Structural variants in Mongolian originated ruminant: role in adaptation of extreme-environment

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1 **Structural variants in Mongolian originated ruminant: role in adaptation of extreme-environment**

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15 **Abstract**

16 **Background:** Mongolian cattle (MC) is one of an ancient livestock breeds with good economic traits such as adaptation to Mongolian Plateau
17 extreme low temperature in winter, resistant to pathogenic organisms infection and high quality meat. To reveal the molecular mechanism
18 underlying these, the whole genome sequencing and comparative transcriptome sequencing of MC were performed.

19 **Results :** By genome sequencing and structure variation analysis, 8 genes related to pathogenic organisms infection, including 4 members of
20 bata-defensins gene family (*LAP*, *DEFB1*, *DEFB2*, and *DEFB5*), 2 members of interferon (IFN) gene family (*IFNW1* and *IFNT2*) and 2 genes
21 coding for BoLA proteins(Mongolian_cattle_21532 and Mongolian_cattle_19448) were found in MC genome inversion region. By

transcriptome-sequencing, it was elucidated that 8 genes (*FATP*, *FABP*, *PEPCK*, *SCP-X*, *ADIPO*, *FABP1*, *SCD-1*, *APO*) related to PPAR α pathway, 23 genes involved in oxidative phosphorylation and 10 P450 genes (*CYP7B1*, *CYP4V2*, *CYP3A5*, *CYP11A1*, *CYP2C18*, *CYP2B6*, *CYP7A1*, *CYP2R1*, *CYP2E1*, *CYP27B1*) were significantly up-regulated in winter MC transcriptomes, comparative to summer MC transcriptomes.

Conclusions: Here, we characterized 41 genes implicated in fatty acid metabolism were up-regulated in winter MC transcriptomes. These genes probably account for the MC adaptation to extreme low temperature. At the same time, 8 genes in MC genome inversion region were discovered. And these genes gave clue to the MC resistant to pathogenic organisms infection. In sum, our revealed genes are of important for us to understand the molecular mechanisms of MC to adapt to their environments and valuable for cattle breeding.

Key words: Mongolian cattle, Genome-sequencing, transcriptome-sequencing, extreme-environment, adaptation.

1. Background

Environmental stress has been a major driving force in the evolution of living organisms (Parsons 2005). Environmental stress may affect species abundance and boundaries, hence affecting biodiversity at all levels, of genes, genomes, individuals, population, species, communities and biota (Nevo 1998).

The Mongolian Plateau (MP) is a highland of the Eurasian continent lying between 87°40'-122°15'N and 37°46'-53°08'E. The varieties of climate and geographical condition in the MP endowed this ancient plateau with high biodiversity. Nevertheless, the harsh environmental condition of this plateau is a big challenge for all organisms lived here. And the animals live here provide optimal models for investigation of how psychrophiles adaptation to its' extreme cold. Polar bears are typical mammals uniquely adapted to life in the High Arctic. Population genomic sequencing of polar bears along with brown bears revealed that in response to Arctic climates and hyperlipid diet, genes on the polar bear lineage have been under stronger positive selection than in brown bears; nine of the top 16 genes under strong positive selection are associated with cardiomyopathy and vascular disease, implying important reorganization of the cardio-vascular system (Liu et al 2014). Arctic fox is another mammal able to survive in Arctic harsh conditions. Several evolutionary adaptations such as insulating and camouflage colored fur, a compact body, and reduced metabolism during starvation or extremely cold weather enable Arctic foxes such capacity (Audet et al. 2002).

46 Transcriptome sequencing of Arctic foxes and their close relative, red foxes, revealed that several genes involved in various metabolic and
47 molecular processes such as energy metabolism, cardiac gene regulation, apoptosis and blood coagulation were under positive selection in both
48 species, whereas four of genes are under positive selection only in Arctic foxes transcriptome, two of which are fat metabolism genes (Kumar et
49 al. 2015). In addition to extreme cold, hypoxia and drought are the other two stresses may affect animals living in MP. The Qinghai-Tibetan
50 Plateau is known for its extreme environment with low atmospheric oxygen pressure, cold climate, and limited resources (Wu et al. 2001). And
51 genome sequencing of Tibetans (Simonson et al. 2010), yak (Qiu et al. 2012), Tibetan antelope (Ge et al 2013), snow leopard (Cho et al. 2013)
52 and Tibetan mastiff (Gou et al. 2014) gave the insights of these extreme high altitude mammals how to adapt to Tibetan hypoxic and extreme
53 cold environments. Drought is another stress with which animals living in MP must be confronted. A few works were reported of mammals lived
54 in desert environments how to adapt to drought. Genomes of sheep in contrasting environments were sequenced and further comparative
55 analyses were preformed. It was revealed that to adapt to desert environments, 11 genes which localized in three pathways, the arachidonic acid
56 metabolism pathway (*ANXA6*, *GPX3*, *GPX7*, and *PTGS2*), the renin-angiotensin system pathway (*CPA3*, *CPVL*, and *ECE1*) and the oxytocin
57 signaling pathway (*CALM2*, *CACNA2D1*, *KCNJ5*, and *COX2*) were positively selected in the Taklimakan desert group sheep. All of these
58 positively selective genes were functionally related to regulating water retention and reabsorption in renal cells and blood vessels in the kidney
59 (Yang et al. 2016). Camelus are uniquely evolved to fit desert harsh environments. Genome sequencing and comparative transcriptome
60 sequencing revealed Na^+/K^+ -ATPase, the epithelial Na^+ channel (ENaC), aquaporin family genes (*AQP1*, *AQP2* and *AQP3*) were involved in
61 water and salt reabsorption which are evolved for camel adaptation to desert extreme drought environments (Wu et al 2014).

62 Cattle had a pivotal position in the advancement of human culture and civilization. Ever since its domestication, cattle distributed almost all
63 continents. To fit for their divergent environments, cattle have involved many breeds with different economic traits and environment adaptation
64 traits. For many cattle breeds, the mechanisms underlying their economic traits were revealed by genome-wide association studies (Takeda et al.
65 2019, Smith et al. 2019, Cruz et al. 2019, Gonzalez-Ruiz et al. 2019, Bedhane et al. 2019). However, few works were reported to address cattle
66 living in different ecosystems how to adapt to their environments, particularly, Mongolian cattle (MC) how to adapt to MP harsh environments.
67 Here, by genome sequencing and comparative transcriptome sequencing, we proved that structure variants play roles in Mongolian cattle
68 adaptation to their extreme environments as well as to apply these knowledge to livestock breeding.

69 2. METHODS

70 2.1 DNA sampling, extraction and sequencing

71 MC living in Khövsgöl Province of Mongolian with pure blood was used in this research. Blood samples collected from target animal's
72 arteria carotis by veterinarian. And genomic DNA was extracted from blood samples according to the instrument of DNA extraction kits
73 (Qiagen). For sequencing, Pair-end libraries of different insert sizes (from 170bp to 20kb) were prepared, and then they were sequenced on
74 IlluminaHiseq 2000 system.

75 2.2 Phylogenetic analyses

76 Previously, including MC, we've sequenced 4 MP livestock genome. The other animals are Mongolian sheep (MS), Mongolian horse (MH)
77 and Alxa Bactrain camel. By aligning MC genome with MS, MH genome and sheep, cattle, horse, mouse, human genome extracted from NCBI
78 data, individually, the divergence among them was revealed and the phylogenetic tree established.

79 2.3 Genome structure variation analyses

80 By comparative analysis of MC genome with published cattle (*Bos taurus*, Hereford breed) genome (Elsik et al. 2010), MC genome
81 structure variations including SNPs (Single Nucleotide Polymorphism), short InDels, CNVs (Copy Number Variations), SDs (Segmental
82 Duplications) and IVs (Inversion Variants) were analyzed.

83 2.4 Transcriptome sequencing

84 For transcriptome sequencing, we choose 3 groups of animals termed B (Cattle living in low altitude), S (MC living in summer) and W
85 (MC living in winter). Each group has 3 replicates. After slaughtered in slaughtering house, four kinds of tissues (skin, liver, back fat, muscle)
86 were carefully collected and quickly put into liquid nitrogen. In lab, the total RNA was extracted from above tissues according to the instrument
87 of RNA extraction kits (Qiagen). Transcriptome sequencing was performed on IlluminaHiseq 2000 system.

88 **2.5 Transcriptome DEGs analysis**

89 By pair-wise comparisons, differentially expressed genes (DEGs) existing in different tissues from different group of animals were revealed.
90 Focused on their functions, DEGs involved in MP harsh environment adaptation were enriched in *PPAR signaling pathway*, *Oxidative*
91 *phosphorylation pathway*, *PI3K-Akt signaling pathway* and *P450 gene family*.

92 **3 RESULTS**

93 **3.1 Genome summary and evolution**

94 We sequenced the genomes of MC using IlluminaHiseq 2000 system. Pair-end libraries of different insert sizes (from 170bp to 20kb) were
95 prepared and generated 292.67 Gb raw sequence data for MC (Supplementary Table 1 and2). Using 17-mer analyzing, the size of genome was
96 estimated to be 3.2Gb (Supplementary Table 3, Supplementary Fig. 1). The total size of the assembled MC was ~ 2.68Gb which close to the
97 2.66Gb and 2.65Gb of sequences of yak and cattle genome (UMD3.1), respectively, with scaffold N50 of 1.58Mb and contig N50 of 27.16kb
98 (Supplementary Table 4, Supplementary Fig. 2-3). From gene structural and functional annotation using genomic data, we obtained in total of
99 22,098 protein coding genes for MC, which is in parallel with that of yak (22,282) (Supplementary Tables 6-8, Supplementary Fig. 4-5). We
100 further compared the gene families of MC, MS, MH, cattle, sheep, horse and human by using CAFE to find the expansion and contracted gene
101 families. We identified 577 expansion genes of MC (Fig. 1a) and GO enrichment analysis revealed they are enriched in the housekeeping gene
102 families, such as 5S rRNA binding and nucleosome assembly (Supplementary Table 9-11).

103 We identified 7,580 one2one orthologous genes by comparing MC, Mongolian sheep (MS), Mongolian horse (MH), sheep, cattle,
104 horse, mouse and human sequences and built the phylogenetic tree. Mongolia mammals and corresponding domestic ones were diverged about
105 2-3 million years ago (Mya, MC-cattle: 1.8 Mya, MS-sheep: 2.6 Mya and MH-horse: 2.7Mya) (Fig. 1a), indicating their divergence maybe
106 influenced with the environment and climate at that time. To identify the population size history, PSMC analysis of MC, MS, MH, cattle, sheep
107 and horse also revealed they diverged about 3 Mya (Fig. 1b). We found population size changes of Mongolia and their domestic ruminants are

similar along the history. Interestingly, all of them decreased to the low about ~0.1 Mya which is fitly overlap the peak of atmospheric surface air temperature distribution, suggesting the substantial population decreasing maybe resulted from the temperature sharply increasing (Fig. 1b).

3.2 Variation analysis

Using cattle genome as reference sequences, we totally detected ~7.62 million single nucleotide variations and short InDels, 4689 copy number variations (block length >5kb, 3750 deletions and 939 duplication) and 32,944 structural variations (19931 deletions, 4343 insertions and 8670 inversions) of MC, which will provide abundant genetic heterogeneity for use in future breeding application (Fig. 2). We also identified the segmental duplication (SD) in MC cattle, and found 251 specific SDs in its' genome. GO analysis showed these SD genes were enriched in the categories including defense response ($P=1.26E-7$), response to stress ($P=3.05E-3$) and response to virus ($P=2.24E-5$), which might be relevant to adaption to extreme environment (Fig. 3a). Genes identified in specific SD area in MC were enriched in a GO term called olfactory receptor activity and they belong to different subfamilies of olfactory receptor proteins (Fig. 3b). Olfactory receptors are members of class-A rhodopsin-like gene family of G protein-coupled receptors, which play important roles in signal transduction cascade (Gaillard et al., 2004, Hussain et al. 2009). In cattle, understanding the OR gene repertoire could lead to link the effects of genetic differences in these genes to variation in olfaction. A study conducted by Lee K. etc. finds that the cattle genome contains 1,071 OR-related sequences including 881 functional, 190 pseudo, and 352 partial OR sequences and they also noticed significant copy number variations are present in the OR repertoire of the cattle (Lee et al. 2013).

We also totally identified 749 inversion variants (IVs) in MC-cattle based on the whole genome alignment results. This is challenging because these inverted regions contain many genes, thus we mainly do enrichment analysis for all the genes in the vicinity of breakpoints of inversion (1kb up- and downstream flank). We found seven genes (Mongolian_cattle_16163, Mongolian_cattle_18647, Mongolian_cattle_03540, Mongolian_cattle_11348, Mongolian_cattle_20851, Mongolian_cattle_19494 and Mongolian_cattle_14394) in MC were enriched in a biological process called defense response in which Beta-defensins gene family and Interferon (IFN) gene family are implicated (Supplementary Fig. 6). In our data, the Beta-defensins genes are *LAP*, *DEFB1*, *DEFB5*, and *DEFB7*. The lingual antimicrobial peptide (LAP) is involved in the innate system and plays an important roles in killing a large variety of microbes, and immunolocalization of it has revealed its existence in both

130 infected and non-infected alveolus in cattle (Isobe et al. 2009). Study pointed out that the mRNA abundance of DEFB1 (Roosen et al. 2004) and
131 DEFB5 in the cattle mammary glands increased, suggesting beta-defensins may play a role in local host defense during under infections. IFNs
132 are members of cytokines and the release of them could trigger the protective defenses of the immune system to help eliminate pathogens
133 (Parkin and Cohen 2001). In our analysis, we found Interferon-omega 1 (IFNW1) and Interferon tau-2 (IFN) located in the breakpoints.
134 Mo_sheep_14980 of MS and Mongolian_cattle_14394 of MC are LOC781948, which is interferon Omega-1 (Type I interferon). Studies showed
135 IFNT2 had antiviral activity in different cell lines and antiluteolytic effect in cyclic ewes (Boue et al. 2000). In general, these two IFNs mainly
136 perform antiviral activity to strengthen the immune system.

137 We also found two genes encoding major histocompatibility complex (MHC) class II protein complex (Mongolian_cattle_21532 and
138 Mongolian_cattle_19448) in the breakpoints (Supplementary Fig. 7). MHC molecules are transmembrane proteins, which localized in cell
139 surface and involved in antigen recognition, immunologic rejection of homotransplantations, immune response and regulation. Amorena and his
140 colleagues first reported MHC class I antigens in cattle, and named it as the bovine leucocyte antigen, BoLA system (Amorena and Stone, 1978).
141 BoLA genes have tight connections to breeding and disease control. The features of BoLA make it become a hot spot in disease resistance area
142 in breeding.

143 **3.3 Transcriptomes analysis**

144 We sequenced transcriptomes of four tissues (skin, liver, back fat, muscle) in three states (B represents cattle, S is the Mongolian cattle
145 sequenced in summer, W is the Mongolian cattle sequenced in winter) (Supplementary table 12). Based on the differentially expressed genes
146 (DEGs) data, we have conducted pathway analysis. By pair-wise comparisons in four tissues, we identified 710, 523, 403, and 383 DEGs in back
147 fat, skin, muscle and liver, respectively. Based on the DEGs, we performed the enrichment analysis and found significantly enriched DEGs with
148 functions terming in response to physiological adaptation (Supplementary Fig. 6-9).

149 **3.4 Enriched DEGs pathway analysis**

150 **3.4.1 *PPAR* signaling pathway**

The first significant enriched pathway of DEGs was PPAR signaling pathway, with 16 DEGs (B-W) and 13 DEGs (S-W) significantly enriched in this pathway, while in B-S, no DEGs were enriched. Peroxisome proliferator-activated receptors (PPARs) are lipid-activated transcription factors belonging to steroid acid receptor superfamily. All of the encoded proteins are involved in lipid homeostasis (Lemberger et al. 1996). PPAR α is the principle transcriptional regulator of FAO enzyme genes, which can control the capacity to produce energy via the utilization of fats by mammalian postnatal heart (Barger et al. 2000). And other researches pointed out that the PPARG/RXRA complex triggers activation of target genes involved in fatty acid oxidation resulting in increased triglyceride formation by ATP production (Lim et al. 2015). In B-W group, genes involved in this pathway like *FATP*, *FABP*, *PEPCK*, *SCP-X*, *ADIPO*, *FABP1*, *SCD-1*, *APO* were all up-expressed in W state cattle, indicating an up-regulating PPAR pathway in Mongolian cattle skin in winter (Fig. 4a and 4b). As for the S-W group, results were consistent with the B-W group, genes such as *SCD*, *ACBP* etc. were up-expressed in W cattle, again showing an enhancement of PPAR pathway in Mongolian cattle skin in winter (Fig. 4a and 4b). Based on the data, we speculated that the synthesis and metabolism of fatty acids in Mongolian cattle skin were greater than normal buffalo, and between Mongolian cattle, the signaling was also more strong in winter, indicating its connection to the cold adaption of Mongolian cattle.

3.4.2 Oxidative phosphorylation pathway

We also found oxidative phosphorylation pathway was enriched by DEGs. Although in S-W group, no DEGs were enriched in this pathway, we did found 23 DEGs in B-S and 20 B-W enriched in this pathway (Fig. 5a). And most of these DEGs were up-regulated expressed in S and W Mongolian cattle, respectively, suggesting a stronger oxidative phosphorylation process in Mongolian cattle than in other cattle breeds. Oxidation phosphorylation is the metabolic pathway in which mitochondria in cells use energy released by nutrients oxidation to form ATP, therefore stronger oxidation phosphorylation reaction in Mongolian cattle means a larger amount of ATP synthesis in Mongolian cattle skin, further indicating a stronger energy use in Mongolian cattle, which may be connected to cold-resistance.

3.4.3 PI3K-Akt signaling pathway

173 We also noticed the downstream part of the PI3K-Akt signaling pathway (Fig. 5B). PI3K-Akt transduction pathway is directly related to cellular
174 quiescence, proliferation, cancer, and longevity. And some studies pointed out that the inhibition of PI3K pathway could indirectly decreases the
175 expression of the glucose transporter GLUT1 at the plasma membrane (Riler et al. 2006). In our data, in S-W group, we could found that GYS,
176 PEPCCK, G6Pase were up-regulated in W Mongolian cattle (5C), showing a more active Glycolysis and Gluconeogenesis process in W cattle,
177 which may indicate in winter, the energy production was more prosperous.

178 **3.4.4 Complement and coagulation cascades pathway**

179 Besides, we also found a totally differentially expressed pathway called complement and coagulation cascades pathway between the skin tissues
180 and muscle tissues, which is connected to the immunocompetence of the species. On skin vs skin group, there was no DEGs enriched in this
181 pathway between B-S group, while 23 and 13 DEGs in B-W and S-W group were significantly enriched, respectively, and all of these DEGs
182 were up-regulated in W state Mongolian cattle (Fig.6A and 6B). On muscle vs muscle group, no DEGs in S-W group were enriched, while 21
183 and 25 DEGs in B-S and B-W group were significantly enriched in this pathway, respectively, and all of these DEGs (except C3AR1) were
184 up-regulated in B cattle, which is different from the results of skin group (Fig. 6a and 6b), suggesting a different immune state in skin and muscle
185 tissues in these two kinds of cattle. Among the up-regulated genes, most encode proteins like coagulation factors, complement components and
186 other proteins related to immunity. Kininogen-1 (KNG1), also known as alpha-2-thiol proteinase inhibitor, Williams-Fitzgerald-Flaujeac factor
187 or the HMWK-kallikrein factor is a protein that in humans is encoded by the KNG1 gene. Kininogen-1 is the precursor protein to
188 high-molecular-weight kininogen (HMWK), low-molecular-weight kininogen (LMWK), and bradykinin. Bradykinin is a potent
189 endothelium-dependent vasodilator, leading to a drop in blood pressure. It also causes contraction of non-vascular smooth muscle in the
190 bronchus and gut, increases vascular permeability and is also involved in the mechanism of pain (Mutschler et al.1997). Bradykinin also causes
191 natriuresis, contributing to the drop in blood pressure.

192 **3.4.5 P450 gene family**

193 Recent studies have indicated that cytochrome P450 is a key enzyme in drug metabolism, and has important effects on cell factor and body
194 temperature regulation. In MC, we found 10 up-expressed P450 genes including *CYP7B1*, *CYP4V2*, *CYP3A5*, *CYP11A1*, *CYP2C18*, *CYP2B6*,

CYP7A1, *CYP2R1*, *CYP2E1*, *CYP27B1*. Cytochromes P450 (CYPs) belong to the superfamily of proteins containing a heme cofactor and, therefore, are hemoproteins. CYPs use a variety of small and large molecules as substrates in enzymatic reactions. It participates in the metabolism of endogenous substances and exogenous substances including drugs and environmental compounds. In the cell, CYPs are mainly distributed in the endoplasmic reticulum and the inner membrane of the mitochondria.

4. DISCUSSION

MC is an ancient cattle breed with valuable economic traits, such as adaptation to harsh environments, resistant to pathogenic organisms infection and high quality meat. By complete mitochondrial DNA D-loop sequences, it's revealed that the MC has the highest genetic diversity (Xia et al 2018), which may account for their varied economic traits. However, the detail molecular mechanism underlying above economic traits remain to be elucidated.

The notable trait of MC is its' tolerance of Mongolian Plateau extreme cold weather in winter. Adipose tissue, including Brown Adipose Tissue (BAT), White Adipose Tissue (WAT) and newly revealed adipocyte termed beige adipocyte, play crucial roles in mammal cold adaptation. In polar bear or belugas, blubbers (deep subcutaneous fat) serve as for insulation keeping heats from lose. Small mammals' BATs are important organs for thermogenesis in cold adaptation. After cold acclimation, a serial of reactions, including releasing of noradrenaline from sympathetic nervous system, binding of it to its' receptor, activating a transcriptional coactivator PGC-1 α , up-regulating genes involved in fatty acid transport, β -oxidation, TCA cycle, electron transport system, glycolysis, lipogenesis and PPAR α activation pathways occur in BATs (Kim et al. 2016). Finally, the proton gradient in mitochondria established and such gradient converted into heats by the function of uncoupling protein1 (UCP1) (Nedergaard et al. 2001). In mammals without BAT, such as cold tolerant pig breeds, Tibetan pig and Min pig, when expose to cold climate, WATs first are browning to be beige adipocytes, where similar thermogenesis process occurred in BAT happening (Lin et al. 2017). Except for WATs, myogenic intermediates are able to differentiate into beige adipocytes (Chen et al. 2019), which implying skeletal muscle implicated in the nonshivering thermogenesis (NST) process, too. In our transcriptome data, we found 8 genes (*FATP*, *FABP*, *PEPCK*, *SCP-X*, *ADIPO*, *FABP1*, *SCD-1*, *APO*) related to PPAR α pathway, 23 genes involved in oxidative phosphorylation and 10 P450 genes (*CYP7B1*, *CYP4V2*, *CYP3A5*, *CYP11A1*, *CYP2C18*, *CYP2B6*, *CYP7A1*, *CYP2R1*, *CYP2E1*, *CYP27B1*) were significantly up-regulated in winter MC transcriptomes. Since all of these genes implicated in fatty acid metabolism, we proposed that similar to cold tolerant pig breeds, MC in cold

218 adaptation could convert the WAT into beige adipocytes, where heats were generated by metabolism of fatty acids and glucose to sustain body
219 core temperature. Unlike polar region climates, where all the year is extreme cold, in summer, the temperature in MP, especially in semiarid
220 regions such as Ordos steppe, is high. Therefore, precious detection of such temperature changes also critical for MC fitting for their
221 environments. Genome structure variation analysis indicated SD area in MC enriched in a GO term called olfactory receptor. The main function
222 of olfactory receptor is perception of chemical and climate factors. Therefor, genome structure variation in MC olfactory receptor probably
223 underlying the molecular mechanism of MC how to preciously detect the temperature change.

224 Resistant to pathogenic organisms infection is another good trait of MC. Via GWAS (genome-wide association study), molecule based on
225 different cattle breeds such as Holstein, *Bos taurus*×*Bos indicus* crossbred cattle and Angus resistant to mastitis ((Kurz et al. 2019),
226 foot-and-mouth disease (FMD) (Lee et al. 2015), tick (Otto et al. 2018), parasite (gastrointestinal nematodes) (Hou et al. 2012) were found out.
227 Here, by whole genome sequencing and genome structure variation analysis, we found millions (~7.62 million) of SNPs and numerous of
228 structure variations (including CNVs, segmental duplications, SDs, inversions). By critical analysis of vicinity of breakpoints of inversion, we
229 found 8 genes related to pathogenic organisms infection. 4 of them (*LAP*, *DEFB1*, *DEFB2*, and *DEFB5*) belong to Beta-defensins gene family.
230 It's well characterized that as an antimicrobial peptide, LAP (lingual antimicrobial peptide) is involved in the innate system and has versatile
231 antimicrobial activities (Isobe et al. 2009). The investigation of cDNA from cattle mammary gland showed that many members of beta-defensins
232 gene family were expressed, which implied these robust antimicrobial peptides playing important roles for cattle resistant to mastitis. 2 of them
233 belong to interferon (IFN) gene family. In our data, they are *IFNW1* and *IFNT2*. Interferon is known for its' anti-virus activities. In this case,
234 *IFNW1* and *IFNT2* are in the vicinity of breakpoints of inversion. Such structure variation probably up-regulated the expression of these
235 anti-virus proteins, which may accounts for MC more resistant to FMD infection than other breeds. Another two genes are coding for MHC class
236 II proteins. In cattle, MHC class I proteins were first found by Amorena and named them BoLA system (For Bovine Leucocyte Antigen). Ever
237 after being found, for their importance in host immunities, BoLAs have been extensively studied and their roles in bovine mastitis (Sharif et al.
238 1998), bovine leukemia virus infection (Stear et al. 1998) and parasitic load (Martinez et al. 2006) were well documented. Here, we found two
239 genes coding for BoLA proteins are localized in MC genome inversion region. Such structure change mostly will affect their expression and in
240 turn affect their anti-pathogenic organism infection activities.

241 MC was considered as a good cattle breed with high quality meat. The criterion used to assess beef includes fat percentage (FAR),
242 unsaturated fat acid (oleic acid) percentage and fatty acid composition. Still by GWAS, candidate genes involved in Japan Black Cattle above
243 trait were revealed respectively (Nakajima et al. 2018, Kawaguchi et al. 2019, Sasago et al. 2016). From our MC genome and transcriptome data,
244 we didn't obtain the direct evidence to support that MC have high quality meat. However, as discussed, FAR is important for mammals living in
245 high altitude to adapt to their environments. To adapt to Arctic extreme cold, half of polar bear mass is composed of fat tissue. And unsaturated
246 fat acid is important for thermogenesis. While COX (Cyclooxygenases)-derived oxylipins (unsaturated fat acid such as omega-3 lipid oxidation
247 products) is required for the formation of beige adipocyte (Vegiopoulos et al. 2010), the P450 epoxygenase and epoxide-derived oxylipins, ($\pm$)
248 12, 13-dihydroxy-9Z-octadecenoic acid (12,13-diHOME) can induce the fatty acid uptake into BAT and skeletal muscle (Lynes et al. 2017). In
249 MC, no BAT were observed, which indicated that in response to extreme cold weather in winter, MC firstly need brown WAT into beige
250 adipocyte, then uptake fatty acid into these nearly formed adipocyte to generate heats. The prerequisite of these two processes is the existence of
251 large amounts of unsaturated fat acid. The indirect evidence is that in winter MC transcriptomes, 10 P450 genes were significantly up-regulated,
252 which implied these up-regulated genes may be involved in the oxidation of unsaturated fat acid into oxylipins.

253 MC is a valuable cattle breed. Nevertheless, so far, few research works performed on this important livestock. By genome sequencing
254 association with comparative transcriptome sequencing, we revealed the molecular mechanisms of MC how to adapt to MP harsh
255 environments as well as resistant to pathogenic organisms. Undoubtedly, these uncovered genes will become cherished genetic resources for
256 cattle breeding.

257

258 **5. Conclusion**

259 In this paper, by whole genome sequencing and comparative transcriptome sequencing, genes localized in MC genome inversion region
260 and genes up-regulated in winter MC transcriptomes were characterized, which probably account for MC adaptation to MP extreme
261 environments and resistant to pathogenic organisms infection. Therefore, these genes are of value for cattle breeding.

262

263

264 **Abbreviations:**

265 MC: Mongolian Cattle; MP: Mongolian Plateau.

266

267 **Declarations**

268

269 **Ethics approval and consent to participate:** Procedures involving animals, their care and humane kill were conducted in conformity with
270 Guidelines on the Humane Treatment of Laboratory Animals (HTLA Pub. Chapter2-6, revised 2006 in China).

271 **Consent for publication:** Not applicable.

272 **Availability of data and material:** All data generated or analyzed during this study are included in this manuscript.

273 **Competing interests:** The authors declare that they have no competing interests.

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275 **Authors' contributions:** YP Xing was a major contributor in writing the manuscript, analyzed and interpreted the genome data. Y Qi analyzed
276 and interpreted the transcriptome data. The collection of tissue samples and extraction of DNA and RNA were performed by C Purev, SY Wang,
277 HB Wang, KF Wu, JW Cao, CX Liu, YY Liu, LU Li. Professor YR Zhang and HM Zhou reviewed the manuscript. All authors read and
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287 References

- 288 Amorena B and Stone WH. 1978. Serologically defined (SD) locus in cattle. *Science*. 201:159-160.
- 289 Audet AM, Robbins CB, Larivière S, Alopexlagopus. 2002. *Mamm Species*. 713:1–10.
- 290 Barger PM, and Kelly DP. 2000. PPAR signaling in the control of cardiac energy metabolism. *Trends in cardiovascular medicine*. 10:238-245.
- 291 Bedhane M, van der Werf J, Gondro C, Duijvesteijn N, Lim D, Park B, Park MN, Hee RS, Clark S. 2019. Genome-Wide Association
292 Study of Meat Quality Traits in Hanwoo Beef Cattle Using Imputed Whole-Genome Sequence Data. *Front Genet*. 10:1235.
- 293 Boue O, Garcia JL, Villar M, Alazo K, Perez A, Ramos E, Morales C, Morera OL, Redondo M, Montero C, Rodríguez M. 2000. Antiviral and
294 antiluteolytic activity of recombinant bovine IFN-omega1 obtained from *Pichia pastoris*. *Journal of interferon & cytokine research*. 20:
295 677-683.
- 296 Chen Y, Ikeda K, Yoneshiro T, Scaramozza A, Tajima K, Wang Q, Kim K, Shinoda K, Sponton CH, Brown Z, et al. 2019. Thermal stress
297 induces glycolytic beige fat formation via a myogenic state. *Nature*. 565: 180-185.
- 298 Cho YS, Hu L, Hou H, Lee H, Xu J, Kwon S, Oh S, Kim HM, Jho S, Kim S. et al. 2013. The tiger genome and comparative analysis with lion
299 and snow leopard genomes. *Nat Commun*. 4: 2433.
- 300 Cruz VAR, Oliveira HR, Brito LF, Fleming A, Larmer S, Miglior F, Schenkel FS. 2019. Genome-Wide Association Study for Milk Fatty Acids
301 in Holstein Cattle Accounting for the DGAT1 Gene Effect. *Animals*. 9: 997-1009.
- 302 Elsie CG, Tellam RL, Worley KC, Gibbs RA, Muzny DM, Weinstock GM, Adelson DL, Eichler EE, Elnitski L, Guigó R. et al. 2009. The
303 genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science*. 324: 522-528.
- 304 Gaillard I, Rouquier S, and Giorgi D. 2004. Olfactory receptors. *Cell Mol Life Sci*. 61: 456-69.

305 Ge RL, Cai QL, Shen YY, San A, Ma L, Zhang Y, Yi X, Chen Y, Yang LF, Huang Y.et al. 2013. Draft genome sequence of the Tibetan
306 antelope. *Nat Commun.* 4: 1858.

307 González-Ruiz S, Strillacci MG, Durán-Aguilar M, Cantó-Alarcón GJ, Herrera-Rodríguez SE, Bagnato A, Guzmán LF, Milián-Suazo F,
308 Román-Ponce SI. 2019. Genome-Wide Association Study in Mexican Holstein Cattle Reveals Novel Quantitative Trait Loci Regions and
309 Confirms Mapped Loci for Resistance to Bovine Tuberculosis. *Animals.* 9: 636-651.

310 Gou X, Wang Z, Li N, Qiu F, Xu Z, Yan D, Yang S, Jia J, Kong X, Wei Z. et al. 2014. Whole-genome sequencing of six dog breeds from
311 continuous altitudes reveals adaptation to high-altitude hypoxia. *Genome Res.* 24: 1308–1315.

312 Hou YL, Liu GE, Bickhart DM, MatukumalliLK, Li CJ, Song JZ, Gasbarre LC, Van Tassell CP, Sonstegard TS. 2012. Genomic regions
313 showing copy number variations associate with resistance or susceptibility to gastrointestinal nematodes in Angus cattle. *Funct*
314 *Integr Genomics.* 12: 81-92.

315 Hussain A, Saraiva LR, and Korsching SI. Positive Darwinian selection and the birth of an olfactory receptor clade in teleosts. 2009. *Proc Natl*
316 *Acad Sci U S.* 106: 4313-4318.

317 Isobe N, Hosoda K, Yoshimura Y. 2009. Immunolocalization of lingual antimicrobial peptide (LAP) in the bovine mammary gland. *Animal*
318 *science journal = Nihon chikusan Gakkaiho.* 80: 446-450.

319 Isobe N, Nakamura J, Nakano H, Yoshimura Y. 2009. Existence of functional lingual antimicrobial peptide in bovine milk. *Journal of dairy*
320 *science.* 92: 2691-2695.

321 Kawaguchi F, Kigoshi H, Fukushima M, Iwamoto E, Kobayashi E, Oyama K, Mannen H, Sasazaki S. 2018. Whole-genome resequencing to

322 identify candidate genes for the QTL for oleic acid percentage in Japanese Black cattle. *Anim Sci J.* 90: 467-472.

323 Kim J, Fernand VE, Henagan TM, Shin J, Huypens P, Newman S, Gettys TW, Chang JS. 2016. Regulation of Brown and White Adipocyte
324 Transcriptome by the Transcriptional Coactivator NT-PGC-1 α . *PLoS ONE.* 11: e0159990.

325 Kumar V, Kutschera VE, Nilsson MA, Janke A. 2015. Genetic signatures of adaptation revealed from transcriptome
326 sequencing of Arctic and red foxes. *BMC Genomics.* 16: 585.

327 Kurz JP, Yang Z, Weiss RB, Wilson DJ, Rood KA, Liu GE, Wang Z. 2019. A genome-wide association study for resistance in phenotypically
328 well-characterized Holstein dairy cattle using a selective genotyping approach. *Immunogenetics.* 71: 35-47.

329 Lee BY, Lee KN, Lee T, Park JH, Kim SM, Lee HS, Chung DS, Shim HS, Lee HK, Kim H. 2015. Bovine genome-wide association study for
330 genetic elements to resist the infection of Foot-and-mouth disease in the field. *Asian-Australas J Animal Science.* 28: 166-170.

331 Lee K, Nguyen DT, Choi M, Cha SY, Kim JH, Dadi H, Seo HG, Seo K, Chun T, Park C. 2013. Analysis of cattle olfactory subgenome: the first
332 detail study on the characteristics of the complete olfactory receptor repertoire of a ruminant. *BMC Genomics.* 14: 596-607.

333 Lemberger T, Desvergne B and Wahli W. 1996. Peroxisome proliferator-activated receptors: a nuclear receptor signaling pathway in lipid
334 physiology. *Annual review of cell and developmental biology.* 12: 335-363.

335 Lim D, Chai HH, Lee SH, Cho YM, Choi JW, Kim NK. 2015. Gene Expression Patterns Associated with Peroxisome Proliferator-activated
336 Receptor (PPAR) Signaling in the Longissimus dorsi of Hanwoo (Korean Cattle). *Asian-Australasian journal of animal sciences.* 28:
337 1075-1083.

338 Lin J, Cao C, Tao C, Ye R, Dong M, Zheng Q, Wang C, Jiang X, Qin G, Yan C et al. 2017. Cold adaptation in pigs depends on UCP3 in beige

339 adipocytes. *J Mol Cell Biol.* 9: 364-375.

340 Liu S, Lorenzen ED, Fumagalli M, Li B, Harris K, Xiong Z, Zhou L, Korneliussen TS, Somel M, Babbitt C. et al. 2014. Population genomics
341 reveal recent speciation and rapid evolutionary adaptation in polar bears. *Cell.* 157: 785–794.

342 Lynes MD, Leiria LO, Lundh M, Bartelt A, Shamsi F, Huang TL, Takahashi H, Hirshman MF, Schlein C, Lee A, et al. 2017. The cold- induced
343 lipokine 12,13-diHOME promotes fatty acid transport into brown adipose tissue. *Nat. Med.* 23: 631–637.

344 Martinez ML, Machado MA, Nascimento CS, Silva MV, Teodoro RL, Furlong J, Prata MC, Campos AL, Guimarães MF, Azevedo AL, et al.
345 2006. Association of BoLA-DRB3.2 alleles with tick (*Boophilus microplus*) resistance in cattle. *Genet. Mol. Res.* 5: 513-524.

346 Mutschler E, Schäfer-Korting, Monika. 1997. Arzneimittelwirkungen (in German) (7 ed.). Stuttgart: Wissenschaftliche Verlagsgesellschaft.
347 ISBN 3-8047-1377-7.

348 Nevo E. 1998. Book review. *Heredity.* 81: 591–597.

349 Nakajima A, Kawaguchi F, Uemoto Y, Fukushima M, Yoshida E, Iwamoto E, Akiyama T, Kohama N, Kobayashi E, Honda T, et al. 2018. A
350 genome-wide association study for fat-related traits computed by image analysis in Japanese Black cattle. *Anim Sci J.* 89:743-751.

351 Nedergaard J, Golozoubova V, Matthias A, Asadi A, Jacobsson A, Cannon B. 2001. UCP1: the only protein able to mediate adaptive
352 non-shivering thermogenesis and metabolic inefficiency. *Biochim Biophys Acta.* 1504: 82–106.

353 Otto PI, Guimarães SEF, Verardo LL, Azevedo ALS, Vandenplas J, Soares ACC, Sevillano CA, Veroneze R, de Fatima A Pires M, de Freitas C,
354 et al. 2018. Genome-wide association studies for tick resistance in *Bos taurus* × *Bos indicus* crossbred cattle: A deeper look into
355 this intricate mechanism. *J Dairy Sci.* 101:11020-11032.

356 Parkin J, Cohen B. 2001. An overview of the immune system. *Lancet.* 357: 1777-1789.

357 Parsons PA. 2005. Environments and evolution: interactions between stress, resource inadequacy and energetic efficiency. *Biol Rev.* 80:89–610.

358 Qiu Q, Zhang G, Ma T, Qian W, Wang J, Ye Z, Cao C, Hu Q, Kim J, Larkin DM. et al. 2012. The yak genome and adaptation to life at high
359 altitude. *Nat Genet.* 44: 946–949.

360 Riley JK, Carayannopoulos MO, Wyman AH, Chi M and Moley KH. 2006. Phosphatidylinositol 3-kinase activity is critical for glucose
361 metabolism and embryo survival in murine blastocysts. *The Journal of biological chemistry.* 281: 6010-6019.

362 Roosen S, Exner K, Paul S, Schroder JM, Kalm E, Looft C. 2004. Bovine beta-defensins: identification and characterization of novel bovine
363 beta-defensin genes and their expression in mammary gland tissue. *Mammalian genome.* 15: 834-842.

364 Sasago N, Abe T, Sakuma H, Kojima T, Uemoto Y. 2017. Genome-wide association study for carcass traits, fatty acid composition, chemical
365 composition, sugar, and the effects of related candidate genes in Japanese Black cattle. *Anim Sci J.* 88:33-44.

366 Sharif S, Mallard BA, Wilkie BN, Sargeant JM, Scott HM, Dekkers JC, Leslie KE. 1998. Associations of the bovine major histocompatibility
367 complex DRB3 (BoLA-DRB3) alleles with occurrence of disease and milk somatic cell score in Canadian dairy cattle. *Anim. Genet.* 29:
368 185-193.

369 Simonson TS, Yang Y, Huff CD, Yun H, Qin G, Witherspoon DJ, Bai Z, Lorenzo FR, Xing J, Jorde LB. et al.2010.
370 Genetic evidence for high-altitude adaptation in Tibet. *Science.* 329:72-74.

371 Smith JL, Wilson ML, Nilson SM, Rowan TN, Oldeschulte DL, Schnabel RD, Decker JE, Seabury CM. 2019. Genome-wide association and
372 genotype by environment interactions for growth traits in U.S. Gelbvieh cattle. *BMC Genomics.* 20: 926-940.

373 Stear MJ, Dimmock CK, Newman MJ, Nicholas FW. 1988. BoLA antigens are associated with increased frequency of persistent lymphocytosis

374 in bovine leukaemia virus infected cattle and with increased incidence of antibodies to bovine leukaemia virus. *Anim Genet.* 19: 151-158.
 375 Takeda M, Uemoto Y, Inoue K, Ogino A, Nozaki T, Kurogi K, Yasumori T, Satoh M. 2019. Genome-wide association study and genomic
 376 evaluation of feed efficiency traits in Japanese Black cattle using single-step genomic best linear unbiased prediction method. *Anim Sci J.*
 377 00:1–11.
 378 Vegiopoulos A, Muller-Decker K, Strzoda D, Schmitt I, Chichelnitskiy E, Ostertag A, Berriel Diaz M, Rozman J, Hrabe de Angelis M,
 379 Nusing RM, et al. 2010. Cyclooxygenase-2 controls energy homeostasis in mice by de novo recruitment of brown adipocytes. *Science.*
 380 328: 1158–1161.
 381 Wu H, Guang X, Al-Fageeh MB, Cao J, Pan S, Zhou H, Zhang L, Abutarboush MH, Xing Y, Xie Z, et al. 2014. Camelid genomes reveal
 382 evolution and adaptation to desert environments. *Nat Commun.* 5:5188.
 383 Wu T. 2001. The Qinghai-Tibetan plateau: how high do Tibetans live? *High Alt. Med. Bio.* 2:489-499.
 384 Xia X, Qu K, Zhang G, Jia Y, Ma Z, Zhao X, Huang Y, Chen H, Huang B, Lei C. 2019. Comprehensive analysis of the mitochondrial DNA
 385 diversity in Chinese cattle. *Anim Genet.* 50:70-73.
 386 Yang J, Li WR, Lv FH, He SG, Tian SL, Peng WF, Sun YW, Zhao YX, Tu XL, Zhang M, Xie XL, Wang YT, Li JQ, Liu YG, Shen ZQ, Wang F,
 387 Liu GJ, Lu HF, Kantanen J, Han JL, Li MH, Liu MJ. 2016. Whole-Genome Sequencing of Native Sheep Provides Insights into Rapid
 388 Adaptations to Extreme Environments. *Mol Biol Evol.* 10: 2576-2592.
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391 **Figure legends**

392

393 **FIG 1 The phylogenetic tree of MP mammals and their divergence.**

394 **(A) The phylogenetic tree of Mongolian Cattle (MC), Mongolian sheep (MS), Mongolian horse (MH), sheep, cattle, horse, mouse and**
395 **human. Mongolia mammals and corresponding domestic ones were diverged about 2-3 million years ago (Mya, MC-cattle:**
396 **1.8 Mya, MS-sheep: 2.6 Mya and MH-horse: 2.7Mya).**

397 **(B) PSMC analysis of MC, MS, MH, cattle, sheep and horse. PSMC analysis revealed MC, MS, MH diverged from their corresponding**
398 **domestic ones about 3 Mya.**

399 **FIG 2 Structure variation analysis of MC genome.**

400 **(A) SNPs (Single Nucleotide Polymorphisms) detection; (B) Indel detection;**

401 **(C) Inversions detection; (D) CNVs (Copy Number Variations).**

402 **Using cattle genome as reference sequences, we totally detected ~7.62 million single nucleotide variations and short InDels, 749 inversion**
403 **variants and 4689 CNVs (block length >5kb, 3750 deletions and 939 duplication). In addition, 32,944 structural variations,**
404 **including 19931 deletions, 4343 insertions and 8670 inversions were also detected.**

405 **FIG 3 Segmental duplications (SDs) analysis and GO enrichment.**

406 **(A) Segmental duplications (SDs) were detected in MC cattle genome and GO enriched in terms related to adaptation to extreme**
407 **environments.**

408 **(B) SDs enriched in a GO term called olfactory receptor activity.**

409 Using cattle genome as reference sequences, 251 specific SDs were identified in MC genome and enriched in GO terms related to
410 adaptation to extreme environments and GO term called olfactory receptor activity.

411 **FIG 4 Differentially Expressed Genes (DEGs) enriched in *PPAR signaling pathway*.**

412 **(A) DEGs enriched in *PPAR signaling pathway*.**

413 **(B) RPKM analysis of DEGs enriched in *PPAR signaling pathway*.**

414

415 **FIG 5 DEGs enriched in *Oxidative phosphorylation pathway* and *PI3K-Akt signaling pathway*.**

416 **(A) DEGs enriched in *Oxidative phosphorylation pathway*.**

417 **(B) DEGs enriched in *PI3K-Akt signaling pathway*.**

418 **(C) RPKM analysis of 3 up-regulated genes related to *PI3K-Akt signaling pathway*.**

419 **FIG 6 DEGs enriched in *Complement and coagulation cascades pathway*.**

420 **(A) DEGs enriched in *Complement pathway*.**

421 **(B) DEGs enriched in *coagulation cascades pathway*.**

422 **(C) RPKM analysis of DEGs enriched in *Complement and coagulation cascades pathway*.**

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426 **Figures.**

427 **(A)**

428

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(B)

Figure 1

Figure 2

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Figure 3

436 (A)

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445 (B)

Figure 4

448 (A)

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460 (B)

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465 (C)

Figure 5

473 (A)

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475 (B)

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Figure 6

Figures

Figure 1

The phylogenetic tree of MP mammals and their divergence. (A) The phylogenetic tree of Mongolian Cattle (MC), Mongolian sheep (MS), Mongolian horse (MH), sheep, cattle, horse, mouse and human. Mongolia mammals and corresponding domestic ones were diverged about 2-3 million years ago (Mya, MC-cattle: 1.8 Mya, MS-sheep: 2.6 Mya and MH-horse: 2.7Mya). (B) PSMC analysis of MC, MS, MH, cattle, sheep and horse. PSMC analysis revealed MC, MS, MH diverged from their corresponding domestic ones about 3 Mya.

Figure 2

Structure variation analysis of MC genome. (A) SNPs (Single Nucleotide Polymorphisms) detection; (B) Indel detection; (C) Inversions detection; (D) CNVs (Copy Number Variations). Using cattle genome as reference sequences, we totally detected ~7.62 million single nucleotide variations and short InDels, 749 inversion variants and 4689 CNVs (block length >5kb, 3750 deletions and 939 duplication). In addition, 32,944 structural variations, including 19931 deletions, 4343 insertions and 8670 inversions were also detected.

Figure 3

Segmental duplications (SDs) analysis and GO enrichment. (A) Segmental duplications (SDs) were detected in MC cattle genome and GO enriched in terms related to adaptation to extreme environments. (B) SDs enriched in a GO term called olfactory receptor activity. Using cattle genome as reference sequences, 251 specific SDs were identified in MC genome and enriched in GO terms related to adaptation to extreme environments and GO term called olfactory receptor activity.

Figure 4

Differentially Expressed Genes (DEGs) enriched in PPAR signaling pathway. (A) DEGs enriched in PPAR signaling pathway. (B) RPKM analysis of DEGs enriched in PPAR signaling pathway.

DEGs enriched in Complement and coagulation cascades pathway. (A) DEGs enriched in Complement pathway. (B) DEGs enriched in coagulation cascades pathway. (C) RPKM analysis of DEGs enriched in Complement and coagulation cascades pathway.

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