

The polymorphism in *ADORA3* decreases transcriptional activity and influences the chronic heart failure risk in Chinese

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List of Supplementary Material for the article

1. Supplementary Table S1: Primers used for SNP genotyping.
2. Supplementary Table S2: Primer lists of real-time PCR.
3. Supplementary Table S3: Genotype distribution of the rs1415792, rs3393 and rs35511654 and their associations with the risk of chronic heart failure under different contrast models.
4. Supplementary Table S4: Logistic regression analysis for rs1415792, rs3393 and rs35511654 under a dominant, recessive, and additive genetic model adjusted for age, sex, and cardiovascular risk factors.

Supplementary Table S1. Primers used for SNP genotyping.

SNP_ID	Allele	1st-PCR	2nd-PCR	UEP_SEQ
rs1415792	T/C	ACGTTGGATGGCAGGTTCTCTGCTCAATTC	ACGTTGGATGGACTTACTGACAAAAGGCTC	TGGTGGTGACTCATTTCAT
rs1544223	G/A	ACGTTGGATGAGAGGACAGTGCAGGATCAG	ACGTTGGATGTTTGCTAAGCTGGCAGAAAG	gaTGGCAGAAAGATTGCATA
rs3393	G/A	ACGTTGGATGGTGAATTGAGCAGAGAACC	ACGTTGGATGTTTCAGCAGTTTAAGTCCCCC	TTCTGTTCCCAACATCT
rs35511654	T/G	ACGTTGGATGAGCACAAAGCTGTGGTACCTC	ACGTTGGATGTGTTTGCTCTGTCATGGCTG	ctcttTCATGGCTGCCTTTATCT

Supplementary Table S2. Primer lists of real-time PCR.

Gene	Forward primer (5'→3')	Reverse primer (5'→3')	Product size (bp)
<i>ADORA3</i>	AGCAAAGCGTCAACTCGTG	ATAAGGAGGCAAACGGGAGA	112
β -actin	TGACGTGGACATCCGCAAAG	CTGGAAGGTGGACAGCGAGG	205

Supplementary Table S3. Genotype distribution of the rs1415792, rs3393 and rs35511654 and their associations with the risk of chronic heart failure under different contrast models.

Population	Genotype	CHF n (%)	Controls n (%)	HWE <i>P</i> ^a	Dominant model <i>P</i> ^a	Recessive model <i>P</i> ^a	Additive model <i>P</i> ^a	Allele contrast <i>P</i> ^a
Xi' an	rs1415792							
	TT (W)	18 (6)	14 (3.5)	0.043	0.117	0.691	0.207	0.826
	CT	105 (35)	156 (39)					
	CC	177 (59)	230 (57.5)					
	rs3393							
	GG (W)	97 (32.33)	146 (36.68)	0.063	0.232	0.996	0.440	0.416
	GA	145 (48.33)	175 (43.97)					
	AA	58 (19.33)	77 (19.35)					
	rs35511654							
	TT (W)	298 (99.33)	398 (99.5)	0.96	0.828 ^b	NA	NA	0.828
	GT	2 (0.67)	2 (0.5)					
	GG	0 (0)	0 (0)					
Kunming	rs1415792							
	TT (W)	15 (4.98)	28 (7)	0.313	0.271	0.526	0.519	0.338
	CT	105 (34.88)	141 (35.25)					
	CC	181 (60.13)	231 (57.75)					
	rs3393							
	GG (W)	78 (25.74)	130 (32.42)	0.076	0.055	0.301	0.147	0.063
	GA	150 (49.5)	185 (46.13)					
	AA	75 (24.75)	86 (21.45)					
	rs35511654							
	TT (W)	302 (99.67)	400 (99.75)	NA	0.606 ^b	NA	NA	0.606
	GT	1 (0.33)	1 (0.25)					
	GG	0 (0)	0 (0)					

Abbreviations: CHF, chronic heart failure; HWE, Hardy-Weinberg equilibrium; NA, not available.

^a *P* values was calculated from two-sided χ^2 -test.

^b *P* values was calculated from two-sided continuity-adjusted χ^2 -test.

Supplementary Table S4. Logistic regression analysis for rs1415792, rs3393 and rs35511654 under a dominant, recessive, and additive genetic model adjusted for age, sex, and cardiovascular risk factors.

SNPs	Contrast models	Xi'an		Kunming	
		Odds ratio (95% CI)	<i>P</i> ^a	Odds ratio (95% CI)	<i>P</i> ^a
rs1415792	Dominant model	0.488 (0.227-1.050)	0.067	1.157 (0.587-2.281)	0.674
	Recessive model	0.931 (0.671-1.290)	0.666	0.997 (0.720-1.381)	0.987
	Additive model	0.865 (0.656-1.140)	0.303	1.021 (0.784-1.329)	0.879
	Allele contrast	0.872 (0.667-1.140)	0.317	1.021 (1.782-1.333)	0.877
rs3393	Dominant model	1.201 (0.854-1.688)	0.292	1.259 (0.883-1.794)	0.203
	Recessive model	1.091 (0.728-1.636)	0.674	1.120 (0.767-1.637)	0.556
	Additive model	1.112 (0.889-1.390)	0.354	1.138 (0.912-1.421)	0.252
	Allele contrast	1.118 (0.889-1.405)	0.342	1.144 (0.913-1.435)	0.242
rs35511654	Dominant model	1.531 (0.205-11.465)	0.678	1.364 (0.078-23.869)	0.832
	Recessive model	NA	NA	NA	NA
	Additive model	NA	NA	NA	NA
	Allele contrast	1.526 (0.205-11.336)	0.680	1.361 (0.078-23.628)	0.832

Abbreviations: CI, confidence interval; NA, not available.

^aAdjusted for age, sex, and cardiovascular risk factors(hypertension, dyslipidemia, diabetes and smoking habit).