

Estimated genetic variances due to QTL candidate regions for carcass traits in Japanese Black cattle

Shinichiro Ogawa^{1,*}, Hirokazu Matsuda¹, Yukio Taniguchi¹, Toshio Watanabe², Akiko Takasuga², Yoshikazu Sugimoto³ and Hiroaki Iwaisaki¹

¹ Graduate School of Agriculture, Kyoto University, Kyoto 606-8502, Japan.

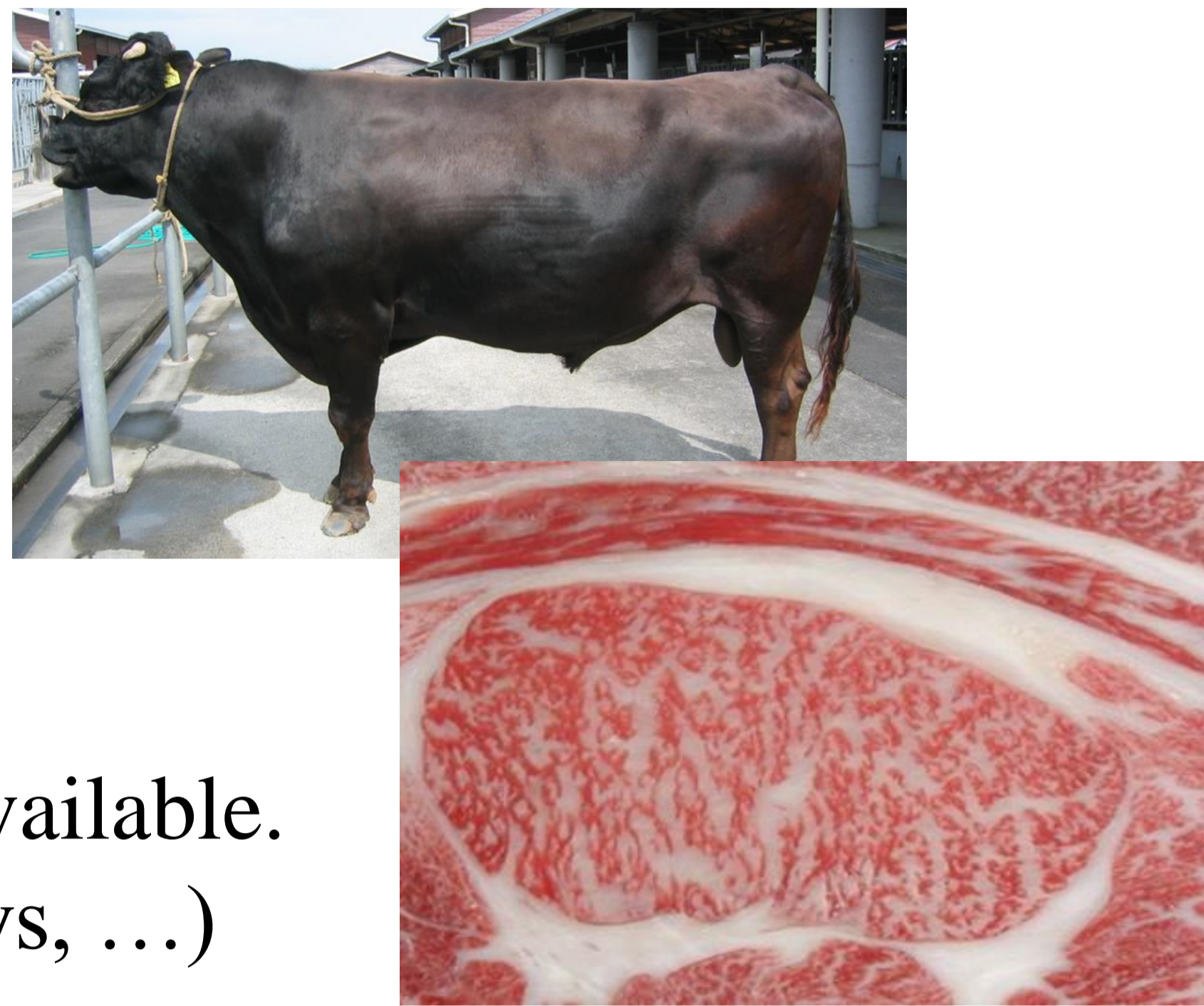
² National Livestock Breeding Center, Fukushima 961-8551, Japan.

³ Shirakawa Institute of Animal Genetics, Fukushima 961-8061 Japan.

*Corresponding author e-mail: sogawa@kais.kyoto-u.ac.jp

Background

Breeding of Japanese Black cattle



Public databases

AnimalQTLdb

Various information is available.
(QTLs, genes, pathways, ...)

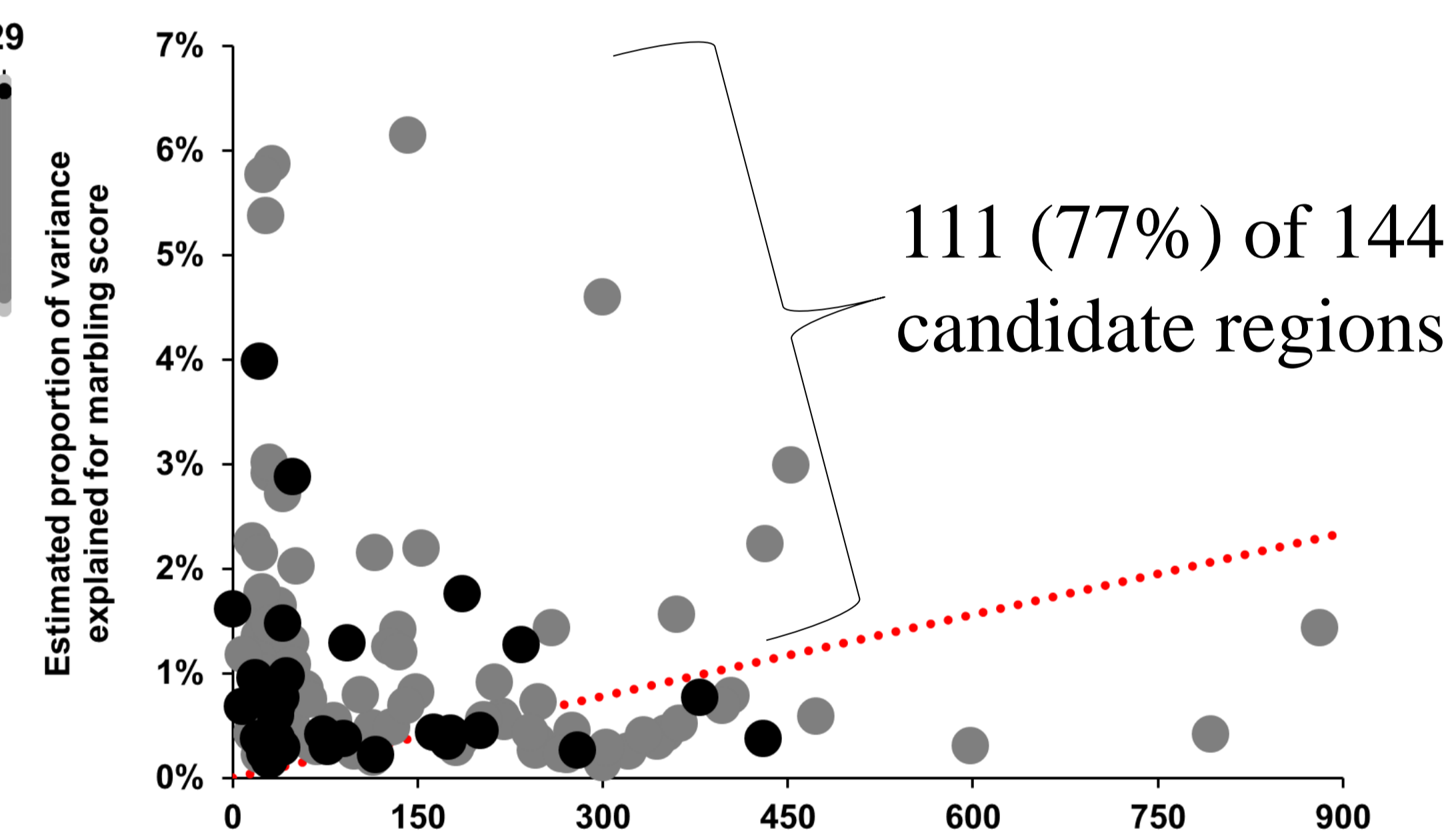
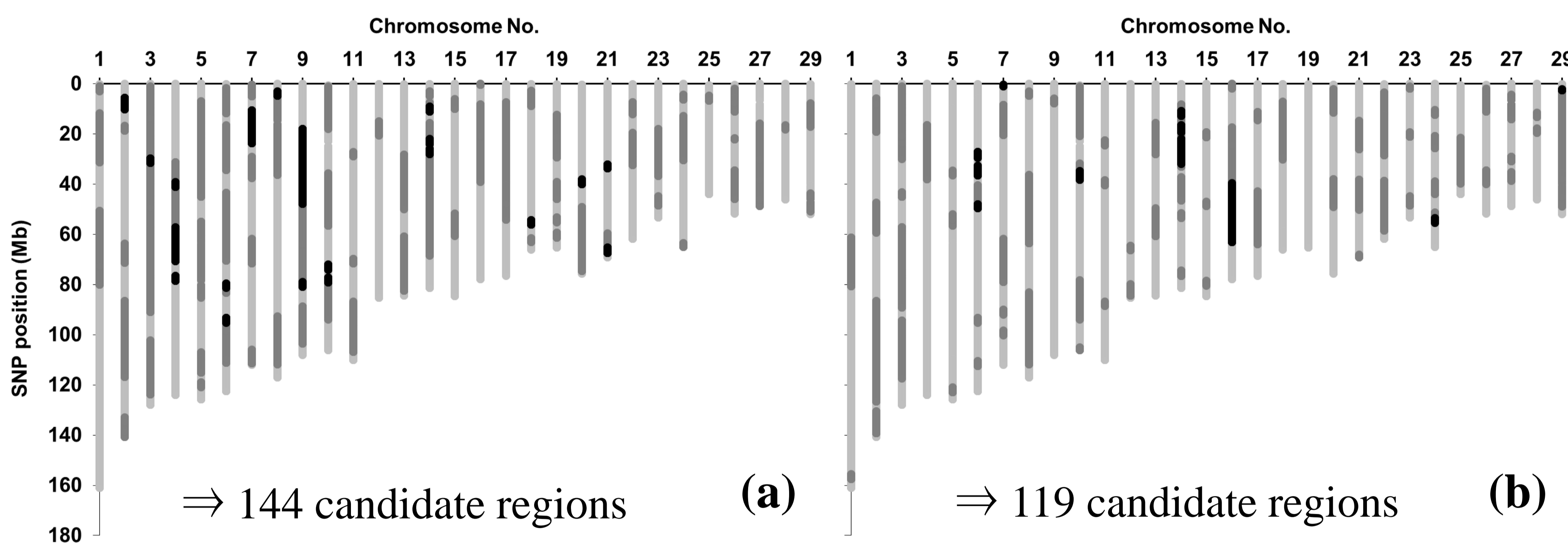
Objective

To estimate the proportions of genetic variances due to the pre-reported QTL candidate regions for the two economically-important carcass traits in Japanese Black cattle.

Materials and Methods

- ◆ Animals: 872 Japanese Black fattened steers
- ◆ Traits: marbling score (MS; 1-12) and carcass weight (CW; kg)
- ◆ Single nucleotide polymorphism (SNP) markers (Btau4.0):
 - 38,467 autosomal SNPs (Illumina BovineSNP50 BeadChip v.1)
 - minor allele frequency > 0.01, call rate > 0.95,
 - p-value for Hardy-Weinberg equilibrium test > 0.001
- ◆ Information on quantitative trait locus (QTL) candidate regions:
 - CW-1, CW-2 and CW-3 and AnimalQTLdb (Hu *et al.*, 2007)
- ◆ Model: $\mathbf{y} = \mathbf{Xb} + \mathbf{g}_1 + \mathbf{g}_2 + \mathbf{e}; \text{Var}(\mathbf{g}_i) = \mathbf{G}_i \sigma_{g_i}^2 (i = 1, 2), \text{Var}(\mathbf{e}) = \mathbf{I} \sigma_e^2$
 - \mathbf{G}_1 and \mathbf{G}_2 = genomic relationship matrix (VanRaden, 2008) constructed using selected n and the remaining (38,467 - n) SNPs, respectively.
- ◆ Estimated proportion of the additive genetic variance explained by the n SNPs located inside a particular region to the total additive genetic variance: $\hat{S} = \hat{\sigma}_{g1}^2 / (\hat{\sigma}_{g1}^2 + \hat{\sigma}_{g2}^2) \times 100$ (%)
- ◆ Analyses: R package BLR (de los Campos *et al.*, 2009)

Results



The distributions of QTL candidate regions registered in AnimalQTLdb for marbling score (a) and carcass weight (b). Black and dark gray circles show the SNPs located inside candidate regions reported in Japanese Black and other cattle breeds, respectively. Light gray circles show the SNPs outside all candidate regions.

The values of \hat{S} due to SNPs located inside each QTL candidate region registered in AnimalQTLdb for marbling score, against the number of SNPs located inside the region. Black and gray circle show the results about candidate regions reported in Japanese Black and other cattle breeds, respectively. Red dotted line shows $y = x / 38,467 \times 100$ (%).

Estimated proportion (\pm standard error) of the additive genetic variance explained by SNPs located inside the pre-reported QTL candidate regions to the total additive genetic variance

Candidate region ¹	Trait	BTA ²	No. of region(s)	No. of SNPs	\hat{S} (%)
CW-1	CW	14	1	18	2.4 \pm 5.2
	MS	14	1	18	0.6 \pm 2.8
CW-2	CW	6	1	10	12.0 \pm 13.5
	MS	6	1	10	1.2 \pm 7.8
CW-3	CW	8	1	112	7.9 \pm 5.0
	MS	8	1	112	0.2 \pm 1.1
CW-1, -2, and -3	CW	-	3	140	22.2 \pm 8.9
QTL	CW	-	119	11,476	42.8 \pm 12.0
	MS	-	144	16,045	53.9 \pm 10.4
QTL + CW-1, -2, and -3	CW	-	122	11,497	49.0 \pm 11.2
QTLJB	CW	-	22	819	19.8 \pm 7.5
	MS	-	31	1,385	7.1 \pm 4.9
QTLJB + CW-1, -2, and -3	CW	-	25	941	28.7 \pm 8.4

✓ The value of \hat{S} due to SNPs located inside all candidate regions (42% and 30% of all available SNPs for MS and CW, respectively) was 54% for MS and 43% for CW.

✓ For CW, the value of \hat{S} due to SNPs located inside the candidate regions reported in Japanese Black cattle was 20%. The proportion of these SNPs was only 2.4% of all available SNPs, and many of these SNPs were on BTA6 and BTA14.

¹ QTL = all pre-reported QTL candidate regions obtained from AnimalQTLdb; QTLJB = all pre-reported QTL candidate regions reported in Japanese Black cattle obtained from AnimalQTLdb. ² BTA = Bos Taurus Autosome.

Proportions of the genetic variance explained by SNPs located inside all candidate regions were estimated in this study as around 50% for the carcass traits, but these are probably an overestimate. Further careful investigation is necessary to select SNPs useful for the valid genomic prediction of carcass traits in Japanese Black cattle.