).

Zebu and taurine cattle (Fig. 1) were found to be fully interfertile. Only difference in their karyotypes is that Y chromosome is metacentric in taurine cattle and acrocentric in zebu cattle. Their F1 hybrids demonstrate high levels of heterosis (McDowell *et al.* 1996). Despite bottlenecks in the domestication events of cattle from among violently hostile aurochs and subsequently during introduction to distant lands thousands of years ago (Felius *et al.* 2014), the sustained zebu and taurine possessed considerable genetic variability. Their progeny responded to a wide variety of selection criteria, including adaptation to diverse agroclimates (Chan *et al.* 2010) and variety of feeds (Church 1984); coat colour (Schmitz 2014); stature (Randhawa *et al.* 2015); body weight (Pinheiro *et al.* 2012); strength and vigour for draught (Joshi *et al.* 2005); tolerance towards pests and diseases (Francis 1966, Qureshi *et al.* 1996, fttp.fao.org/docrep/fao); polledness and horn size (Schmitz 2013); high milk yield (Kiplagat *et al.* 2012, IAEA-TECDOC–1670); high content of protein (Zhou *et al.* 2015) and fat (Winter *et al.* 2002, Kaupe *et al.* 2004, Kuhn *et al.* 2004, Glaser *et al.* 2010) in the milk (Ibeagha *et al.* 2007); and high meat yield (Pinheiro *et al.* 2012, O'Rourke *et al.* 2013, Publication 8130 ANR Univ Cal). The major genes controlling certain important traits linked to positive selection sweeps in cattle include the following: *POLL* for horn development, *MSTN, AKA* and *GDF8* genes for muscular hypertrophy, *KIT* and *MCIR* for coat colour pattern, *PDGFRA* and *KDR* for fertility, *NCAPG-LCORL* and *PLAG1-CHCHD7* genes for stature, *R3HDM1, ZRANB3* genes for feed efficiency, *ABCG2*, *DGAT1* and *GHR* genes for milk yield and its protein quality and *HSPA9, CD14, ARAP3* and *PCDM* genes for immune response (Randhawa *et al.* 2016). Complementary nature of their characters allowed worldwide spread of taurine, zebu and their hybrids. However, cattle populations of taurine and zebu breeds in Eurasia and Asia remained susceptible to rinderpest transmission (Yadav 2011).

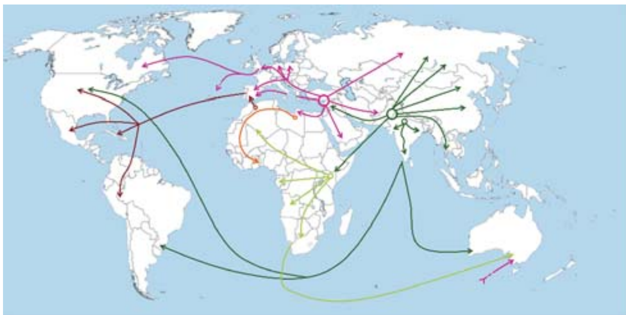

Fig. 2. Diagrammatic representation of centres of origin (domestication) and approximate migration routes of *Bos taurus* (Taurine) and *Bos indicus* (Zebu) cattle. Red and green circles respectively depict Fertile Crescent (Near East) area, the centre of origin of Taurines and Greater Indus valley/Indian subcontinent centres of origin of Zebus. The migration routes of Zebu to parts of Indian subcontinent, Southeast Asia, China, Mongolia, Near East, Africa, Americas and Australia are shown by arrows of green colour. Red coloured arrows show the migaration routes of taurine to different parts of Europe via Mediterranean coast and Danube basin, Russia, Northeast Asia, India, Africa, North America and Australia. Light green coloured arrows show migratory routes of Taurine introgressed with zebu in Africa and movement into Australia. Orange coloured arrows depict the route of Aurochs introgressed Taurine or African Taurine in Africa. The entry of African Taurine × zebu introgressed cattle into Portugal and Spain and from there to America is shown by brown coloured arrows.

Following their origin, taurine and zebu cattle were dispersed in ancient times in different directions, via their co-migration with farmers and explorers moving to new farmable areas for greater opportunities. In recent times, cattle have been traded between different countries. Thus cattle got introduced to wherever human populations came to reside on different continents and islands. Discussed below is the paleogenetical and/or historiogenetical evidence about the times and routes of initial dispersal of zebu, taurine and their admixed lines to various parts of continents and to islands of human habitation (Fig. 2).

Introduction of taurine into Europe, Africa and Northeast Asia from Fertile Crescent

Starting from ~ 10,000 ya, Neolithic farmers rapidly distributed the domesticated taurines world over. There is evidence that bulk of the taurines from Fertile Crescent were taken away by the then farmers to different parts of Europe, resided hitherto by hunter gatherers (Evershed *et al.* 2008). Cattle were transported by boat to southwestern areas of Europe lying along the Mediterranean coast. Land route along the Danube river was used to reach the cattle to areas of central and northern Europe. Neolithism and cattle finally reached western Europe and England + Ireland around 6,000 ya. Genetic variability among the cattle, progressively introduced westwards and northwards, decreased among the onwards moving cattle. There was no gene flow from taurine cattle left in Fertile Crescent to taurine cattle moved towards Europe, from about 7,000 ya. The cattle that arrived in Europe from Fertile Crescent were predominantly the T3 haplogroup derivatives of the taurine domesticates (Lanstra and Bradley 1999, Troy *et al.* 2001, Balasse and Tresset 2002, Kuhn *et al.* 2004, Arbuckle and Makarewicz 2009, Decker *et al.* 2014, Felius *et al.* 2014, Orzco-ter Wengel *et al.* 2015, Scheu *et al.* 2015). Taurine had introgression from aurochs in Europe. Ancient taurine cattle of P haplogroup and R haplogroup (originating from matings of European auroch females and taurine males) have been respectively found in Slovakia, Spain, Switzerland and Italy (Bollingino *et al.* 2006, Achilli *et al.* 2009, Ajmone-Marson *et al.* 2010, Bonfiglio *et al.* 2010, Schibler *et al.* 2014). It is also known that significant gene flow occurred from male aurochs to taurine females in England and Ireland (Orlando 2015, Park *et al.* 2015). Application of breeding procedure, from about 250 ya, on all of genetic variability accumulated in Europe has made the genetic base of modern European cattle much broader, thus somewhat overcoming the founding bottlenecks faced during introduction of taurine cattle into Europe (Felius 1995, Felius *et al.* 2014, Felius *et al.* 2015, Scheu *et al.* 2015).

Taurine cattle of T1 haplogroup (a variant of T3 haplogroup) migrated to Africa from Fertile Crescent (Bonfiglio *et al*. 2012b). Taurine cattle entered, along with southward migrating farmers, into Africa from an area near Suez in northeast of continent ~ 8,500 ya. Before the taurines spread in Africa, the introduced taurines inter-bred with males of *Bos primigenius africanus* (Linseele 2004), the African aurochs, which were genetically variant from European and Indian aurochs. The European taurines possessing high level of aurochs introgression are called African taurines. Because of introgression from aurochs, the African taurines acquired a very important trait, resistance towards trypanosomiasis (Stewart 1951). African taurines spread from northeast to west and central parts of Africa (Epstein and Mason 1984, Payne and Hoges 1997, Lenstra and Bradley 1999, Blench and McDonald 2000, Troy *et al.* 2001, Hanotte *et al.* 2002, Ajmone-Marson *et al.* 2010, Decker *et al.* 2014, Felius *et al.* 2014, 2015, Lenstra *et al.* 2014, Magee *et al.* 2014). Further, it has been ascertained that although rare, there are pure European/ Fertile Crescent type taurines present in Africa (Decker *et al.* 2014).

Neolithic pastoralists of Fertile Crescent took taurine cattle of T2, T3 and T4 haplogroup (latter a subgroup of T3) to Northeast Asia (North China and Mongolia) about 5000 ya. During bronze age (4000–2700 ya) taurine were exclusive cattle in Northern China. From North China, taurine cattle migrated to Japan 1,800 ya via Korean peninsula. T4 haplogroup taurine cattle are present only in Siberia, Mongolia, China, Korea and Japan (Mannen *et al.* 2004, Ajmone-Marson *et al.* 2010, Li *et al.* 2013, Cai *et al.* 2014, Lenstra *et al.* 2014, Magee *et al.* 2014, Yonesaka *et al.* 2015).

Zebu introgressed African Taurine spread in Africa and entered Southwest Europe

Spread of cattle in highly diverse agro-environments of African continent, such as hot and dry, temperate to tropical, became possible with the derivation of African Taurine × zebu hybrids (Lenstra and Bradley 1999, Ajmone-Marson *et al.* 2010, Magee *et al.* 2014, Mwai *et al.* 2015). Zebu cattle were introduced into Africa from India in waves, first 4000 ya, second 1300 ya and third 128 ya (Epstein and Mason 1984, Felius 1995, Payne and Hoges 1997, Hanotte *et al.* 2002, MacHugh *et al.* 1997, Marshall 1989, Ajmone-Marson *et al.* 2010, Decker *et al.* 2014, Mwai *et al.* 2015, Orzoco-ter Wengel *et al.* 2015). Pure zebu cattle do not occur in African continent (Decker *et al.* 2014, Mwai *et al.* 2015). The zebu introgressed African taurine carry T1 mt DNA suggesting that zebu males were crossed with African taurine females to obtain Taurine × zebu hybrids (Troy *et al.* 2001, Edwards *et al.* 2007). Absence of zebu mt DNA in zebu admixed African taurines is intriguing and requires an explanation. The zebu introgressed cattle are distributed all over Africa, but with varying zebu content. Zebu introgression is poorly represented in West and South-Africa, it is predominant in East and Central-Africa (McHugh *et al.* 1997, Payne and Hoges 1997, Freeman *et al.* 2004).

Zebu introgressed African taurine cattle (carrying genes from Fertile Crescent taurine, African aurochs and Indian Zebu) were introduced into Portugal and Spain, from Morocco via the strait of Gibralter, during Moorish occupation (1300 ya); such cattle also reached Italy from Spain (Cymbrom *et al.* 1999, 2005, Beja-Pereira *et al.* 2006, Decker *et al.* 2014, Mwai *et al.* 2015). Zebu introgressed African taurine perhaps served as a source of indicine genes into European and American cattle (Orzoco-ter Wengel *et al.* 2015).

Zebu and taurine cattle admixture in Middle- and Near-East and in India

The cattle present in the Fertile Crescent Area of Near East/Middle East are not the original taurine domesticates since the migratory Neolithic farmers had spread most of the genetic variability of the taurines domesticated in Fertile Crescent into Europe, North Africa and Northeast Asia (Ajmone-Marson *et al.* 2010, Decker *et al.* 2014). Over time cattle of the entire area from Italy to Iran through Fertile Crescent got admixed with African taurine and Zebu genetic variability. Zebu cattle had reached the region by 6500 ya (Decker *et al.* 2014). Both males and females participated in contributing the zebu gene flow into taurines of the area (Loftus *et al.* 1994, Lenstra and Bradley 1999, Troy *et al.* 2001, Edwards *et al.* 2007, Ajmone-Marson *et al.* 2010, Akis and Oztabak 2013, Ozsensoy and Kurar 2014). Reciprocally, taurine cattle reached Indus Valley 6200 ya and introgressed with zebu. Important zebu breeds have been shown to possess taurine genes (Naik 1978, Kumar *et al.* 2003, Baig *et al.* 2005, Magee *et al.* 2014).

Introduction of cattle into Americas

Human colonization and dispersal of cattle were concurrent in Americas. Between 1493 and 1521 (28 calender years), cattle were shipped in large numbers from Portugal, Spain and southern France and dispersed in areas of southern North America (state of Texas) and northern South America (Mexico, Columbia and Venezuela) (Rouse 1977, Barragy 2003). These cattle were either T3 mt DNA bearing European taurines or T1 mt DNA bearing Iberian taurines, the latter possessing tripartite genome with components of European taurine, African aurochs and Indian zebu, received in Portugal and Spain from Africa via strait of Gibralter (Barragy 2003, McTavish *et al.* 2013, Decker *et al.* 2014, Magee *et al.* 2014). These cattle ranged freely in the wild for about 400 years and thus became naturally selected for adaptation to local conditions. Subsequently, breeds such as Corriente in Mexico, Longhorns in Texas and Romosinuanos in Columbia emerged from them (Rouse 1977). The prime Indian zebu breeds were brought to Brazil in 1813 and these were redistributed to North America in 1880. Zebu breeds were brought directly from India to North America in 1906 and also European breeds were brought around that time from Europe continent (Hoyt 1982). Widespread crossing of taurine and zebu in Americas provided the genetic variability needed for adoption of cattle to environments in Americas varying from temperate to tropical (Magee *et al.* 2014).

Cattle introduction into Australia

Cattles are not indigenous to Australia, like they are to Eurasia. First batch of taurines and zebu types of cattle arrived, with first batch of European settlers in Australia in 1788, these cattle had been obtained from South Africa. This introduction was successful and animals thrived in the wild. A bigger batch of cattles were brought from India in 1795. Subsequently Australia imported most of the important breeds from America, Asia and Europe (darken berger.com.au/…-us/history-of-beef-cattle).

Cattle in India and adjoining Southeast Asia

Climates in the Indian subcontinent (South Asia, areas of ancient Indus Valley Civilizations included) and Southeast Asia are as varied as alpine, montane, arid, semi-arid, semi-temperate, dry tropical and humid tropical. The parent species of *Bos indicus* (zebu/indicine) cattle, the Indian aurochs *Bos primigenius namadicus* which ranged in Indian subcontinent was adapted to the climate associated with alpine, grassland, savanna and rainforest agro-ecological conditions. The wide environment adaptability of zebu cattle stemmed from its parentage. In addition to zebu cattle, the Neolithic farmers of the region domesticated several sister species viz. *Bos grunniens* (yak), *Bos frontalis* (mithun/gayal) and *Bos javanicus* (Bali-banteng). They experimented and successfully used interspecific hybrids of zebu (or taurine) as one parent and yak, mithun, wild yak (*Bos mutus*) or wild gaur (*Bos gaurus*) as the other parent and hybrids of wild gaur with mithun and banteng and of wild yak with domesticated yak (Table 1). Genetic variability present in the cattle of the region is enormous and awaits conservation and characterization.

Of the two zebu domesticated populations, the I1 mt DNA carrying zebu population spread from the greater Indus valley eastwards. Migratory farmers brought the I1 haplotype zebu to Haryana, Uttar Pradesh, Bihar, Odisha and West Bengal states of the present Indian geography, Bangladesh, Myanmar and Thailand and adjoining mainland countries. Zebu cattle were present in Thailand 6000 ya (Wangkumhang *et al.* 2015), and had reached Indonesian islands before 1000 ya (Mohamad *et al.* 2009, 2012). Some Thai breeds of Zebu cattle have *Bos javanicus* admixture (Wangkumhang *et al.* 2015). Zebu were introduced from India into Central and Northern China and Mongolia and were present in Southern China 3500 ya (Naik 1978, Payne and Hoges 1997, Cai *et al.* 2014, Decker *et al.* 2014, Magee *et al.* 2014). The haplotype I2 of Zebu spread from the Indo-Gangetic plains southwards and became the main cattle of all parts of India and of Srilanka and Bangladesh (Edea *et al.* 2015). There are zebu or zebu × taurine breeds in all milk producing countries. India has 37 well characterized zebu breeds for milk (Sahiwal, Gir, Red Sindhi, Tharparkar and Rathi), milk and draught (Kankrej, Ongole and Haryana) and draught (29 breeds), selected by farmers in various parts of India over antiquity (Naik 1978, Baig *et al.* 2005, Decker *et al.* 2014, Felius *et al.* 2014, Magee *et al.* 2014, Sharma *et al.* 2015, allindiadairy.com/cattle-breeds). From the time of origin to present, different breeds have introgressed each other giving rise to non-descript cattle in India. In recent years many Indian zebu breeds have been introgressed with taurines to improve milk yield. Use of cattle as means of transportation and traction having declined, steps are needed to conserve the purity of prominent Indian zebu milk and milk and draught breeds in such a way that much sought combination of alleles for disease and pest tolerance, heat and water stress tolerance and effective utilization of low quality and rough material as feed in indigenous Indian zebu varieties are not eroded.

Concluding remarks

Bos taurus (taurine) and *Bos indicus* (zebu) domesticates inherited from *Bos primigenius* only a small fraction of genetic variability. Since their domestication 8500 ya, both taurine and zebu cattle have spread worldwide. There were many bottlenecks in the process of introduction of domestic cattle to new geographic areas, and thus the genetic variability got reduced. The domesticates have undergone natural selection and artificial selection by their owners, based on the needs of the latter for various combinations of characters, including superior adaptation to local abiotic and biotic stresses, nature of feed, fertility, milk and meat production, draught power, docility, social behaviour, coat colour and size and shape of horns. In the last 250 years, production properties of cattle have been improved by application of general, molecular and biometrical genetic procedures for selections of progeny from crosses between pre-characterized parent animals, using conventional mating, artificial insemination, *in vitro* fertilization and embryo cloning and transfer procedure. Use of CRISPR/ Cas 9 nuclease gene editing to mediate directed changes in specific genes has also begun. Following the application of strong selection criteria for specific trait(s) multiple times, cattle have been exposed to further depletion of genetic variability. To conserve all the prevailing alleles with large favourable effects, there is need to identify individual genes controlling such properties in the available genetic resources. Now that modern technologies of controlled reproduction are available, it has become possible to utilize worldwide genetic resources of cattle in any one place. Genomic information from minor cattle species and other mammals, including man, will be useful in this direction.

Pre- and post- domestication history of zebu cattle of Indian sub-continent is less understood than that of taurine cattle in Europe and Africa. Archaeological investigations in Indus valley areas of India in Himachal Pradesh, Haryana, Punjab, Uttar Pradesh and Rajasthan and in areas of Pakistan and Afganistan are needed to recover any remnants of ancient cattle for their paleogenetic analysis and comparison with modern zebu breeds. The ancient cattle genomes need to be treated as reservoirs of novel genes/alleles for cattle improvement.

All the genetic analysis carried out so far, about cattle domestication process, distribution worldwide and breeds available in different countries, has shown the following with reference to properties in Zebu cattle. In antiquity (5000–10000 ya), the sedented Indian farmers located in the latitudinal areas of Sarswati-cum-Indo-gangetic plains domesticated the Indian aurochs *Bos primigenius* into *Bos indicus* cattle whose progeny had qualities of adapting to draught in climates of all the inhabited continents and islands of earth and producing milk that had health promoting properties.

ACKNOWLEDGEMENT

SK wishes to thank Indian National Science Academy for grant of its Honorary Scientistship to him. Facilities provided by NIPGR are also gratefully acknowledged.

REFERENCES

Achilli A, Bonfiglio S, Olivieri A, Malusà A, Pala M, Hooshiar Kashani B, Perego U A, Ajmone-Marsan P, Liotta L, Semino O, Bandelt H J, Ferretti L and Torroni A. 2009. The multifaceted origin of taurine cattle reflected by the mitochondrial genome. *PLoS One* **4**:e5753.

Adbullah M H, Idris I and Hilmi M. 2009. Karyotype of Malayan Gaur (*Bos gaurus* Hubbacki), Sahiwal-Friesian cattle and Gaur × cattle hybrid backcrosses. *Pakistan Journal of Biological Sciences* **12**: 896–901.

Ajmone-Marson, Garcia F J and Lenstra J A. 2010. The globaldiv consortium on the origin of cattle: How aurochs became cattle and colonized the world. *Paolo Evolutionary Anthropology* **19**: 148–57.

Akis I and Oztabak K. 2013. *Bos indicus* associated alleles in Anatolian cattle breeds support zebu introgression into Near East. *Journal of Biological Research -Thessalon* **19**: 131–38.

Alan D and Muir G W. 1935. *Hybridization of Domestic Cattle, Bison and Yak.* Report of the Wainwright Experiment Technical Bulletin 2. Dominion of Canada, Department of Agriculture, Ottawa.

Arbuckle B S and Makarewicz C A. 2009. The early management of cattle (*Bos taurus*) in Neolithic central Anatolia. *Antiquity* **83**: 669e686.

Bahbahani H, Clifford H, Wrag D, Mbole-Karuki M N, Van Tassel C *et al.* 2015. Signatures of the positive selection in East African Short horn zebu: A genome-wide single nucleotide polymorphism analysis. *Scientific Reports* **5**: Article number 11729.

Baig M, Beja-Pereira A, Mohammad R, Kulkarni K, Farah S and Luikart G. 2005. Phylogeography and origin of Indian domestic cattle. *Current Science* **89**: 38–40.

Balasse M and Tresset A. 2002. Early weaning of Neolithic domestic cattle (Bercy, France) revealed by intra-tooth variation in nitrogen isotope ratios. *Journal of Archaeological Science* **29**: 853–59.

Barragy T G. 2003. Gathering Texas Gold. Cayo Del Grullo Press, Cayo de Grullo, Texas.

Beales P E, Elliott R B, Flohé S, Hill J P, Kolb H, Pozzilli P, Wang G S, Wasmuth H and Scott F W. 2002. A multi-centre, blinded international trial of the effect of A(1) and A(2) beta-casein variants on diabetes incidence in two rodent models of spontaneous Type I diabetes. *Diabetologia* **45**: 1240–46.

Beja-Pereira A, Caramelli D, Lalueza-Fox C, Vernesi C, Ferrand N, Casoli A, Goyache F, Royo L J, Conti S, Lari M, Martini A, Ouragh L, Magid A, Atash A, Zsolnai A, Boscato P, Triantaphylidis C, Ploumi K, Sineo L, Mallegni F, Taberlet P, Erhardt G, Sampietro L, Bertranpetit J, Barbujani G, Luikart G and Bertorelle G. 2006. The origin of European cattle: evidence from modern and ancient DNA. *Proceedings of National Academy of Sciences USA* **103**: 8113–18.

Blench R M and MacDonald K C. 2000. *The origin and development of African Livestock: archaeology, genetics, linguistics and ethnography.* Routledge, NY.

Bollongino R, Burger J, Powell A, Mashkour M, Vigne J D and Thomas M G. 2012. Modern taurine cattle descended from small number of near-eastern founders. *Molecular Biology and Evolution* **29**: 2101–04.

Bollongino R, Edwards C J, Alt K W, Burger J and Bradley D G. 2006. Early history of European domestic cattle as revealed by ancient DNA. *Biological Letters* **2**: 155–59.

Bollongino R, Nehlich O, Richards M P, Orschiedt J, Thomas M G, Sell C, Fajkosová Z, Powell A and Burger J. 2013. 2000 years of parallel societies in Stone Age Central Europe. *Science* **342**: 479–81.

Bonfiglio S, Achilli A, Olivieri A, Negrini R, Colli L, Liotta L, Ajmone-Marsan P, Torroni A and Ferretti L. 2010. The enigmatic origin of bovine mtDNA haplogroup R: sporadic interbreeding or an independent event of *Bos primigenius* domestication in Italy? *PLoS One* **5**:e15760.

Bonfiglio S, De Gaetano A, Tesfaye K, Grugni V, Semino O and Ferretti L. 2012a. A novel USP9Y polymorphism allowing a rapid and unambiguous classification of *Bos taurus* Y chromosomes into haplogroups. *Animal Genetics* **43**: 611–13.

Bonfiglio S, Ginja C, De Gaetano A, Achilli A, Olivieri A, Colli L, Tesfaye K, Agha S H, Gama L T, Cattonaro F, Penedo M C, Ajmone-Marsan P, Torroni A and Ferretti L. 2012b. Origin and spread of *Bos taurus*: new clues from mitochondrial genomes belonging to haplogroup T1. *PLoS One* **7**:e38601.

Bradley D G, Loftus R T, Cunningham P and MacHugh D E. 1998. Genetics and domestic cattle origins. *Evolutionary Anthropology* **6**: 79–86.

Bradley D G and Magee D A. 2006. Genetics and the origins of domestic cattle. (Eds) Zeder M A, Bradley D G, Emshwiller E, Smith B D. Documenting domestication: new genetic and archaeological paradigms. pp.317–328. University of California Press, London.

Cai D, Sun Y, Tang Z, Hud S, Li W, Zhao X, Xiang H and Zhou H. 2014. The origins of Chinese domestic cattle as revealed by ancient DNA analysis. *Journal of Archaeological Science* **41**: 423–34.

Canavez F C, Luche D D, Stothard P, Leite K R, Sousa-Canavez J M, Plastow G, Meidanis J, Souza M A, Feijao P, Moore S S and Camara-Lopes L H. 2012. Genome sequence and assembly of *Bos indicus*. *Journal of Heredity* **103**: 342–48.

Chan E K, Nagaraj S H and Reverter A. 2010. The evolution of tropical adaptation: comparing taurine and zebu cattle. *Animal Genetics* **41**: 467–77.

Chen S, Lin B Z, Baig M, Mitra B, Lopes R J, Santos A M, Magee D A, Azevedo M, Tarroso P, Sasazaki S, Ostrowski S, Mahgoub O, Chaudhuri T K, Zhang Y P, Costa V, Royo L J, Goyache F, Luikart G, Boivin N, Fuller D Q, Mannen H, Bradley D G and Beja-Pereira A. 2010. Zebu cattle are an exclusive legacy of the South Asia neolithic. *Molecular Biology and Evolution* **27**: 1–6.

Christian D. 2000. Silk Roads or Steppe Roads? The Silk Roads in World History. *Journal of World History* **11**: 1–26.

Church D E. 1984. *Livestock Feeds and Feeding*. Corvallis, O&B books.

Clutton-Block J. 1999. *A Natural History of Domesticated Mammals. Cambrige University Press, Cambridge, UK.*

Colledge S, Conolly J, Dobney K, Manning K and Shennan S. 2013. The Origins and Spread of Domestic Animals in Southwest Asia and Europe. *Left Coast Press. Walnut Cred, CA, USA.*

Copley M S, Berstan R, Dudd S N, Docherty G, Mukherjee A J, Straker V, Payne S and Evershed R P. 2003. Direct chemical evidence for widespread dairying in prehistoric Britain. *Proceedings of National Academy of Science USA* **100**: 1524–29.

Curry A. 2013. Archaeology: The milk revolution. *Nature* **500**: 20–22.

Cymbron T, Freeman A R, Isabel Malheiro M, Vigne J D and Bradley D G. 2005. Microsatellite diversity suggests different histories for Mediterranean and Northern European cattle populations. *Proceedings of Biological Sciences* **272**: 1837–84.

Cymbron T, Loftus R T, Malheiro M I and Bradley D G. 1999. Mitochondrial sequence variation suggests an African influence in Portuguese cattle. *Proceedings of Biological Sciences* **266**: 597–603.

Daetwyler H D, Capitan A, Pausch H, Stothard P, van Binsbergen R, Brøndum R F, Liao X, Djari A, Rodriguez S C, Grohs C, Esquerré D, Bouchez O, Rossignol M N, Klopp C, Rocha D, Fritz S, Eggen A, Bowman P J, Coote D, Chamberlain A J, Anderson C, VanTassell C P, Hulsegge I,Goddard M E, Guldbrandtsen B, Lund M S, Veerkamp R F, Boichard D A, Fries R and Hayes B J. 2014. Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle. *Nature Genetics* **46**: 858–65.

Decker J E, McKay S D, Rolf M M, Kim J, Molina Alcala A, Sonstegard T S, Hanotte O and Gotherstrom A. 2014. Worldwide patterns of ancestry, divergence, and admixture in domesticated cattle. *PLoS Genet* **10**: e1004254.

Decker J E, Pires J C, Conanta G C, McKaya S D, Heaton M P, Chen K, Cooper A, Vilkki J, Seabury C M, Caetano A R, Johnson G S, Brenneman R A, Hanotte O, Eggert L S, Wiener P, Kim J J, Kim K S, Sonstegard T S, Van Tassell C P, Neibergs H L, McEwan J C, Brauning R, Coutinho L L, Babar M E, Wilson G A, McClure M C, Rolf M M, Kim J, Schnabel R D and Taylor J F. 2009. Resolving the evolution of extant and extinct ruminants with high-throughput phylogenomics. *Proceedings of National Academy of Science USA* **106**: 1864449.

Diamond J. 2002. Evolution, consequences and future of plant and animal domestication. *Nature* **418**: 700–07.

Drew K R and Baskin L M. 1989. Wildlife Production Systems: Economic Utilisation of Wild Ungulates. *CUP Archives* p354.

Dunne J, Evershed R P, Salque M, Cramp L, Bruni S, Ryan K, Biagetti S and di Lernia S. 2012. First dairying in green Saharan Africa in the fifth millennium BC. *Nature* **486**: 390–94.

Edea Z, Bhuiyan M S, Dessie T, Rothschild M F, Dadi H and Kim K S. 2015. Genome-wide genetic diversity, population structure and admixture analysis in African and Asian cattle breeds. *Animal* **9**: 218–26.

Edwards C J, Bollongino R, Scheu A, Chamberlain A, Tresset A, Vigne J D, Baird J F, Larson G, Ho S Y, Heupink T H, Shapiro B, Freeman A R, Thomas M G, Arbogast R M, Arndt B, Bartosiewicz L, Benecke N, Budja M, Chaix L, Choyke A M, Coqueugniot E, Döhle H J, Göldner H, Hartz S, Helmer D, Herzig B, Hongo H, Mashkour M, Ozdogan M, Pucher E, Roth G, Schade-Lindig S, Schmölcke U, Schulting R J, Stephan E, Uerpmann H P, Vörös I, Voytek B, Bradley D G and Burger J. 2007. Mitochondrial DNA analysis shows a Near Eastern Neolithic origin for domestic cattle and no indication of domestication of European aurochs. *Proceedings Biological Science* **274**: 1377–85.

Ellis E C, Kaplan J O, Fuller D Q, Vavrus S, Klein Goldewijk K and Verburg P H. 2013. Used planet: a global history. *Proceedings of the National Academy of Sciences USA* **110**: 7978–85.

Elsik C G, Tellam R L and Worley K C. 2009. Bovine Genome Sequencing and Analysis Consortium. The genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science* **324**: 522–28.

Epstein H and Nason I L. 1984. *Cattle. Evolution of domesticated Animals.* (Ed.) Mason I L. Long man Group, Essex, UK.

Evershed R P1, Payne S, Sherratt A G, Copley M S, Coolidge J, Urem-Kotsu D, Kotsakis K, Ozdoðan M, Ozdoðan A E, Nieuwenhuyse O, Akkermans P M, Bailey D, Andeescu R R, Campbell S, Farid S, Hodder I, Yalman N, Ozbaºaran M, Biçakci E, Garfinkel Y, Levy T and Burton M M. 2008. Earliest date for milk use in the Near East and southeastern Europe linked to cattle herding. *Nature* **455**: 528–31.

Felius M. 1995. *Cattle Breeds-An Encyclopedia.* Misset: Doetinchem, The Netherlands.

Felius M, Beerling M-L, Buchanan D S, Theunissen B, Koolmees P A and Lenstra J A. 2014. On the history of cattle genetic resources. *Diversity* **6**: 705–50.

Felius M, Theunissen B and Lenstra J A. 2015. Conservation of cattle genetic resources: the role of breeds. *Journal of Agricultural Science* **153**: 152–62.

Francis J. 1966. Resistance of zebu and other cattle to tick infestation and babesiosis with special reference to Australia: an historical review. *British Veterinary Journal* **122**: 301–07.

Freeman A R, Meghen C M, MacHugh D E, Loftus R T, Achukwi M D, Bado A, Sauveroche B and Bradley D G. 2004. Admixture and diversity in West African cattle population. *Molecular Ecology* **13**: 3477–87.

Frisch J E and Vercoe J E. 1977. Food intake, eating rate, weight gains, metabolic rates and efficiency of feed utilization in *Bos taurus* and *Bos indicus* cross-breed cattle. *Animal Production* **25**: 353–58.

Fuller D Q. 2006. Agricultural origins and frontiers in South Asia: a working synthesis. *Journal of World Prehistory* 2**0**: 1–86.

Fuller D Q, Denham T, Arroyo-Kalin M, Lucas L, Stevens C J, Qin L, Allaby R G and Purugganan MD. 2014. Convergent evolution and parallelism in plant domestication revealed by an expanding archaeological record. *Proceedings of the National Academy of Sciences USA* **111**: 6147–52.

Fuller D Q and Murphy C. 2014. Overlooked but not forgotten: India as a center for agricultural domestication. *General Anthropology* **21**: 1–8.

Galbreath G J, Mordacq J C and Weiler F H. 2006. Genetically solving a zoological mystery: was the kouprey *(Bos sauveli)* a feral hybrid? *Journal of Zoology London* **270**: 561– 64.

Galbreath G J, Mordacq J C and Weiler F H. 2007. An evolutionary conundrum involving kouprey and banteng: a response from Galbreath, Mordacq and Weiler. *Journal of Zoology* **271**: 253–54.

Gentry A, Clutton-Brock J and Groves C P. 2004. The naming of wild animals and their domestic derivatives. *Journal of Archaeological Science* **31**: 645–51.

Giasuddin M, Huque K and Alam J. 2003. Reproductive potentials of gayal (*Bos frontalis*) under semi-intensive management. *Asian Australasian Journal of Animal Sciences* **16**: 331–34.

Glaser C, Heinrich J and Koletzko B. 2010. Role of FADS1 and FADS2 polymorphisms in polyunsaturated fatty acid metabolism. *Metabolism* **59**: 993–99.

Gou X, Wang Y, Yang S, Deng W and Mao H. 2010. Genetic diversity and origin of Gayal and cattle in Yunnan revealed by mtDNA control region and SRY gene sequence variation. *Journal of Animal Breeding Genetics* **127**: 154–60.

Gray K A, Cassady J P, Huang Y and Maltecca C. 2012. Effectiveness of genomic prediction on milk flow traits in dairy cattle. *Genetics, Selection, Evolution* **44**: 24.

Grigson C. 1980. The craniology and relationships of four species of *Bos.5. Bos indicus. Journal of Archeological Sciences* **7**: 3–32.

Grigson C. 1991. An African origin for African cattle? — some archaeological evidence. *African Archaeological Review* **9**: 119–14.

Groves C and Grubb P. 2011. Ungulate Taxonomy. John Hopkins Press, Baltimore.

Guo S, Savolainen P, Su J, Zhang Q, Qi D, Zhou J, Zhong Y, Zhao X and Liu J. 2006. Origin of mitochondrial DNA diversity of domestic yaks. *BMC Evolutionary Biology* **6**: 73.

Gupta S C, Gupta N and Nivsarkar A E. 1999. *Mithun—A Bovine of Indian Origin.* Directorate of Information and Publication on Agriculture, ICAR, New Delhi, India.

Hall S J G. 2004. *Livestock biodiversity: genetic resources for the farming of the future show extra info.* Oxford: Blackwell Science.

Hammerton J A. 1930. Wonders of Animal Life.

Hanotte O, Bradley D G, Ochieng J W, Verjee Y, Hill E W, Rege J E. 2002. African pastoralism: genetic imprints of origins and migrations. *Science* **296**: 336–39.

Hansen P J. 2004. Physiological and cellular adaptations of zebu cattle to thermal stress. *Animal Reproduction Science* **82–86**: 349–60.

Hassanin A, An J, Ropiquet A, Nguyen T T and Couloux A. 2013. Combining multiple autosomal introns for studying shallow phylogeny and taxonomy of Laurasiatherian mammals: Application to the tribe Bovini (Cetartiodactyla, Bovidae). *Molecular Phylogenetics and Evolution* **66**: 766–75.

Hiendleder S, Lewalski H and Janke A. 2008. Complete mitochondrial genomes of *Bos taurus* and *Bos indicus* provide new insights into intra-species variation, taxonomy and domestication. *Cytogenetic and Genome Research* **120**: 150–56.

Hill J P. 2003. The influence of consumption of A1 beta-casein on heart disease and type 1 diabetes. *New Zealand Medical Journal* **116**: U346.

Ho S Y W and Shapiro B. 2011. Skyline-plot methods for estimating demographic history from nucleotide sequences. *Molecular Ecology Resources* **11**: 423–34.

Hongo H. 2011. The process of ungulate domestication at Çayönü, Southeastern Turkey: A multidisciplinary approach focusing on Bos sp. and *Cervus elaphus*. *Anthropozoologica* **44**: 63–78.

Hoyt Am. 1982. History of Texas Longhorns. *Texas Longhorn Journal* 1–48.

Huque K S, Rahman M M and Jalil M A. 2001. Study on the growth pattern of gayals (*Bos frontalis*) and their crossbred calves. *Asian Australasian Journal of Animal Sciences* **14**: 1245–49.

Ibeagha-Awemu E M, Prinzenberg E M, Jann O C, Lühken G, Ibeagha A E, Zhao X and Erhardt G. 2007. Molecular characterization of bovine CSN1S2*B and extensive distribution of zebu-specific milk protein alleles in European cattle. *Journal of Dairy Science* **90**: 3522–29.

IUCN. 2012. IUCN Red list of threatened species. Version 2012.2.www.iucn.elist.org.

Jarrige C and Quivron G. 2006. Mehrgarh Neolithic: the updated sequence. In C.Jarrige & V. Lefevre, eds., *South Asian Archaeology* 2001.

Joshi B K, Singh A and Mukherjee S. 2005. Genetic improvement of indigenous cattle for milk and draught: A review. *Indian Journal of Animal Sciences* **75**: 335–48.

Kantanen J, Edwards C J, Bradley D G, Viinalass H, Thessler S, Ivanova Z, Kiselyova T, Cinkulov M, Popov R, Stojanoviæ S, Ammosov I and Vilkki J. 2009. Maternal and paternal genealogy of Eurasian taurine cattle (*Bos taurus*). *Heredity*

(*Edinb*) **103**: 404–15.

Kantanen J, Olsaker I, Adalsteinsson S, Sandberg K, Eythorsdottir E, Pirhonen K and Holm L E. 1999. Temporal changes in genetic variation of north European cattle breeds. *Animal Genetics* **30**: 16–27.

Kaupe B, Winter A, Fries R and Erhardt G. 2004. DGAT1 polymorphism in *Bos indicus* and *Bos taurus* cattle breeds. *Journal of Dairy Research* **71**: 182–87.

Kieffer A M and Cartwright T C. 1968. Sex chromosome polymorphisms in domestic cattle. *Journal of Heredity* **39**: 35–36.

Kiplagat S K, Limo M K and Kosgey I S. 2012. Genetic improvement of livestock for milk production. www.gbcbiotech.com>bovinos>acervo

Koks S, Lilleoja R, Reimann E, Salumets A and Reemann P U. 2013. Sequencing and annotated analysis of the Holstein cow genome. *Mammalian Genome* **24**: 309–21.

Kuhn C, Thaller G, Winter A, Bininda-Emonds O R, Kaupe B, Erhardt G, Bennewitz J, Schwerin M and Fries R. 2004. Evidence for multiple alleles at the DGAT1 locus better explains a quantitative trait locus with major effect on milk fat content in cattle. *Genetics* **167**: 1873–81.

Kumar P, Freeman A R, Loftus R T, Gaillard C, Fuller D Q and Bradley D G. 2003. Admixture analysis of South Asian cattle. *Heredity* (*Edinb*) **91**: 43–50.

Kumar S and Kumari R. 2016. Mutant alleles whose natural selection protected Eurasian against diseases resulting from their occupation of dairy farming and crop cultivation (agriculture): Evidence for co-evolution of culture and human genome (submitted).

Larson G and Burger J. 2013. A population genetics view of animal domestication. *Trends in Genetics* **29**: 197–205.

Lenstra J A, Ajmone-Marsan P, Beja-Pereira A, Bollongino R, Bradley D, Colli L, Gaetano A D, Edwards C J, Felius M, Ferretti L, Ginja C, Hristov P, Kantanen J, Lirón J P, Magee D A, Negrini R and Radoslavov G A. 2014. Meta-analysis of mitochondrial DNA reveals several population bottlenecks during worldwide migrations of cattle. *Diversity* **6**: 178–87.

Lenstra J A and Bradley D G. 1999. Systematics and phylogeny of cattle. In: Ruvinsky RFA, editor. *The genetics of cattle. Wallingford: CAB Int.* pp. 1–14.

Lenstra J A and Felius M. 2014. Genetic aspects of domestication. *The Genetics of Cattle*, 2nd Edition, Ed: D Garrich and A. Ruvinsky. CABI

Leslie D M Jr and Schaller G B. 2009. *Bos grunniens* and *Bos mutus* (Artiodactyla: Bovidae). *Mammalian Species* **836**: 1–17.

Li R, Zhang X M, Campana M G, Huang J P, Chang Z H, Qi X B, Shi H, Su B, Zhang R F, Lan X Y, Chen H and Lei C Z. 2013. Paternal origins of Chinese cattle. *Animal Genetics* **44**: 446–49.

Linseele V. 2004. Size and size change of the African aurochs during the Pleistocene and Holocene. *Journal of African Archaeology* **2**: 165–85.

Loftus R T, Ertugrul O, Harba A H, El-Barody M A, MacHugh D E, Park S D and Bradley D G. 1999. A microsatellite survey of cattle from a centre of origin: The Near East. *Molecular Ecology* **8**: 2015–22.

Loftus R T, MacHugh D E, Bradley D G, Sharp P M and Cunningham P. 1994. Evidence for two independent domestications of cattle. *Proceedings of the National Academy of Sciences USA* **91**: 2757–61.

MacHugh D E, Shriver M D, Loftus R T, Cunningham P and Bradley D G. 1997. Microsatellite DNA variation and the evolution, domestication and phylogeography of taurine and zebu cattle (*Bos taurus* and *Bos indicus*). *Genetics* **146**: 1071–86.

Magee D A, MacHugh D E and Edwards C J. 2014. Interrogation of modern and ancient genomes reveals the complex domestic history of cattle. *Animal Frontiers* **4**: 7–22.

Mamatha-Midi K, Idris I and Hilmi M. 2009. Karyotype of Malayan Gaur (*Bos gaurus hubbacki*), Sahiwal-Friesian Cattle and Gaur × Cattle Hybrid Backcrosses. *Pakistan Journal of Biological Science* **12**: 896–901.

Mannen H, Kohno M, Nagata Y, Tsuji S, Bradley D G, Yeo J S, Nyamsamba D, Zagdsuren Y, Yokohama M, Nomura K and Amano T. 2004. Independent mitochondrial origin and historical genetic differentiation in North Eastern Asian cattle. *Molecular Phylogenetics and Evolution* **32**: 539–44.

Martojo H. 2012. Indigenous Bali cattle is most suitable for sustainable small farming in Indonesia. *Reproduction in Domestic Animals* **47** Suppl **1**: 10–14.

Marshall F. 1989. Rethinking the role of *Bos indicus* in Sub-Saharan Africa. *Current Anthropology* **30**: 235–40.

Mathieson I, Lazaridis I, Rohland N, Mallick S, Patterson N, Roodenberg S A, Harney E, Stewardson K, Stewardson K, Fernandes D, Novak M, Sirak K, Gamba C, Jones E R, Llamas B, Dryomov S, Pickrell J, Arsuaga J L, de Castro J M, Carbonell E, Gerritsen F, Khokhlov A, Kuznetsov P, Lozano M, Meller H, Mochalov O, Moiseyev V, Guerra M A, Roodenberg J, Vergès J M, Krause J, Cooper A, Alt K W, Brown D, Anthony D, Lalueza-Fox C, Haak W, Pinhasi R and Reich D. 2015. Genome-wide patterns of selection in 230 ancient Eurasians. *Nature* **528**: 499–503.

McDowell R E, Wilk J C and Talbott C W. 1996. Economic viability of crosses of *Bos taurus* and *Bos indicus* for dairying in warm climates. *Journal of Dairy Science* **79**: 1292–1303.

McKenna M C and Bell S K. 1997. *Classification of mammals above the species level.* Columbia University Press, NY.

McTavish E J, Decker J E, Schnabel R D, Taylor J F and Hillis D M. 2013. New World cattle show ancestry from multiple independent domestication events. *Proceedings of National Academy of Sciences USA* **110**:E1398–1406.

Mc Tavish E J and Hillis D M. 2014. A genomic approach for distinguishing between recent and ancient admixture as applied to cattle. *Journal of Heredity* **105**: 445–56.

Md. Uzzaman R, Md. Bhuiyan S A, Edea Z and Kim K-S. 2014. Semi-domesticated and irreplaceable genetic resource Gayal (*bos frontalis*) Needs effective genetic conservation in Bangladesh: A Review. *Asian Australasian Journal of Animal Sciences* **27**: 1368–72.

Meagher M. 1986. *Bison bison*. *Mammalian sp* **268**:1–8.

Melleti M and Burton J (Eds) 2014. Ecology, Evolution and Behaviour of Wild Cattle: Implications for Conservation. Cambridge University Press.

Mohamad K, Olsson M, Andersson G, Purwantara B, van Tol H T, Rodriguez-Martinez H, Colenbrander B and Lenstra J A. 2012. The origin of Indonesian cattle and conservation genetics of the Bali cattle breed. *Reproduction in Domestic Animals* **47** Suppl 1: 18–20.

Mohamad K, Olsson M, van Tol H TA, Mikko S, Vlamings B H, Andersson G, Rodríguez-Martínez H, Purwantara B, Paling R W, Colenbrander B and Lenstra J A. 2009. On the origin of Indonesian Cattle. *PLoS ONE* **4**: e5490.

Mona S, Catalano G, Lari M, Larson G, Boscato P, Casoli A, Sineo L, Di Patti C, Pecchioli E, Caramelli D and Bertorelle G. 2010.

Population dynamic of the extinct European aurochs: genetic evidence of a north-south differentiation pattern and no evidence of post-glacial expansion. *BMC Evolutionary Biology* **10**:83.

Mondal M, Baruah K K and Rajkhowa C. 2014. Mithun: An Animal of Indian Pride. *Livestock Research for Rural Devlopment* 26 article #6.

Mondal M, Karunakaran M, Lee K B and Rajkhowa C. 2010. Characterization of Mithun (*Bos frontalis*) ejaculates and fertility of cryopreserved sperm. *Animal Reproduction Science* **118**: 210–16.

Murray C, Huerta-Sanchez E, Casey F, Daniel G and Bradley D G. 2010. Cattle demographic history modelled from autosomal sequence variation. *Philosophical Transections of Royal Society of London B Biological Sciences* **365**: 2531–39.

Mwai O, Hanotte O, Kwon Y-J and Cho S. 2015. African indigenous cattle: Unique genetic resources in a rapidly changing world. *Asian Australasian Journal of Animal Sciences* **28**: 911–21.

Naik S N. 1978. Origin and domestication of zebu cattle (*Bos indicus*). *Journal of Human Evolution* **7**: 23–30.

Nijman I J, van Boxtel D C J, van Cann L M, Marnoch Y, Cuppen E and Lenstra J. 2008. Phylogeny of Y chromosomes from bovine species. *Cladistics* **24**: 723–26.

Orlando L. 2015. The first aurochs genome reveals the breeding history of British and European cattle. *Genome Biology* **16**:225.

O'Rourke B A, Greenwood P L, Arthur P F and Goddard M E. 2013. Inferring the recent ancestry of myostatin alleles affecting muscle mass in cattle. *Animal Genetics* **44**: 86–90.

Orozco-ter Wengel P, Barbato M, Nicolazzi E, Biscarini F, Milanesi M, Davies W, Williams D, Stella A, Ajmone-Marsan P and Bruford M W. 2015. Revisiting demographic processes in cattle with genome-wide population genetic analysis. *Frontiers in Genetics* **6**: 191.

Ozsensoy Y and Kurar E. 2014. Genetic diversity of native Turkish cattle breeds: Mantel, AMOVA and Bottleneck analysis. *Journal in Advancement of Veterinary Animals Research* **1**: 86–93.

Park S D, Magee D A, McGettigan P A, Teasdale M D, Edwards C J, Lohan A J, Murphy A, Braud M, Donoghue M T, Liu Y, Chamberlain A T, Rue-Albrecht K, Schroeder S, Spillane C, Tai S, Bradley D G, Sonstegard T S, Loftus B J and MacHugh D E. 2015. Genome sequencing of the extinct Eurasian wild aurochs, *Bos primigenius*, illuminates the phylogeography and evolution of cattle. *Genome Biology* **16**:234.

Pathak S and Kieffer N M. 1979. Sterility in hybrid cattle. 1. Distribution of constitutive heterochromatin and nucleolus organizer regions in somatic and meiotic chromosomes. *Cytogenet Cell Genetics* **24**: 42–52.

Pavuk J. 2005. *Typologische Geschichte der Linearbandkeramik.* (Eds) J. L•uning, C. Friedrich, A. Zimmermann. Die Bandkeramik im 21. *Jahrhundert: Symposium in der Abteil Brauweiler bei K•oln* 17–39.

Payne W J A and Hodges J. 1997. *Tropical cattle, origins, breeds and breeding policies.* Oxford: Blackwell Science. 333 p.

Pehrsson P R, Haytowitz D B, Holden J M, Perry CR and Beckler D G. 2000. USDA's national food and nutrient analysis program: food sampling. *Journal of Food Composition and Analysis* **12**: 379–89.

Perkins D Jr. 1969. Fauna of Catal Hüyük: evidence for early cattle domestication in Anatolia. *Science* **164**: 177–79.

Pertoldi C, Tokarska M, Wójcik J M, Kawako A, Randi E, Kristensen T N, Loeschcke V, Coltman D, Wilson G A, Gregersen Vivi R and Bendixen C. 2010. Phylogenetic relationships among the European and American bison and seven cattle breeds reconstructed using the Bovine SNP50 Illumina Genotyping BeadChip. *Acta Theriologica* **55**: 97–108.

Peters J, von den Driesch A and Helmer D. 2005. The upper Euphrates-Tigris Basin, cradle of agro-pastoralism? *The First Steps of Animal Domestication.* (Eds) Vigne J D, Peters J and Helmer D. Oxford: Oxbow Books, 96–124.

Pinheiro T R, Mercadante M E Z, Albuquerque L G, Bonilha S F M and Monteiro F M. 2012. Selection for higher body weight in Nellore cattle is effective in achieving an increase of longissimus muscle area without reducing subcutaneous fat thickness. *Revista Brasileira de Zootecnia* **41**: 1426–32.

Pucek Z, Belousova I P, Krasiñska M, Krasiñski Z A and Olech W (comps.). 2004. *European Bison. Status Survey and Conservation Action Plan.* (Ed.) Pucek Z., IUCN/SSC Bison Specialist Group. IUCN, Gland, Switzerland and Cambridge, UK. ix + 54 pp.

Qi X B, Jianlin H, Wang G, Rege J E and Hanotte O. 2010. Assessment of cattle genetic introgression into domestic yak populations using mitochondrial and microsatellite DNA markers. *Animal Genetics* **41**: 242–52.

Qiu Q, Zhang G, Ma T, Qian W, Wang J, Ye Z, Cao C, Hu Q, Kim J, Larkin D M, Auvil L, Capitanu B, Ma J, Lewin H A, Qian X, Lang Y, Zhou R, Wang L, Wang K, Xia J, Liao S, Pan S, Lu X, Hou H, Wang Y, Zang X, Yin Y, Ma H, Zhang J, Wang Z, Zhang Y, Zhang D, Yonezawa T, Hasegawa M, Zhong Y, Liu W, Zhang Y, Huang Z, Zhang S, Long R, Yang H, Wang J, Lenstra J A, Cooper D N, Wu Y, Wang J, Shi P, Wang J and Liu J. 2012. The yak genome and adaptation to life at high altitude. *Nature Genetics* **44**: 946–49.

Qureshi T, Templeton J W and Adams L G. 1996. Intracellular survival of *Brucella abortus*, *Mycobacterium bovis* BCG, *Salmonella dublin*, and *Salmonella typhimurium* in macrophages from cattle genetically resistant to *Brucella abortus. Veterinary Immunology and Immunopathology* **50**: 55–65.

Randhawa I A, Khatkar M S, Thomson P C and Raadsma H W. 2015. Composite selection signals for complex traits exemplified through bovine stature using multibreed cohorts of European and African *Bos taurus*. *G3* (*Bethesda*) **5**: 1391–1401.

Randhawa I A, Khatkar M S, Thomson P C and Raadsma H W. 2016. A-meta assembly of selection signatures in cattle. *PLoS One* **11**: e0153013.

Reich D, Thangaraj K, Patterson N, Price A L and Singh L. 2009. Reconstructing Indian population history. *Nature* **461**: 489–94.

Riggs P K, Owens K E and Rexroad C E 3rd, Amaral M E and Womack J E. 1997. Development and initial characterization of a *Bos taurus* × *B. gaurus* interspecific hybrid backcross panel. *Journal of Heredity* **88**: 373–79.

Rollinson D H L. 1984. Bali cattle. *Evolution of Domesticated Animals,* Pages 28–34. (Ed.) Mason I L. Longman, London.

Rouse, J.E. 1970. *World Cattle.* Vol.

Ropiquet A, Gerbault-Seureau M, Deuve J L, Gilbert C, Pagacova E, Chai N, Rubes J and Hassanin A. 2008. Chromosome evolution in the subtribe Bovina (Mammalia, Bovidae): the karyotype of the Cambodian banteng (*Bos javanicus birmanicus*) suggests that Robertsonian translocations are related to interspecific hybridization. *Chromosome*

Research **16**: 1107–18.

Rouse J E. 1977. *The Criollo Spanish cattle in the Americas.* Norman, OK, USA: University of Oklahoma Press, 303 pp.

Scheu A, Powell A, Bollongino R, Vigne J D, Tresset A, Çakýrlar C, Benecke N and Burger J. 2015. The genetic prehistory of domesticated cattle from their origin to the spread across Europe. *BMC Genetics* **16**: 54.

Schibler J, Elsner J and Schlumbaum A. 2014. Incorporation of aurochs into a cattle herd in Neolithic Europe: single event or breeding? *Scientific Reports* **4**: 5798.

Schmitz S. 2013a. The genetics of polled/horned/scurred in cattle. Homepage.usask.ca/~schmitz/polled.html

Schmitz S. 2013b. Genetics of coat colour in cattle. Homepage.usask.ca/~schmitz/colors.html

Sharma G P. 1954. Yak in Nepal Himalayas. *Indian Farming no.* 3124–26.

Sharma R, Kishore A, Mukesh M, Ahlawat S, Maitra A, Pandey A K and Tantia M S. 2015. Genetic diversity and relationship of Indian cattle inferred from microsatellite and mitochondrial DNA markers. *BMC Genetics* **16**: 73.

Simoons F J and Simoons E S. 1968. *A Ceremonial Ox of India: The Mithan in Nature, Culture, and History.* The University of Wisconsin Press, Madison, Wisconsin.

Singh U. 2008. *A History of Ancient and Early Medieval India: From the Stone Age to the 12th Century*. New Delhi. Pearson Education, India.

Sodhi M, Mukesh M, Kataria R S, Mishra B P and Joshii B K. 2012. Milk proteins and human health: A1/A2 milk hypothesis. *Indian Journal of Endocrinology Metabolism* **16**: 856.

Srivastav A and Nigam P. 2010. *Indian National Studbook of Gaur* (*Bos gaurus*). Wildlife Institute of India, Dehradun, India.

Steklenev E P. 1995. The characteristics of the reproductive capacity of hybrids of the bison (*Bison bison* L.) with the domestic cow (*Bos* (*Bos*) *primigenius taurus*). 1. The reproductive capacity of hybrid males. *Tsitoliia i Genetkca* **29**: 66–76.

Steklenev E P and Elistratova T M. 1992. The characteristics of the reproductive capacity of hybrids of banteng (*Bos* (Bibos) javanicus d'Alton) with the domestic cow (*Bos* (*Bos*) *primigenius taurus*). *Tsitologiia i Genetika* **26**: 45–57.

Stewart J L. 1951. The West African Shorthorn cattle. Their value to Africa as trypanosomiasis-resistant animals. *Veterinary Record* **63**: 45.

Stock F and Gifford-Gonzalez D. 2013. Genetics and African Cattle Domestication. *African Archaeological Review* **30**: 51–72.

Taberlet P, Coissac E, Pansu J and Pompanon F. 2011. Conservation genetics of cattle, sheep, and goats. *Comptes Rendus Biologies* **334**: 247–54.

Takeda K, Satoh M, Neopane S P, Kuwar B S, Joshi H D, Shreshtha N P *et al.* 2004. Mitochondrial DNA analysis of Nepalese domestic dwarf cattle Lulu. *Animal Science Journal* **75**: 103–10.

Troy C S, MacHugh D E, Bailey J F, Magee D A, Loftus R T, Cunningham P, Chamberlain A T, Sykes B C and Bradley D G. 2001. Genetic evidence for Near-Eastern origins of European cattle. *Nature* **410**: 1088–91.

Turner J W. 1980. Genetic and biological aspects of Zebu adaptability. *Journal of Animal Sciences* **50**: 1201–05.

Utech K B W, Wharton R H and Kerr J D. 1978. Resistance to *Boophilus microplus* (Canestrini) in different breeds of cattle. *Australian Journal of Agricultural Research* **29**: 885–95.

Van Gelder R G. 1977. Mammalian hybrids and generic limits. *American Museum Novitates* **2653**: 1–25.

van Vuure C. 2005. Retracing the Aurochs: History, Morphology and Ecology of an Extinct Wild Ox Sofia and Moscow: Pensoft Publishers. 431pp

van Vuure T. 2002. History, morphology and ecology of the Aurochs (*Bos primigenius*). Lutra 45–1.

Verkaar E L, Nijman I J, Beeke M, Hanekamp E and Lenstra J A. 2004. Maternal and paternal lineages in cross-breeding bovine species. Has wisent a hybrid origin? *Molecular Biology and Evolution* **21**: 1165–70.

Verkaar E L, Vervaecke H, Roden C, Romero Mendoza L, Barwegen M W, Susilawati T, Nijman I J and Lenstra J A. 2003. Paternally inherited markers in bovine hybrid populations. *Heredity* (*Edinb*) **91**: 565–69.

Vigne J D. 2011. The origins of animal domestication and husbandry: a major change in the history of humanity and the biosphere. *Comptes Rendus Biologies* **334**: 171–81.

Wangkumhang P, Wilantho A, Shaw P J, Flori L, Moazami-Goudarzi K, Gautier M, Duangjinda M, Assawamakin A and Tongsima S. 2015. Genetic analysis of Thai cattle reveals a Southeast Asian indicine ancestry. *Peer Journal* **3**: e1318

Ward A E. 1924. The mammals and birds of Kashmir and adjacent hill provinces. *Journal of the Bombay Natural History Society* **29**: 879–87.

Ward T J, Bielawski J P, Davis S K, Templeton J W and Derr J N. 1999. Identification of domestic cattle hybrids in wild cattle and bison species: a general approach using mtDNA markers and the parametric bootstrap. *Animal Conservation* **2**: 51–57.

Ward T J, Skow L C, Gallagher D S, Schnabel R D, Nall C A, Kolenda C E, Davis S K, Taylor J F and Derr J N. 2001. Differential introgression of uniparentally inherited markers in bison populations with hybrid ancestries. *Animal Genetics* **32**: 89–91.

Winter H, Kalat M, Mayr B, Dworak E and Schleger W. 1988. Mithun cross siri hybrids: cyto- and immunogenetic examinations and characterisation of abnormal spermatogenesis. *Research in Veterinary Sciences* **45**: 86–100.

Winter A, Kramer W, Werner F A, Kollers S, Kata S, Durstewitz G, Buitkamp J, Womack J E, Thaller G and Fries R. 2002. Association of a lysine–232/alanine polymorphism in a bovine gene encoding acyl-CoA:diacylglycerol acyltransferase (DGAT1) with variation at a quantitative trait locus for milk fat content. *Proceedings of National Academy of Sciences U S A* **99**: 9300–05.

Woodford K. 2009. *Devil in the Milk Illness, Health, and the Politics of A1 and A2 Milk.* Keith Woodford Chelsea Green Publishing, Vermonk, USA.

Yadav M P. 2011. Laboratory contributions for rinderpest eradication in India. *Technical Report for FAO under the Global Rinderpest Eradication Programme* (*GREP*) (*GCP/GLO/302/EC*) 58 p.

Yonesaka R, Sasazaki S, Yasue H, Niwata S, Inayoshi Y, Mukai F and Mannen H. 2015. Genetic structure and relationships of 16 Asian and European cattle populations using DigiTag2 assay. *Animal Science Journal* doi: 10.1111/asj.12416.

Zeder M A, Emshwiller E, Smith B D and Bradley D G. 2006. Documenting domestication: the intersection of genetics and archaeology. *Trends in Genetics* **22**: 139–55.

Zhang H, Paijmans J L, Chang F, Wu X, Chen G, Lei C, Yang X, Wei Z, Bradley D G, Orlando L, O'Connor T and Hofreiter M. 2013. Morphological and genetic evidence for early Holocene cattle management in northeastern China. *National Communication* **4**: 2755.

Zhang R C. 2000. Interspecies Hybridization between Yak, *Bos taurus* and *Bos indicus* and Reproduction of the Hybrids. *Recent Advances in Yak Reproduction*. (Eds) Zhao X X and Zhang R C. International Veterinary Information Service.

Zhang R C and Duan L C. 1991. Study on sperm producing level for yak and cattle-yak bull. *Journal of Animal and Veterinary Sciences* **22**: 231–34.

Zhou H, Cheng L, Azimu W, Hodge S, Edwards G R and Hickford J G H. 2015. Variation in the bovine FABP4 gene affects milk yield and milk protein content in dairy cows. *Scientific Reports* **5**: 10023.

Zimin A V, Delcher A L, Florea L, Kelley D R, Schatz M C, Puiu D, Hanrahan F, Pertea G, Van Tassell C P Sonstegard T S, Marçais G, Roberts M, Subramanian P, Yorke J A and Salzberg S L. 2009. A whole-genome assembly of the domestic cow, *Bos taurus*. *Genome Biology* **10**: R42.