Clinical Study on MYH9 Gene Singe Nucleotide Polymorphism and IgA Nephropathy among Han Chinese in Inner Mongolia

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OBJECTIVES

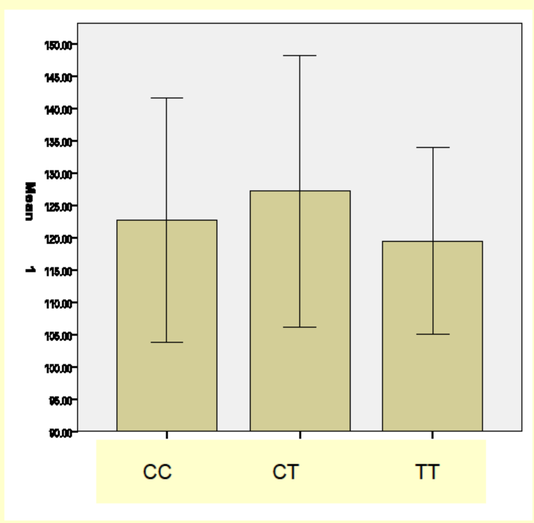
To Study on the relationship between the single nucleotide polymorphism (SNP) in MYH9 and the following: pathological clinical features, pathological type and progression in patients, with IgA Nephropathy of Han nationality in Inner Mongolia Autonomous Region .

METHODS

Collect one hundred and forty-eight cases in which patients were proven to IgA nephropathy by biopsy. Fifty-six of the patients had been followed up for 1-97 months. DNA was extracted from the peripheral blood of the above patients. The SNP in MYH9 gene of Rs3752462、Rs4821480 site were determined by PCR-restriction fragment length polymorphisms (PCR-RFLP). Analysis of different genotypes and clinical features of IgA nephropathy, pathology and progression was made. SPSS17.0 software was used for data analysis.

RESULTS

grapy1



Table

	genetype	
	GG	GT+ TT
Systolic blood pressure (mmHg)	116.00±13.03	124.74±18.81*
diastolic blood pressure (mmHg)	76.33±9.19	81.37±12.43*
age (year)	29.67±7.43	34.46±12.68*

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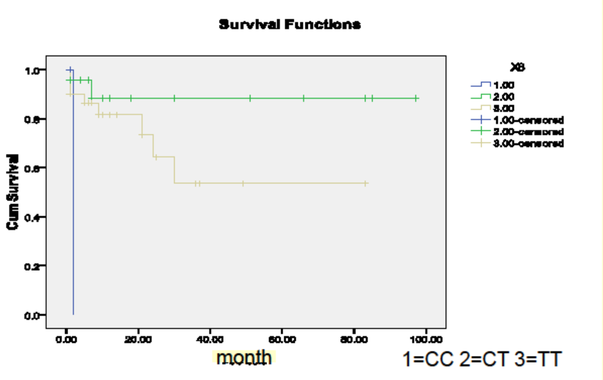
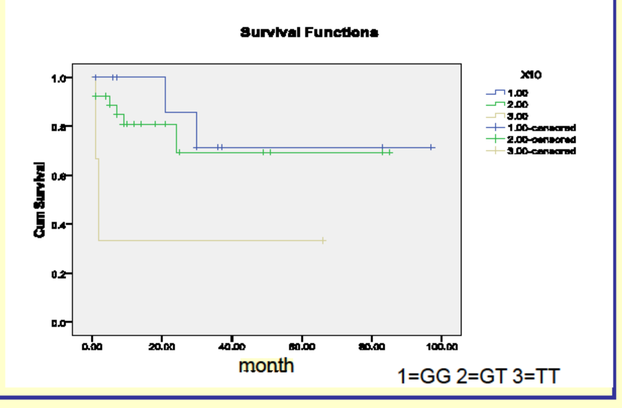
grapy2



grapy3



1.Rs3752462 site groups in Hardy Weinberg equilibrium (P> 0.05), Rs4821480 site does not meet the Hardy Weinberg equilibrium.

2. IgA nephropathy in patients with MYH9 gene Rs3752462 site TT genotype in patients with systolic blood pressure is less than the other two genotypes *(P<0.05)(Graph1*). Rs4821480 site three genotypes were statistically significant between different ages *(P<0.05)(Table*). Two sites of gender, Serum Creatinine, Creatinine clearance rate, plasma protein, hemoglobin, renal pathology immunofluorescence IgA, immunofluorescence C3, microscopic hematuria, pathological HASS grade, degree of proteinuria and other clinical parameters between the three genotypes was no statistical differences.

3. Kaplan-Meier analysis of overall survival compared to kidney dysfunction from the time of renal biopsy, Rs3752462 site CC genotype faster than other genotypes; genotype pair compared, CC genotype and CT genotype were significantly different *(P<0.05) (Graph2);* RS4821480 site TT genotype faster than other genotypes , genotype pair compared, GG genotype with the TT genotype were significantly different *(P<0.05) (Graph3).*

4. Grouped according to whether hypertension as the dependent variable, the age at onset, 24h urine protein, genotype, Haas grade assignment as the independent variable, respectively, Logistic regression analysis. Rs3752462 site TT genotype is a protective factor for the increase in IgAN hypertension.

CONCLUSIONS

1.MYH9 gene Rs3752462, Rs4821480 polymorphism on the effects of the disease with obvious racial differences. The findings, to further deepen our MYH9 gene and IgA nephropathy understanding of genetics;
2.IgA nephropathy in patients with MYH9 gene SNP Rs3752462 genotype TT is not susceptible to high blood pressure, C allele is the damage caused by IgA nephropathy patients with hypertension were independent risk factors;
3. MYH9 gene locus Rs4821480 the age of three genotypes were statistically significant, the polymorphisms affect the prognosis, natural selection caused by the gene, resulting in an imbalance of the site javin ；
4.The study found that C allele carrying Rs3752462 sites, Rs4821480 locus T allele in patients with poor prognosis, requires further validation.

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