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국내 과학자의 아프리카소 진화 논문, 세계적 관심 받아

- 서울대 농업생명과학대학 김희발 교수팀과 (주) 조앤김지노믹스는 아프리카와 유럽 6개국이 참여한 아프리카소 진화 유전체 연구를 8년간 주도하여 유전학 최고의 권위지 네이처 지네틱스에 9월 28일 (영국시간 오후 4시) 온라인으로 발표하였다. 본 논문은 네이처 지네틱스 10월호 표지 논문으로 선정되었다 (서울대 보도자료 10월 5일).
- 관련 연구의 화제성 우수성이 인정되어 네이처 리뷰 지네틱스의 리서치 하이라이트에 선정되어 온라인에 소개되었다 (2020년 10월 5일).
- 국내 연구진의 유전체 연구에서 표지논문뿐 아니라 네이처 리뷰지에 리서치 하이라이트로 동시에 선정된 것은 아주 드문 사례로 보여진다.
- 본 연구는 영국, 프랑스, 케냐, 호주, 중국, 브라질 등 20여 개국에 BBC Newsday를 비롯한 50여 매체에 보도되었다.
- 국내 연구진이 제1저자와 교신저자를 비롯한 많은 공저자가 포함되어 우리나라 연구진이 주도한 국제적으로 중요 논문임에도 국내에는 잘 소개되지 않고 해외에서 더 많은 관심을 받고 있다.

[붙임] 리서치 하이라이트

리서치 하이라이트

 GENOMICS

African cattle adaptations

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genetic history
of African
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The African continent is home to >150 indigenous cattle breeds that exhibit diverse phenotypic and adaptive characteristics. Now, a study in *Nature Genetics* describes the analysis of 172 genomes from 16 representative indigenous cattle breeds that maps the genetic history of African cattle and their unique adaptations.

The majority of African cattle are crossbreeds of the humpless *Bos taurus* (taurine cattle) and *Bos indicus* (indicine or zebu cattle), which are characterized by a large hump of fat tissue on their shoulders and are well adapted to dry climates and high temperatures. Domestic cattle are not native to the African continent, and both species are

thought to have descended from distinct subspecies of aurochs (*Bos primigenius*), a now extinct species of cattle.

In this study, the authors generated whole-genome sequences for 114 cattle from 12 indigenous African cattle populations and 2 African buffalo (*Syncerus caffer caffer*) as reference. These genomes were combined with 58 previously sequenced genomes from 4 additional African cattle populations to yield a genomic resource representative of the main African cattle groups.

The team first established the level of taurine versus indicine admixture among African cattle, before using admixture linkage disequilibrium (LD) decay to estimate the timing of its generation. A major taurine × indicine admixture event was identified and dated to approximately 750–1,050 years (around 150 generations) ago. This event markedly shaped the genome of today's crossbreeds living in the Horn of Africa, the main entry point of Asian zebu on the African continent.

Both taurine and indicine cattle were introduced onto the African continent after domestication in different regions, thus likely facing distinct new environmental challenges. To identify loci or haplotypes of either taurine or indicine ancestry that may have undergone

selection for conferring adaptive advantages under given environmental pressures, the authors used the integrated haplotype score; this statistic detects evidence of recent positive selection on the basis of differential levels of LD around a positively selected allele compared with the background allele at the same position. Along with inferences of local ancestry across the genome, this analysis revealed that the admixed cattle populations harbour candidate selected regions in haplotypes originating from indicine cattle that include genes related to the immune response and heat tolerance. Haplotypes of taurine origins containing genes associated with inflammatory responses and trypanotolerance also showed signatures of positive selection.

Taken together, the findings suggest that the success of African cattle pastoralism followed the arrival of indicine cattle and their crossbreeding with local taurine cattle and that selection shaped the admixture proportion of *B. taurus* × *B. indicus* crossbreeds to increase diversity and facilitate evolutionary adaptation. The authors propose “further crossbreeding of indigenous African cattle with exotic cattle ... as one of the pathways for the continent's food security”.

Linda Koch

ORIGINAL ARTICLE Kim, K. et al. The mosaic genome of indigenous African cattle as a unique genetic resource for African pastoralism. *Nat. Genet.* **52**, 1099–1110 (2020)

