**INTRODUCTION**

Hypertension is the main factor for morbidity and mortality worldwide (Kearney et al., 2005; Staessen, Wang, Bianchi, & Birkenhager, 2003; Stokes, Kannel, Wolf, D'Agostino, & Cupples, 1989). However, the specific pathogenesis of hypertension is still unclear. (Mein, Caulfield, Dobson, & Munroe, 2004). Several studies have shown that the etiology and pathogenesis of hypertension are likely to comprise a multifactorial disorder resulting from environmental factors...
(overweight, alcohol, and smoke) and genetic factors or their interaction (Carretero & Oparil, 2000; Lu et al., 2015). Recently, hypertension has been found to be the main factor in the occurrence of myocardial infarction, stroke, cardiac and renal failure and later lesions of the retina of the eyes (Mosterd et al., 1999), and that has also been steadily increasing in China for the past several years.

Hypertension can reduce the function of which is easy to form atherosclerosis (Fujimaki et al., 2015), and atherosclerosis is the main pathological basis of coronary heart disease (Lefevre & Puymirat, 2017; Savoia et al., 2017). SMARCA4 (OMIM: 603254) and ZC3HC1 (OMIM: 603254) are high-risk genes for coronary heart disease. At present, there are many researches about the association between SMARCA4 and ZC3HC1 and coronary heart disease. For examples, GWAS study showed that SMARCA4 was related to coronary heart disease (Kathiresan, Voight, et al., 2009) and myocardial infarction (Martinelli et al., 2010). Previous studies were also identified rs11879293, rs12232780, rs2072382, and rs1529729 variants' effect on hypertension and dyslipidemia-related disease (Fujimaki et al., 2015; Liu et al., 2011). Guo et al. (2017) found the variant in the SMARCA4 was associated with coronary heart disease susceptibility in Han Chinese population. Linseman et al. (2017) identified that ZC3HC1 was associated with protection from coronary artery disease. However, few studies have examined the association between SMARCA4 and ZC3HC1 and coronary heart disease. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk. For the current study, we evaluated the association between eight SNPs in SMARCA4 and ZC3HC1 and hypertension risk.

All subjects were from the Chinese Han population living in Shaanxi province. Hypertensive subjects were defined as having a systolic blood pressure (SBP) of at least 140 mmHg and a diastolic blood pressure (DBP) of at least 90 mmHg (de Menezes, Oliveira, & Ma, 2014). All the hypertensive patients were not only required to be free of other cardiovascular diseases, metabolic diseases, cancers or familial hereditary disease, but diagnosed with hypertension before the age of 70 years. Normotensive controls were recruited from the same hospital. These individuals were never treated with antihypertensive medications, and their SBP were less than 140 mmHg and DBP less than 90 mmHg. They had no family history of hypertension.

### 2.3 SNP selection and genotyping

Eight SNPs in ZC3HC1 and SMARCA4 had minor allele frequencies greater than 5% in the 1000 Genomes Project (http://www.internationalgenome.org/). A GoldMag-Mini Purification Kit (GoldMag Co. Ltd.) was performed to extract genomic DNA from whole blood. DNAs were stored at −80°C until analysis. DNA concentrations were measured using a NanoDrop 2000 (Thermo Scientific). The primers were designed online (https://agenax.com/online-tools/). Agena MassARRAY Assay Design 4.0 software was used to design multiplexed SNP MassEXTEND assay, and SNP genotyping was performed utilizing the Agena MassARRAY RS1000 as recommended by the manufacturer. Agena Typer 4.0 software was used to perform data management and analyses.

### 2.4 Statistical analysis

All statistical analyses were performed using Microsoft Excel and SPSS 19.0 (SPSS). All p values were two-sided (p < .05 was considered as achieving the threshold of statistical significance). Each SNP frequency in the control subjects was tested by deviation from Hardy–Weinberg equilibrium by the Fisher’s test. Allele frequencies and genotype frequencies for each SNP in cases and controls were compared by the chi-squared test/Fisher’s exact test to determine the associations between genotypes and hypertension risk. Odds ratio (OR) values and 95% confidence intervals (CIs) measured the risk allele effect size using unconditional logistic regression analysis (Bland & Altman, 2000). Four genetic models (codominant, dominant, recessive, and log-additive) were used to evaluate the potential association of ZC3HC1 and SMARCA4 polymorphisms with risk and clinical parameters of hypertension. Finally, the Haploview was used to construct haplotype and genetic association at significant polymorphism loci and to estimate the pairwise linkage disequilibrium (LD), haplotype software (version4.2) and SHEsis software platform (http://...
for significant deviation from Hardy–Weinberg equilibrium ($p < .05$), a chi-square analysis revealed that no significant differences in allele frequency distributions of SNPs between the hypertension patients group and the healthy control analyzed. In other words, there is no statistically significant association between allele and hypertension risk.

### 3.3 Associations between genotype frequencies and hypertension risk

As shown in Table 3, logistic regression analyses revealed that the genotype “T/C” of rs1464890 in ZC3HC1 was associated with a decreased risk of hypertension in the codominant model (OR = 0.48, 95% CI, 0.47–0.98, $p = .044$) and dominant model (OR = 0.65, 95% CI, 0.46–0.93, $p = .016$), respectively. Rs4507692 in ZC3HC1 was associated with a 0.69-fold and a 0.66-fold decreased risk of hypertension under the codominant model and dominant model, respectively. The genotype “G/A-A/A” of rs11879293 in SMARCA4 was significantly associated with decreasing the risk of hypertension under the dominant model (OR = 0.70; 95% CI = 0.49–0.99, $p = .044$). Rs1122608 in SMARCA4 was also significantly associated with a decreased risk of hypertension in the dominant model (OR = 0.61; 95% CI = 0.38–0.99, $p = .047$ for the “G/T-T/T” genotype) and log-additive model (OR = 0.61; 95% CI = 0.38–0.98, $p = .038$), respectively. Furthermore, the statistical power of our study was more than 80%.

### 3.4 Associations between haplotype analyses and hypertension risk

Linkage disequilibrium and haplotype analyses of the SNPs in the case and control samples were further studied. Haplotype analysis detected the block in ZC3HC1 (Figure 1). Rs2242487, rs1464890, and rs4507692 had very strong

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**TABLE 1** General characteristics of the study population

| variable   | Cases ($n = 350$) | Controls ($n = 483$) | $p$ value |
|------------|-------------------|----------------------|-----------|
| Gender     |                   |                      |           |
| Male       | 204               | 183                  | 37.9      |
| Female     | 146               | 300                  |           |
| Age, yr (mean ± SD) | 62.68 ± 10.7 | 50.37 ± 7.9 | $<.01^b$ |

$^a$ $p$ values were calculated by Student’s $t$ tests.

$^b$ $p$ values were calculated from two-sided chi-squared tests.

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**TABLE 2** Allele frequencies in cases and controls and odds ratio estimates for hypertension risk

| SNP          | Gene(s) | Locus | Alleles (A/B) | MAF   | Case | Control | $p$ values | OR (95%CI) | $p^a$ value | $p^b$ value |
|--------------|---------|-------|---------------|-------|------|---------|------------|------------|------------|------------|
| rs2242487    | ZC3HC1  | 7q32.2| A/G           | 0.233 | 0.270| 0.249  | 0.82 (0.66–1.03) | .088       | .011       |
| rs1464890    | ZC3HC1  | 7q32.2| T/C           | 0.277 | 0.314| 0.247  | 0.94 (0.68–1.04) | .102       | .013       |
| rs4507692    | ZC3HC1  | 7q32.2| T/C           | 0.277 | 0.314| 0.246  | 0.84 (0.68–1.04) | .108       | .014       |
| rs11879293   | SMARCA4 | 1p13.2| A/G           | 0.237 | 0.259| 0.097  | 0.89 (0.71–1.12) | .313       | .039       |
| rs12232780   | SMARCA4 | 1p13.2| A/G           | 0.199 | 0.213| 0.135  | 0.91 (0.72–1.16) | .466       | .058       |
| rs2072382    | SMARCA4 | 1p13.2| T/C           | 0.337 | 0.280| 0.018  | 0.018b       | 1.31 (1.06–1.62) | .012       | .002       |
| rs1529729    | SMARCA4 | 1p13.2| C/T           | 0.224 | 0.228| 0.091  | 0.98 (0.78–1.24) | .871       | .109       |
| rs1122608    | SMARCA4 | 1p13.2| T/G           | 0.066 | 0.084| 0.561  | 0.77 (0.53–1.12) | .169       | .021       |

Abbreviations: Alleles A/B, Minor/major alleles; CI, confidence interval; HWE, Hardy–Weinberg equilibrium; MAF, minor allele frequency; OR, odds ratio; SNP, single-nucleotide polymorphism.

$^a$Site with HWE $p \leq .05$ excluded; $^b$ $p$ values were calculated using two-sided chi-squared test. $^p$ values were adjusted by Bonferroni correction. $^p < .05$ indicates statistical significance; $^p < .05$ indicates statistical significance.
| SNP        | Model     | Genotype       | Genotype frequency | p²-value | OR (95% CI) | Study power |
|------------|-----------|----------------|--------------------|----------|-------------|-------------|
|            |           |                | Control (%)        | Case (%) |             |             |
| **ZC3HC1** |           |                |                    |          |             |             |
| rs2242487  | Codominant| G/G            | 262 (54.4)         | 209 (59.7) | .158 1     |             |
|            |           | A/G            | 180 (37.3)         | 119 (34.0) | 0.71 (0.49–1.03) |  |
|            |           | A/A            | 40 (8.3)           | 22 (6.3)  | 0.69 (0.35–1.38) |  |
|            | Dominant  | G/G            | 262 (54.4)         | 209 (59.7) | .054 1     |             |
|            |           | A/G-A/A        | 220 (45.6)         | 141 (40.3) | 0.71 (0.50–1.01) |  |
|            | Recessive | G/G-A/G        | 442 (91.7)         | 328 (93.7) | .479 1     |             |
|            |           | A/A            | 40 (8.3)           | 22 (6.3)  | 0.78 (0.40–1.54) |  |
|            | Log-additive | —             | —                 | —         | .069 0.77 (0.59–1.02) |  |
| rs1464890  | Codominant| C/C            | 232 (48.1)         | 183 (52.3) | .044 1     | .925        |
|            |           | T/C            | 197 (40.9)         | 140 (40.0) | 0.68 (0.47–0.98) | .014 0.72 (0.55–0.94) |
|            |           | T/T            | 53 (11.0)          | 27 (7.7)  | 0.55 (0.29–1.02) |  |
|            | Dominant  | C/C            | 232 (48.1)         | 183 (52.3) | .016 1     | .978        |
|            |           | T/C-T/T        | 250 (51.9)         | 167 (47.7) | 0.65 (0.46–0.93) |  |
|            | Recessive | C/C-T/C        | 429 (89.0)         | 323 (92.3) | .149 1     |             |
|            |           | T/T            | 53 (11.0)          | 27 (7.7)  | 0.65 (0.35–1.18) |  |
|            | Log-additive | —             | —                 | —         | .014 0.72 (0.55–0.94) |  |
| rs4507692  | Codominant| C/C            | 233 (48.2)         | 183 (52.3) | .049 1     | .905        |
|            |           | C/T            | 197 (40.8)         | 140 (40.0) | 0.69 (0.48–0.99) | .015 0.72 (0.55–0.94) |
|            |           | T/T            | 53 (11.0)          | 27 (7.7)  | 0.55 (0.29–1.03) |  |
|            | Dominant  | C/C            | 233 (48.2)         | 183 (52.3) | .019 1     | .969        |
|            |           | C/T-T/T        | 250 (51.8)         | 167 (47.7) | 0.66 (0.47–0.93) |  |
|            | Recessive | C/C-C/T        | 430 (89)           | 323 (92.3) | .158 1     |             |
|            |           | T/T            | 53 (11.0)          | 27 (7.7)  | 0.65 (0.36–1.19) |  |
|            | Log-additive | —             | —                 | —         | .015 0.72 (0.55–0.94) |  |
| **SMARCA4**|           |                |                    |          |             |             |
| rs11879293 | Codominant| G/G            | 258 (53.4)         | 204 (58.3) | .110 1     |             |
|            |           | G/A            | 200 (41.4)         | 126 (36.0) | 0.68 (0.47–0.97) |  |
|            |           | A/A            | 25 (5.2)           | 20 (5.7)  | 0.87 (0.41–1.81) |  |
|            | Dominant  | G/G            | 258 (53.4)         | 204 (58.3) | .044 1     | .898        |
|            |           | G/A-A/A        | 225 (46.6)         | 146 (41.7) | 0.70 (0.49–0.99) |  |
|            | Recessive | G/G-G/A        | 458 (94.8)         | 330 (94.3) | .960 1     |             |
|            |           | A/A            | 25 (5.2)           | 20 (5.7)  | 1.02 (0.49–2.09) |  |
|            | Log-additive | —             | —                 | —         | .101 0.79 (0.59–1.05) |  |
| rs12232780 | Codominant| G/G            | 293 (60.7)         | 221 (63.1) | .210 1     |             |
|            |           | G/A            | 174 (36.0)         | 119 (34.0) | 0.72 (0.50–1.04) |  |
|            |           | A/A            | 16 (3.3)           | 10 (2.9)  | 0.72 (0.26–2.00) |  |
|            | Dominant  | G/G            | 293 (60.7)         | 221 (63.1) | .073 1     |             |
|            |           | G/A-A/A        | 190 (39.3)         | 129 (36.9) | 0.72 (0.51–1.03) |  |
|            | Recessive | G/G-G/A        | 467 (96.7)         | 340 (97.1) | .678 1     |             |
|            |           | A/A            | 16 (3.3)           | 10 (2.9)  | 0.81 (0.30–2.22) |  |
|            | Log-additive | —             | —                 | —         | .080 0.76 (0.55–1.04) |  |

(Continues)
linkage disequilibria; compared to the “GCC” wild-type, the haplotype “ATT” was associated with a decreased risk of hypertension (OR = 0.75; 95% CI = 0.56–0.99; \( p = .044 \)) after adjustments for age and gender (Table 4).

4 | DISCUSSION

Genetic studies have provided insight into numerous diseases, including hypertension. Eight SNPs in ZC3HC1 and SMARCA4 have been investigated in other diseases. In this study, we examined 833 subjects (350 patients with hypertension and 483 healthy controls) to determine whether they were associated with the risk of hypertension in the Han Chinese population. Our results suggest that rs1464890 and rs4507692 (ZC3HC1), rs11556924 (SMARCA4) and rs1122608 (SMARCA4) were conducive to play a protective role against the risk of hypertension. In addition, the “ATT” ZC3HC1 haplotype was associated with a 0.75-fold decreased risk of hypertension.

ZC3HC1 (zinc finger, C3HC-type containing 1) was also called NIPA (nuclear interaction partner of ALK), which could monitor the timing of mitotic entry and was thought to contribute to the development of carcinogenesis together with oncogenic proteins (Li & Morris, 2008). Studies have been shown that mediators of angiogenesis may play an important role in the regulation of endothelial integrity and inflammation and it was possible that changes in the stability and functional properties of ZC3HC1 protein may play a role in the endothelial dysfunction (Schunkert et al., 2011), especially in the coronary heart disease and hypertension. Recently, a genome-wide association study, reported by Linseman et al. (2017), found that ZC3HC1 polymorphism was associated with a protective role in coronary artery disease. Kunnas and Nikkari (2015) reported the association of ZC3HC1 rs11556924 genetic variant with hypertension in a Finnish population. However, in previous studies, many reports only focused on the association of genetic variant in ZC3HC1 (rs11556924) with diseases, the genetic polymorphism of other locus in ZC3HC1 were little reported. Therefore, in our research, we studied the relationship between

![FIGURE 1](Image) Linkage disequilibrium (LD) plots containing four SNPs from ZC3HC1
ZC3HC1 SNPs (rs2242487, rs1464890, and rs4507892) and hypertension in Chinese Han population, and we found that the polymorphism of ZC3HC1 (rs1464890) has a strong protective effects on the hypertension.

SMARCA4 (also known as BRG1) is located in chromosomal region of 19p13.2, and its protein is the important catalytic component of the SWI/SNF complexes (Moes-Sosnowska et al., 2015). It is composed of multiple domains, a conserved C-terminal bromodomain, the less characterized N-terminal region which has crucial effect on DNA binding, recruitment of SWI/SNF, and the recognition of modified histone proteins (Singh, D’Silva, & Holak, 2006). SMARCA4 is located closely to the low-density lipoprotein receptor gene and disrupting chromatin structure regulates the transcription of various genes using the chemical energy of adenosine triphosphate hydrolysis (Mulholland, Xu, Sugiyama, & Zhao, 2012). In our research, we found rs11879293 and rs1122608 in SMARCA4 seemed to have strong protective effects on the hypertension. However, the previous studies, Guo et al. (2017) found rs11879293 was associated with decreasing the risk of coronary heart disease, and another study found rs11879293 was associated with increasing the risk of hepatocellular carcinoma is more pronounced in males, younger individuals, and nondrinkers (Pan et al., 2007). Kathiresan, Willer, et al. (2009) found the loci rs1122608 was associated with elevating the risk of low-density lipoprotein cholesterol and coronary heart disease in Caucasian population. At present, there were no relevant reports on the relationship between rs11879293 and rs1122608 in SMARCA4 seemed to have strong protective effects on the hypertension. However, the previous studies, Guo et al. (2017) found rs11879293 was associated with decreasing the risk of coronary heart disease, and another study found rs11879293 was associated with increasing the risk of hepatocellular carcinoma is more pronounced in males, younger individuals, and nondrinkers (Pan et al., 2007). Kathiresan, Willer, et al. (2009) found the loci rs1122608 was associated with elevating the risk of low-density lipoprotein cholesterol and coronary heart disease in Caucasian population. At present, there were no relevant reports on the relationship between rs11879293 and rs1122608 with hypertension. Therefore, in future studies, we will consider that the SMARCA4 may function differently in varying disease mechanisms.

To sum up, in our study, we confirmed two genes (ZC3HC1 and SMARCA4) are associated with risk of hypertension in Han Chinese population for the first time, which may provide new data to facilitate earlier diagnosis and promote early prevention, and shed light on the new candidate genes and new ideas for the study of subsequent occurrence mechanism of hypertension. Some potential limitations of our current study should be considered when interpreting the results. Investigating these SNPs should use more clinical data with bigger samples. Our current research is fundamental; further functional studies and larger population-based prospective studies are required to understand the genetic factors underlying hypertension.

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CONFLICT OF INTEREST

The authors have no conflict of interest to disclose.

ORCID

Tianbo Jin https://orcid.org/0000-0001-8378-6624

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### TABLE 4 Haplotype analysis results in this study

| Haplotypes | Without adjusted | With adjusted |
|------------|------------------|---------------|
|            | OR (95% CI)      | p-value       | OR (95% CI)      | p* -value |
| rs2242487  | rs1464890        | rs4507692     | Freq             | p         | Adjusted by gender and age. |
| G          | C                | C             | 0.701            | —         | —                           |
| A          | T                | T             | 0.253            | 0.83 (0.66–1.03) | .095 | 1 | — |
| G          | T                | T             | 0.045            | 0.94 (0.58–1.53) | .810 | 0.75 (0.56–0.99) | .044 | 0.55 (0.29–1.02) | .056 |

Note: The bold values and p < .05 indicate statistical significance.

Abbreviations: CI, confidence interval; OR, odds ratio; SNP, single nucleotide polymorphism.
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