

Analysis of Genetic Molecular Processes in Animals

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Abstract: *This article describes the molecular genetic and genomic processes in animals and the studies carried out. It is worth saying that the scope of work in this area is very wide, and this article briefly covered the work in this area.*

Keywords: *genome, breed, animal, gene, phenotype*

Introduction. Genomic origin and traceability are being used to address issues of species management and product quality. Tracking can also address food safety issues, but this has not been addressed in the US livestock industry as it has been in other countries. As another example, cultivated and wild aquaculture species are often at risk of interbreeding. With the development of marine aquaculture [eg in the Gulf of Mexico where 18 species are considered for cultivation], genome analysis is needed to verify the region of origin of the breeding fish. This reduces the risk to wild fish if farmed fish escape and provides a means of monitoring in the event of a major escape event. Genomic genotyping of breeding populations is attractive in some aquaculture species where breeding candidates are limited to selection of wild animals or F1 offspring to alleviate fears of escape.[1]

Genome-based technologies have been developed for several species with high economic value and investment in research. However, many of these species can be improved, and the application of these technologies to additional species and sectors has great potential to improve livestock production. For example, although the United States has contributed to the development of genomic tools for sheep, the use of genomic data such as sheep is large and widely used. Limited compared to New Zealand. Similarly, the use of genomic data to improve goat genetics is not currently used in the United States, but is used in Europe to improve dairy goat populations. Since genome-based technologies are applied where there is a clear economic benefit, it makes sense to make similar investments in other species. Consumers and producers are also poised to benefit from the application of genome-based technologies to fish species that have recently begun local production, such as oysters and California yellowfin tuna. To improve genome-wide selection in more animal species, scientists need to:

- (1) Use genomic data to determine relatedness between individuals to calculate genetic traits.
- (2) Use genomic marker data to conduct genomic selection.
- (3) Complementing genomic selection using identified causative mutations.
- (4) Supplement genotyping with genome sequence data to identify all common DNA variations in humans.
- (5) Expand datasets to include transcriptomic, proteomic, and metabolomic data related to traits.
- (6) Develop and implement strategies to reduce the impact of inbreeding.[2]

In transgenic animals, the foreign gene is permanently integrated into the animal's genetic material, i.e., DNA, reproductive (i.e., germ) cells and non-reproductive (i.e., somatic) cells, resulting in expression and reproduction of the gene. This method is mainly used to assess the role of specific genes in fetal development or to apply and study human disease in animals. In the second case, scientists introduce a human disease-causing gene into an animal and then study how the disease develops in the animal. Examples of human diseases studied in transgenic animals include cystic fibrosis and muscular dystrophy. A detailed

study of the mechanism of disease development allows scientists to develop better approaches to prevention or treatment, and then study them in these animals.[3]

Results. The development of new technologies that improve aspects of livestock production requires a deep understanding of animal biology. Over the past decade, US scientists and their international colleagues and partners have used genomic approaches to greatly expand the biological knowledge base of farm animal species. Since 2008, 7,558 peer-reviewed publications indexed by PubMed have reported work related to the genomics of the 13 species in the 2008 roadmap, nearly doubling the volume of work from the previous decade and increasing from 1949 to almost 44 percent of publications of this type.[4]

Conclusion. In the course of these studies, all efforts were properly highlighted and analyzed. Because of the additional challenges posed by genetically modified animals, policy makers often begin to develop appropriate policies requiring increased vigilance and monitoring of potential impacts on animal welfare.

References:

1. Bogliotti, Y. S., Wu, J., Vilarino, M., Okamura, D., Soto, D. A., Zhong, C., et al. (2018). Эффективное получение стабильно примированных плюрипотентных эмбриональных стволовых клеток из бычьих бластоцист. Proc. Natl. Acad. Sci. USA.
2. Carillier, C., Hélène, L. and Larroque, H. (2013). Первый шаг к геномной селекции в популяции мультипородных французских молочных коз. J. Dairy Sci. 96, 7294–7305
3. NAS (2015). Важнейшая роль исследований в области зоотехники в обеспечении безопасности и устойчивости пищевых продуктов. Washington, DC: National Academy of Sciences.
4. MacHugh, D. E., & Larson, G. (2017). Sustaining the Past: Exploring Ancient DNA and Animal Domestication. Annu. Rev. Anim. Biosci. 5, 329–351