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Migration led to the microevolution of Chinese short fat-tailed Sheep

China has a long history of sheep domestication and rich resources of sheep breeds. Based on tail type, the Chinese domesticated sheep can be divided into five types: short fat-tailed sheep, long fat-tailed sheep, short thin-tailed sheep, long thin-tailed sheep and buttock-tailed sheep. According to archaeological and genetic research, Mongolian sheep is the common ancestor of Chinese short fat-tailed sheep breeds. Mongolian sheep evolved from the wild Argali sheep in the mountain regions of Central Asia. More than 2000 years ago, with the development of free trade, inter-ethnic war and the southward migration of steppe tribes, a large number of populations had moved south of the Great Wall. As a result, Mongolian sheep also migrated to North China villages and were introduced into Gansu, Xinjiang, Qinghai, Shandong and other provinces.

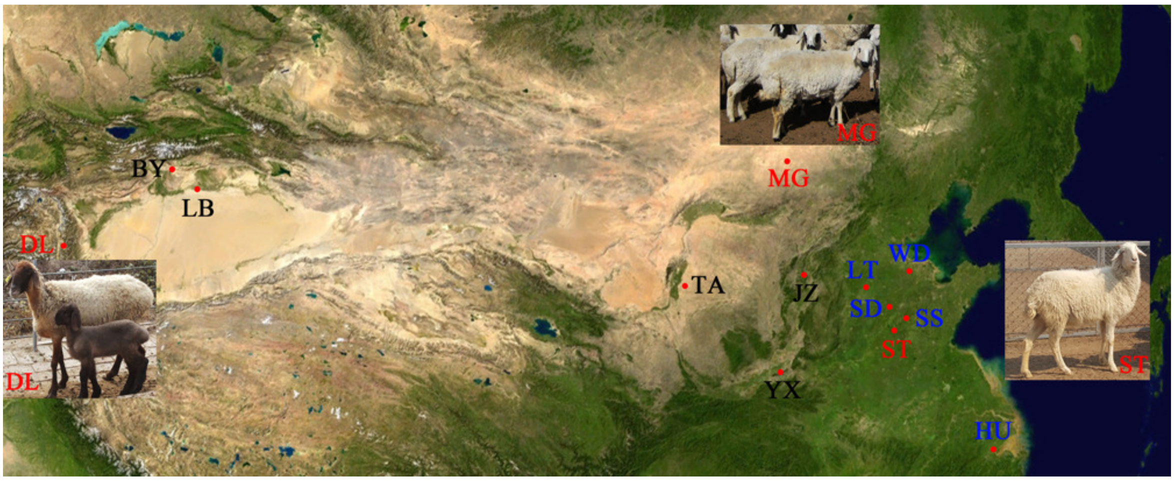

Fig. 1. Geographic distribution of Chinese short fat-tailed sheep. MG, DL, LB, BY, JZ, TA, YX, ST, LT, WD, SD, SS and HU are abbreviations for Mongolian sheep, Duolang sheep, Luobu sheep, Buyinbuluk sheep, Jinzhong sheep, Tan sheep, Yuxi fat-tailed sheep, Small-tailed Han sheep, Large-tailed Han sheep, Wandi sheep, Luzhong Shandi sheep, Sishui Fur sheep and Hu sheep, respectively. The 3 breeds used for whole-genome resequencing are labeled in red, and the additional 5 breeds used for genotyping are labeled in blue. This figure has been modified from China 100.78713E 35.63718N.jpg (https://commons.wikimedia.org/wiki/File:China_100.78713E_35.63718N.jpg). This image is in the public domain because it is a screenshot from NASA's globe software World Wind using a public domain layer, such as Blue Marble, MODIS, Landsat, SRTM, USGS or GLOBE.

Thus, most modern Chinese sheep breeds have a relationship to Mongolian sheep. Small-tailed Han sheep, Duolang sheep, Hu sheep, Tan sheep and others are all Mongolian sheep subspecies (Fig. 1). However, from the Mongolian plateau to various ecoregions around almost the entire country, Mongolian sheep have experienced changes in climate, environment and feeding conditions (from pastoral areas to rural areas) and been subjected to artificial selection in different directions. All of these factors have the potential to drive changes in selection and thereby cause microevolution. The subspecies of Mongolian sheep show significant differences in a number of traits, especially related to reproduction. Mongolian sheep exhibits seasonal estrous and singleton breeding, whereas Small-tailed Han sheep, Hu sheep and Duolang sheep exhibit year-round estrous and prolificacy in breeding. However, how species differ genetically in relation to these traits is not well understood. What different selection signals did these species get exactly during the migration? What kind of genetic diversities did these selection signals caused to the various species? How did the complex or tiny genetic mutation lead to the trait variations? Chinese short fat-tailed sheep are an excellent model for genetic studies on phenotypic evolution and adaptations to various ecoregions.

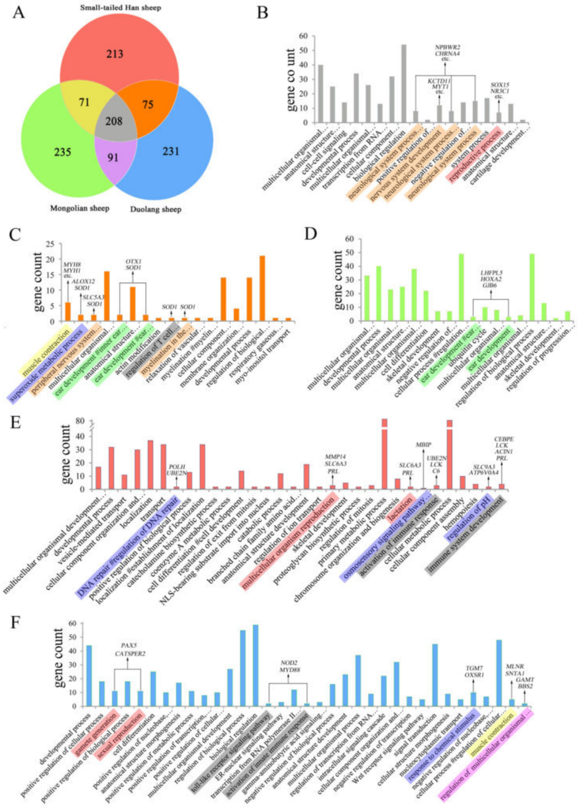

Fig. 2. Biological processes enrichment of genes located in regions with a Z(HP) < -4. A, All of the genes in regions with a Z(HP) < -4 were divided into 3 groups: I, Z(HP)M.

In this study we performed pooled whole-genome resequencing of 3 sheep breeds (Mongolian sheep, Small-tailed Han sheep and Duolang sheep) distributed over a wide range of geographical distance to examine the genetic variation among them. A 43.2-fold coverage of the reference genome, with a 14.4 X average sequencing depth for each breed was achieved. This effort identified 17,420,695 putative SNPs and 2,912,131 indels for the three breeds. We were able to experimentally validate 100 out of 102 tested SNPs. Selective sweep analysis revealed 143 genomic regions with reduced pooled heterozygosity or increased genetic distance to each other breed that represent likely targets for selection during the migration. These regions harbor genes related to developmental processes, cellular processes, multicellular organismal processes, biological regulation, metabolic processes, reproduction, localization, growth and various components of the stress responses (Fig. 2). Furthermore, we examined the haplotype diversity of 3 genomic regions involved in reproduction and found significant differences in TSHR and PRL gene regions among 8 sheep breeds. The substantial genomic resources provided here are useful for identifying genetic variations for phenotypic diversity and for revealing different signatures of selection associated with adaptation to various ecoregions.

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