

Identification of genetic basis underlying egg and growth traits in chickens

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Abstract

Chickens are well known as the most abundant livestock animals in the world, and widely spread and adapted to varieties of environmental conditions. To overcome world food problem of hunger situation, it will be important to utilize genetically divergent adapted genetic resources of livestock. Chickens have a large potential as food source of animal proteins throughout the world, because of low food taboo. Therefore, I have researched what kinds of genetic differences regulate egg and growth traits in chickens. A large scale F₂ resource population based on Japanese Large Game (Oh-Shamo) have been used to identify quantitative trait loci (QTLs) for egg production traits, egg quality traits, and growth traits¹). These traits are generally controlled by many main-effect QTLs, epistatic interaction-effect QTLs, and environmental factors. Revealing QTLs underlying egg and growth traits will be effective to understand genetic basis of quantitative traits and to apply to enhance future livestock production.

For egg production traits (age at first egg and egg production ratios), 5 main-effect QTLs and 3 pairs of epistatic QTLs were found on chromosomes 1, 2, 4, 7, 8, 11, 17, and 19. For external egg traits (egg weight, egg sizes, eggshell weight, eggshell thickness, eggshell strength, and eggshell colors) measured at three different egg laying states, 44 main-effect QTLs were identified on chromosomes 1, 2, 4, 5, 8, 10, 11, 12, 17, and Z. For internal egg traits (albumen sizes, albumen weight, yolk sizes, yolk weight, and yolk colors) collected at three stages, 49 main-effect QTLs and 3 pairs of epistatic QTLs were detected. Moreover, statistical method of causal inference revealed three independent phenotypic networks based on 17 main-effect QTLs and 24 egg traits. For growth traits (body weight and shank length) measured at from 0 to 64 weeks of age, 48 main-effect QTLs and 19 pairs of epistatic QTLs were found on 22 different chromosomes²). Taken together, many QTLs interacted with each other and their age-specific expression are common feather in genetic basis underlying egg and growth traits in chickens. In addition, I have started to investigate genetic factors in egg component traits. Using a variety of chicken breeds, my team found that yolk amino acid traits and yolk and albumen metabolite traits are significantly altered by genetic factors³).

In summary, genetic basis underlying egg and growth traits in chickens has been revealed. These findings will lead to understand genetic basis of quantitative traits and be potential use for enhancing world livestock production.

References

- 1) **Goto T*** and Tsudzuki M*. (2017) Genetic mapping of quantitative trait loci for egg production and egg quality traits in chickens: a review. *Journal of Poultry Science* 54: 1-12.
- 2) **Goto T***, Ishikawa A, Nishibori M, Tsudzuki M*. (2019) A longitudinal quantitative trait loci mapping of chicken growth traits. *Molecular Genetics and Genomics* 294: 243-252.
- 3) **Goto T***, Mori H, Shiota S, Tomonaga S. (2019) Metabolomics approach reveals the effects of breed and feed on the composition of chicken eggs. *Metabolites* 9: 224.