

Research Paper

## Genome-wide Association Study of Porcine Hematological Parameters in a Large White × Minzhu F2 Resource Population

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### Abstract

Hematological traits, which are important indicators of immune function in animals, have been commonly examined as biomarkers of disease and disease severity in humans and animals. Genome-wide significant quantitative trait loci (QTLs) provide important information for use in breeding programs of animals such as pigs. QTLs for hematological parameters (hematological traits) have been detected in pig chromosomes, although these are often mapped by linkage analysis to large intervals making identification of the underlying mutation problematic. Single nucleotide polymorphisms (SNPs) are the common form of genetic variation among individuals and are thought to account for the majority of inherited traits. In this study, a genome-wide association study (GWAS) was performed to detect regions of association with hematological traits in a three-generation resource population produced by intercrossing Large White boars and Minzhu sows during the period from 2007 to 2011. Illumina PorcineSNP60 BeadChip technology was used to genotype each animal and seven hematological parameters were measured (hematocrit (HCT), hemoglobin (HGB), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), mean corpuscular volume (MCV), red blood cell count (RBC) and red blood cell volume distribution width (RDW)). Data were analyzed in a three step Genome-wide Rapid Association using the Mixed Model and Regression-Genomic Control (GRAMMAR-GC) method. A total of 62 genome-wide significant and three chromosome-wide significant SNPs associated with hematological parameters were detected in this GWAS. Seven and five SNPs were associated with HCT and HGB, respectively. These SNPs were all located within the region of 34.6-36.5 Mb on SSC7. Four SNPs within the region of 43.7-47.0 Mb and fifty-five SNPs within the region of 42.2-73.8 Mb on SSC8 showed significant association with MCH and MCV, respectively. At chromosome-wide significant level, one SNP at 29.2 Mb on SSC1 and two SNPs within the region of 26.0-26.2 Mb were found to be significantly associated with RBC and RDW, respectively. Many of the SNPs were located within previously reported QTL regions and appeared to narrow down the regions compared with previously described QTL intervals. In

current research, a total of seven significant SNPs were found within six candidate genes *SCUBE3*, *KDR*, *TDO*, *IGFBP7*, *ADAMTS3* and *AFP*. In addition, the *KIT* gene, which has been previously reported to relate to hematological parameters, was located within the region significantly associated with MCH and MCV and could be a candidate gene. These results of this study may lead to a better understanding of the molecular mechanisms of hematological parameters in pigs.

Key words: genome-wide association study, porcine, hematological parameters

## Introduction

Hematological traits are important indicators of immune function in animals [1, 2]. Some hematological traits i.e. hematocrit (HCT), hemoglobin (HGB), mean corpuscular hemoglobin concentration (MCHC) and red cell distribution width (RDW) are similar between humans and pigs (normal and mini pigs) [3-5]. These hematological traits are commonly examined as biomarkers of disease and disease severity in human and animals. Besides being an agriculturally important resource for meat production, pig is also a large-animal model for human genetic diseases due to the high degree of similarity with human physiological characteristics.

Genome-wide significant quantitative trait loci (QTL) for hematological parameters (hematological traits) have been detected on all pig chromosomes (<http://www.animalgenome.org/cgi-bin/QTLdb/SS/index>). However, QTLs are often mapped by linkage analysis to a large interval of 20 centimorgans (cM) or more [6]. Single nucleotide polymorphisms (SNPs) provide more markers covering the genome than microsatellite markers and are the common form of genetic variation among individuals. Genome-wide association studies (GWAS) that survey most of the genome using genetic variants [7] have been developed and applied widely in analysis of human disease and complex traits. As a result of the development of Illumina SNP genotyping technology, 50000 to 60000 SNPs have been detected among domestic animals for GWAS of complex traits in chickens [8, 9], dairy cattle [10-12] and pigs [13]. Although many studies have identified QTLs for porcine hematological traits, GWAS of these traits are yet to be performed. In this study, a GWAS was undertaken using the PorcineSNP60 Genotyping BeadChip technology (Illumina, San Diego, CA, USA) to detect potential genetic variants associated with hematological traits in a porcine Large White  $\times$  Minzhu intercross population.

## Materials and Methods

### Animals

In this study, a three-generation resource population was produced by intercrossing Large White

boars and Minzhu sows during the period from 2007 to 2011. All animal procedures were performed according to guidelines developed by the China Council on Animal Care, and protocols were approved by the Animal Care and Use Committee of Beijing, China. The approval ID or permit numbers are SYXK (Beijing) 2008-007 and SYXK (Beijing) 2008-008. Four Large White boars were mated to 16 Minzhu sows. Nine boars and 46 sows of their offspring were used (avoiding full-sib mating) to produce 430 F<sub>2</sub> animals (90 litters) in three parities. Male pigs of the F<sub>2</sub> generation were castrated 15 days after birth. The average number of half-sibs per sire was 64. All animals were raised under identical feeding conditions at the experimental farm of the Institute of Animal Science, Chinese Academy of Agricultural Sciences. All parental animals were apparently healthy.

### Blood samples collection and analysis of hematological traits

Blood samples (2 ml) were obtained from F<sub>2</sub> animals at 240 days of age in 49 batches (blood collection group). Blood samples were obtained by venipuncture and immediately injected into tubes containing K3-EDTA anti-coagulant for measurement of hematological parameters. All blood samples were conserved in a condition of 4 °C and sent to the Xi-yuan Hospital of the China Academy of Chinese Medical Sciences and analyzed within 24 hours.

Seven hematological parameters, including hematocrit (HCT), hemoglobin (HGB), mean corpuscular hemoglobin (MCH), mean corpuscular hemoglobin concentration (MCHC), mean corpuscular volume (MCV), red blood cell count (RBC) and red cell distribution width (RDW), were measured using a fully automatic Hematology Analyzer (MEK-6318K, Nihon-Kohden, Tokyo, Japan). All traits were analyzed by professional researchers in order to assure accuracy of the results.

### Genotyping and quality control

A total of 20 F<sub>0</sub>, 55 F<sub>1</sub>, and 430 F<sub>2</sub> animals were genotyped using the PorcineSNP60 BeadChip (Illumina). Pedigree mismatching was first checked by the

Cervus program [14] using the SNPs information. Data were quality controlled for sample call rate, SNP call rate, minor allele frequency (MAF) and deviation from Hardy-Weinberg Equilibrium (HWE). Quality control procedures were performed for the F<sub>2</sub> individuals using GenABEL package [15] within the R statistical environment. Gender errors were identified and SNPs were excluded according to the following criteria: (1) MAF < 3%, (2) call rate < 90%, (3) significant divergence from HWE with *p*-values < 10<sup>-6</sup>. Genotyping efficiency for samples was also verified and individuals were excluded with threshold call rates < 90%.

Following quality control, 112 X-linked SNPs were excluded because they were likely to be autosomal (odds > 1000), 11211 SNPs were excluded due to MAF < 3%, 3993 SNPs were excluded due to call rate < 90%, 1367 SNPs were excluded with divergence from HWE with *p* < 10<sup>-6</sup> and one animal was excluded with a call rate < 90%. The final data set used in this GWAS contained 429 animals and 48355 SNPs. The distribution of SNPs after quality control and the average distance between adjacent SNPs on each chromosome are shown in Table 1.

**Table 1.** Distribution of SNPs after quality control and average distances on each chromosome.

Chromosome	No. SNPs	Average distance (kb) <sup>a</sup>
1	5165	61.05
2	2108	77.12
3	1672	86.60
4	2910	49.30
5	1778	62.71
6	1510	104.48
7	2846	47.35
8	1772	83.80
9	2095	73.35
10	1096	72.17
11	1486	59.01
12	895	71.05
13	2864	76.34
14	3161	48.67
15	2031	77.64
16	1262	68.86
17	1318	52.88
18	901	67.95
X	669	215.68
Y	1	1637.72
0 <sup>b</sup>	10815	
Total	48355	

<sup>a</sup>Derived from *Sus scrofa* Build 10.2 ([http://pre.ensembl.org/Sus\\_scrofa\\_map/Info/Index](http://pre.ensembl.org/Sus_scrofa_map/Info/Index)).

<sup>b</sup>These SNPs are not assigned to any chromosome according as Illumina PorcineSNP60 Beadchip.

## Statistical analysis

Genome-wide association analysis was performed using a three step GRAMMAR-GC approach (Genome-wide Rapid Association using the Mixed Model and Regression-Genomic Control) [15, 16] as follows:

Firstly, data were analyzed using the mixed model:

$$y=1\mu+Xb+Tc+Za+e$$

where *y* is the vector of phenotypes of 429 F<sub>2</sub> animals, *b* is the vector of fixed effects (consisting of sex, parity and batch effects), *c* is the vector of litter effect (considered as a random effect,  $c \sim N(0, \sigma_c^2)$ ), *a* is the vector of random additive genetic effects with  $a \sim N(0, A\sigma_a^2)$  (where *A* is the relationship matrix calculated from the corrected pedigree and  $\sigma_a^2$  is the additive genetic variance) and *e* is the vector of residual errors with  $e \sim N(0, I\sigma_e^2)$ , where *I* is the identity matrix and  $\sigma_e^2$  is the residual variance. *X*, *T* and *Z* are incidence matrices relating records in *y* to fixed and random effects. The herd-year-season effect was contained in the batch effect. The vector of residuals *y*<sup>\*</sup> is estimated as:

$$y^*=y-(1\mu^{\wedge}+Xb^{\wedge}+Tc^{\wedge}+Za^{\wedge})$$

where *b*<sup>^</sup>, *c*<sup>^</sup> and *a*<sup>^</sup> are estimates and predictors for *b*, *c* and *a*, respectively.

Secondly, the residuals were used as the dependent trait and the associations were tested using the single locus regression analysis:

$$y^*=1\mu+kg+e^*$$

where *g* is the vector of genotypes, *k* is the regression coefficient and *e*<sup>\*</sup> is the vector of random residuals.

Thirdly, in the GC procedure, the unadjusted test statistic factor of the *i*<sup>th</sup> SNP *T*<sub>*i*</sub><sup>2</sup> was calculated as:

$$T_i^2=k_i^{\wedge}/\text{var}(k_i^{\wedge})$$

where *k*<sup>^</sup><sub>*i*</sub> and  $\text{var}(k_i^{\wedge})$  are the estimate and sample variance of *k*, respectively. The deflation factor  $\lambda^{\wedge}$  was estimated as  $\lambda^{\wedge}=\text{median}(T_1^2, T_2^2, \dots, T_i^2)/0.456$ , where 0.456 is the median of  $\chi_{(1)}^2$  [17]. Association of the *i*<sup>th</sup> SNP with the trait was examined by comparison of *T*<sub>*i*</sub><sup>2</sup>/ $\lambda^{\wedge}$  with  $\chi_{(1)}^2$ .

The first step was performed using DMU software [18] and the remainder of the analysis was performed using GenABEL package within the R statistical environment [14]. The genome-wide significance threshold was determined by the Bonferroni method, in which the conventional *p*-value was divided by the number of tests performed [19]. A SNP was considered to have genome-wide significance at *p* < 0.05/*N*, where *N* is the number of SNPs tested in the analyses. In this study, *N* was 48355 and the genome-wide sig-

nificant threshold was  $1.03e-6$ . The chromosome-wide significant thresholds for SSC1 and SSC12 were  $9.63e-6$  and  $5.67e-5$ , respectively.

### Population stratification

Population stratification for GWAS can lead to false positive results [6]. In this study, the influence of population stratification was assessed in a quantile-quantile (Q-Q) plot by examining the distribution of test statistics generated from association tests and the deviation from the null hypothesis of no SNP association with the trait was assessed. Comparison of the GWAS results with and without the GC procedure were shown in the Q-Q plot to assess the validity of this method for adjustment of population stratification. The Q-Q plot was constructed within the R statistical environment.

## Results

### Phenotype description

Means, standard deviations, minimum, and maximum values of the traits measured in the current experiment were presented in Table 2. Means for HCT, HGB, MCH, MCHC, MCV, RBC and RDW were 44.20%, 142.29 g/L, 17.56 pg, 321.68 g/L, 53.72 fL,  $7.97 (10^{12}/L)$  and 16.94%, respectively.

**Table 2.** Descriptive statistics of seven hematological parameters for 430 individuals.

Traits	Mean	Standard deviation	Minimum	Maximum
HCT(%)	44.20	5.29	15.00	76.10
HGB(g/L)	142.29	22.67	12.50	208.00
MCH(pg)	17.56	1.02	15.00	21.20
MCHC(g/L)	321.68	43.35	30.40	375.00
MCV(fL)	53.72	4.11	44.10	74.00
RBC( $10^{12}/L$ )	7.97	1.43	0.02	9.96
RDW(%)	16.94	0.92	14.30	22.10

HCT, hematocrit; HGB, hemoglobin; MCV, mean corpuscular volume; MCH, mean corpuscular hemoglobin concentration; MCHC, mean corpuscular hemoglobin concentration; RBC, red blood cell count; RDW, red cell distribution width.

### Population stratification assessment

The Q-Q plots that compared the distribution of observed  $\chi^2$  statistics with the distribution of those expected under the null hypothesis for the seven traits are shown in Fig.1A-1G. The deflation factors  $\lambda$  for HCT, HGB, MCH, MCHC, MCV, RBC and RDW were

1.55, 1.63, 2.05, 1.01, 2.26, 0.80 and 0.99, respectively. From these plots, it was observed that there were early and dramatic deviations from the null hypothesis expectation for the results without adjustment of deflation factors, which indicated population stratification. Deviations were reduced in the Q-Q plots using the GC adjustment, which suggested proper type I error control. These results indicated that the potential influence of population stratification was reduced to a certain degree by using the GRAMMAR-GC method.

### Hematological parameters

#### Hematocrit

Seven genome-wide significant SNPs for HCT were located within a 1.9 Mb segment (34.6-36.5 Mb) on SSC7 (Table 3 and Fig.2A). Two of these (MARC0039836 and H3GA0020849) were located in an annotated genes *signal peptide*, *CUB domain*, *EGF-like 3 (SCUBE3)*. One SNPs H3GA0020739 was located in the predicted gene *ENSSSCP00000001643*. The remaining SNPs were located 21.3 Kb to 47.7 Kb from the nearest genes.

#### Hemoglobin

The results of significant SNPs detected in this GWAS and Manhattan plot for HGB were presented in Table 3 and Fig.2B. Five SNPs were located in the region from 34.6 Mb to 36.5 Mb on pig chromosome 7 (SSC7). Only one SNP (MARC0033464) was located in a predicted gene *ENSSSCP00000001643*. The remaining SNPs were located 21.3 Kb to 47.7 Kb from the nearest genes.

#### Mean corpuscular hemoglobin concentration

The SNPs significantly associated with MCH were presented in Table 3 and Manhattan plot was shown in Fig.2C. These SNPs were all located in the region of 43.7-47.0 Mb on chromosome 8 (SSC8). Four significant SNPs were identified in this region, of which, only one SNP (MARC0075425) was located within *tryptophan 2,3-dioxygenase (TDO)* gene. The most significant SNP (MARC0029724) was located near *guanylate cyclase 1, soluble, beta 3 (GUCY1B3)* gene.

#### Mean corpuscular hemoglobin concentration, Red blood cell count and red cell distribution width

Except for MCHC, there were chromosome-wide significant associations of SNPs with RBC and RDW in current study (Table 3 and Fig.2D, 2F and 2G). Only one SNP ALGA0009920, which was located at 292414075 bp on SSC1 and 40.8 Kb away from *CDK5 regulatory subunit associated protein 2 (CDK5RAP2)* gene, showed significant association with RBC. Two

significant SNPs associated with RDW were located in the region from 26.0 Mb to 26.2 Mb on SSC12. The most significant SNP was MARC0049315 and located in a predicted gene *LOC100511101*.

#### Mean corpuscular volume

Fifty-five SNPs showed significant association with MCV (Table 4). The Manhattan plot was shown

in Fig.2E. These significant SNPs were located within a 31.6 Mb segment (42.2-73.8 Mb) on SSC8. Five of the 55 SNPs were located within regions of known genes, while the remainders were located 0.9 kb to > 1Mb away from the nearest known genes. The most significant SNP MARC0029724 was located 270.3 Kb from the *GUCY1B3* gene on SSC8.

**Table 3.** Significant SNPs associated with HCT, HGB, MCH, RBC and RDW.

Trait	SNP	Chr. <sup>1</sup>	Position <sup>2</sup>	Nearest Gene <sup>3</sup>	Distance (bp) <sup>4</sup>	P-Value
HCT*	H3GA0020739	7	34556148	ENSSSCP00000001643	within	2.54E-07
	H3GA0020765	7	34755602	ENSSSCP00000001643	47403	2.45E-07
	MARC0058766	7	34803564	GRM4	35680	2.10E-07
	MARC0033464	7	35177641	ENSSSCP00000001654	47720	1.94E-07
	MARC0039836	7	35935629	SCUBE3	within	4.75E-07
	H3GA0020849	7	36004578	SCUBE3	within	3.99E-07
	ASGA0032595	7	36497507	LOC100157423	21323	4.33E-07
HGB*	H3GA0020739	7	34556148	ENSSSCP00000001643	within	9.27E-07
	H3GA0020765	7	34755602	ENSSSCP00000001643	47403	6.56E-07
	MARC0058766	7	34803564	GRM4	35680	6.24E-07
	MARC0033464	7	35177641	ENSSSCP00000001654	47720	3.53E-07
	ASGA0032595	7	36497507	LOC100157423	21323	8.92E-07
MCH*	ALGA0115258	8	43651607	KIT	51004	1.02E-06
	MARC0039159	8	46447819	GUCY1A3	42366	1.03E-06
	MARC0075425	8	46706900	TDO	within	1.03E-06
	MARC0029724	8	47035822	GUCY1B3	270324	8.83E-07
RBC†	ALGA0009920	1	292414075	CDK5RAP2	40830	6.15E-06
RDW†	MARC0049315	12	26022727	LOC100511101	within	1.94E-05
	MARC0036181	12	26162083	ENSSSCP00000018640	12305	3.83E-05

\*Genome-wide significant.

†Chromosome-wide significant.

<sup>1</sup>SNP location adjusted on chromosome in *Sus scrofa* Build 10.2 assembly.

<sup>2</sup>SNP position derived from *Sus scrofa* Build 10.2 assembly.

<sup>3</sup>Gene location on the *Sus scrofa* Build 10.2 assembly. Gene names starting with ENSSSCG represent Ensembl nomenclature while other gene symbols represent GenBank nomenclature.

<sup>4</sup>SNP designated as in a gene or distance (bp) from a gene region in *Sus scrofa* Build 10.2 assembly.

**Table 4.** Genome-wide significant SNPs associated with MCV.

SNP	Chr. <sup>1</sup>	Position <sup>2</sup>	Nearest Gene <sup>3</sup>	Distance (bp) <sup>4</sup>	P-Value
DRGA0008574	8	42150857	ENSSSCP00000009423	112244	7.62E-07
ALGA0115258	8	43651607	KIT	51004	2.70E-07
ALGA0047798	8	43730377	KIT	129777	5.37E-07
MARC0053405	8	43955459	KDR	within	1.40E-07
ALGA0047813	8	44927836	TLL1	6928	1.53E-07
ASGA0038785	8	45310709	CPE	84772	1.25E-07
MARC0039159	8	46447819	GUCY1A3	42366	8.66E-08
MARC0075425	8	46706900	TDO	within	8.66E-08
MARC0029724	8	47035822	GUCY1B3	270324	7.98E-08
ALGA0047834	8	47498650	ENSSSCP00000009463	179502	4.03E-07

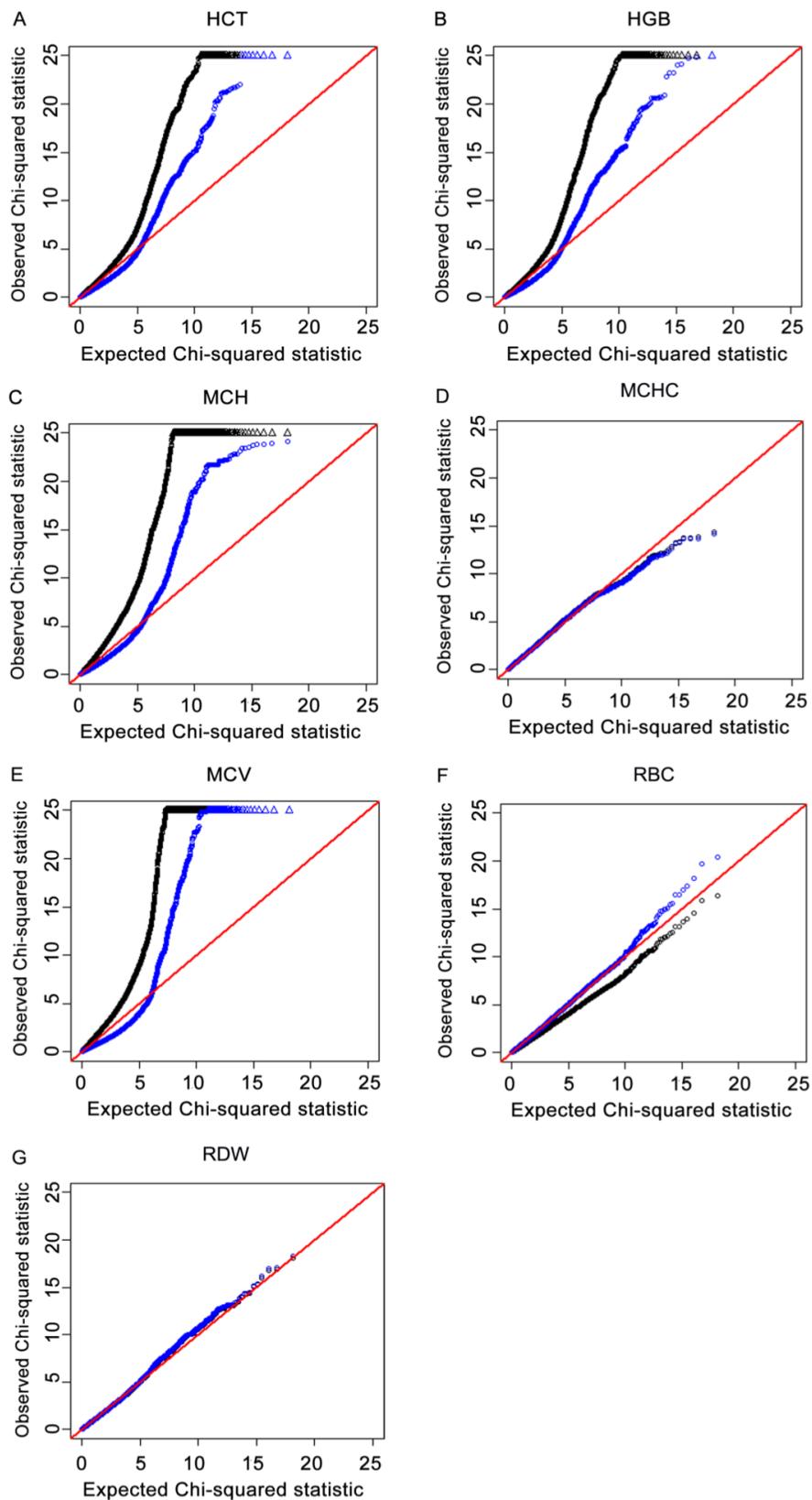
ALGA0047829	8	47560329	ENSSSCP00000009463	117823	2.11E-07
INRA0029810	8	49000633	ENSSSCP00000009465	266787	3.01E-07
MARC0085941	8	49027286	ENSSSCP00000009465	240134	3.01E-07
MARC0007151	8	50562134	LOC100517409	64593	2.68E-07
ALGA0108841	8	50670176	LOC100517409	within	2.91E-07
MARC0063673	8	51018121	ENSSSCP00000009476	148401	4.26E-07
MARC0038980	8	51070662	LOC100517409	388568	3.40E-07
ASGA0038810	8	51093615	ENSSSCP00000009476	223895	5.35E-07
INRA0029816	8	51235665	ENSSSCP00000009476	365945	5.35E-07
MARC0056888	8	51623467	ENSSSCP00000009476	753747	5.51E-07
ALGA0047879	8	52301582	NONE	>1Mb	6.15E-07
DBWU0000619	8	52565396	NONE	>1Mb	5.94E-07
MARC0087739	8	52958719	ENSSSCP00000009478	635959	6.15E-07
MARC0071439	8	53555323	ENSSSCP00000009478	39600	2.80E-07
MARC0024662	8	54201619	O62706	310552	8.40E-07
MARC0076384	8	54466796	O62706	45375	7.44E-07
ALGA0047889	8	55181102	LOC100518673	32491	7.36E-07
INRA0029827	8	55332803	ENSSSCP00000009481	22346	6.15E-07
MARC0017124	8	55529571	LOC100517956	31601	6.15E-07
ALGA0047893	8	55690977	ENSSSCP00000009483	29672	6.15E-07
ALGA0047912	8	57588232	HOPX	40950	3.42E-07
ALGA0047931	8	58493225	LOC100523263	81173	6.15E-07
ASGA0100508	8	59002762	REST	13690	6.15E-07
MARC0041089	8	59080961	IGFBP7	within	6.15E-07
MARC0036671	8	59578284	IGFBP7	438883	6.15E-07
ALGA0047954	8	59813269	IGFBP7	673868	6.15E-07
MARC0020164	8	60101923	IGFBP7	962522	6.15E-07
DRGA0008593	8	60847500	NONE	>1Mb	2.30E-07
H3GA0024898	8	61863927	NONE	>1Mb	2.30E-07
H3GA0024902	8	63746669	ENSSSCP00000009510	504438	2.30E-07
H3GA0024903	8	64355935	ENSSSCP00000009510	within	2.30E-07
MARC0051033	8	66027078	NONE	>1Mb	2.88E-07
DRGA0008614	8	68524361	ENSSSCP00000009514	984471	5.75E-07
MARC0005619	8	70772472	ENSSSCP00000009529	69642	5.55E-07
MARC0070956	8	70907832	ENSSSCP00000009529	205002	5.55E-07
INRA0029885	8	71603584	LOC100517174	within	6.35E-07
ASGA0038909	8	72656941	ADAMTS3	within	3.80E-07
ASGA0038910	8	72893479	ADAMTS3	112533	5.57E-07
ASGA0038912	8	73265823	LOC100520317	77758	5.57E-07
MARC0029095	8	73279054	LOC100520317	64527	7.58E-07
ALGA0048087	8	73286056	LOC100520317	57525	5.57E-07
DIAS0000495	8	73355105	LOC100520317	within	5.57E-07
MARC0109837	8	73611944	ALB	903	5.57E-07
ASGA0100173	8	73675216	ALB	45136	5.57E-07
DIAS0002183	8	73783363	AFP	within	8.26E-07

<sup>1</sup>SNP location adjusted on chromosome in *Sus scrofa* Build 10.2 assembly.

<sup>2</sup>SNP position derived from *Sus scrofa* Build 10.2 assembly.

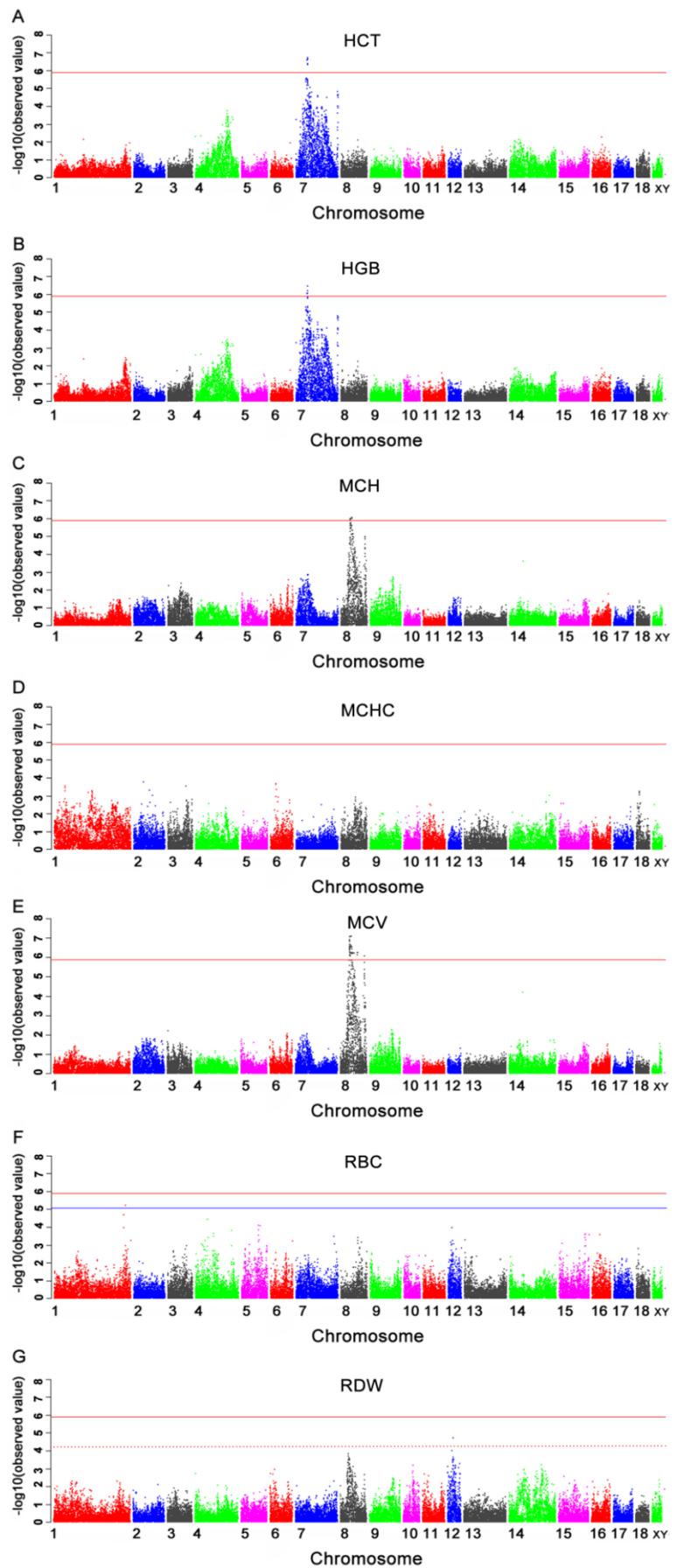
<sup>3</sup>Gene location on the *Sus scrofa* Build 10.2 assembly. Gene names starting with ENSSSCP represent Ensembl nomenclature while other gene symbols represent GenBank nomenclature.

<sup>4</sup>SNP designated as in a gene or distance (bp) from a gene region in *Sus scrofa* Build 10.2 assembly.



**Fig. I** For each of the four immune traits, a quantile-quantile (Q-Q) plot of the results derived without adjustment for the inflation factor ( $\lambda$ ) are shown in black. Results derived using the genomic control (GC) procedure are shown in blue. SNPs for which the test statistic exceeds 25 are represented by triangles. IA, IB, IC, ID, IE, IF and IG refer to Q-Q plots for HCT, HGB, MCH, MCHC, MCV, RBC and RDW, respectively. Results indicated that population stratification was reduced to a certain degree by using the GC method.

**Fig.2** Manhattan plots of genome-wide association study of seven immune traits. Chromosomes 1-18, X and Y are represented by different colors. 2A, 2B, 2C, 2D, 2E, 2F and 2G refer to plots for HCT, HGB, MCH, MCHC, MCV, RBC, and RDW, respectively. Values above  $-\log_{10}(\text{Observed value}) > 5.88$  (red horizontal) are of genome-wide significance. Values above  $-\log_{10}(\text{Observed value}) > 5.02$  (blue horizontal) and  $-\log_{10}(\text{Observed value}) > 4.25$  (dashed horizontal) are of chromosome-wide significance on SSC1 and 12, respectively.



## Discussion

In the present research, genome-wide association studies were performed for seven hematological parameters. A total of 62 SNPs showed significant association with four hematological parameters (HCT, HGB, MCH and MCHC) in this GWAS. Although some QTLs for MCHC be mapped to chromosomes 2, 3, 4, 6, 7, 9, 11, 14, 16, 17 and X (<http://www.animalgenome.org/cgi-bin/QTLdb/SS/index>), no SNPs was found to be associated with this trait significantly in our work. Comparing to the population size in human GWAS (over 10,000), a small population (430 animals) was used in this work. The limitation of population size might decrease the power of GWAS.

The QTLs for HCT have been located on pig chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 10, 12, 13 and 18, and for HGB on chromosomes 1, 2, 3, 4, 5, 7, 8, 9, 10, 12, 13, 16 and X [20-23]. In this study, significantly associated SNPs for HCT and HGB were detected within regions on pig chromosome 7 (SSC7). SSC7 has been widely investigated and the QTLs for HCT and HGB have been located in the regions of 27.65-101.73 Mb and 12.01-72.54 Mb [22, 23]. In contrast with previous studies, these significant SNPs for the two traits have been located to a shorter region (34.6-36.5 Mb) on SSC7 in this study. However, there are no reports for association of these SNPs with HCT and HGB in the pig previously. When the genome-wide significance level was adopted, the significant associated SNPs for HCT were located in the region from 34.6 Mb to 36.5 Mb. Two SNPs (MARC0039836 and H3GA0020849), which were located within intron of *SCUBE3* gene, were detected to associate with HCT. The *SCUBE3* gene may act locally and/or distantly through a proteolytic mechanism, and may play an important role in bone cell biology [24]. In addition, two significant SNP, MARC0058766 for HCT and MARC0058766 for HGB, in this study were near the *glutamate receptor, metabotropic 4 (GRM4)* gene. The GRM4 is preferentially localized in presynaptic terminals and negatively regulates glutamate release [25] and adaptive immunity and modulates restrains neuroinflammation [26]. However, the association of SNP in the two genes with hematological parameters was not reported previously and need to be studied further.

The QTLs for MCH have been located on pig chromosomes 2, 3, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16 and X, and for MCV on chromosomes 3, 4, 6, 7, 8, 9, 10, 12 and 13 [20-23]. In this study, the significantly associated SNPs for MCH and MCV were located in regions of 43.7-47.0 Mb and 42.2-73.8 Mb on pig chromosome 8 (SSC8), respectively. Four significant SNPs for MCH

were located in the vicinity of, or within, four annotated genes. Fifty-five significant SNPs for MCV were located in the vicinity of, or within, 13 annotated genes. Five SNPs MARC0053405, MARC0075425, MARC0041089, ASGA0038909 and DIAS0002183 were found within five annotated genes *kinase insert domain receptor (KDR)*, *TDO*, *insulin-like growth factor binding protein 7 (IGFBP7)*, *ADAM metalloproteinase with thrombospondin type 1 motif, 3 (ADAMTS3)* and *alpha-fetoprotein (AFP)*, respectively. Through checking the annotated gene functions, except for *KDR* gene, these genes were not found to affect erythropoiesis. Vascular endothelial growth factor (VEGF) and its receptor [fetal liver kinase 1 (Flk-1)/kinase insert domain-containing receptor (KDR)] play an important role in vascular permeability and tumor angiogenesis [27]. Binding with KDR, VEGF can also modulate erythropoiesis through regulation of adult hepatic erythropoietin synthesis [28]. So, *KDR* gene could be an important candidate gene for MCV to be studied further. Eight genes (*c-kit (KIT)*, *tolloid-like 1 (TLL1)*, *carboxypeptidase E (CPE)*, *guanylate cyclase 1, soluble, alpha 3 (GUCY1A3)*, *GUCY1B3*, *HOP homeobox (HOPX)*, *RE1-silencing transcription factor (REST)* and *albumin (ALB)*) were found near the significant SNPs for MCV. For these genes, it was notable that only *KIT* gene could relate to erythropoiesis from gene function information. The *KIT* gene, also known as *c-kit* or *CD117*, encodes a tyrosine kinase (mast/stem cell growth factor receptor) essential for the development of hematopoietic stem cells and melanocytes in the human, mouse and pig [29-32] and has been shown to be expressed in hemoatopoietic cells [32]. Many reports have demonstrated *KIT* gene mutation association with the dominant white (I) coat color in the pig [34-36]. Moreover, a strong association of the *KIT* locus with blood phenotypes (MCH and MCV) has been confirmed using dense single nucleotide polymorphism marker data on SSC 8 and marker-assisted association tests [37]. Johansson *et al.* [38] found that pigs with different *KIT* genotypes differ in hematological parameters and homozygous dominant white (I/I) piglets had larger erythrocytes with lower hemoglobin concentrations. However, Fésüs *et al.* [39] found that there was no significant association between porcine *KIT* mutations and hematological parameters. That blood samples were taken at different ages in the first and second farrowing might be the reason of no significant association in their work. Haase *et al.* [40] did not detect any statistically significant differences in peripheral blood parameters between different *KIT* genotypic horses due to the limited statistical power in the small cohorts (15 dominant white and 18 solid-coloured horses). Therefore,

further investigation is required to study the influence of the *KIT* gene on hematological parameters in pigs.

Although no QTL was mapped on SSC1 (<http://www.animalgenome.org/cgi-bin/QTLdb/SS/index>), one SNP ALGA0009920 showed chromosome-wide significant association with RBC in this study. The *CDK5 regulatory subunit associated protein 2* (*CDK5RAP2*) gene is near the SNP. *CDK5RAP2* is a  $\gamma$ -tubulin complex-binding protein and functions in  $\gamma$ -tubulin attachment to centrosomes [41-43]. It localizes to the Golgi complex in an ATP- and centrosome-dependent manner and associates with Golgi membranes independently of microtubules [44]. While no report about this gene was found to relate to RBC previously. For RDW, the QTL was mapped to the region of 26.4-41.9 Mb on SSC12 [21]. Near the QTL region, two significant SNPs MARC0049315 and MARC0036181 were located within the region 26.0-26.2 Mb on SSC12 in the present work. However, no annotated gene was found in this region. So, it is necessary to study the two traits in a larger population in future.

There are certain logic relationships among red blood cell related parameters. Hemoglobin (HGB) equals red blood cell count (RBC) multiplied by mean corpuscular hemoglobin (MCH). Red blood cell count (RBC) is a variate instead of a constant. And one SNP ALGA0009920 on SSC1 was found to be chromosome-wide significantly associated with RBC in this work. Moreover, the phenotypic correlations between HGB and MCH was low (0.28) in this research (data not shown). As a result of significant SNPs for HGB located on SSC7 while those for MCH located on SSC8, different genetic mechanisms and a certain interaction might exist between HGB and MCH.

Population stratification is a confounding component known to affect GWAS results. False associations could result from the use of two different genetic parental lines, a complex population structure due to the high level of relatedness and absence of pedigree information [45]. In this study, GRAMMAR-GC analysis was used to consider within-family and between-family variation. Trait phenotypes were adjusted for the fixed and random effects and the test statistic was adjusted by the inflation factor. In this work, Q-Q plots were used to assess the effectiveness of GC method for population stratification. Results indicated that this method could adjust population stratification and the F<sub>2</sub> intercross population design was suitable for use in this GWAS.

In summary, 62 genome-wide significant and three chromosome-wide significant SNPs associated with hematological parameters were detected in this GWAS. Many of the SNP effects overlapped with

previously reported QTL regions in the pig, providing evidence towards confirmation of QTL effects. Furthermore, these results appeared to narrow down the regions compared with previously described QTL intervals. Therefore, these results are of importance for identification of exact QTL locations using the much improved map resolution provided by analysis of this 60k SNP panel. To date, this type of GWAS study of hematological parameters has not been conducted in pigs and these results may lead to a better understanding of the molecular mechanisms of hematological parameters.

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## Competing Interests

The authors have declared that no competing interest exists.

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