after the predicted stop codon and do not interfere with the amino acid composition of the new protein. The generated sequences were deposited at NCBI under accession nos MZ361079 and MZ361080.

Polymorphisms in the *MC1R* gene are frequently associated with changes in the coat color of domestic animals, including cattle.[6,7] We therefore believe that this deletion is the mutation responsible for the red coat of the Guzerat cow studied. The frequency of occurrence of this coat color is very low. The biological knowledge provided by the report highlights the importance of the gene for coat color and should encourage future studies investigating similar variations using this gene as a candidate gene.

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Conflicts of interest

The authors declare no potential conflicts of interest.

Data availability statement

Data are available at GenBank, accession nos MZ361079 and MZ361080.

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Correspondence: G. M. F. de Camargo
(gregorio.camargo@ufba.br)

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Novel insight into linkage disequilibrium and additive effect of *GBP1* and *GBP5* SNP haplotypes associated with porcine reproductive and respiratory syndrome virus susceptibility in Korean native pigs

Sangwook Kim*, Eun-Seok Cho†, Young-Sin Kim†, Youngjo Lim‡, Seul-A Jeong‡, Minji Song‡, Kyung-Tai Lee‡ and Jun-Mo Kim*

*Department of Animal Science and Technology, Chung-Ang University, Anseong, Gyeonggi-do 17546, Korea; †Swine Science Division, National Institute of Animal Science, RDA, Cheonan 31000, Korea; ‡Animal Genomics and Bioinformatics Division, National Institute of Animal Science, RDA, Wanju 55365, Korea

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Brief note

The major quantitative trait loci related to host resistance to porcine reproductive and respiratory syndrome virus (PRRSV) and weight gain have been identified by genome-wide association studies.[1–3] In addition, the viral load and weight gain traits of PRRSV-infected pigs have strong negative phenotypic and genetic correlations.[3,4] Several studies have shown that SNPs (rs712180276, WUR10000125, and rs340943904) in the *guanylate binding protein 1* (*GBP1*) and 5 (*GBP5*) genes have significant correlations with the viral load and weight gain of PRRSV-infected pigs.[2,5–7] In particular, WUR10000125 in *GBP1* and rs340943904 in *GBP5* have complete or strong linkage disequilibrium (LD; $r^2 > 0.70$) in many pig breeds[8–10] and individual with homozygous recombinant haplotypes have so far not been reported. This precludes an estimation of additive genetic effects of the *GBP1* and *GBP5* SNPs.

This study analyzed, in 113 Korean native pigs (KNPs), associations of the three SNPs (Table S1) with three phenotypes of days to 90 kg, backfat thickness (BF), and average daily gain (ADG; Table S2), considering sex and genotype as fixed effects and slaughter age as a covariate. The degree of LD between *GBP5* (rs340943904) and *GBP1* (WUR10000125) SNPs, D', and r^2 between the variations were estimated.[11]

Individuals with rs340943904 genotype GT genotyped pigs grew more slowly than those with GG genotype (Tables S3, S4; TT has not been observed). Two SNPs (rs712180276 and WUR10000125) in *GBP1* were also in complete LD in our KNPs. The WUR10000125 GG genotype had a significant effect on ADG and BF ($P < 0.05$). Unlike in previous studies, the two SNPs *GBP5*: rs340943904 and *GBP1*: WUR10000125 showed very low LD ($r^2 = 0.203$, Tables S5, S6a). The frequencies of haplotype (ht) 1 (-GA-), ht2 (-GG-), and ht3 (-TG-) were 0.814, 0.142, and 0.044, respectively (Table S5b). Ht1 confers a significantly better BF ($P = 0.021$) than ht2, while it had faster growth in days to 90 kg and ADG than ht3 (Table 1). Ht2 showed clearly faster growth than ht3 ($P < 0.001$), suggesting that individuals with the rs340943904 SNP T and WUR10000125 SNP G alleles, which are associated with high resistance to PRRSV, grow more slowly.

Lack of LD in KNP results indicated rs340943904 and WUR10000125 SNPs have independent effects on growth traits, with the allele effect size of *GBP5* is larger than for

Sangwook Kim and Eun-Seok Cho equally contributed this work.

Table 1 Differences in phenotypes between the *GBP5* (rs340943904) and *GBP1* (WUR10000125) haplotypes in 113 Korean native pigs.

Haplotype estimate	D90 (days) least squares means ± S.E (*p*-value)	BF (mm)	ADG (kg)
ht1 (GA) vs. ht2 (GG)	4.54 ± 2.37 (0.336)	0.15 ± 0.03 (0.021)	–0.02 ± 0.01 (0.107)
ht1 (GA) vs. ht3 (TG)	–20.06 ± 4.02 (0.004)	–0.22 ± 0.05 (0.012)	0.04 ± 0.01 (0.010)
ht2 (GG) vs. ht3 (TG)	–24.60 ± 6.49 (0.002)	–0.36 ± 0.09 (<0.001)	0.05 ± 0.01 (<0.001)

D90, days to 90 kg; BF, backfat thickness; ADG, average daily gain (kg); SE, standard error; ht, haplotype structure in *GBP5* (rs340943904) and *GBP1* (WUR10000125) polymorphisms.

GBP1. Hence, we suggest that the KNP is a suitable population for studies of the mechanism of PRRSV resistance.

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Correspondence: G. M. F. de Camargo (gregorio.camargo@ufba.br)

Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Table S1 The candidate genes and polymorphisms examined in this study.

Table S2 Summary statistics for the four phenotypes in Korean native pigs.

Table S3 Genotype and allele frequency of three polymorphisms in the *GBP5* and *GBP1* genes genotyped in 113 Korean native pigs.

Table S4 Associations of three *GBP5* and *GBP1* polymorphisms with phenotypic data of Korean native pigs (n = 113).

Table S5 Linkage disequilibrium and haplotypes between *GBP5* (rs340943904) and *GBP1* (WUR10000125) SNPs in 113 Korean native pigs.

Table S6 Combined frequencies of the *GBP5* (rs340943904) and *GBP1* (WUR10000125) polymorphisms in 113 Korean native pigs.

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Genome-wide association for plasma albumin concentration in sheep

Taiana Cortez de Souza*, Tatiana Cortez de Souza*, Gerson Barreto Mourão†, Luiz Lehmann Coutinho†, Gregorí Alberto Rovadoscki†, Victor Breno Pedrosa‡, Raphael Bermal Costa*, Gregório Miguel Ferreira de Camargo*, Gleidson Giordano Pinto de Carvalho* and Luís Fernando Batista Pinto*

*Federal University of Bahia – 500, Av. Adhemar de Barros, Salvador, BA 40170110, Brazil; †University of São Paulo – 11, Av. Pádua Dias, Piracicaba, SP 13635900, Brazil; ‡State University of Ponta Grossa – 4748, Av. General Carlos Cavalcanti, Ponta Grossa, PR 84030900, Brazil

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Low plasma albumin concentration (PAC) may indicate either liver or kidney diseases in lambs.[2] Although PAC has both clinical and biochemical importance, its genetic control is poorly studied in farm animals. We genotyped 491 Santa Inês healthy lambs with a 50k SNP chip and carried out a association study for PAC (Table S1). We found an average ± standard deviation of 35.1 ± 5.9 g/L, which is similar to previous values reported for healthy lambs.[2] Moreover, the present study shows that a part of the PAC variation can be attributed to additive genetic variance (V_A) since the estimate of heritability was 0.29 ± 0.03, which is close to the value reported in pigs (0.25 ± 0.06).[3]

We identified three genomic windows that individually explained at least 1.5% of V_A (Figure 1), which harbor 32 protein coding genes (Table 1). These genomic windows overlapping QTL for body weight and growth rate (in OAR3), birth weight and stature (in OAR5), and