



Symposium mini review

Genomic Prediction in Japanese Black Beef Cattle: Some Topics

Shinichiro OGAWA

Graduate School of Agricultural Science, Tohoku University, Sendai, Miyagi, Japan

Keywords

Japanese Black cattle,
single nucleotide polymorphism,
breeding value prediction,
the degree of marbling,
genome-wide high-density DNA marker

Corresponding Author

Shinichiro OGAWA,
shinichiro.ogawa.d5@tohoku.ac.jp

Abstract

The Japanese Black is a representative of the beef cattle breeds constructing Wagyu in Japan. The beef produced are high quality, especially highly marbled (shimofuri), and they are also famous overseas. Carcass traits including the degree of marbling have been remarkably improved through use of a low number of elite sires with high predicted genetic abilities (breeding values) for meat quality. Breeding values are predicted by using a deep pedigree information and a large amount of carcass performance data of fattened steers and heifers. Breeding values for growth performance and feed efficiency of young bulls and those for female reproductivity of cows have been also evaluated using pedigree information. Recently, prediction of breeding values by using genotype information on genome-wide high-density single nucleotide polymorphisms (SNPs) as DNA markers, also referred to as genomic prediction, have been studied in Japanese Black cattle. Genomic prediction is believed to have a potential to achieve more efficient breeding in livestock species. In this review, some relevant topics for genomic prediction in Japanese Black cattle, as well as the possibility of genomic prediction and the future issues in this breed, will be discussed.

Japanese Black cattle as the primary beef breed of Wagyu

Wagyu is a general term used for modern native Japanese beef cattle breeds in Japan. Wagyu cattle consist of four beef breeds: the Japanese Black, Japanese Brown, Japanese Shorthorn, and Japanese Polled. The Japanese Black cattle is the primary Wagyu breed and is well known to excel in meat quality, especially in marbling. For the detailed description about establishing the Japanese Black breed, see, for example, Hirooka (2014), Motoyama *et al.* (2016), and Gotoh *et al.* (2018). In short, native Japanese cattle in Japan were crossed with British and Continental breeds during an approximately 10-year period in the early 1900s. And then, under a completely closed breeding system, the four breeds of Wagyu were fixed through strict selection over many years (Namikawa, 1992).

In Japanese Black cattle, the genetic abilities (breeding values) have been evaluated for several economically important traits relating to carcass performance of fattened progeny, growth and feed efficiency of young bulls, and female reproductive efficiency of dams. For the detailed explanation about the progeny-testing for the representative

carcass traits in this breed, see, for example, Inoue (2004) and Sasaki (2007). Beef quality traits including the degree of marbling have received more emphasis in domestic beef production of Japanese Black cattle since the relaxation of beef import restrictions in Japan in 1991. In the same year, genetic evaluation of carcass traits using a mixed model methodology (Henderson, 1973) based on a deep pedigree information was introduced using relevant field data collected at carcass markets (Wagyu Registry Association, 2007). Assuming the infinitesimal model to breeding value (Fisher, 1918; Bulmer, 1980), the whole genome is targeted in the genetic evaluation but is treated as an unobserved black box. Subsequently, while there has been steady genetic improvement attained in carcass traits, it is known that there is a sharp decline occurred in effective population size of this breed, because of intensive use of few sires with higher predicted breeding values for degree of marbling (e.g., Nomura *et al.*, 2001; Nomura, 2002; Honda *et al.*, 2004).

Numerous studies have reported the estimated heritabilities of, and genetic correlations among various kinds of traits in Japanese Black cattle. Oyama (2011) summarized the estimated values of direct and maternal heritabilities for body weight and daily gain traits of calves, those of direct

heritability for body weight, daily gain, feed intake, and feed conversion traits of young bulls, those of direct heritability for and genetic correlation among carcass traits of fattened steers and heifers, and those of direct and maternal heritabilities for female reproductive traits of dams. In general, carcass and growth traits were moderately to highly heritable but female reproductive traits had low heritabilities, and the genetic correlation between two fat deposition traits, marbling and subcutaneous fat thickness, was low (Oyama, 2011).

Genetic parameters for different traits have been also estimated. For example, several studies estimated the heritabilities of body measurement traits and their genetic correlation with carcass and female reproductive traits (e.g., Baco *et al.*, 1997; Kuchida *et al.*, 1994; Munim *et al.*, 2012; Oyama *et al.*, 1996). Heritabilities of traits relating to meat quality and their genetic correlations with carcass traits have been also reported (e.g., Inoue *et al.*, 2008; Komatsu *et al.*, 2014; Nogi *et al.*, 2011; Onogi *et al.*, 2017; Sakuma *et al.*, 2016). Heritabilities of image analysis traits for the shape of ribeye and marbling in ribeye and other muscles have been estimated (e.g., Goto *et al.*, 2020; Kuchida *et al.*, 2006; Osawa *et al.*, 2008). Moderate to high heritability has been estimated for growth curve parameters (e.g., Inoue *et al.*, 2020; Onogi *et al.*, 2019; Takeda *et al.*, 2018; Wada & Nishida, 1987), residual feed intake, residual daily gain, and residual feed intake and daily gain (e.g., Hoque & Oikawa, 2004; Okanishi *et al.*, 2008; Takeda *et al.*, 2018), and predicted methane emission traits (Uemoto *et al.*, 2020). For female reproductive efficiency for heifer, Inoue *et al.* (2020) estimated the heritability of first service conception rate to be 0.03 and Setiaji and Oikawa (2020) estimated the heritability of non-return rate, the number of inseminations, and interval from first to successful insemination to be 0.027, 0.019, and 0.011, respectively. Ogawa and Satoh (2021) reported that the estimated heritability of calving interval was low but the genetic correlation between different ages of dam was consistently high. Inoue *et al.* (2017) estimated the direct and maternal heritabilities of calving difficulty to be 0.24 and 0.61, respectively. Nishida *et al.* (2006) estimated the heritability of the number of services per conception at different parity to be ~0.1 in most cases. Nishimura *et al.* (2010) estimated the heritability for semen characteristics traits in bulls to be around 0.1. Nishi *et al.* (2016) estimated the heritabilities of carcass defects including blood splash, intramuscular edema, muscle steatosis, bruising, trim loss, and other defects, and Oyama *et al.* (2020) estimated the heritabilities of defective appearances including white spotting, tongue defect, and nipple defect. Inoue *et al.* (2015) estimated the heritabilities of internal diseases of fattened steers and their genetic correlations with carcass traits. Takeda *et al.* (2017) estimated the heritability of temperament of calves and its genetic correlation with carcass traits. These estimates could provide valuable information for the development of appropriate, sound future breeding plans in Japanese Black cattle (Oyama, 2011).

Studies for genomic prediction for carcass traits in Japanese Black cattle

In the late twentieth-century, breakthroughs occurred in molecular biology and genetic engineering that established the

technological basis for modern genomics and biotechnology. This facilitated quantitative trait locus (QTL) mapping and marker-assisted selection (MAS). The MAS assumes the use of a small number of DNA markers for major causative genes with large effects. However, there is now a general consensus that most complex and quantitative traits are usually affected by a large number of small-effect genes (de los Campos *et al.*, 2013).

Meuwissen *et al.* (2001) proposed the idea of a new type of MAS that simultaneously treats all chromosome segments by using genome-wide DNA markers such as single nucleotide polymorphisms (SNPs). Genome-wide high-density SNPs are used with the expectation of tracing all underlying QTLs, or to explain all additive genetic variances of a trait by exploiting the status in linkage disequilibrium between QTLs and SNPs. Prediction of breeding values using genome-wide DNA markers is often referred to as genomic prediction (GP), and selection based on the result of GP is genomic selection (GS). For the detailed explanation for GP and GS written in Japanese, see, for example, Matsuda *et al.* (2013) and Nagamine (2012).

After developing the commercial SNP chip which can determine the genotypes of SNPs identified using samples other than Japanese Black cattle (Matukumalli *et al.*, 2009), GS following GP was introduced into routine genetic evaluation and selection of dairy cattle, especially Holstein cattle (e.g., Hayes *et al.*, 2009; VanRaden *et al.*, 2009); this is partly because of the possibility of reducing the costs of progeny testing schemes (Schaeffer, 2006). Even though the potential for GS to improve genetic gain in beef cattle would be substantial (Pimentel *et al.*, 2012; Van Eenennaam *et al.*, 2011), there are no reports providing the information on GP accuracy for Japanese Black cattle. Ogawa *et al.* (2014) estimated the variance of carcass weight and marbling score explained by the genome-wide 38,502 SNP markers using 872 fattened steers (Fig. 1). This study showed that the genome-wide SNP markers genotyped by using the commercial chip can capture most additive genetic variances of carcass weight and marbling score in Japanese Black cattle. Ogawa *et al.* (2016a) assessed the accuracy of GP for carcass weight and marbling score, using 1,791 steers as the training population and 189 animals as the validation population (Fig. 2). The accuracy of GP was middle to high for both traits, implying

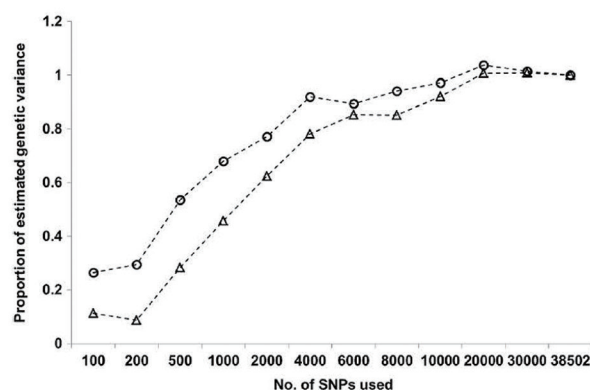


Fig. 1. Changes in proportions of estimated genetic variances with increasing SNP marker density. Circles: carcass weight; triangle: marbling score (Ogawa *et al.*, 2014).

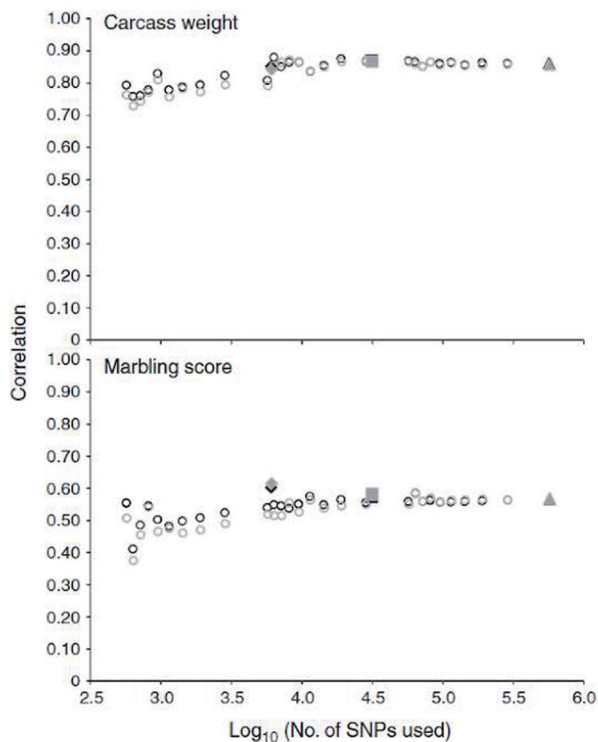


Fig. 2. Changes in the accuracy of genomic prediction. Triangles, squares and rhombuses show the results obtained using high-density, 50K and low-density single nucleotide polymorphism (SNP) sets, respectively (Ogawa *et al.*, 2016a).

that GP for carcass traits could be available in pre-selecting young Japanese Black breeding animals. Watanabe (2016) compared the accuracies of GP for six carcass traits with those of parent average of breeding value, which is used as a classical indicator for pre-selection, and showed that the accuracy was higher for GP than parent average.

Some possible future challenges in this breed

In Japanese Black cattle, the study about GP for fatty acid composition in meat (Onogi *et al.*, 2015), semen production traits (Atagi *et al.*, 2017), and feed efficiency traits (Takeda *et al.*, 2020) were also reported. In the future, GP for other traits including female reproductive efficiency, resistance to disease and heat stress, and traits related to environmental load should be performed.

Integrating multi-omics data is a hot topic (e.g., Snelling *et al.*, 2013; Suravajhala *et al.*, 2016; Takagi *et al.*, 2014). Okada *et al.* (2018) estimated candidate gene-gene interaction network for feed efficiency in cattle combining the results of the genome-wide association study for seven feed utilization traits in Japanese black cattle and public RNA-expression data from different tissues of multiple foreign breeds (**Fig. 3**). The results could give meaningful insight into the trait, and GP incorporating such a biological information might increase the performance of GP in cattle (e.g., Gao *et al.*, 2017; Melzer *et al.*, 2013; Tiezzi *et al.*, 2018).

The study about long-term implementation of GP and GS in Japanese Black cattle is essential (e.g., Maltecca *et al.*, 2020; Neyhart *et al.*, 2017; Ogawa *et al.*, 2016b). For example,

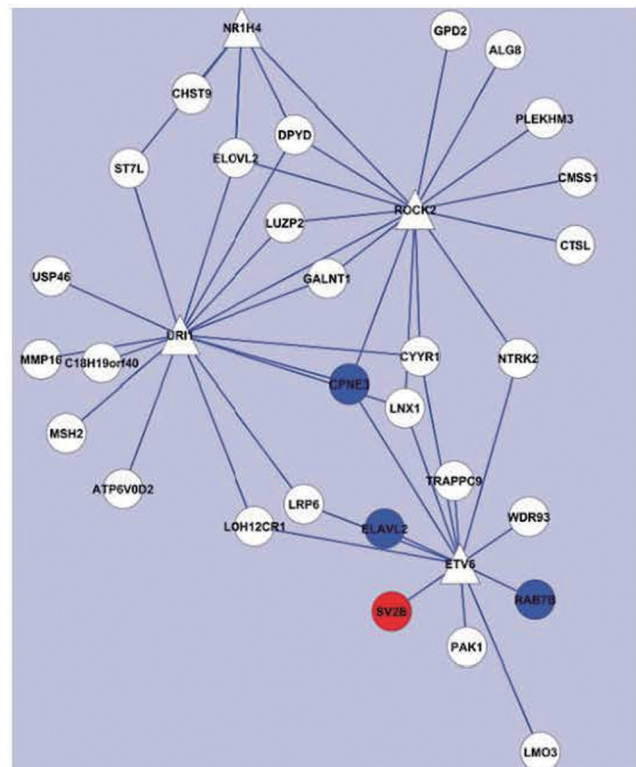


Fig. 3. Subnetwork extracted from the top 3 hub transcription factors (TFs) and their neighboring genes (Okada *et al.*, 2018). Node colors correspond to gene tissue specificity: gland (red), nervous system (blue), and nontissue-specific genes (white). Node shapes indicate gene classification: triangle (TF) and circle (other genes).

GS can boost the speed of genetic improvement, while this might also bring further decrease in genetic diversity of this breed, as already observed in dairy cattle (Doekes *et al.*, 2018; Doublet *et al.*, 2019). High-density SNP markers could be also available for assessing the genetic diversity of cattle populations (e.g., Decker *et al.*, 2014; Eusebi *et al.*, 2019; VanRaden *et al.*, 2011). Therefore, genome-wide DNA markers might be a powerful tool to achieve the efficient genetic improvement while considering the genetic diversity of Japanese Black cattle (e.g., Gómez-Romano *et al.*, 2016; Thomasen *et al.*, 2013; Wang *et al.*, 2017).

Acknowledgements

The works of Ogawa *et al.* (2014, 2016a,b) were partly supported by the Japanese Ministry of Agriculture, Forestry, and Fisheries, by the Japanese Racing and Livestock Promotion Foundation (H20-5), and by the Research Fellowship of the Japanese Society for the Promotion of Science for Young Scientists (No.15J02417). The author thanks the staff of the Shirakawa Institute of Animal Genetics for their technical assistance for collecting SNP genotype data. The work of Ogawa and Satoh (2021) was supported by the Sasakawa Scientific Research Grant from The Japan Science Society (2018–2019). The author thanks the Miyagi Prefectural Government Livestock Industry division for kindly providing the data.

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