ISSN:2790-1688 DOI: 10.56028/aetr.3.1.510

Review of whole genome sequencing technology on the selected signals of local chickens

Changsheng Deng[1], Momo Li[2], Wanqing Duan[3], Aiwei Guo[1], Fenfen Chen[1], Lili Liu[1], Yajing Yang[1] and Qingqing Li[1,3,*]

[1]Life Science College, Southwest Forestry University, Kunming 650224, China

[2]School of Mathematics and Computer Science, Yunnan Nationalities University, Kunming 650031, China

[3]College of Veterinary Medicine, China Agricultural University Beijing 100193, China

[4]Kunming Xianghao Technology Co. Ltd., Kunming 650204, China

*Corresponding author e-mail: doublelqq@163.com

Abstract. Genome sequencing has become one of the most rapid and effective methods to study molecular breeding of animals and plants. Chickens and chicken products are the necessary production for people and play an important role in our lives. Chickens are the first species of birds to get the whole genome sequence. This paper reviewed the research situation of domestic chicken reference genome and whole genome sequencing, which revealed the selective genes of special traits of local chicken breeds. It is believed that with the development of science and technology, whole genome sequencing combined with data from other sources can continuously promote the progress of this discipline.

Key words: whole genome sequencing; local chicken; selection; review

1. Introduction

The range and quantity of domestic chickens is wide, and the total quantity is about six times of the total human population [1]. Chicken accounts for the highest proportion of meat consumption in the world. Due to the differences in natural ecological environment and the development of society, economy and culture, people have different purposes for selecting and using chickens. Therefore, through long-term artificial domestication and selection, chicken genetic resources with different shapes, appearances and uses have been formed [2]. More importantly, chicken genome size is about 1G, which is about 1/3 of the total genome size of other domestic animals [2]. Therefore, Gallus gallus spadiceus [3] became the first livestock and poultry to complete the whole genome sequencing among amniotic animals.

Whole genome sequencing can obtain the whole genome sequence of an organism, which is characterized by rapidity, accuracy, high sensitivity and automation [3-7]. Through genome comparison, we can find a large number of gene differences, find the genetic basis related to good traits, realize genetic evolution analysis and predict candidate genes of importance, and discuss the adaptability of species and resistance to adverse environmental pressure [8-9]. Therefore, genome sequencing has become one of the most rapid and effective methods for studying animal and plant molecular breeding [9].

2. Chicken reference genome

In 2004, the International Chicken Genome Sequencing Consortium published the whole genome sequence sketch of Gallus gallus spadiceus [10]. They selected an inbred strain of Gallus gallus spadiceus hen (UCD001) for whole genome shotgun sequencing. The sequencing depth was about 6.6X, and the N50 was 36Kb. Combined with the comprehensive analysis of plasmid, fosmid and BAC terminal sequences, 1.05G sequencing data was obtained after assembly. 933Mb was located on a specific chromosome 907Mb is arranged along the chromosome, and 20000-23000

ISSN:2790-1688 DOI: 10.56028/aetr.3.1.510
genes are annotated. Compared with the genome similarity between domestic chicken and human, the aligned segment is more likely to be located in the conservative collinear large segment, and the frequency of chromosome translocation is lower than the frequency of chromosome inversion; The co linear relationship between non coding RNA and coding protein genes was different; The chicken chromosome size spans two orders of magnitude and is negatively correlated with the recombination rate, GC and CpG content, but the gene density is positively correlated with the duplication density; The synonymous substitution rate of small chromosome and large chromosome subthromosome region was higher in domestic chickens; Compared with mammalian genome, chicken genome lacks degenerated pseudogenes, simplifying the classification of chicken gene content; Analysis of chicken and human genome sequences shows that at least 70Mb long sequences are likely to function in both species.

In the same year when the draft of the whole gene sequence of Gallus gallus spadiceus was published, the International Chicken Polymorphism Map Consortium sequenced broilers, layers and silky fowls based on the strategy of whole genome re sequencing, and combined with the comparative analysis of the reference genome sequence of Gallus gallus spadiceus, a total of 2.8 million single nucleotide polymorphisms (SNPs) were obtained. Subsequent studies showed that 90% of the SNPs were reliable 70% SNPs are distributed in many domesticated species. By comparing the SNPs between red grouse and domestic chickens, between domestic chickens and within domestic chickens, it was found that the variation density was only 5 SNP/kb, indicating that domestication did not significantly reduce genetic diversity [11].

3. Whole genome sequencing reveals selected genes for special traits of local chicken breeds

Local chicken breeds are rare precious materials in the genetic resource pool of livestock and poultry. Local chicken breeds with different phenotypes in the world have different domestication histories [12, 13]. Through long-term artificial domestication, they have gradually formed local chicken breeds with diverse uses such as meat, egg, dual use and appreciation, as well as body and appearance. Local chicken breeds have the genetic characteristics of wide adaptability, strong resistance to stress, rough feeding tolerance, strong foraging ability and good egg and meat quality [12].

Yellow feather chickens are called "three yellow chickens" because of their yellow beak, yellow feathers, yellow feet and other physical characteristics. Because their meat is delicious and their meat color meets consumer needs, they are loved by many countries in Asia, especially in South Korea, southern China and other cities. Huang et al. [14] conducted a full genome analysis of 10 local yellow feather chicken breeds in China, and found that the genetic similarity between yellow feather broilers is higher than that between yellow feather broilers and other local chicken breeds; RALY, LGR4, SLC23A2, SLC2A14 and BCDO2 genes were screened as pigment candidate genes of yellow feather chickens. The ladybird chicken is a good material for studying the structural degradation of the tail of livestock and poultry. Its tail vertebrae, tail fat glands, tail feathers and other important main tail structures are missing. Based on the whole genome sequencing and transcriptome data, candidate genes (IRX4, IL-18, HSPB2 and CRYAB) for the deletion of the tail of the ladybird chicken were screened. Wang et al. proposed that strong selection pressure on regulatory elements may lead to changes in the activity of tail mesenchymal stem cell genes, Moreover, by hindering the proliferation and differentiation of stem cells, it finally led to the loss of tail structure of ladybugs [15]. Because of its aggressive character, cockfighting is often used as an ornamental chicken species for competition. Based on the whole genome re sequencing technology, candidate genes [16] (BDNF, NTS, APP, SNCA and PPT1) related to cockfighting have been preliminarily screened. Dulong chicken is a local characteristic chicken breed raised by a very small ethnic group in China, Dulong, for generations. It is only distributed in Gongshan County, Nujiang Prefecture, Yunnan Province, China. The local environment is harsh, with high mountains and

ISSN:2790-1688 DOI: 10.56028/aetr.3.1.510
valleys, fast rivers, high altitude (~3000m), and high humidity (annual average humidity 90%). Historically, the local area has been closed for a long time, thus forming a typical three-dimensional microclimate environment [10, 17], Our team conducted genome re sequencing analysis on Dulong chicken and preliminarily screened candidate genes for Dulong chicken to adapt to special environment (PAIP1, MIPOL1, TLE1, FGF10, RICTOR, NFIB and MRPS30, etc.) and to be artificially selected (KIF18A, ADAMTSL1, NNT, AGTPBP1 and ADAMTSL1, etc.) [11]. Based on the whole genome sequencing, the silkiness trait associated gene (PDSS2) of Jinyang silky fowl was screened; Regulate the growth and development related genes (SMPD3 and GLI3) of Muchuan black bone chickens and asbestos grass chickens; Genes related to laying performance (KIF18A) of Tianfu black bone chickens and Pengxian yellow chickens [14]; Candidate genes for black feather and black bone traits (BMP7, EDN3 and TUBB1) of Tianfu black bone chickens, Muchuan black bone chickens and Jiuyuan black chickens [10, 12], and black bone traits of Xichuan black bone chickens in Henan [15].

4. Conclusion

The development of any technology is from simple to deep, and the whole genome sequencing technology is no exception, starting from the first complete virus genome (bacteriophage MS2) measured by Walter; When the Human Genome Project was officially launched in the United States, whole genome sequencing became the "darling of the times" in the field of biological research at that time. Biological research gradually ushered in the era of big data, providing more detailed data support for biological disciplines, but it still could not avoid the emergence of controversy, which was in line with the development law of "spiral rise and zigzag progress", and also promoted the continuous and healthy development of whole genome sequencing technology.

Based on the whole genome sequencing technology, candidate genes selected by the sample can be preliminarily screened, which provides a good guide for subsequent research. In addition, we can also obtain SNPs, Insertion/Deletion (InDels), Structural variants (SV), CNV, etc., of which SVs are increasingly attracting researchers' interest by changing the number of gene copies and their expression, This may lead to the generation of new genes, which may even affect the evolution of organisms' phenotypes and their adaptability to the local environment [18-20]; CNVs are also associated with phenotypic evolution, and can provide important guidance for research on complex diseases and important economic traits [21, 22]. Now is the era of genomics and even the era of big data. Whole genome sequencing can provide early basic data well, and combine with transcriptome, proteome, macrogenome and other multi genomics, and use the deep mining of bioinformatics to continuously promote the progress of this discipline.

References

[1] M. Tixier-Boichard, B. Bed'hom, X. Rognon, Chicken domestication: from archeology to genomics. C R Biol, 2011. 334(3): pp. 197-204.

[2] S.Y. Liang, Z.K. Zhou, S.S. Hou, The research progress of farm animal genomics based on sequencing technologies. Yi Chuan, 2017. 39(4): pp. 276-292.

[3] H.A. Lewin, G.E. Robinson, W.J. Kress, et al., Earth BioGenome Project: Sequencing life for the future of life. Proc Natl Acad Sci U S A, 2018. 115(17): pp. 4325-4333.

[4] L. Donghua, W. Xinlei, L. Zhuanjian, et al., Research progress in sequencing the whole genome of domestic chickens. Biotechnology Bulletin, 2017. 33(07): pp. 35-39.

[5] Z. Yuchen, L. Shuai, G. Wenjin, et al., Important application and progress of poultry molecular breeding technology. Chinese Journal of Veterinary Medicine, 37(12): pp. 2430-2433.

[6] D. Berner and W. Salzburger, The genomics of organismal diversification illuminated by adaptive radiations. Trends Genet, 2015. 31(9): pp. 491-9.

ISSN:2790-1688 DOI: 10.56028/aetr.3.1.510
[7] B.N. Keel, D.J. Nonneman, G.A. Rohrer, A survey of single nucleotide polymorphisms identified from whole-genome sequencing and their functional effect in the porcine genome(). Anim Genet, 2017. 48(4): pp. 404-411.

[8] N. Vijay, M. Weissensteiner, R. Burri, et al., Genomewide patterns of variation in genetic diversity are shared among populations, species and higher-order taxa. Mol Ecol, 2017. 26(16): pp. 4284-4295.

[9] C.J. Rubin, M.C. Zody, J. Eriksson, et al., Whole-genome resequencing reveals loci under selection during chicken domestication. Nature, 2010. 464(7288): pp. 587-91.

[10] Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. Nature, 2004. 432(7018): pp. 695-716.

[11] G.K. Wong, B. Liu, J. Wang, et al., A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. Nature, 2004. 432(7018): pp. 717-22.

[12] D. Li, Y. Li, M. Li, et al., Population genomics identifies patterns of genetic diversity and selection in chicken. BMC Genomics, 2019. 20(1): pp. 263.

[13] C.S. Ekarius, Illustrated Guide to Poultry Breeds: Chickens, Ducks, Geese, Turkeys, Emus, Guinea Fowl, Ostriches, Partridges, Peafowl, Pheasants, Quails, Swans. City: Storey publishing, 2007.

[14] X. Huang, N.O. Otecko, M. Peng, et al., Genome-wide genetic structure and selection signatures for color in 10 traditional Chinese yellow-feathered chicken breeds. BMC Genomics, 2020. 21(1): pp. 316.

[15] Y.M. Wang, S. Khederzadeh, S.R. Li, et al., Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait. Genomics Proteomics Bioinformatics, 2021. 19(5): pp. 787-799.

[16] R.A. Lawal, R.M. Al-Atiyat, R.S. Aljumaah, et al., Whole-Genome Resequencing of Red Junglefowl and Indigenous Village Chicken Reveal New Insights on the Genome Dynamics of the Species. Front Genet, 2018. 9: pp. 264.

[17] L. Suyun, Z. Zhengkui, H. Shuisheng, Research progress in livestock and poultry genomics based on sequencing technology %J inheritance. 2017. 39(04): pp. 276-292.

[18] X. Zhang, K. Wang, L. Wang, et al., Genome-wide patterns of copy number variation in the Chinese yak genome. BMC Genomics, 2016. 17: pp. 379.

[19] S. Xu, Z. He, Z. Zhang, et al., The origin, diversification and adaptation of a major mangrove clade (Rhizophoreae) revealed by whole-genome sequencing. Natl Sci Rev, 2017. 4(5): pp. 721-734.

[20] Y. Paudel, O. Madsen, H.J. Megens, et al., Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. BMC Genomics, 2013. 14: pp. 449.

[21] G. Yi, L. Qu, J. Liu, et al., Genome-wide patterns of copy number variation in the diversified chicken genomes using next-generation sequencing. BMC Genomics, 2014. 15(1): pp. 962.

[22] S. Lin, X. Lin, Z. Zhang, et al., Copy Number Variation in SOX6 Contributes to Chicken Muscle Development. Genes (Basel), 2018. 9(1).