Dan Med J 61/5 May 2014

Genotyping increases the yield of angiotensinconverting enzyme in sarcoidosis – a systematic review

Andreas Fløe¹, Hans Jürgen Hoffmann¹, Peter H. Nissen², Holger Jon Møller² & Ole Hilberg¹

ABSTRACT

INTRODUCTION: The diagnosis of sarcoidosis is challenging and involves radiological, clinical and paraclinical evaluation, the latter including the measurement of serum angiotensin-converting enzyme activity (s-ACE), which is elevated in about 60% of sarcoidosis patients. The normal inter-individual biological variation of s-ACE is large. Approximately 50% of the variation is due to a genomic insertion/deletion (I/D) polymorphism in the ACE gene.

METHODS: We searched the MEDLINE library for articles presenting genotype-based reference intervals for s-ACE in healthy people. We summarised the results as weighted mean DD/II ratios of s-ACE. We also summarised the presented frequencies of the genotypes.

RESULTS: We identified nine studies presenting genotypebased reference intervals. All studies found a significant difference between mean s-ACE in the three genotype groups DD, ID and II. The mean DD/II ratio was 1.85 (range: 1.79-1.92) for all studies, 2.01 (1.92-2.10) for Caucasians and 1.64 (1.55-1.73) for Asians. The median frequencies of genotypes among Caucasians were 23% II, 45% ID and 30% DD, and 45% II, 49% ID and 14% DD among Asians. **CONCLUSION:** Genotyping for the I/D polymorphism increases the benefit of s-ACE since all studies found significantly different levels between genotype groups in healthy subjects. Genotyping is of special value if s-ACE is between the upper 97.5 percentile for genotype II and DD since values in this interval are at risk of being misclassified. Due to assay variation, genotype-specific reference levels should be verified locally.

Sarcoidosis is an inflammatory, granulomatous disease. Its pathogenesis is unknown, but probably involves genetic predisposition as well as external factors [1]. Approximately 500 new cases are diagnosed in Denmark annually. Diagnosing sarcoidosis is challenging and includes radiological changes, clinical manifestations and paraclinical findings, including measurement of serum angiotensin-converting enzyme activity (s-ACE, peptidylpeptidase A). ACE has a number of metabolic effects; most notably it catalyses the modification of angiotensin I to angiotensin II, a potent vasoconstrictor [2] and inactivates bradykinin through the kallikrein-kininogen system [3]. It is also a potent pro-inflammatory modulator [4] secreted by activated cells of the monocyte-macrophage cell lineages, which are crucial in the process of granuloma formation. S-ACE is elevated in about 60% of sarcoidosis patients [5], but also in other granulomatous diseases like Gaucher's disease and tuberculosis [6]. Though the level of s-ACE reflects the mass of granuloma in the body [7], the clinical use of s-ACE in monitoring disease activity is controversial, and recommendations differ between guidelines.

The activity of ACE can be measured by enzyme kinetic methods which most commonly utilise the polypeptide FAPGG (furyl-acryloyl-phenylalanyl-glycyl-glycine), which acts as a synthetic substrate for ACE. The degradation of FAPGG to FAP is visualised by a changed absorption spectrum by spectrophotometry [8]. Several commercial kits for automatic analysis are available.

The normal level of ACE depends on genetic variation in the ACE gene. In intron 16, a common *insertion/ deletion* polymorphism, varying in a 287 base pair sequence, is of importance [9]. The genotypes are termed DD (homozygote for deletion), ID (heterozygote) and II (homozygote for insertion).

The I/D polymorphism is responsible for almost half of the biological variation in s-ACE among healthy individuals [10], s-ACE being highest in individuals carrying the genotype DD and lowest in genotype II.

Analysis of the genotype was previously performed by restriction fragment length polymorphism (RFLP) [9], which has now been replaced by PCR-based methods for identification of the I and D alleles [11] and most recently by high-resolution melting (HRM) technique [12].

Since the I/D polymorphism impacts the normal level of s-ACE, we aimed to summarise current evidence for genotype-based differences in mean values of s-ACE in different ethnic populations.

METHODS

We used PubMed to search the MEDLINE library for articles providing genotype-based reference intervals of s-ACE until June 2013. We applied the following search terms: "sarcoidosis, pulmonary" (Mesh) AND "peptidyldipeptidase A" (Mesh), and "sarcoidosis" AND "ace" AND "genotype" (free text search). We restricted the search to articles in English, German and Danish. No limits were set regarding entry year

From the studies selected, genotype-based mean

SYSTEMATIC REVIEW

1

 Department of Pulmonary Medicine, Aarhus University Hospital
Department of Clinical Biochemistry, Aarhus University Hospital

Dan Med J 2014;61(5):A4815

Dan Med J 61/5 May 2014

TABLE 1

Genotype-based reference intervals. Overall reference interval refers to non-genotype based reference interval.

						Overall	ref. interval	Genoty	pe II	
Reference	n	Ethnicity	Assay for s-ACE	Genotyping technique	Unit	lower	upper	mean	lower	upper
Tomita et al [20]	314	Asian	Fujizoki Assay, Tokyo, Japan (colorimetric)	Real-time PCR	IU/I	8.3	21.4	10.8	9	12.5
Furuya et al [16]	341	Asian	ACE Color, Fujirebio Inc, Tokyo (colorimetric)	PCR and agarose electrophoresis	IU/I	7.6	24.2	11.8	6.8	18.2
Kruit et al [17]	200	Caucasian	Bühlmann ACE kinetic test, Bühlmann Laboratories AG, CH	Real-time PCR	U/I	-	-	25.9	9	43
Camos et al [15]	147	Caucasian	BEN srl, Milan, Italy (kinetic test)	Real-time PCR	U/I	13.3	63.9	19.1	9.6	28.7
Sharma et al [19]	146	Caucasian	-	-	U/I			17.6	4.6	30.6
Ruprecht et al ^a [18]	262	Caucasian	Bühlmann ACE kinetic test, Bühlmann Laboratories AG, CH	PCR and agarose electrophoresis	U/I	15	80.9	32.2	13.7	50.7
Rigat et al [9]	80	Caucasian	Radio-immunoassay	RFLP	μg/l	-	-	299.3	220.5	397
Biller et al [14] Assay 1 ^b	159	Caucasian	Bühlmann ACE kinetic test, Bühlmann Laboratories AG, CH	Real-time PCR	U/I	12	82	34.8	8	62
Assay 2 ^b	159	Caucasian	Trinity Biotech, Bray, Ireland (kinetic test)	Real-time PCR	U/I	7	44	25.4	7	44
Nissen et al [12]	400	Caucasian	Infinity ACE, Thermo Fischer Scientific, MA, USA	High-resolution melting	U/I	12	60	21.3	6.5	36.1

DD = homozygous for deletion; ID = heterozygous; II = homozygous for insertion; PCR = polymerase chain reaction; RFLP = restriction fragment length polymorphism; s-ACE = serum angiotensin-converting enzyme activity.

a) 95% CI constructed by the authors from In-transformed mean value and SD.

b) s-ACE was measured with two individual assays.

TABLE 1 CONTINUES

values of s-ACE and standard deviations were obtained, as well as size and ethnicity of the study populations. Between-laboratory and between-assay variation in measurement of s-ACE is substantial [8] and, furthermore, results were reported in different units between

🖌 🛛 FIGURE 1

Flow-chart demonstrating the selection of studies. Adopted in revision from Prisma 2009.



studies. Aa quantitative meta-analysis of the mean s-ACE levels would therefore not provide useful information for comparing the genotype groups. Instead, we used Intransformed mean values of s-ACE from each study for the groups II, ID and DD to calculate ratios of s-ACE between the groups. These ratios (II/DD, II/ID and ID/DD) do not provide clinically meaningful information in themselves, but they serve to evaluate whether the differences between the groups are significant. This is the case if the confidence interval does not include the value one.

We summarised II/DD, II/ID and ID/DD ratios as weighted mean values as the sample sizes varied considerably. Data were expressed as means and two-sided 95% confidence intervals. Furthermore, we calculated ethnicity-stratified, weighted estimates of the II/DD ratio.

Finally, we summarised genotype frequencies from studies in which such data were reported, and ethnicity-grouped median values were obtained.

Where applicable, the review process complied with the Prisma guidelines [13].

Ethics approval

The review included only data from prior studies. Therefore, ethics approval was not needed. All included studies documented that appropriate ethics approvals had been obtained.

📕 | TABLE 1, CONTINUEI

Continued.

Genoty	vpe ID		Genoty	vpe DD	p-value for differ-		
mean	lower	upper	mean	lower	upper	ence between means (test)	
13.8	10.5	17.1	17.2	11.9	22.6	< 0.0001 (Kruskal-Wallis)	
15.2	9.3	23.5	19.3	11.5	26.9	< 0.0001 (Anova)	
38.1	14	62	53.1	24	82	< 0.0001 (Anova)	
29.5	9.5	49.5	39	12.3	65.6	< 0.05 (Anova)	
28.8	10	47.6	41.1	17.9	64.3	< 0.0001 (Mann-Whitney)	
47.7	18.6	76.8	59.8	31.8	87.8	< 0.0001 (Mann-Whitney)	
392.6	277.8	540.4	494.1	336.2	708	0.001 (One-way analysis)	
45.5	16	75	59.3	12	82	< 0.0001 (Anova)	
33.7	10	57	43.7	7	62	< 0.0001 (Anova)	
32.5	11.4	53.6	43.8	20.1	67.4	< 0.0001 (Anova)	

FIGURE

Ratio of mean s-ACE between genotypes for each study, and weighted mean ratio for each genotype with 95% Cl. Mean values: DD/II 1.88, DD/ ID 1.31, ID/II 1.43. For Biller et al [14], the mean s-ACE measured by two different assays is shown.



RESULTS

The study selection process is outlined in **Figure 1**. We identified 102 journal articles. By review of title and abstract, 12 articles were relevant for this analysis. Seven articles [14-20] presented new genotype-based reference intervals for s-ACE based on genotyping and s-ACE measurements in healthy individuals. Furthermore, one article [9] presenting genotype-based reference intervals was identified from reference lists and, in addition, data from a recent Danish study [12] were included. The nine studies represented 2,052 healthy individuals. Genotype-based mean values of s-ACE, and standard deviations for all nine studies are shown in **Table 1**. One study [14] measured ACE activity with two assays. These are provided individually in Table 1.

All studies found significantly different levels of s-ACE between genotype groups, with DD having the highest mean ACE value, II having the lowest mean ACE value and ID having intermediate values. The distribution of ratios of s-ACE (DD/II, DD/ID and ID/II) is shown in **Figure 2**. The weighted mean DD/II ratio was 1.85 (range: 1.79-1.92) for all studies, 2.01 (1.92-2.10) for Caucasians and 1.64 (1.55-1.73) for Asians. The mean DD/ID ratio and ID/II ratio were both significantly different from one. Therefore, the mean s-ACE was significantly higher for the DD genotype than for the ID genotype, which was again significantly higher than that for the II genotype.

Two studies [16, 20] provided genotyping and s-ACE data for 310 sarcoidosis patients. These are shown in

CI = confidence interval; DD = homozygous for deletion; ID = heterozygous II = homozygous for insertion; s-ACE = serum angiotensin-converting enzyme activity.

Table 2. Weighted mean DD/II ratio was 1.45 (1.30-1.62) for these patients. Severity of sarcoidosis was indicated roentgenologically ad modem DeRemee, but genotype-based s-ACE levels were not stratified for roentgenologic disease stage.

All included papers documented that none of the participants were being treated with ACE inhibitors.

Frequency of I/D genotypes was reported in eight of nine study populations. These are shown in **Table 3**. When adjusting for ethnicity, the mean frequency of I/D genotypes among Caucasians was 27.6% II, 45.7% ID and 26.7% DD, while the mean frequencies among two Asian studies was 36.1% II, 49.9% ID and 14.0% DD.

DISCUSSION

This review revealed that significant differences of s-ACE between I/D genotype groups were seen in all included studies. On this basis, it seems rational to recommend genotyping of patients if the value of s-ACE is considered part of the diagnostic process for sarcoidosis or for monitoring disease activity in confirmed cases. It is important to note, though, that the benefit of I/D genotyping is primarily derived from the significant differences of s-ACE

TABLE 2

Sarcoidoses patients only: genotype-based mean values of s-ACE from prior studies.

					Mean value by genotype				
	Reference	n	Ethnicity	Assay for s-ACE	Unit	П	ID	DD	p-value
	Tomita et al [20]	207	Asian	Fujizoki Assay, Tokyo, Japan (colorimetric)	IU/I	21.4	23.9	27.3	< 0.01
	Furuya et al [16]	103	Asian	ACE Color, Fujirebio lnc , Tokyo (colorimetric)	IU/I	18.7	27.5	32.7	< 0.0001

DD = homozygous for deletion; ID = heterozygous; II = homozygous for insertion; s-ACE = serum angiotensin-converting enzyme activity.



The frequency of the I/D genotypes between studies.

			Freque	Frequency of genotype		
Reference	n	Ethnicity	П	ID	DD	
Sarcoidosis						
Tomita et al [20]	207	Asian	37.2	48.8	14.0	
Furuya et al [16]	103	Asian	35.0	51.0	14.0	
Mean			36.1	49.9	14.0	
Healthy						
Tomita et al [20]	314	Asian	43.3	44.3	12.4	
Furuya et al [16]	341	Asian	46.0	40.0	14.0	
Kruit et al [17]	200	Caucasian	21.5	53.5	25.0	
Camos et al [15]	147	Caucasian	20.4	42.9	36.7	
Sharma et al [19]	146	Caucasian	26.7	43.2	30.1	
Ruprecht et al [18]	262	Caucasian	21.0	49.6	29.4	
Rigat et al [9]	80	Caucasian	17.5	46.3	36.3	
Biller et al [14]	159	Caucasian	24.5	45.9	29.6	
Mean			27.6	45.7	26.7	

DD = homozygous for deletion; ID = heterozygous; II = homozygous for insertion.

between the genotypes in healthy people. In this analysis, two studies supported that genotyping will also improve the yield of s-ACE in sarcoidosis patients, but more clinical studies are needed to clearly confirm this finding.

The mean s-ACE level for the genotype DD is almost twice that of genotype II. Variance analyses od previous data have shown that almost 50% of the normal variation in s-ACE in healthy people is attributable to the polymorphism [9, 17]. It is noteworthy that by evaluating s-ACE in 129 sarcoidosis patients and sarcoidosis suspect patients after genotyping Kruit et al [17] found that 8.5% of these were misclassified as having either normal or elevated s-ACE by application of standard (non-genotype based) reference intervals. Sharma et al [19] evaluated their genotype-based reference intervals on 47 sarcoidosis patients and found 33.5% more patients to have elevated s-ACE than by applying standard reference intervals. These findings indicate that routine genotyping would increase the yield of s-ACE in diagnosing sarcoidosis, though they do not show whether routine genotyping will have a similar impact on the clinical management of these patients. More prospective studies are needed to clarify this.

There is a considerable variation in the results obtained by photometric measurement of s-ACE between analytical methods. This has potential implications for the ability to compare values between laboratories for clinical as well as for scientific purposes. This variation is reduced by using commercial kits, traceable calibrators and by applying external quality control programmes for laboratories [5]. The introduction of routine genotyping increases the clinical significance of small variations in s-ACE, which makes efforts to reduce between-laboratory variation even more important. Whenever I/D genotyping is introduced, genotype-based reference values should be verified with the laboratory kits used for genotyping as well as for measurement of s-ACE activity, preferably at the laboratory performing the analyses, but at least with identical kits in a comparable population group.

Genotyping will certainly incur additional costs to the investigation of sarcoidosis. This has to be taken into account when considering the rationale for performing genotyping. In this context, one approach would be to restrict genotyping to the group of patients in which the impact would expectedly be greatest; at least theoretically, this would be in persons in whom s-ACE is between the upper 97.5 percentile for the genotype II and DD since values in this interval are at the greatest risk of being misclassified as normal or elevated if genotyping is not performed. Prospective studies of the clinical impact of genotyping would help clarify the cost-effectiveness of the analysis and would also help define whether a routine or a selective genotyping approach should be chosen. The use of s-ACE in diagnosing and monitoring of sarcoidosis is challenging itself since it is neither specific, nor sensitive [21], and the clinical justification of the test is a matter of ongoing debate. Since genotyping seems to improve the accuracy of the test, this may very well be cost-effective, though no present studies clearly address this question.

As shown in Table 2, a significant difference in s-ACE between genotypes was also present among a smaller number of verified sarcoidosis cases. It has been demonstrated that the genotype DD is associated with a higher increase in s-ACE than the genotype II [22] in sarcoidosis. The data included in this review did not confirm this trend as the DD/II ratio of s-ACE was lower in sarcoidosis populations than in healthy study populations. However, this assumption is based on two studies only, and it only represents Asian patients. In neither of the two studies were the genotype-based ACE levels stratified for severity of sarcoidosis; therefore, they did not reveal whether the impact of the I/D genotype on s-ACE reflects sarcoidosis severity.

We found the I-allele to be more frequent in Asian than in Caucasian populations, which is in concordance with prior findings [23]. As there is also a well-known geographical and ethnic variation in the incidence of sarcoidosis, it has been hypothesised that the I/D polymorphism may play a role in the pathogenesis of sarcoidosis [16, 24]. Data are conflicting, but most recent studies generally do not support such a correlation [25, 26]. The function of the I/D polymorphism, though, is not clearly understood, but its location in an intronic position suggests a linkage disequilibrium with other transcriptionregulating genes [27].

For genotyping of the I/D polymorphism to be used routinely, the method has to be stable and reliable. Previous data have shown that prior PCR techniques misclassified 4-5% [28, 29] of heterozygote individuals because the shorter D-allele is amplified more efficiently that the I-allele. The vast majority of these can be detected by running a confirmatory genotyping on all DD patients. A recently introduced high-resolution meltingtechnique provides more robust genotyping results, with primary HRM results performing at par with primary and confirmatory RT-PCR results in combination [12].

Certain limitations apply to this review. Since the studies were performed over a span of 23 years, the methods for genotyping and ACE measurement have changed, which makes direct comparison of studies difficult. Also, this review only included Asian and Caucasian subjects. As the I/D prevalence varies between ethnic groups, the external validity in other ethnic groups might be limited. All studies showed a significant difference of s-ACE between genotype groups. We assume that this effect is due to the I/D genotype playing a major role for the normal level of s-ACE. This effect could potentially be

FACT BOX

Serum-angiotensin converting enzyme (s-ACE) is elevated in about 60% of sarcoidosis patients.

The yield of measuring s-ACE is halted by large normal inter-individual variation.

About 50% of the normal variation is due to an insertion/deletion (I/D) polymorphism in the ACE gene.

The normal level of s-ACE is significantly different between the genotypes II, ID and DD.

Genotype-based reference intervals increase the clinical benefit of s-ACE.

Due to assay variation, genotype-specific reference levels should be verified locally.



enforced by publication bias if studies showing no significant difference between groups have not been published. At the single study level, results could be biased by misclassification of genotypes. In all the identified studies except one [18], PCR-based genotyping (RT-PCR or conventional PCR with agarose gel electrophoresis) was confirmed with a second genotyping.

CONCLUSION

This literature search unequivocally demonstrates that among Asian and Caucasian persons, the mean s-ACE activity is significantly higher in individuals with the DD genotype than in individuals with the II genotype, with the ID genotype having intermediate values. Few studies have evaluated the impact of genotyping on the management of sarcoidosis and though more studies are clearly needed, the present data suggest that a significant amount of sarcoidosis patients are misclassified because non-genotype-based reference values are applied. Genotyping will expectedly be of greatest impact if s-ACE is between the upper 97.5 percentile for the genotypes II and DD since values in this interval are at risk of being misclassified, but clinical validation studies are needed to clarify cost-effectiveness.

Whenever implementing I/D genotyping, genotypespecific reference levels should always be verified locally due to great assay variation.

CORRESPONDENCE: Andreas Fløe, Lungemedicinsk Afdeling LUB, Hjertecentret, Aarhus Universitetshospital, Nørrebrogade 44, 8000 Aarhus C, Aarhus, Denmark. E-mail: andrniel@rm.dk ACCEPTED: 30 January 2014

CONFLICTS OF INTEREST: none. Disclosure forms provided by the authors are available with the full text of this article at www.danmedj.dk. **ACKNOWLEDGEMENTS**: The study was financed by the Department of Clin-

ical Biochemistry, Aarhus University Hospital, and Department of Pulmonary Medicine, Aarhus University Hospital. It did not involve any external funding. FUNDING: The study was financed by the Department of Clinical Biochemistry, Aarhus University Hospital, Denmark, and the Department of Pulmonary Medicine, Aarhus University Hospital, Denmark. No external funding was received.

LITE ATURE

1. Costabel U, Hunninghake GW. ATS/ERS/WASOG statement on sarcoidosis.

Bilateral hilar lymphadenopathy. A typical finding in sarcoidosis (stadium I). Sarcoidosis Statement Committee. American Thoracic Society. European Respiratory Society. World Association for Sarcoidosis and Other Granulomatous Disorders. Eur Respir J 1999;14:735-7.

- Coates D. The angiotensin converting enzyme (ACE). Int J Biochem Cell Biol 2003;35:769-73.
- Bryant JW, Shariat-Madar Z. Human plasma kallikrein-kinin system: physiological and biochemical parameters. Cardiovasc Hematol Agents Med Chem 2009;7:234-50.
- Song GG, Kim JH, Lee YH. Associations between the angiotensinconverting enzyme insertion/deletion polymorphism and susceptibility to sarcoidosis: a meta-analysis. J Renin Angiotensin Aldosterone Syst 2013 May 15 (e-pub ahead of print).
- McGrath DS, Foley PJ, Petrek M et al. Ace gene I/D polymorphism and sarcoidosis pulmonary disease severity. Am J Respir Crit Care Med 2001;164:197-201.
- Brice EA, Friedlander W, Bateman ED et al. Serum angiotensin-converting enzyme activity, concentration, and specific activity in granulomatous interstitial lung disease, tuberculosis, and COPD. Chest 1995;107:706-10.
- Luisetti M, Beretta A, Casali L. Genetic aspects in sarcoidosis. Eur Respir J 2000;16:768-80.
- 8. Muller BR. Analysis of serum angiotensin-converting enzyme. Ann Clin Biochem 2002;39:436-43.
- Rigat B, Hubert C, Alhenc-Gelas F et al. An insertion/deletion polymorphism in the angiotensin I-converting enzyme gene accounting for half the variance of serum enzyme levels. J Clin Invest 1990;86:1343-6.
- Pietinalho A, Furuya K, Yamaguchi E et al. The angiotensin-converting enzyme DD gene is associated with poor prognosis in Finnish sarcoidosis patients. Eur Respir J 1999;13:723-6.
- 11. Sayed-Tabatabaei FA, Oostra BA, Isaacs A et al. ACE polymorphisms. Circ Res 2006;98:1123-33.
- Nissen P, Campbell NB, Højskov C et al. Development of a high-resolution melting genotyping assay for the angiotensin I converting enzyme (ACE) insertion/deletion variant and establishment of genotype specific reference intervals in a Danish population. Ann Clin Biochem 2014 (in press)
- Liberati A, Altman DG, Tetzlaff J et al. The PRISMA statement for reporting systematic reviews and meta-analyses of studies that evaluate healthcare interventions: explanation and elaboration. BMJ 2009;339:b2700.
- Biller H, Zissel G, Ruprecht B et al. Genotype-corrected reference values for serum angiotensin-converting enzyme. Eur Respir J 2006;28:1085-90.
- Camos S, Cruz MJ, Morell F et al. Genetic-based reference values for angiotensin-converting enzyme (ACE) according to I/D polymorphism in a Spanish population sample. Clin Chem Lab Med 2012;50:1749-53.
- Furuya K, Yamaguchi E, Itoh A et al. Deletion polymorphism in the angiotensin I converting enzyme (ACE) gene as a genetic risk factor for sarcoidosis. Thorax 1996;51:777-80.
- Kruit A, Grutters JC, Gerritsen WB et al. ACE I/D-corrected Z-scores to identify normal and elevated ACE activity in sarcoidosis. Respir Med 2007;101:510-5.
- Ruprecht B, Schurmann M, Ziegenhagen MW et al. Corrected normal values for serum ACE by genotyping the deletion-/insertion-polymorphism of the ACE gene. Pneumologie 2001;55:326-32.
- 19. Sharma P, Smith I, Maguire G et al. Clinical value of ACE genotyping in diagnosis of sarcoidosis. Lancet 1997;349:1602-3.
- Tomita H, Ina Y, Sugiura Y et al. Polymorphism in the angiotensinconverting enzyme (ACE) gene and sarcoidosis. Am J Respir Crit Care Med 1997;156:255-9.
- 21. Valeyre D, Prasse A, Nunes H et al. Sarcoidosis. Lancet 2013 Sep 30 (e-pub ahead of print).
- Schurmann M. Angiotensin-converting enzyme gene polymorphisms in patients with pulmonary sarcoidosis: impact on disease severity. Am J Pharmacogenomics 2003;3:233-43.
- 23. Lee EJ. Population genetics of the angiotensin-converting enzyme in Chinese. Br J Clin Pharmacol 1994;37:212-4.
- Maliarik MJ, Rybicki BA, Malvitz E et al. Angiotensin-converting enzyme gene polymorphism and risk of sarcoidosis. Am J Respir Crit Care Med 1998;158:1566-70.
- Yilmaz D, Karkucak M, Coskun F et al. ACE gene I/D polymorphism and risk of sarcoidosis development in Turkish patients. Tuberk Toraks 2012:60:201-6.
- Alia P, Mana J, Capdevila O et al. Association between ACE gene I/D polymorphism and clinical presentation and prognosis of sarcoidosis. Scand J Clin Lab Invest 2005;65:691-7.
- 27. Baudin B. New aspects on angiotensin-converting enzyme: from gene to disease. Clin Chem Lab Med 2002;40:256-65.
- Fogarty DG, Maxwell AP, Doherty CC et al. ACE gene typing. Lancet 1994;343:851.
- Lindpaintner K, Pfeffer MA, Kreutz R et al. A prospective evaluation of an angiotensin-converting-enzyme gene polymorphism and the risk of ischemic heart disease. N Engl J Med 1995;332:706-11.