ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics



BRIEF NOTE

doi: 10.1111/age.13134

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

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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 genomewide 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 stud-SNPs have shown that (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 *GBP*5 (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 *GBP1*. Hence, we suggest that the KNP is a suitable population for studies of the mechanism of PRRSV resistance.

Acknowledgements: This work was carried out with the support of the "Cooperative Research Program for Agriculture Science and Technology Development (Project No. PJ015611)" Rural Development Administration, Republic of Korea.

References

- 1 Yang T et al. (2016) Sci Rep 6, 1-14.
- 2 Waide E et al. (2017) J Anim Sci 95, 16-38.
- 3 Boddicker N et al. (2012) J Anim Sci 90, 1733-1746.
- 4 Hess AS et al. (2016) Genet Sel Evol 48, 1-20.
- 5 Boddicker NJ et al. (2014) Anim Genet 45, 48-58.
- 6 Boddicker NJ et al. (2014) Genet Sel Evol 46, 1-14.
- 7 Niu P et al. (2016) Vet Microbiol 182, 187-195.
- 8 Koltes JE et al. (2015) BMC Genom 16, 1-13.

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 \pm S.E (p -value)	BF (mm)	ADG (kg)
ht1 (GA) vs. ht2 (GG)	$4.54 \pm 2.37 \ (0.336)$	$0.15 \pm 0.03 \ (0.021)$	-0.02 ± 0.01 (0.107)
ht1 (GA) vs. ht3 (TG) ht2 (GG) vs. ht3 (TG)	$-20.06 \pm 4.02 \ (0.004)$ $-24.60 \pm 6.49 \ (0.002)$	-0.22 ± 0.05 (0.012) -0.36 ± 0.09 (<0.001)	$0.04 \pm 0.01 \ (0.010)$ $0.05 \pm 0.01 \ (<0.001)$

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.

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2 Kim *et al*.

- 9 Jeon R et al. (2021) Livest Sci 224, 104399.
- 10 Khatun A et al. (2020) Vet Res 51, 1-14.
- 11 Barrett JC et al. (2005) Bioinformatics 21, 263-265.

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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).

TableS5LinkagedisequilibriumandhaplotypesbetweenGBP5(rs340943904)andGBP1(WUR10000125)SNPs in 113 Korean native pigs.