

Research progress of domestication and origin in chicken by whole genome sequencing

Changsheng Deng¹, Momo Li², Wanqing Duan³, Aiwei Guo¹, Fenfen Chen¹, Lili Liu¹, Yajing Yang¹, Qiongyao Zeng⁴ and Qingqing Li^{1,5,*}

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

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

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

⁴Yunnan Hospital of Traditional Chinese Medicine, Kunming 650021, China

⁵Kunming Xianghao Technology Co. Ltd., Kunming 650204, China

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

Abstract. Whole genome sequencing technology started in the middle and late 20th century. In recent years, with the rapid development of high-throughput sequencing technology, the further reduction of sequencing costs and the continuous improvement of assembly methods, it has penetrated into various fields of modern biological research and played a revolutionary role in promoting. Chickens and chicken products have become the necessary means of production and life for people, and chickens are the first species of birds to have the whole genome sequence. In this paper, we reviewed the research progress of whole genome sequencing technology in chicken origin and domestication, especially discussed the significance and problems in the research of candidate genetic signals of chicken breeds.

Key words: whole genome sequencing; Chicken; Domestication; Origin; Research progress

1. Introduction

Whole genome sequencing can obtain the whole genome sequence of an organism, which is characterized by rapidity, accuracy, high sensitivity and automation [1-5]. 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 [6-8]. Therefore, genome sequencing has become one of the most rapid and effective methods for studying animal and plant molecular breeding [1-5, 9]. In 1990, the Human Genome Project (HGP) [10] was launched by the National Human Genome Research Center of the United States and relevant multinational institutions. The project took 13 years and mapped 3 billion base pairs of human beings, which is a milestone and a new starting point for the development of life science. Among them, Chinese scientists participated in the "1% Plan" and undertook the sequencing and analysis task of about 30cM (centromorgan) on the telomere side of the short arm of chromosome 3. At the same time of completing the first sketch of the human genome, we also completed the sequencing of genome sequences of seven model organisms, including *Saccharomyces cerevisiae* [11], *Escherichia coli* [12], *Caenorhabditis elegans* [13], *Arabidopsis thaliana* [14], *Drosophila melanogaster* [15], *Fuku rubripes* [16] and *Mus musculus* [17]. With the rapid development and wide application of genome sequencing technology, the mechanisms of domestication and character difference of domestic animals have been deeply interpreted at the genome level, which has pushed the research on domestic animals to a new level.

2. The domestication and origin in chicken by whole genome sequencing

Domesticated by humans for thousands of years, domestic chickens have been serve agricultural production [18] and provide high-quality meat and eggs for humans. Rubin et al [9] found that there was a mutation at Gly558Arg site in domestic chickens and the mutation site was also fixed on *Gallus gallus spadiceus* (*G. g. spadiceus*), a subspecies of red broilers. The mutation frequency of this site was *G. g. Spadiceus* (94%) and Thai red jungle fowl (90.5%) are very high, but the mutation frequency is very low in other subspecies of red jungle fowl (5.4%) [19]. In addition, there is a 239 bp deletion in the seventh intron of TSHR gene (thyroid stimulating hormone receptor, TSHR) (chr5: 40080509 – 4008074). The deletion frequency of this site is the same as that of Gly558Arg mutation, indicating that the changes of these two sites are likely to be genetically related. Recently, based on the whole genome re sequencing strategy, the TSHR gene has also been strongly positive selected in other local chicken breeds [20]. The mutation of this site may weaken the impact of photoperiodic changes on domestic chickens, leading to seasonal reproduction loss, which is a common feature in domestic animals, but rarely in wild animals. Therefore, it is speculated that TSHR may be a selected gene during domestication of domestic chickens. However, the analysis of chicken ancient DNA from the 12 European archaeological sites from 280 BC to the 18th century AD shows that the allelic variation in the TSHR gene did not play an important role in the early domestication of chickens, and the fixation of the mutation site only occurred in the last 500 years[21] - 1100 years[22], which is roughly consistent with the beginning of the industrial revolution [21, 22], but thousands of years later than the domestication process of domestic chickens [23].

Rubin et al [9] also found that the SH3 domain-containing ring finger 2 (SH3RF2) containing two zinc rings was located in the quantitative trait locus (QTL) region. The deletion of the coding sequence of SH3RF2 gene was most likely the main locus causing allometric growth in domestic chickens. This study screened candidate genes associated with meat production traits. Based on previous studies, Jing et al [24] detected copy number variations (CNV) of SH3RF2 gene in 4079 samples of 17 chicken populations (including Chinese native chicken breeds, commercial laying hens and commercial broilers), and the native chickens and commercial laying hens are wild homozygous; Except for Hubbard broilers, commercial broilers are mutated individuals, which indicates that SH3RF2 gene of commercial broilers mutates in the process of human continuous selection; The team took the hybrid strain F2 of Gushi chicken and Anka chicken as the research object, and found that the CNV of SH3RF2 gene was related to the weight gain at 2, 6, 10 and 12 weeks, and the CNV of SH3RF2 gene was significantly related to the weight and sternum length at 8 weeks.

To sum up, we can preliminarily screen and identify the selected candidate genes of domestic chickens through the whole genome sequencing strategy, which provides basic materials and direction for the subsequent research work [25-28]. However, domestic chickens are characterized by a wide variety and wide distribution. Rubin et al, It may not be possible to accurately estimate the approximate time when candidate genes are selected and determine whether the selected genes are the main genes of domesticated chickens. In addition, due to the lack of direct radiocarbon dating, the early archaeological relics have some limitations in estimating the domestication time of domestic chickens.

3. Conclusion

With the continuous improvement and maturity of whole genome sequencing technology, the gradual decline of sequencing price has promoted the leapfrog development of sequencing, which has enabled the genetic information of the most widely distributed livestock and poultry in the world - domestic chickens (with diverse domestication backgrounds and different morphological and physical characteristics) to be gradually deciphered [29-31]. Depending on the whole genome sequencing technology, we can learn more comprehensively the genetic information of different

chicken breeds, even the domestication history, geographical origin and distribution characteristics of domestic chickens. 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.

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