Influence of Serum Amyloid A (SAA1) and SAA2 Gene Polymorphisms on Renal Amyloidosis, and on SAA/C-Reactive Protein Values in Patients with Familial Mediterranean Fever in the Turkish Population

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ABSTRACT. ***Objective.*** To evaluate the effect of serum amyloid A (SAA) 1 and SAA2 gene polymorphisms on SAA levels and renal amyloidosis in Turkish patients with familial Mediterranean fever (FMF).

Methods. SAA1 and SAA2 gene polymorphisms and SAA levels were determined in 74 patients with FMF (39 female, 35 male; median age 11.5 yrs, range 1.0–23.0). All patients were on colchicine therapy. SAA1 and SAA2 gene polymorphisms were analyzed using polymerase chain reaction restriction fragment length polymorphism (PCR-RFLP). SAA and C-reactive protein (CRP) values were measured and SAA/CRP values were calculated.

Results. The median SAA level was 75 ng/ml (range 10.2–1500). SAA1 gene polymorphisms were: α/α genotype in 23 patients (31.1%), α/ß genotype in 30 patients (40.5%), α/γ genotype in one patient (1.4 %), ß/ß genotype in 14 patients (18.9%), ß/γ genotype in 5 patients (6.8 %), and γ/γ genotype in one patient (1.4%). Of the 23 patients who had α/α genotype for the SAA1 polymorphism, 7 patients had developed renal amyloidosis (30.4%) compared to only one patient without this genotype (1/51; 2.0%); $p < 0.001$. SAA2 had no effect on renal amyloidosis. SAA1 and SAA2 genotypes had no significant effect on SAA levels. SAA/CRP values were significantly lower in patients with the SAA1α/α genotype, compared to other SAA1 genotypes: 0.16 (0.025–1.96) versus 0.23 (0.012–28.20), $p < 0.05$.

Conclusion. SAA1α/α genotype is one genetic factor that confers a significant risk for amyloidosis in the Turkish FMF population. Neither the SAA1 nor SAA2 genotypes had a significant effect on SAA level. (J Rheumatol 2004;31:1139–42)

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Familial Mediterranean fever (FMF) is a recessively inherited disorder. The diagnosis is based on the occurrence of recurrent episodes of fever and serous inflammation manifested by sterile peritonitis, arthritis, and pleurisy. The disease primarily affects Sephardic Jews, Armenians, Turks, and North African Arabs. Amyloidosis of AA type, mainly renal, is the major complication of FMF[1]. It develops over years and progresses to renal failure.

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In 1997, 2 independent groups (French FMF Consortium and International FMF Consortium) identified the gene responsible for FMF, designated MEFV, on chromosome 16 (16p13.3)[2,3]. The most common MEFV mutations are M694V, M680I, V726A, and M694I located on exon 10 and E148Q located on exon 2. Genotype-phenotype correlation is not well established. There are unexplained ethnic differences in the rates of amyloidosis[1,4-6]. Although early data suggested that M694V mutation was a risk factor for amyloidosis, there are also patients with FMF who have renal amyloidosis and do not carry the M694V homozygous genotype[7-10]. Unidentified genetic and environmental factors might have a protective or exacerbating effect on renal amyloidosis.

Serum amyloid A (SAA) protein family is known to contain a number of differentially expressed apolipoproteins that are synthesized primarily by the liver. The concentration of acute phase SAA can increase to more than 1000-fold during inflammation[11]. Its sensitivity was shown to be equal or more than that of C-reactive protein (CRP) in

several studies; persistently high SAA levels were correlated with activity of rheumatic disease, rapid progression of secondary amyloidosis, and poor outcome in patients undergoing certain surgical interventions[12,13].

Acute phase isotypes of human SAA are encoded at 2 different loci, SAA1 and SAA2. SAA3 is a pseudogene[14]. It has been suggested that AA-fibrils deposited in tissues were predominantly derived from SAA1α[15]. SAA1 and SAA2 are serum precursors of amyloid A1 (AA1) and A2 (AA2) proteins, the principal components of the secondary amyloid plaques. Although prolonged high plasma levels of SAA may lead to the deposition of its products, AA proteins, in tissues, high concentrations of SAA are not sufficient to promote the development of amyloidosis. Recent studies have focused on the polymorphisms of SAA as the genetic background for amyloidogenesis[16-18].

Recently, Cazeneuve, *et al* showed in a group of Armenian patients with FMF that the SAA1α/α genotype was associated with a 7-fold increased risk for renal amyloidosis, compared with other SAA1 genotypes[19]. No correlation with SAA levels was examined.

There is continuous subclinical inflammation in patients with FMF[20]. Our group has previously shown that FMF patients homozygous and compound heterozygous for MEFV mutation had higher SAA levels compared to heterozygotes[21]. Elevated SAA levels in FMF patients can be secondary to either subclinical inflammation or to SAA1 genotype. It is well known that CRP correlates markedly with SAA in most inflammatory disorders, and that no study has reported the effect of a genetic factor in producing a variation in serum CRP levels. The SAA/CRP ratio can be a useful measure when evaluating the relation between SAA values and SAA1 genotypes in patients with continuous inflammation[22].

We evaluated the influence of SAA1 and SAA2 polymorphisms on renal amyloidosis, SAA level, and SAA/CRP values in Turkish patients with FMF.

MATERIALS AND METHODS

Patients. SAA1 and SAA2 gene polymorphisms and SAA levels were determined in 74 FMF patients (39 female, 35 male; median age 11.5 yrs, range 1.0–23.0) who were homozygous or compound heterozygous for MEFV mutation (M694V, M694I, M680I, V726A, and E148Q). Homozygous or compound heterozygous patients were recruited in order to clarify the effect of MEFV genotype on SAA level[21].

The clinical data were registered on a standardized form that included age, sex, familial consanguinity, history of the disease, age at onset of symptom(s), presence of fever, abdominal pain, pleurisy, joint pain, duration of FMF disease, duration of colchicine prophylaxis, and colchicine dosage. All patients were on colchicine therapy and drug compliance was estimated to be good. Informed consent was obtained from the patient or the parents.

Mutation analysis. Our strategy for mutation analysis included 2 steps. The hot spot, exon 10, which harbors 18 mutations, was first analyzed by denaturing gradient gel electrophoresis (DGGE). According to the band pattern, subsequent analysis was done either by restriction endonuclease enzyme digestion or sequencing. Further, E148Q in exon 2 was analyzed by restriction endonuclease enzyme digestion.

SAA measurement. SAA levels were measured by solid phase sandwich ELISA method (Cytoscreen, Human SAA immunoassay kit; Biosource International, Camarillo, CA, USA). The normal SAA level was < 10 ng/ml. Blood samples for SAA and CRP measurements were drawn at least 2 weeks after an FMF attack. This period was chosen since we aimed to measure subclinical inflammation in these patients and not levels during an attack. The SAA/CRP ratio was calculated.

Analysis of polymorphisms in SAA1 and SAA2 genes. The SAA1 α, ß, and γ isoforms are encoded by the V52-A57, A52-V57, and A52-A57 SAA1 alleles, respectively. The SAA2 α and ß isoforms are encoded by the H71 and R71 SAA2 alleles. These polymorphisms are located in the coding region of the gene. SAA1 and SAA2 gene polymorphisms were analyzed using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP), as described[23]. SAA2 gene polymorphism was available in 69 patients.

Statistical analysis. Results were expressed as median (minimum-maximum) for data not showing normal distribution and as mean ± standard deviation (SD) for data showing normal distribution. Mann-Whitney U and chi-squared tests were used for comparison. P values < 0.05 were considered significant.

RESULTS

Clinical features, MEFV mutation analysis, and distribution of SAA1 and SAA2 gene polymorphisms are summarized in Table 1. Median age at onset of clinical symptoms was 3 (0.5–13) years, median age at diagnosis was 7 (1–16) years. The mean duration of FMF was 7.5 ± 4.40 years (range 1–15) and duration of colchicine prophylaxis 3.50 ± 3.64 years (range 1–13). Colchicine dosage ranged from 0.5 to

Table 1. Clinical characteristics, MEFV mutation analysis, and SAA1 and SAA2 gene polymorphisms of 74 patients with FMF.

Features	n (%)
M/F	35/39
Current age, yrs median, (minimum-maximum)	11.5 (1–23)
Amyloidosis	8/74 (10.8)
Consanguinity	20/74 (27.0)
Family history	34/74 (45.9)
History of appendectomy	7/74 (9.5)
Clinical features	
Fever	70/74 (94.6)
Abdominal pain	69/74 (93.2)
Pleurisy	34/74 (45.9)
Arthritis/arthralgia	59/74 (69.7)
MEFV mutations	
M694V/M694V	44/74 (59.5)
M694V/M680I	21/74 (28.4)
M694V/V726A	9/74 (12.2)
SAA1 genotypes	
α/α	23/74 (31.1)
α/ß	30/74 (40.5)
α/γ	1/74 (1.4)
ß/ß	14/74 (18.9)
ß/γ	5/74 (6.8)
γ/γ	1/74 (1.4)
SAA2 genotypes	
α/α	55/69 (79.7)
α/ß	13/69 (18.8)
ß/ß	1/69 (1.4)

1.5 mg/day. Frequency and duration of attacks before colchicine treatment were 12 (0–52)/year and 2 (0–15) days, respectively. Eight patients (10.8%) presented with renal amyloidosis; their MEFV mutation analysis revealed M694V/M694V genotype in 6 patients, and M694V/M680I in 2 patients. They all had typical recurrent attacks before the diagnosis.

Of the 23 patients who had α/α genotype for SAA1 polymorphism, 7 patients had developed renal amyloidosis (30.4%), whereas only one patient without this genotype developed renal amyloidosis (1/51, 2.0%; $p < 0.001$) (Table 2).

Although all of the amyloidosis patients were in the SAA2α/α genotype group, and none of the 14 patients with non-α/α genotype for SAA2 had developed amyloidosis, the difference was not statistically significant (7/55, 12.7% vs 0/14, 0%; $p > 0.05$) (Table 2).

The median SAA level was 75 ng/ml (range 10.2–1500). The difference between SAA levels of patients with α/α and non-α/α genotypes for both SAA1 and SAA2 genes was not statistically significant (Table 2). The groups were comparable for duration of FMF, duration of colchicine prophylaxis, and colchicine dosage. Of the 13 patients who were homozygous for M694V and SAA1α alleles, only 5 patients had renal amyloidosis.

The median CRP levels were not different between SAA1α/α and non-α/α genotypes. On the other hand SAA/CRP values were significantly lower in patients with SAA1α/α genotype, compared to other SAA1 genotypes (Table 2).

SAA1 and SAA2 genotypes had no significant effect on the presence of fever, abdominal pain, pleurisy, arthritis, consanguinity, and family history. There was no correlation between the MEFV genotype and SAA1 and SAA2 gene polymorphisms.

DISCUSSION

Previous studies focused on SAA1 genotype effect on secondary amyloidosis. SAA1α/α genotype was associated with an increased risk of renal amyloidosis in Caucasian patients with juvenile chronic arthritis[17]. SAA1γ/γ genotype and γ-allele frequency were associated with an increased risk of renal amyloidosis in Japanese patients with rheumatoid arthritis (RA)[16,18].

Cazeneuve, *et al* showed that the SAA1α/α genotype was associated with a higher risk of renal amyloidosis in FMF[19]. They studied 137 Armenian FMF patients; 47 patients had renal amyloidosis. Their results showed a 7-fold increased risk of amyloidosis in patients with SAA1α/α genotypes, compared to other genotypes. Another striking point was that all 11 patients who were homozygous for both M694V and SAA1α alleles had developed renal amyloidosis[19].

Mutation analysis may give different results in different ethnic groups. It is of particular importance to evaluate the effect of the SAA1α/α genotype in different FMF populations. In our study, SAA1α/α genotype was significantly associated with the development of renal amyloidosis: 7/23 (30.4%) versus 1/51 (2.0%); $p < 0.001$. In contrast to the observation by Cazeneuve, *et al*, 5 out of 13 patients who were homozygous for M694V and SAA1α alleles had renal amyloidosis in our study. These data support the view that genetic factors other than MEFV and SAA1 genotype and/or environmental factors play a role in the pathogenesis of renal amyloidosis in patients with FMF. Early and regular use of colchicine in our study population may be another factor responsible for a lower rate of amyloidosis in this selected subgroup, compared to Armenian patients.

We propose 3 hypotheses to explain the increased risk of renal amyloidosis with SAA1α/α genotype. First, a greater macrophage uptake of SAA1α isoform: this hypothesis is supported by Meek, *et al*[24] and Kluve-Beckerman, *et al*[25], who showed that in mice the plasma clearance of α/α isoform was increased. Second, the α/α isoform may also have a high intrinsic potential to promote (RA) fibrilogenesis, compared with the ß and γ isoforms. Lastly, the product of the α/α genotype may somehow be more prone to deposition[19]. Since the polymorphisms for which we screened are not in the promoter region, we cannot be sure that the levels of the protein are affected.

As described above, the SAA1γ/γ genotype was associated with renal amyloidosis in Japanese patients with RA[16], but SAA levels of healthy Japanese subjects carrying

Table 2. The effect of SAA1 and SAA2 genotypes on amyloidosis and SAA levels.

Genotypes	Amyloidosis n (%)	SAA ng/ml median (minimum–maximum)	CRP ng/ml median (minimum–maximum)	SAA/CRP
SAA1				
α/α	7/23 (30.4)*	56 (10.2–1500)	367.5 (100–8210)	0.16 (0.025–1.96)**
Non-α/α	1/51 (2.0)*	160 (16.4–1500)	312.5 (10–9710)	0.23 (0.012–28.20)**
SAA2				
α/α	7/55 (12.7)	196 (10.2–1500)	120 (100–351)	0.18 (0.160–0.31)
Non-α/α	0/14 (–)	125 (15.6–1400)	292 (100–1600)	0.17 (0.012–2.4)

* $p < 0.001$, ** $p < 0.05$.

SAA1γ/γ genotype were lower than those of individuals with other SAA1 genotypes[22].

In our study, SAA values did not depend on SAA1 genotype. Since they were receiving colchicine, our patients' SAA levels were affected by the drug as well. The SAA/CRP values were even lower in patients with the SAA1α/α genotype, compared to other SAA1 genotypes. Observations by Yamada, *et al*[22] and our results suggest that the increased risk for renal amyloidosis is not directly related to SAA level. The question of why the SAA1γ/γ genotype is associated with renal amyloidosis in Japanese patients with RA and the SAA1α/α genotype is associated with renal amyloidosis in FMF patients remains to be answered.

Our study confirms an association between the SAA1α/α genotype and renal amyloidosis in patients with FMF. SAA/CRP value is a better measure for evaluating the influence of SAA1α/α genotype on SAA level in patients with FMF. Whether greater macrophage uptake or increased (RA) fibrilogenesis of the α/α isoform plays a role in the pathogenesis of amyloidosis in FMF merits further study.

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