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American Journal of Medical Genetics 136A:249–253 (2005)

Variations of the *CFTR* Gene in the Hanoi-Vietnamese

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In order to investigate polymorphic backgrounds of the cystic fibrosis transmembrane conductance regulator gene (*CFTR*) in the Vietnamese, we analyzed 495 blood samples of randomly selected healthy individuals in Hanoi for the delta F508 mutation and TG-repeats, poly-T, and M470V polymorphisms. We compared their distributions with those of Caucasians and other Asian populations. No delta F508 mutation was found, being consistent with the extremely low incidence of cystic fibrosis (CF) in Vietnam. Allele frequency of the T5 allele promoting exon 9 skipping was 0.037. Greater number of TG-repeats, which is known to facilitate this aberrant splicing, was a predominant trend in the Vietnamese and other Asians. A "T5-TG12-V470" haplotype was most common (29/37) among T5—bearing haplotypes. Three major haplotypes, T7-TG12-M470, T7-TG11-V470, and T7-TG12-V470, estimated by PHASE program, related to 92% of the population. This is the first study of the *CFTR* gene among the Vietnamese.

KEY WORDS: cystic fibrosis transmembrane conductance regulator gene; polymorphism variation; Vietnamese

INTRODUCTION

Cystic fibrosis (CF), also called mucoviscidosis or CF of the pancreas, is an autosomal recessive disease. CF classically involves the lungs, sinuses, pancreas, liver/bile ducts, intestines, reproductive tract, and sweat glands. The disease is most common among Caucasian populations and is caused by mutations in the CF transmembrane conductance regulator gene (*CFTR*) [Welsh and Fick, 1987; Doull, 2001]. More than 1,000 mutations and 200 sequence variations in *CFTR* have been identified (http://www.genet.sickkids.on.ca). In Asians, the prevalence of CF is very low and there are few data on *CFTR*, especially in South East Asia (http://www.genet.sickkids.on.ca). Recently, articles on relations within other *CFTR* mutations and polymorphisms in CF-like diseases such as congenital bilateral absence of the vas deferens (CBAVD), bronchiestasis (BE), chronic rhinosinusitis, allergic bronchopulmonary aspergillosis (ABPA), and unexplained recurrent pancreatitis have been reported [Chillón et al., 1995; Casals et al., 2000; Marchand et al., 2001; Casals et al., 2004]. Bombieri et al. [1998] found *CFTR* mutations in 11 of 23 patients with disseminated bronchiestasis (DBE) of unknown cause, in 7 of 25 emphysema, and in 1 of 4 tuberculosis patients. It was mentioned especially that poly-thymidine (poly-T), TG-repeats, and M470V polymorphisms play a role in developing CF-like diseases. Poly-T and TG-repeats at the junction of intron 8 and exon 9 affect transcription of exon 9 mRNA by exon skipping, and alter the level of normal CFTR protein. On the other hand, an M470V polymorphism on exon 10 influences the intrinsic chloride activity [Cuppens et al., 1998; Tzetis et al., 2001; Lee et al., 2003; Fujiki et al., 2004].

Vietnam is a country located in South East Asia. It has about 82.7 million inhabitants estimated in 2004. The majority of Vietnamese ethnicity is Kinh people, accounting for 85%–90% of the population, and there are nearly 60 ethnic groups (http://www.emwg.org.vn/04_v.html). No reports on *CFTR* among the Vietnamese have been published. In order to explore polymorphic backgrounds of *CFTR* in the Vietnamese population, we analyzed blood samples of 495 healthy individuals among the general population in Hanoi under the auspices of the research cooperation with Japan.

MATERIALS AND METHODS

Subjects

Approximately 500 healthy unrelated subjects were randomly selected from 15,000 individuals in 20 communes among the population of Hanoi City, consisting of about 2.9 million people. As regards the Ethnic rate, Kinh people account for more than 99% of the population of Hanoi. Ethical approval for this research was obtained from the ethics committees of both the Vietnamese Ministry of Health and the International Medical Center of Japan.

Male/female ratio was 1.00/1.03. Mean age was 37.4 year (range 15–60 years), and the median age was 38 year. The subjects were interviewed, a chest X-ray test was conducted, and 10 ml of blood samples were collected for genotyping. For comparison, we also genotyped DNA samples from 50 Caucasians in North America provided by Human Variation Collection of the Human Genetic Cell Repository (National Institute of General Medical Sciences-Camden, NJ) and from 50 Japanese in Health Science Research Resources Bank (Osaka, Japan).

DNA Analysis

DNA was extracted from 495 samples of whole blood with the QIAamp™ DNA Blood Midi kit. (QIAGEN GmbH, Max

Grant sponsor: Ministry of Health, Labour, and Welfare of Japan (for International Health Cooperation Research); Grant number: 14C-9.

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Received 20 November 2004; Accepted 27 April 2005

DOI 10.1002/ajmg.a.30826

Published online 9 June 2005 in Wiley InterScience (www.interscience.wiley.com)

TABLE I. Allele Frequencies of the Poly-T Tract

Ethnic groups	Number (frequency) of individuals with alleles of poly-T tract			
	T5	T6	T7	T9
Vietnamese (2n = 990)	37 (0.037)	1 (0.001)	946 (0.946)	6 (0.006)
Japanese (2n = 100)	1 (0.01)	0 (0.00)	98 (0.98)	1 (0.01)
Caucasians (2n = 100)	7 (0.07)	0 (0.00)	86 (0.86)	7 (0.07)

Four alleles T5, T6, T7, and T9 depend on the number of thymidines in the poly-T tract, located in intron 8 of the *CFTR* gene.

Volmer Straße 4, Germany). The PCR protocol was 35 cycles using a Gene Amp PCR System (model 9700; Applied Biosystems, Foster, CA) at 95°C for 9 min for preheat, 95°C for 15 sec, 60°C for 15 sec, and 72°C for 1 min with oligonucleotide primer pairs 5′-GAG GCA AGT GAA TCC TGA GCG-3′ and 5′-CCA TTG AGG ACG TTT GTC TCA C-3′ [Haga et al., 2002], and Ampli Taq Gold 5 U/μl (Applied Biosystems). The PCR products were 553 bp and RFLP with *Hph*I was used to detect the M470V polymorphism.

The delta F508 mutation was screened by PCR 45 cycles' protocol at 95°C for 15 sec, 54°C for 15 sec, and 72°C for 30 sec with primer pairs 5′-CAT TAA AGA AAA TAT CAT CGG-3′ and 5′-CCA TTG AGG ACG TTT GTC TCA C-3′. This was a slight modification to the method described previously [Ballabio et al., 1990]. Poly-T, TG repeats, and haplotypes consisting of two these loci were directly identified by bi-directional nucleotide sequencing as described previously [Arduino et al., 1999; Lucarelli et al., 2002], with primer pairs, intron 8 and exon 9 junction sense primer, 5′-GAT CAT GTC CTC TAG AAA CCG-3′, antisense primer, 5′-CAA ATT AAG TTC TTA ATA GTG-3′ [Haga et al., 2002]. PCR products were purified using Exo SAP-IT (Amersham Biosciences, Tokyo, Japan) and provided for sequencing by automated sequencer (ABI Prism3100, Applied Biosystems) using a Big Dye Terminator kit (Applied Biosystems).

Statistics

Conformity of the genotype distribution of the polymorphisms to Hardy–Weinberg equilibrium was examined in the population under study. Haplotypes consisting of three loci investigated, that is, poly-T, TG repeats, and the M470V polymorphism were estimated by the use of the PHASE algorithm (PHASE, version 2.1) based on Bayesian inference with the default settings [Stephens et al., 2001; Stephens and Donelly, 2003]. Estimated haplotype frequencies in PHASE program were obtained from the _freqs file. Probabilities of the most likely pairs of haplotypes for each individual were obtained from the _pairs file. Fst values and pairwise linkage disequilibrium were evaluated by using Arlequin ver. 2.000, software for population genetics data analysis with the default settings [Schneider et al., 2000].

RESULTS

Frequencies of Variations on CFTR

No deltaF508 mutation was found in the 990 *CFTR* alleles from 495 normal subjects. In the Vietnamese, more than 90% (0.956) of poly-T tract in intron 8 consisted of the T7 allele. The T5 (0.037) and T9 alleles (0.006) were much less frequent than the T7 allele (Table I). Homozygotes for the T5 allele were not detected in the population tested. The T6 allele was found with a frequency of 0.001. Predominance of T7, compared to other alleles, in the Vietnamese population was comparable to that in the Japanese and Caucasians. The TG11 and TG12 alleles accounted for more than 95% in the Vietnamese and the Japanese. Especially, TG12 was most frequent in the Vietnamese (Table II). By contrast, in Caucasians, TG11 is the predominant allele and followed by TG10. The M470V polymorphic site in exon 10 was also genotyped. The V allele was slightly more frequent than the M allele in the Vietnamese population (Table III). Large difference of allele frequencies was not observed among the three ethnic populations. Frequencies of MM, MV, and VV genotypes were in the Hardy–Weinberg equilibrium (data not shown).

Haplotype Analysis

Haplotypes consisting of the three loci were estimated by PHASE v2.1 (Table IV). Three major haplotypes including two TG12-containing haplotypes accounted for more than 90% in the Vietnamese and the Japanese populations. Especially, "T7-TG12-M470" was a predominant haplotype in the Vietnamese. In Caucasians, two major haplotypes, "T7-TG11-V470" and "T7-TG10-M470," accounted for 73%.

T5-bearing haplotypes were further analyzed in the Vietnamese population. Among four haplotypes containing the T5 allele, "T5-TG12-V470" was most common (78.4%) in the Vietnamese (Table V). Majority of the T5 allele were associated with the TG12 or the TG13 alleles. In contrast, T5 was mainly associated with the TG11 allele in Caucasians [Groman et al., 2004]. However, the sample size of the Japanese and Caucasians in our study was too small to estimate the proportion of T5-containing haplotypes.

TABLE II. Allele Frequencies of TG-Repeat Polymorphisms

Ethnic groups	Number (frequency) of individuals with alleles of TG repeats			
	TG10	TG11	TG12	TG13
Vietnamese (2n = 990)	6 (0.006)	406 (0.410)	557 (0.563)	21 (0.021)
Japanese (2n = 100)	0 (0.00)	54 (0.54)	46 (0.46)	0 (0.00)
Caucasians (2n = 100)	25 (0.25)	67 (0.67)	8 (0.08)	0 (0.00)

Four alleles TG10, TG11, TG12, and TG13 depend on the number of tandem TG repeats adjacent to the poly-T tract in intron 8 of the *CFTR* gene.

TABLE III. Genotypes and Allele Frequencies at the M470V Polymorphic Site

Ethnic groups	Number (frequency) of individuals with genotypes			Number (frequency) of individuals with alleles	
	MM	MV	VV	M	V
Vietnamese (2n = 990)	106 (0.214)	250 (0.505)	139 (0.281)	462 (0.467)	528 (0.533)
Japanese (2n = 100)	8 (0.16)	19 (0.38)	23 (0.46)	35 (0.350)	65 (0.650)
Caucasians (2n = 100)	9 (0.18)	22 (0.44)	19 (0.38)	40 (0.400)	60 (0.600)

M470V is a non-synonymous single nucleotide polymorphism in exon 10 of the *CFTR* gene.

We further computed genetic distance among the three ethnic populations using allelic distribution of these three loci. A parameter showing genetic distance, Fst between the Vietnamese and the Japanese was 0.046, whereas Fst between the Vietnamese and Caucasians was 0.179. We also evaluated strength of linkage disequilibrium for all pairs of loci applying the likelihood ratio test. A pair of poly-T and TG repeats and a pair of TG repeats and M470V showed the presence of linkage disequilibrium ($P = 0.03$ and $P < 0.00001$, respectively), whereas poly-T and M470V did not ($P = 0.49$).

DISCUSSION

The present study is the first comprehensive report on the functional polymorphisms of *CFTR* in the Vietnamese population. Considering the genetic data on the Japanese and Koreans [Lee et al., 2003; Fujiki et al., 2004] and an apparently low CF prevalence in Vietnam, we first thought that the delta F508 mutation must be very rare in the Vietnamese. In fact, it was not found among 990 alleles tested. In Caucasians, such a mutation is strongly associated with the T9-M470 haplotype [Cuppens et al., 1994], but in the Vietnamese, the same haplotype was rarely found.

The frequency of the T5 allele in the Vietnamese was 3.7%, which was similar to 3%–7% in Caucasians reported by us and others [Chillón et al., 1995; Tzetis et al., 2001], but higher than those in other Asian populations including the Japanese population (0.7%) and Koreans (1.7%) [Lee et al., 2003; Fujiki et al., 2004]. The T6 allele has not been reported in Caucasians and may be widely distributed in Asia including Koreans [Lee et al., 2003] and Japanese [Fujiki et al., 2004], although it is also rare. Homozygotes for the T5 alleles are known to produce non-functional exon 9-*CFTR* mRNA and thus reduce the amount of normal CFTR protein to less than 10% [Chu et al., 1993]. It has been suggested that homozygotes or heterozygotes for the T5 alleles and another mutant allele of *CFTR* are associated with CF or CF-related diseases [Chu et al., 1993; Chillón et al., 1995; Pignatti et al., 1996; Cuppens et al., 1998; Noone et al., 2000; Casals et al., 2004; Wu et al., 2004]. In our study, 37 individuals who had the T5 allele were all heterozygotes and never showed any clear bronchiectasis on chest X-ray films.

TABLE IV. Estimated Frequencies of Three-Locus Haplotypes

Haplotype	Frequency		
	Vietnamese	Japanese	Caucasians
T7-TG12-M470	**0.424**	**0.34**	0.06
T7-TG11-V470	**0.391**	**0.53**	**0.54**
T7-TG12-V470	**0.108**	**0.11**	0.01
T5-TG12-V470	0.029	0.01	0
T7-TG11-M470	0.017	0	0.04
T7-TG13-M470	0.012	0	0
T5-TG13-M470	0.006	0	0
T9-TG10-M470	0.004	0	0.03
T7-TG13-V470	0.002	0	0
T5-TG11-V470	0.001	0	0.01
T5-TG13-V470	0.001	0	0
T7-TG10-M470	0.001	0	**0.19**
T9-TG10-V470	0.001	0	0.02
T9-TG11-M470	0.001	0.01	0.02
T5-TG11-M470	0	0	0.05
T7-TG10-V470	0	0	0.02
T5-TG12-V470	0	0	0.009
Others[a]	0.002	0	0

Predominant haplotypes accounting for more than 10% of each ethnic population are depicted in bold letters.
[a]Haplotypes with frequencies lower than 0.001 are combined.

The Vietnamese population had strikingly high frequency (56.3%) of the TG12 allele. This was even higher than 46%–48% among the Japanese reported by us and others [Fujiki et al., 2004]. In Caucasians, the TG10 allele was predominant and the frequency of the TG12 allele was only 1%–8% as reported by us and others [Ruiz et al., 1999; Tzetis et al., 2001]. Together with the T5 allele, longer TG repeats are known to suppress normal splicing and to increase the proportion of non-functional exon 9-transcripts [Chu et al., 1993; Cuppens et al., 1998]. In South-Asian countries, where infectious diarrhoeal diseases are the major causes of mortality in children, it is plausible that decreased production of intact CFTR protein due to longer TG repeats minimizes fluid loss and helps survival from diarrhoeal diseases. Electrolyte loss due to increased sweat fluid in warm and humid Asian countries could also be involved [Fujiki et al., 2004].

The M470V polymorphisms also appear to affect chloride channel activity; V470 CFTR proteins had a lower activity than M470 [Cuppens et al., 1998]. The frequency of the V470 allele was 53.8% among the Vietnamese, which is comparable to those among the Japanese (60%–65%) [Fujiki et al., 2004] and Caucasians (36%–64%) [Ruiz et al., 1999; Tzetis et al., 2001].

We found three major haplotypes, T7-TG12-M470, T7-TG11-V470, and T7-TG12-V470, in both the Vietnamese and the Japanese populations, although some differences in frequency were observed. The two major TG12-bearing haplotypes in these Asian populations may correspond to low CFTR activity as discussed earlier. In Caucasians, two haplotypes, T7-TG11-V470 and T7-TG10-M470, were predominant from our data and others [Ruiz et al., 1999]. Linkage disequilibrium was obvious between the TG repeat and the M470V loci, whereas it was not found between the poly-T tract and M470V, presumably because the M470 and V470 alleles were equally distributed in combination with the major T7 allele in the populations tested. A parameter showing genetic distance, Fst between the Vietnamese and the Japanese was much lower than the value between the Vietnamese and Caucasians, which corresponded to the similarity and difference of the major haplotypes observed in the three populations. These findings indicate that the genetic distance between the two Asian populations was much shorter than that between Asians and Caucasians.

Considering the size of population of Vietnam, we made a rough estimate that 113 thousand individuals are homozygous

TABLE V. Estimated Frequency of T5-Containing Haplotypes

Three locus haplotypes	Number of haplotypes in the Vietnamese	Two locus haplotypes	Number (frequency) of haplotypes	
			Vietnamese	Caucasians[a]
T5-TG11-M470	0	T5-TG11	1 (0.03)	83 (0.77)
T5-TG11-V470	1			
T5-TG12-M470	0	T5-TG12	29 (0.78)	23 (0.21)
T5-TG12-V470	29			
T5-TG13-M470	6	T5-TG13	7 (0.19)	2 (0.02)
T5-TG13-V470	1			

[a]The relative frequencies of T5 and TG combinations were estimated among 1,269 DNA samples from United States, Czech Republic, Poland, Italy, and Germany [Groman et al., 2004].

for the T5 allele. The most frequent T5-containing haplotypes in the Vietnamese was "T5-TG12-V470," accounting for 78.4% of all T5-bearing haplotypes. A combination of the T5 allele with TG12 or TG13 alleles is known to further increase the proportion of non-functional exon 9-transcripts [Chu et al., 1993; Chillón et al., 1995; Cuppens et al., 1998]. The haplotype T5-TG13 occupied 18.9% of the Vietnamese, but it was not found in Caucasians of this study and only 2% in a previous report [Groman et al., 2004]. Thus, Vietnamese T5 may have a strong effect on the reduction of normal CFTR protein, even if the allele frequency of T5 is similar. Although detailed information was not available, we found a 40-year-old man without children among 29 samples having a T5-TG12-V470 genetic background.

In conclusion, this is the first large-scale *CFTR* analysis of functional polymorphisms in the Vietnamese population. We found that there are marked differences among frequencies of three-locus haplotypes consisting of poly-T, TG-repeats, and M470V polymorphisms of *CFTR* compared with Caucasian populations. Long TG repeats may be a characteristic of Asian populations. Significance of the potentially pathogenic T5 allele with greater number of TG-repeats should be investigated in the future.

ACKNOWLEDGMENTS

The authors thank Dr. Nguyen Le Hang, Pham Thi Phuong Thuy, and Nguyen Thi Thu Ha for their help in the management and coordination of this study in Vietnam. The authors also thank Kazuko Tanabe for her critical reading of this manuscript and Izumi Matsumoto for her excellent technical support. Mai Hai Nam is a JICA long-term training participant.

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J Mol Hist (2005) 36:77–87

The cell cycle associated protein, HTm4, is expressed in differentiating cells of the hematopoietic and central nervous system in mice

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Received 23 July 2004 and in revised form 15 September 2004

Summary

HTm4 is a member of a newly defined family of human and murine proteins, the MS4 (membrane-spanning four) protein group, which has a distinctive four-transmembrane structure. MS4 protein functions include roles as cell surface signaling receptors and intracellular adapter proteins. We have previously demonstrated that HTm4 regulates the function of the KAP phosphatase, a key regulator of cell cycle progression. In humans, the expression of HTm4 is largely restricted to cells of the hematopoietic lineage, possibly reflecting a causal role for this molecule in differentiation/proliferation of hematopoietic lineage cells. In this study, we show that, like the human homologue, murine HTm4 is also predominantly a hematopoietic protein with distinctive expression patterns in developing murine embryos and in adult animals. In addition, we observed that murine HTm4 is highly expressed in the developing and adult murine nervous system, suggesting a previously unrecognized role in central and peripheral nervous system development.

Introduction

HTm4 is a member of a newly defined, extensive family of human and murine proteins. Each member of the MS4 (membrane-spanning four) protein group has a distinctive four-transmembrane structure. To date, few members of this family are well understood, but a diverse functionality is beginning to emerge. These functions include roles as cell surface signaling receptors and intracellular adapter proteins (Hulett *et al.* 2001, Ishibashi *et al.* 2001, Liang *et al.* 2001, Liang & Tedder, 2001, Barnhill *et al.* 2004). We demonstrated that HTm4 is an adapter molecule that regulates the function of the KAP phosphatase, a key regulator of cell cycle progression (Donato *et al.* 2002). HTm4, in humans, is a 214 amino acid protein whose expression is largely restricted to both mature and precursor cells of the hematopoietic lineage, which may reflect a causal role in driving the differentiation/proliferation of hematopoietic lineage-specific cells (Adra *et al.* 1994, 1999, Donato *et al.* 2002, Nakajima *et al.* 2004).

A second important feature of the biology of human *HTm4* is its genetic localization. Human *HTm4* maps to chromosome 11q13.1 (Adra *et al.* 1994), in close

**JLK and XY contributed equally to this work.

proximity to the FcεRI antigen receptor beta chain gene (Ra *et al.* 1989, Ravetch & Kinet 1991) and the gene for CD20 (Tedder *et al.* 1988), both of which are MS4 family members. The 11q13.1 region is linked significantly to human atopic phenotypes (Collee *et al.* 1993, Shirakawa *et al.* 1994, van Herwerden *et al.* 1995, Folster-Holst *et al.* 1998, Adra *et al.* 1999). Specifically, TaqI restriction fragment length polymorphism (RFLP) in the 3rd intron of the human *HTm4* showed a strong association with atopic asthma. This variant showed similar odds ratios to that of intron 2 of the FcεRIβ gene in severe asthma, as well as in severe atopy phenotypes. Interestingly, we found that HTm4 is highly expressed in basophils at both the mRNA and protein levels (Nakajima *et al.* 2004); hence, human *HTm4* is considered an atopy gene candidate on locus 11q13.1 (Adra *et al.* 1999).

In this report, we present data on the genetic sequence, genomic organization, protein structure prediction, biochemistry and tissue expression pattern of the murine HTm4 homologue. Our data show that, like the human homologue, murine HTm4 is also predominantly a hematopoietic protein with distinctive expression patterns in developing murine embryos and adults. We also report the unexpected finding that murine HTm4 is expressed in the developing murine nervous system. Moreover, we demonstrate that the functional interaction with the KAP phosphatase, previously demonstrated by our group in human cells, is also present in the murine system. Our work suggests a conservation of structure and function for HTm4 between the mouse and human systems.

Materials and methods

Cloning of murine HTm4 cDNA

Rapid Amplification of cDNA Ends (RACE)-PCR was used for the cloning of murine *HTm4* cDNA. Marathon-Ready BALB/c mouse spleen cDNA library (Clontech Laboratories Inc, Palo Alto, CA) was used as the template. Two gene specific primers were derived from a single EST sequence that was highly homologous to human *HTm4*. A gene specific antisense primer, 5′-CAT TCG TGT GGG GTT TCT CCT GC-3′, was paired with the 5′ primer supplied by the manufacturer to generate PCR product that would cover the 5′ end region of cDNA of interest, murine *HTm4*. In the same manner, a gene specific sense primer, 5′-GTT TAC AAC ACG TGT CCC ACC ACT TCA G-3′, was used to generate PCR product that would cover the 3′ end region of murine *HTm4* cDNA, when paired with the 3′ primer from the manufacturer. PCR products from both experiments were sequenced and compared. The longest contiguous murine *HTm4* cDNA sequence was generated through the merging of largest 5′ and 3′ PCR fragments at the overlapping region that was flanked by the aforementioned gene specific primers. Based on this sequence, a pair of murine *HTm4* specific primers was generated for the procurement of a full-length cDNA. The sequences for this pair of primers were 5′-CAA AGA AGA GAT TCG TTA AGC CTG AGG-3′, the sense primer, and 5′-CGC CTA AGG AAA TAT ATT TAT TCA TCC AGA TC-3′, the antisense primer. The final full-length murine *HTm4* cDNA was cloned into the pGEM-T vector (Promega, Madison, WI) and analyzed by DNA sequencing.

Cloning and sequencing of the murine HTm4 genomic sequence

A BAC genomic library of murine 129/SvJ DNA (Genome Systems Inc., St. Louis, MO) was screened by PCR using primers designed for the 5′ and 3′ ends of the gene. The positive clone was isolated, and its DNA purified, restricted and sub-cloned in the pBluescript vector (Stratagene, CA). The mouse genomic DNA insert (accession number: AY258288) was sequenced by direct BAC sequencing and also by sequencing the sub-clones using the BigDye Terminator Cycle Sequencing Kit and ABI prism-377 DNA sequencer (PE Applied Biosystems, Foster City, CA).

Murine HTm4 protein modeling

Murine HTm4 protein modeling was predicted and compared to human HTm4 by program 'SOSUI' (http://sosui.proteome.bio.tuat.ac.jp/sosuiframe0.html) which was made for prediction of existence of transmembrane helices and determination of transmembrane helical regions in the proteins based on physicochemical properties of amino acid sequences such as hydrophobicity and charges. A 'primary' transmembrane helix is composed of the highly hydrophobic and successive region of the AA sequence by a hydropathy profile based on the Kyte–Doolittle hydropathy index (Kyte & Doolittle 1982), while a 'secondary' transmembrane helix is composed of less hydrophobic and some polar AA sequences of which parameters are calculated with amphiphilicity index of polar amino acids (Mitaku *et al.* 1995).

Generation of a polyclonal antiserum directed against murine HTm4

A peptide derived from the amino-terminus of murine HTm4 (amino acids 4–19: EETGGSVYQPLDESRH) was coupled to keyhole limpet hemocyanin and used to generate a rabbit polyclonal antiserum. We produced amino- and carboxyl-terminal fusion proteins (aa 4–19 and aa 197–213) of murine HTm4 with the GST protein using pGEX6P1 vector (Amersham

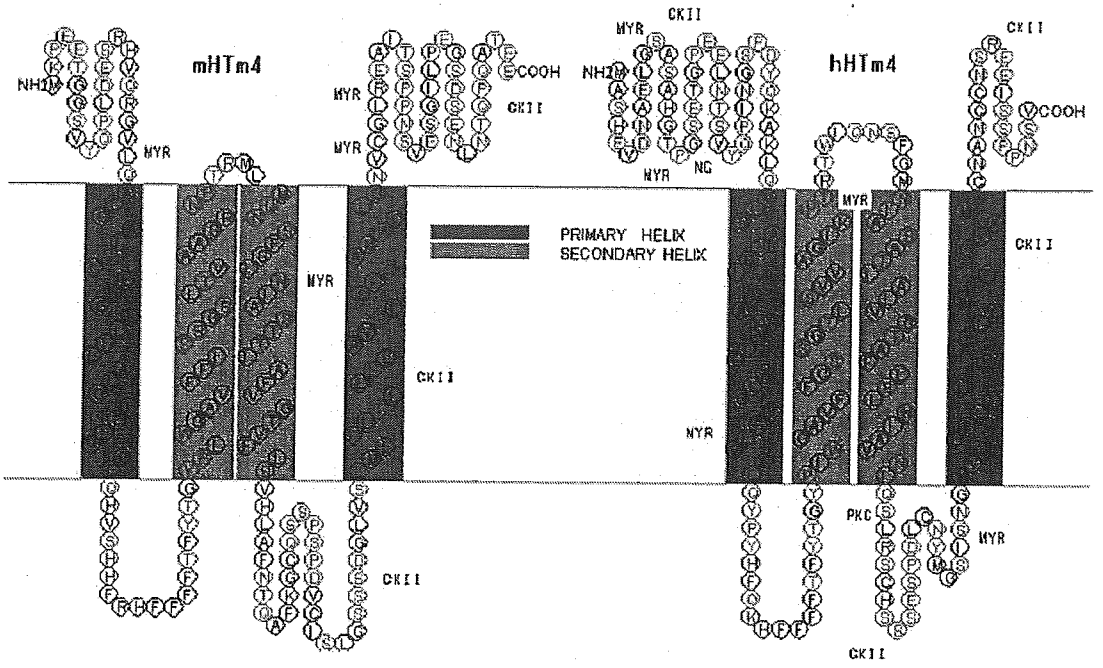

Figure 1. Comparison of the predicted model of murine HTm4 and human HTm4 proteins. The predicted murine (m)HTm4 (left panel) and human (h)HTm4 (right panel) protein structures were compared. Each figure shows topology with AA sequence from outer to inner side through membrane portion. Two outside loops are predicted for each protein as 'primary' transmembrane helixes (dark green loops), while two inside loops are predicated as 'secondary' transmembrane helixes (light green loops).

Pharmacia Biotech, Piscataway, NJ) in order to screen the reactivity of these antibodies. Affinity purification was performed by standard methods using the immunizing peptide.

Immunoprecipitation and western blotting

Samples consisted of either 5 µg murine HTm4 GST fusion proteins, or 20 µg proteins derived from BALB/c mouse spleen cells lysed in a standard SDS buffer. Protein samples were boiled for 8 min before loading. Cells were pelleted in a microcentrifuge (2000*g*, 2 min) and washed once in 1 ml ice cold phosphate buffered saline to remove serum proteins. 10^7 cells were lysed on ice for 30 min in 350 µl of the following buffer: 50 mM HEPES pH 7.4, 75 mM NaCl, 20 mM NaF, 10 mM iodoacetamide, 0.5% (w/v) Triton X-100, 1 mM phenlymethylsulfonyl fluoride (PMSF), 500 mg/ml Aprotinin, 1.0 mg/ml Leupeptin and 2.0 mg/ml Chymostatin. Lysates were clarified by microcentrifugation (10,000*g*, 5 min). Supernatants were transferred to clean tubes and either mixed with 1.4 volumes acetone and placed at −20 °C for 1 h (to pellet total protein) or tumbled at 4 °C for 2 h with the indicated antibody. Acetone precipitates were harvested by centrifugation at 10,000*g* for 5 min. Immunocomplexes were captured using 15 µl/tube Protein G-sepharose beads and washed using two rounds of microcentrifugation and re-suspension in 1 ml lysis buffer. Beads and protein pellets were dried by aspiration and then incubated at 95 °C for 8 min in a reducing SDS polyacrylamide gel electrophoresis (PAGE) loading buffer. After 10% SDS–PAGE, the resolved proteins were transferred to PVDF membrane by electroblotting and the membrane was blocked for 1 h using 5% BSA bovine serum albumin (Figure 3B) or 5% non-fat milk (Figure 5) in PBS pH 7.0. The membrane was then probed for either 2 h at RT (Figure 3B) using 1:1000 dilution of murine HTm4 antiserum, or 16 h at 4°C (Figure 5) using 1:2000 dilution monoclonal anti-KAP (BD Pharmingen, San Diego, CA.). After extensive washing (4 × 5 min in PBS/0.5% Tween-20) a developing antibody was applied (1 h at RT, 1:10,000 dilution of donkey anti-rabbit (Amersham, Piscataway, NJ) or sheep anti-mouse (Amersham, Piscataway, NJ) IgG coupled to HRP). After further washing bands were visualized using ECL according to the manufacturer's instructions (Amersham, Piscataway, NJ).

Northern blotting procedures

Northern blot filters of Poly (A)+ RNA from normal mouse tissues were purchased from BD Biosciences, CLONTECH, Palo Alto, CA. The filters were probed with 32p-labelled full-length murine cDNA according to the published protocols (Adra *et al.* 1994, 1997). The blots have been normalized to beta-actin by the manufacturer.

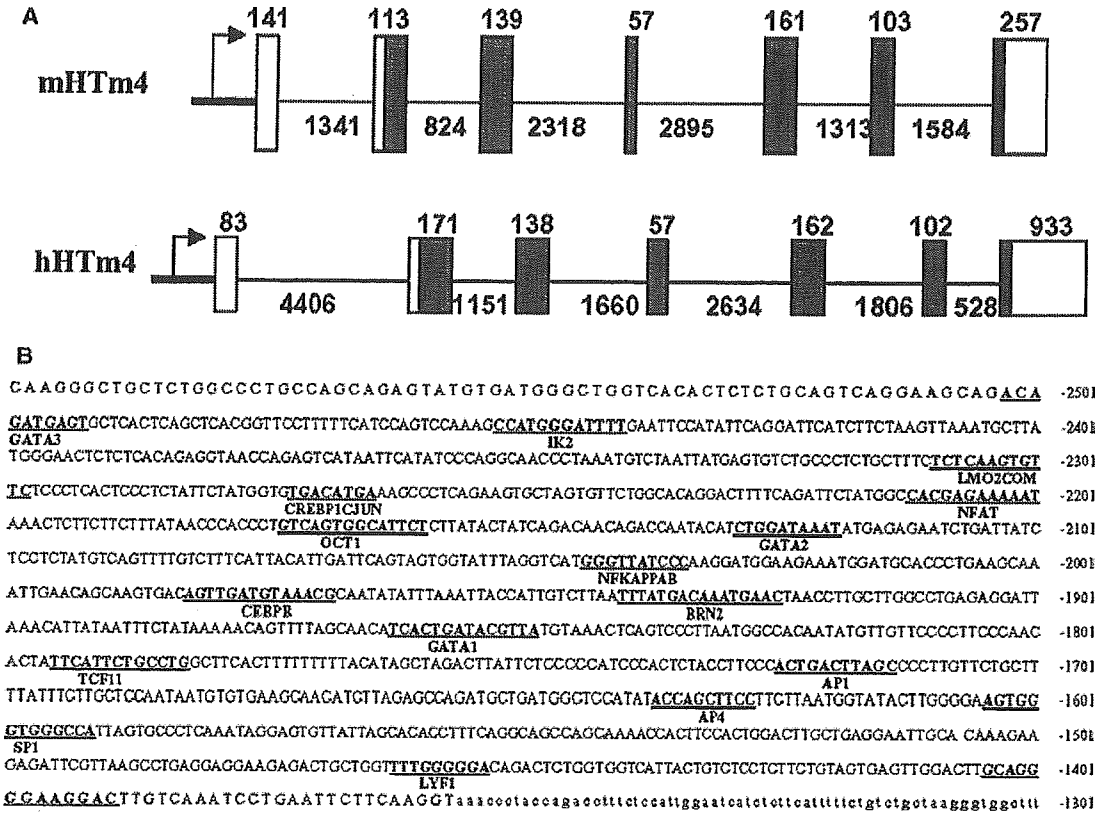

Figure 2. Structure and 5′ nucleotide sequence of the murine HTm4 gene. (A) Comparison of the complete gene structure of mouse HTm4 and human HTm4. Exons are shown as boxes and introns are connecting lines. The coding region is shaded. Exon and intron lengths are marked. Arrows are used to indicate the direction of transcription. (B) 5′nucleotide sequence of the murine HTm4 gene.
Accession number is AY258288. Sequence analysis started up to 1 kb upstream from the ATG (+1). The potential transcription factor binding sites were searched using MatInspector V2.2 (http://transfac.gbf.de/cgi-bin/matSearch/matsearch.pl) (Quandt *et al.* 1995) and are shown in boldface and underlined.

Immunohistochemical studies for murine HTm4

All staining was performed by standard immunoperoxidase methods. Briefly, either embryonic murine tissue slides from day 8-day 16 or adult murine BALB/c tissue (Novagen, Madison, WI) were deparaffinized and pre-treated in 10 mM sodium citrate, pH 6.0 using a pressure cooker system (Decloaking chamber, Biocare Medical, Walnut Creek, CA as per manufacturer's instructions). All further steps were performed at room temperature in a hydrated chamber. Slides were pre-treated with Peroxidase Block (DAKO, Carpinteria, CA) for 5 min to quench endogenous peroxidase activity, and a 1:5 dilution of goat serum in 50 mM Tris-Cl, pH 7.4, for 20 min to block non-specific binding sites. Affinity purified rabbit anti-murine HTm4 antibody (1:100 dilution in 50 mM Tris–Cl, pH 7.4 with 3% goat serum) was applied at room temperature for 1 h. After washing in 50 mM Tris–Cl, pH 7.4, secondary goat anti-rabbit horseradish peroxidase-conjugated antibody (Envision detection kit, DAKO, Carpinteria, CA) was applied for 30 min. After further washing, immunoperoxidase staining was developed using a DAB chromogen kit (DAKO, Carpinteria, CA), per manufacturer's instruction, and counterstained with hematoxylin. To assure specificity, murine HTm4 antibody was pre-incubated with the immunizing peptide in most experiments and applied to identical tissues, revealing complete blocking of staining.

Bone marrow cell preparation for flow cytometry analysis

C57/BL6 mice were used. Either femurs or tibias were harvested from mice without exsanguinations following cervical dislocation. The bone marrow contents were flushed with 4 °C PBS using a 26G hypodermic needle, thoroughly resuspended by gentle pipetting several times, and filtered through 30-μm-nylon mesh to remove remaining particulate material. Bone marrow cells were then washed twice with PBS buffer, pelleted by centrifugation at 1000 rpm for 10 min at 4 °C, resuspended, and counted. Cells were permeabilized with the Fix & Cell Permeabilization Kit, as described

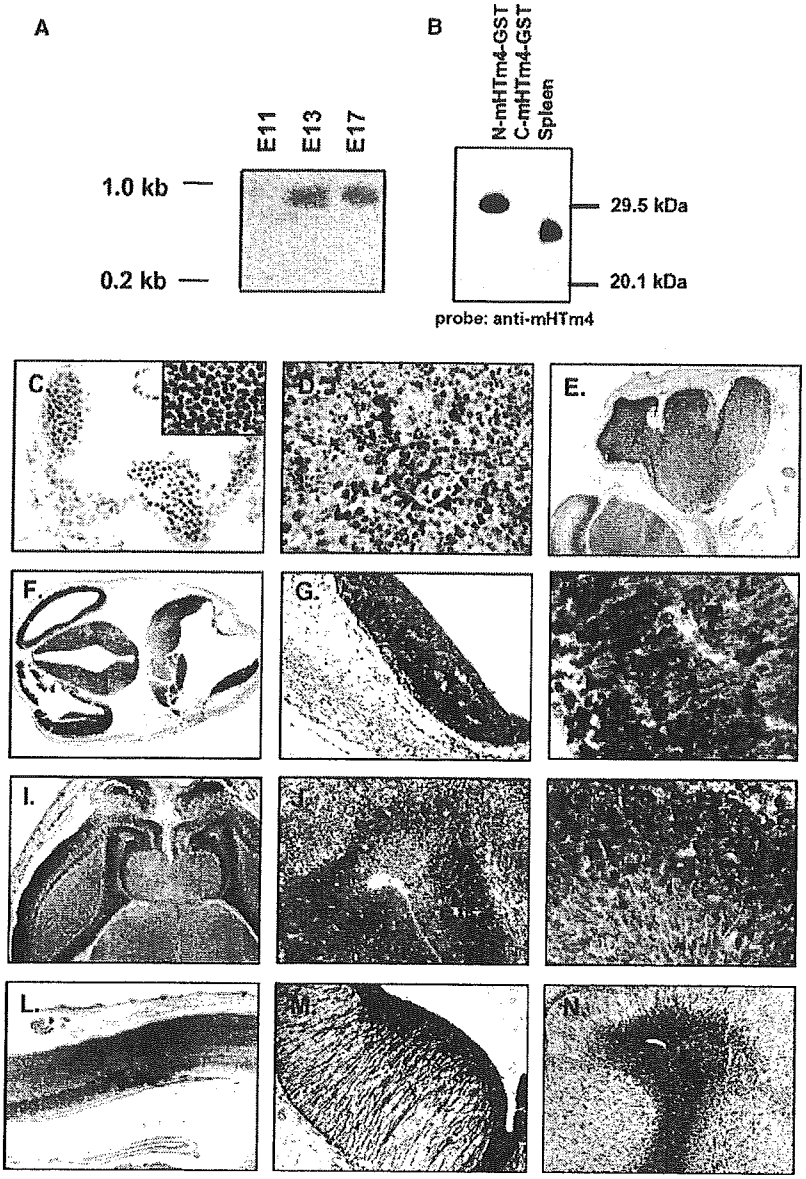

Figure 3. Murine HTm4 expression patterns in the embryonic mouse. (A) Northern blot analysis of HTm4 transcription during mouse embryogenesis. Poly A^+ RNA (approximately 2 μg/lane) was prepared from mouse embryos at the indicated stage of development (The Northern membrane was probed as described in Methods to detect the 1.0 kb HTm4 transcripts, which are detectable by this technique after day E11. This commercial blot has been normalized to beta-actin by the manufacturer (BD Biosciences, CLONTECH, Palo Alto, CA). (B) Validation of anti-murine HTm4 antibody by specific western blot. Polyclonal anti-murine HTm4 was generated against N-terminal amino acids 4-19 in rabbit as described in Methods. Protein samples corresponding to 5 μg/lane GST fusion proteins of either the amino- or carboxyl-terminal cytoplasmic tails of murine HTm4 (N-murine HTm4-GST, C-murine HTm4-GST), or total lysate from $1x10^6$ murine spleen cells, were resolved by 10% SDS–PAGE. After electrotransfer to PVDF membrane, western analysis was performed with 1 μg/ml anti-murine HTm4. Note the presence of approximately 25 kDa band in murine spleen and immunoreactivity for only the N-murine HTm4-GST fusion protein, which contains the immunogenic peptide. (C–N) Immunohistochemisty for murine HTm4 in embryonic murine hematopoietic and neural tissues. Representative sections of formalin-fixed paraffin embedded embryonic (E) murine tissues were stained with anti-murine HTm4 antibody. Positive staining (DAB chromogen with hematoxylin counterstain) was restricted to either developing hematopoietic cells within the blood islands (C; E8; 400× original magnification; inset 1000×) and liver (D; E14; 400× original magnification), or neural derived cells within the developing brain (E for E15, sagittal section, 40× original magnification; F–H for E12, cross-section, 20×, 100×, or 400× original magnifications, respectively; and I–K for E16, cross section, 20×, 100×, or 400× original magnifications, respectively). Strong expression of murine HTm4 was also detected within the spinal cord and dorsal and ventral ganglia starting at E14 (L; representative E15 embryo, 40× original magnification). Nestin staining is shown in panel M (E12, 40× original magnification) and panel N (E16 original magnification, 100×). Note the distinct patterns of murine HTm4 and nestin expression (panel G versus M for E12 and panel H versus N for E16) indicating diminished murine HTm4 protein expression in the more primitive periventricular cells of the developing brain compared to nestin.

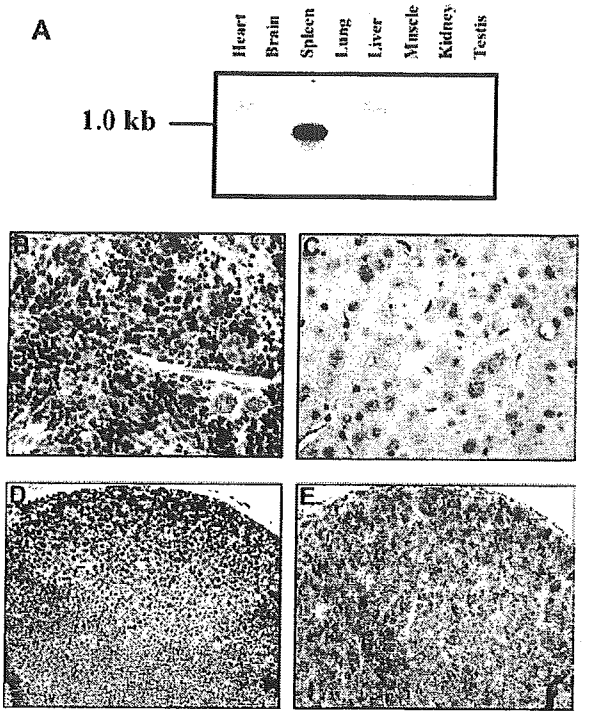

Figure 4. Murine HTm4 expression patterns in the adult mouse. (A) Northern analysis of HTm4 transcript distribution in adult mouse. Adult mouse multiple tissue Northern blot was probed with 32P labeled full length HTm4 cDNA. Of the tissue RNA extracts present on this membrane, only the spleen sample displayed significant hybridization. Visualized band corresponds to the approximately 1 kb murine HTm4 transcript. This commercial blot has been normalized to beta-actin by the manufacturer (BD Biosciences, CLONTECH, Palo Alto, CA). (B–E). Immunohistohemical staining of adult murine spleen, brain and lymph node for murine HTm4. Representative sections of formalin-fixed paraffin embedded adult murine spleen, lymph node, or brain were stained with anti-murine HTm4 antibody as described in Methods. Positive cytoplasmic staining of cells (DAB chromogen with hematoxylin counterstain) was restricted to either hematopoietic cells within the red pulp of the spleen (B; 400× original magnification) or neurons of the cerebral cortex of the adult murine brain (C; 400× original magnification). Germinal center B-lymphocytes within secondary lymphoid follicles also express murine HTm4 (D; 200× original magnification). The pattern of expression is identical to that of the murine HTm4 interacting protein KAP (E; 200× original magnification). (F) Flow cytometric analysis of HTm4 expression in cell populations derived from adult murine bone marrow. Mouse bone marrow cells were isolated as described in Methods. Aliquots of cells were co-stained with either control rabbit IgG or anti-murine HTm4 and antibodies to specific surface markers for various bone marrow subpopulations. Cell-type specific co-stains were as follows: B-lymphocytes (CD19), T-lymphocytes (CD3), monocytes (CD11b), nucleated red blood cells (Ter119), and granulocytes (GR-1).

by the manufacturer (Caltag Laboratories Inc., Burlingame, CA, USA). Cells were labeled with 2 μg/ml of polyclonal anti-murine HTm4 for 20 min, followed by the incubation with anti-rabbit IgG-FITC (Fab) (Caltag, Burlingame, CA), along with CD19-PE (BD Pharmingen, San Diego, CA), CD3-PE (BD Pharmingen), Ter119 (BD Pharmingen), Gr1-PE (BD Pharmingen) and CD11b-PE (Caltag). The flow cytometry analyses were performed on a FACScan flow cytometer (Becton Dickinson Immunocytometry Systems, San Diego, CA). In the control group, bone marrow cells were labeled with 2 μg/ml of Rabbit IgG (Sigma, St. Louis, MO) for 20 min, followed by the incubation with anti-rabbit IgG-FITC (Fab) (Caltag).

Results

cDNA, genomic and protein sequence of murine HTm4

Our database analysis identified a murine expressed sequence tag (EST) that was highly homologous to the human *HTm4* cDNA sequence. This enabled the design of a specific PCR primer that was used to isolate a clone from a murine cDNA library. After several rounds of RACE-PCR and DNA sequence analysis, we obtained a single contiguous cDNA corresponding to murine *HTm4*. The cDNA and translated protein sequence of murine HTm4 was deposited in Gene Bank (accession number AY184359).

Murine HTm4 is a 213 amino acid protein with a predicted molecular weight of approximately 25 kDa. Proscan analysis reveals that murine HTm4 has no obvious enzymatic or protein–protein interaction domains, but does contain a single consensus sequence for *N*-glycosylation. Human HTm4 is similarly devoid of amino acid sequence clues to its functional role, and also contains a single *N*-glycosylation site and a PKC substrate motif.

We compared the protein sequences of murine HTm4 and human HTm4 using ClustalW alignment (Oxford Molecular and MacVector, Accelrys, San Diego, CA). Across the ~220 amino acid sequence, 119 identities (55%) and 27 functional similarities (12%) were found. Murine HTm4, like its human counterpart, has four putative transmembrane domains resulting in very similar predicted structures (Figure 1). Both murine HTm4 and human HTm4 proteins can be defined as members of the MS4A protein family, on the basis of their four-transmembrane structure and sequence homology. Murine HTm4 is designated MS4A3.

We have previously assigned the chromosomal location of human *HTm4* to 11q13.1 (Donato *et al.* 2002). Location of the murine gene for *HTm4* was assigned using genomic BLAST against the available mouse genome (NCBI BLAST facility). Probes were murine *HTm4* genomic sequence and human *HTm4* cDNA sequence, which gave identical results. Using this analysis, the murine *HTm4* gene was localized to chromosome 19A. We note that the murine *HTm4* gene is clustered in this location with the *MS4A2* gene, corresponding to the mouse *FcεRIβ* subunit and the gene for *MS4A6D*. This cluster is highly reminiscent of that

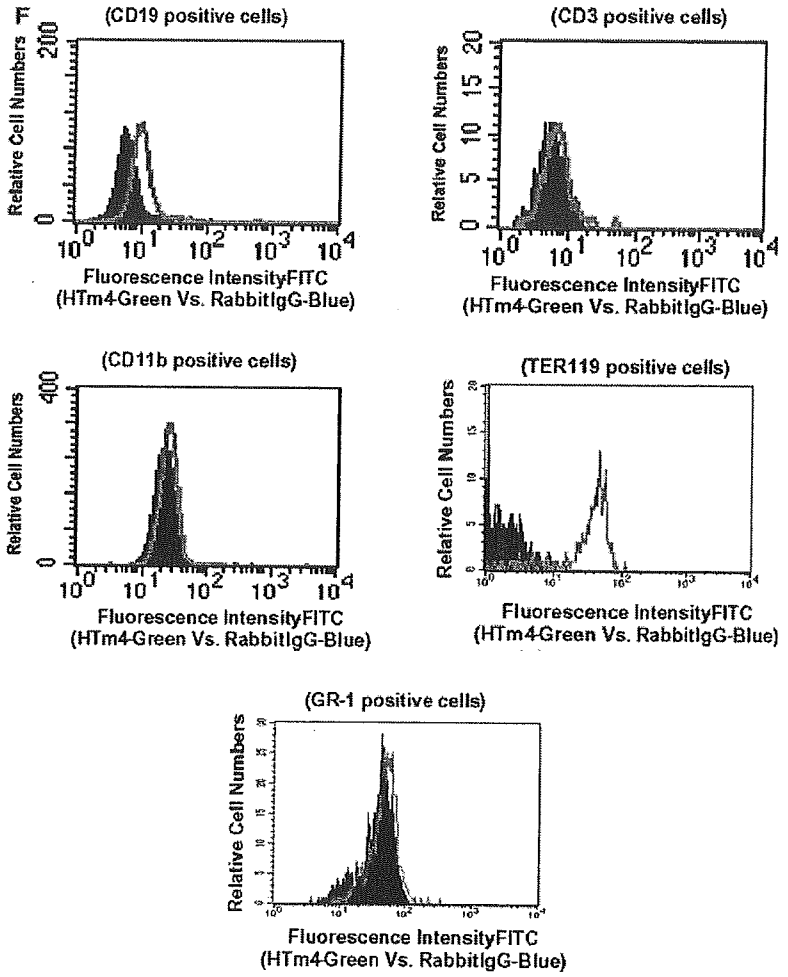

Figure 4. (Continued).

located in humans at chromosome 11q13.1, which has been linked to atopic/allergic disorders (Adra *et al.* 1999). Other members of the MS4A family are located at more distal locations also on the mouse chromosome 19, including *MS4A10, MS4A8 and MS4A7* (Ishibashi *et al.* 2001, Liang *et al.* 2001, Liang and Tedder, 2001).

Further analysis of the murine genomic sequence revealed that the murine *HTm4* gene has the same six-intron and seven-exon gene structure as the human HTm4 gene (Figure 2A). In addition, the full length of murine *HTm4* gene (Gene Bank accession number AY258288) spans approximately 11 kb, which is also comparable to the human *HTm4* gene (Adra et al., 1999). Sequence analysis up to 1 kb upstream from the ATG (Figure 2B) showed that the putative promoter region contains many potential binding sites for transcription factors that are involved in hematopoiesis, immune response and cell proliferation, such as AP1 (Mathas *et al.* 2002), CEBPB (Akira *et al.* 1990), IK1-2 (Georgopoulos *et al.* 1994) and GATA1-3 (Tsai *et al.* 1994, Pandolfi *et al.* 1995, McDevitt *et al.* 1997).

Murine HTm4 expression pattern in developing mouse embryos reveals restriction to hematopoietic and neural tissues

One of the most notable features of the human HTm4 protein is its relatively restricted tissue expression pattern. Current data suggest that human HTm4 is expressed, in adult tissues, in cells of the hematopoietic lineage. In our characterization of murine HTm4, we asked if this tissue specificity is also a feature of the mouse system. We first probed Northern blots for the presence of murine *HTm4* transcripts in RNA extracts from whole murine embryos at defined stages of development (Figure 3A). Sufficient levels of a ~1.0 kb murine HTm4 transcript are present for detection by at least day 13 and continue to be expressed at day 17. Northern analysis provides a valuable, but low-resolution, picture of the expression levels of a given transcript during development. In order to localize expression of murine HTm4 within specific tissuetypes, we performed immunohistochemistry on tissue from various embryonic stages. Initially, we validated the

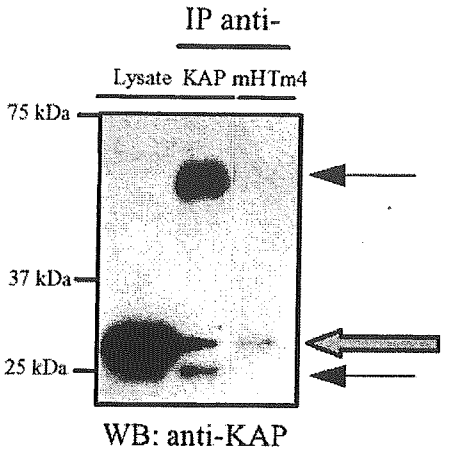

Figure 5. Co-immunoprecipitation of HTm4 and KAP proteins in murine leukocytes. P815 mouse mast cells (10^7 cells per lane) were lysed as described in Methods. Total protein precipitates (lysate) were produced by acetone precipitation or immunoprecipitation was performed using either 2 μg/lane anti-KAP (mouse monoclonal) or 11 μg/lane anti-murine HTm4 (rabbit polyclonal). Samples were resolved by 10% SDS-PAGE and visualized using anti-KAP western blot. KAP appears as a 32 kDa band in lysate from these cell (open arrow). KAP is also present in anti-KAP and anti-murine HTm4 immunocomplexes. Filled arrows mark presence of antibody heavy (55 kDa) and light (26 kDa) chains in immunoprecipitations using mouse anti-KAP and visualized with the same antibody.

specificity of our anti-murine HTm4 antibody raised against the N-terminal amino acids 4-19 via western blot. Figure 3B shows that our anti-murine HTm4 antibody specifically recognizes a 25-kDa protein from adult murine spleen cells (right lane). Importantly, anti-murine HTm4 also recognizes the amino-terminus of murine HTm4 when expressed as a glutathione *S*-transferase fusion protein (Figure 3B, left lane). A carboxy-terminal murine HTm4 fusion protein is not recognized (center lane). These data confirm the specificity of the antiserum for the amino-terminus of murine HTm4.

Immunohistochemical analysis was performed for murine HTm4 expression in formalin-fixed, paraffin-embedded day 8–16 embryonic murine tissues. As anticipated, hematopoietic expression was confirmed in murine development. We observed that from embryonic days (E) 8–10, murine HTm4 expression appears in small numbers of hematopoietic cells resident in blood islands and vessels (Figure 3C top left panel and inset). By E12–13, murine HTm4 expression is seen within the hematopoietic cells now resident in the liver, where mononuclear cells show positive staining (Figure 3D). Morphologically, these cells are compatible with both erythroid and myeloid precursors, with some staining also noted in megakaryocytes. At E14, expression persists in the liver hematopoietic cells and appears in splenic red pulp hematopoietic cells for the first time (data not shown). Staining was not present within non-germinal center B-cells of the spleen. Scattered cortical thymocyte staining was also noted, later in development (E15–16) (data not shown).

In addition to staining of murine embryonic hematopoietic cells, embryos from E8 through 16 stained with murine HTm4 show a developmental pattern of expression in the central nervous system (CNS) (Figure 3E–L). In general, murine HTm4 is expressed only in regions outside the ventricular zone, suggesting upregulation as cells begin to differentiate (Figure 3F–K). Specifically, at E8 and E9, the CNS is negative. By E10, however, expression is visible at the periphery of the neural tube (i.e., away from the ventricular zone neuropithelium) at all levels. Sagittal sections at E11–12 show expression that is somewhat stronger, particularly within the dorsal prosencephalon, mesencephalon, isthmal plate, cerebellar plate, and pontine plate, and along the ventral aspect of the spinal cord. Faint expression of murine HTm4 is noted in the trigeminal and paravertebral ganglia. At E12, faint expression appears in the anterior prosencephalon, and at E13, additional positivity is noted in the neocortex rostrally, the diencephalon ventral to the neuroepithelium, and along the peripheral (subpial) regions caudally, corresponding to dorsal and ventral gray matter columns. At this stage, the peripheral nerve roots are now faintly positive. At E14, sagittal sections demonstrate strong immunoreactivity in the ventral telencephalon and diencephalon, tegmentum of the mesencephalon, anterior and posterior pons, medulla, and ventral spinal cord, but absence of staining in the ventricular zone neuroepithelium. There is also staining in the peripheral nerves and paravertebral ganglia (Figure 3L). The tectum and the eye are negative. E15 sagittal sections show staining as in the E14 embryo, additionally with faint staining in the pretectum and dorsal root ganglia, and in the ganglion cell layer of the retina (Figure 3E). The ependyma of the fourth ventricle and the myenteric plexus of the gut are also positive. E16 sagittal sections additionally revealed staining in the olfactory bulb (a structure not identified in earlier age sections). To determine whether the HTm4-expressing cells were undifferentiated neural progenitor cells, serial sections were stained for nestin at E12 and E16 (Figure 3M and N). In these sections, nestin highlights ventricular zone neuroepithelial cells and radial (possibly glial) cell processes, but do not stain the presumed differentiating cells in the primitive neocortex and ventral diencephalon (at E12 and E16), the caudoputamen, anterior and posterior pontine nuclear groups, superior tectal neuroepithelium, superior central raphe and reticular formation of the midbrain and pons, or the subventricular zone (at E16) that are positive on HTm4 immunostaining (Figure 3F–K) Thus, an apparently non-overlapping pattern of expression is noted with these two antibodies. For all ages studied, appropriate negative controls (sections incubated with preimmune serum and/or

peptide, or with the secondary antibody only) showed no staining.

Murine HTm4 is expressed in cells of the hematopoietic lineage and brain in adult mouse

We analyzed the expression pattern of murine *HTm4* mRNA in adult animals using Northern blot. Assaying multiple tissues revealed that of the tissue RNA preparations probed in this experiment, only the spleen extract contained sufficient RNA for detection with the murine *HTm4* probe (Figure 4A). Transcript size of approximately 1 kb is consistent with the human *HTm4* mRNA. We also performed a dot blot analysis on adult mouse tissues and observed a similar degree of restriction in *HTm4* expression pattern (data not shown).

Immunohistochemical analysis of adult murine tissues yielded similar patterns to that seen in developing embryos. Strong cytoplasmic staining for murine HTm4 was noted within maturing hematopoietic cells of the spleen (Figure 4B) and in lymphoid cells (presumably B-lymphocytes) within germinal centers of lymphoid tissue of lymph nodes (Figure 4D) and Peyer's patches of the gut (not shown). As was previously demonstrated in human lymphoid tissue (Donato *et al.* 2002), murine HTm4 co-localized within germinal centers with mKAP protein (Figure 4E), a putative functional regulator of HTm4 activity. Additionally, in adult murine brain, murine HTm4 expression is identified in cells morphologically consistent with neurons in the hypothalamus, thalamus, cerebral cortex (Figure 4C), and, more faintly, in the hippocampus.

To further characterize the specific lineages of hematopoietic cells expressing murine HTm4, we isolated cells from murine bone marrow and spleen and assessed their expression of intracellular murine HTm4 by flow cytometry. Staining patterns from isolated hematopoietic cells were identical in both tissues. Representative data from bone marrow studies is shown in Figure 4F. Murine HTm4 expression was noted in Ter119 positive erythroid precursors and a smaller fraction of CD19-positive B-lymphocytes. Minimal murine HTm4 detection was observed in GR-1 positive granulocytic forms, CD11b-positive monocytic elements, or CD3 positive T-lymphocytes.

Association of murine HTm4 with the KAP phosphatase

In the human, we have proposed that HTm4 is involved in cell cycle regulation in hematopoietic cells, based on the association between HTm4 and the KAP phosphatase (Hannon *et al.* 1994, Poon & Hunter 1995) in human hematopoietic cells (Donato *et al.* 2002). In murine germinal centers, the cell populations that express murine HTm4 and KAP co-localize as assessed by immunohistochemical staining for these proteins (Figure 4D and E), raising the possibility that these proteins may be functionally associated. We asked if murine HTm4 is also physically associated with KAP. We identified a murine leukocytic line, P815, with expression of murine HTm4 and KAP. Co-immunoprecipitation using the P815 cell line demonstrates that immunocomplexes isolated using either anti-KAP or anti-murine HTm4 antibodies contain KAP protein (Figure 5). These data indicate that in the murine system, as in human cells, murine HTm4 and KAP form a physiological complex.

Discussion

In this study, we asked whether the cell cycle-associated protein HTm4, previously characterized by us in the adult human (Adra *et al.* 1994; Adra *et al.* 1999, Donato *et al.* 2002; Nakajima *et al.* 2004), shared similar structural, biochemical and functional features, in the developing and adult mouse. To that end, we undertook the cloning, genomic organization, and expression analysis of murine HTm4, and demonstrated its interaction with a protein known to interact with the human homologue of HTm4.

In our previous work, we cloned the human *HTm4* gene and assigned two key features to the protein. First, the expression of human HTm4 appears largely restricted to the hematopoietic cell lineages (Adra *et al.*, 1994). Second, a function for human HTm4 as an adapter protein that contributes to cell cycle progression was supported (Donato *et al.* 2002). Murine HTm4 is highly similar to human HTm4 at the DNA and amino acid level, and both proteins display a similar predicted four-transmembrane structure (Figure 1). Comparison to two reported HTm4 cDNA sequences (Hulett *et al.* 2001; Liang *et al.* 2001) revealed two amino acid sense variants (Ser162Ala and Ser211Thr). CLUSTAL alignment analysis and chromosomal grouping places murine *HTm4*, like human *HTm4*, in the MS4 protein superfamily (Hulett *et al.* 2001, Ishibashi *et al.* 2001, Liang *et al.* 2001, Liang & Tedder 2001). A similar genomic structure between the two genes is also identified with both genes containing a six-intron and seven-extron arrangement. Several promoter regions for transcription factors important for hematopoiesis, immune response and cell proliferation, such as AP1, CEBPB, IK1-2, and GATA1-3 are also identified. The presence of the GATA promoter regions is particularly interesting given the critical role of these transcription factors in erythopoiesis (Tsai *et al.* 1994, Pandolfi *et al.* 1995, McDevitt *et al.* 1997). The high level of expression of murine HTm4 in erythroid progenitors suggests GATA-regulated transcriptional regulation of HTm4 and a potential role for HTm4 in erythroid differentiation. Additionally, GATA-3 appears to be critical for neural development

as well (Pandolfi *et al.* 1995). Overall, we have found a high degree of conservation of structure and function of this gene and its protein across species, suggesting a fundamentally conserved biological function.

In addition to similarities at the genomic and protein level, the tissue expression pattern of murine HTm4 also has similarities to that seen in the human. Immunohistochemical techniques reveal expression of murine HTm4 within early hematopoietic cells of the blood islands starting at E8. Hematopoietic cell expression persists as hematopoiesis moves to the liver then spleen later in embryonic life. Immunohistochemical analysis of adult murine tissues confirms that murine HTm4 appears to continue to be largely hematopoietically restricted. Clusters of predominantly mononuclear cells present within the spleen react with antibody directed against murine HTm4. These cells morphologically appear most consistent with nucleated erythroid, myeloid and lymphoid elements. To confirm this morphologic impression and define more specifically the hematopoietic cell lineages expressing murine HTm4, multicolor flow cytometric analysis was performed on permeabilized, disaggregated spleen and bone marrow cells. These studies reveal that the majority of Ter119-expressing nucleated erythroid precursors display positive staining for murine HTm4. Very weak expression was noted within cells co-expressing the myeloid markers GR-1 and CD11b by flow cytometry. In addition, murine HTm4 co-expression was also noted in CD19-positive B-lymphocytes within the marrow. Further evidence for expression in the B-lymphoid population comes from the strong immunoreactivity for murine HTm4 antibody in germinal center B-cells in lymph nodes and Peyer's patches. The predominance of staining in germinal center cells as opposed to surrounding mantle or marginal zone cells suggests an upregulation of murine HTm4 during the germinal center reaction. Minimal staining was seen in the T-lymphoid cell population by immunohistochemistry or flow cytometry.

In contrast to previous human studies in which analysis of expression was restricted to mature tissues, the current work includes extensive study of both embryonic and adult murine tissues. Examination of the developing mouse has expanded the tissue distribution of expression from being solely hematopoietic, as in adult human tissues, to include prominent expression in the developing and mature murine nervous system, a novel and unexpected finding. By E10, immunohistochemical staining can detect murine HTm4 expression within cells that are morphologically consistent with differentiating neuronal and glial cells of the developing central nervous system, and by E15–16, prominent expression is seen as well in the peripheral nervous system. Importantly, there is no overlap in the expression of murine HTm4, most highly expressed in more mature neuronal and glial cells, and nestin, a protein that is associated with primitive neural cells. The strong expression of murine HTm4, and non-overlapping pattern of expression with nestin, in the developing brain suggests a role of murine HTm4 in CNS development and neural cell differentiation. Once a site expresses HTm4, it appears to retain expression into adulthood. Further analysis of the specific role of murine HTm4 expression in CNS cells is needed. These data also suggest that a CNS-based phenotype, in addition to an effect on hematopoiesis, may be a feature of experimental murine HTm4 deficient mice.

Our previous work on human HTm4 has suggested that this is an intracellular protein. Unlike several other MS4 family members (Tedder *et al.* 1988, Ravetch & Kinet, 1991), HTm4 is not present on the cell surface, but rather resides in the perinuclear compartment within the ER/Golgi apparatus. We have shown that human HTm4 is part of a complex containing the KAP phosphatase (Donato *et al.* 2002). Immunoprecipitation studies and western blotting confirm a similar biochemical association between murine HTm4 and KAP protein in a murine leukocyte cell line, P815, suggesting that murine HTm4 plays a similar role in mouse and human leukocytes. Although we have already detected HTm4 expression in primary human mast cells, basophils, eosinophils (Adra *et al.* 1994, Nakajima *et al.* 2004), and also in murine P815, another group did not detect HTm4 mRNA in P815 by PCR (Hulett *et al.* 2001). This could be due to a very low copy number of mRNA that nevertheless corresponds to a very high level or protein. It is also possible that HTm4 mRNA may not have been detectable in their experiments. We have not yet been able to conduct similar studies on CNS cells that express murine HTm4, and thus we do not know if murine HTm4 in the embryonic CNS cells also physically interacts with KAP. Interestingly, preliminary data (not shown) using immunohistochemical staining suggest that murine HTm4 and KAP may co-localize in developing CNS, but proof of this interaction will require co-purification from dissociated embryonic CNS cells.

In summary, we have examined the distribution of murine HTm4 in murine tissues. Murine HTm4 distribution in adult mice closely resembles the highly restricted pattern seen in adult human tissues. In studying the murine embryo, we have revealed a potentially exciting facet of HTm4 biology and function, namely, the strong expression in the developing CNS, and apparent persistence in a subset of adult neural cells. Other aspects of HTm4 biology are closely parallelled between murine and human systems. In hematopoietic cells from both systems, HTm4 binds with KAP and therefore, likely functions as a component of the cell cycle machinery. These data will aid in the creation and analysis of a murine HTm4 deficient

mouse in an attempt to address the role of HTm4 in both hematopoietic and CNS development. In addition, further analysis of the protein interactions and cell-cycle regulatory capability of HTm4 will identify its importance in both contexts.

Acknowledgements

This work was supported by NIH Grant AI 43663 from the National Institute of Allergy and Infectious Diseases and by Grant RSG-01-241-01-LIB from the American Cancer Society (to C. Adra). Histological and immunohistochemical services were provided by the DF/HCC cancer center Hematopathology core lab supported by NIH-P30CA6516; NIH-HL44851, NIH-HL65909, and the Richard Saltonstall Charitable Foundation (to D.T. Scadden). This work was also supported by the Adra family and is dedicated to the memories of Dr. Ramzi Cotran and Dr. Stephen H. Robinson. We would like to acknowledge the technical assistance of Ms. Vuong Nguyen.

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Hum Genet (2005) 117: 16–26
DOI 10.1007/s00439-005-1285-0

ORIGINAL INVESTIGATION

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Functional promoter polymorphism in the *TBX21* gene associated with aspirin-induced asthma

Received: 25 November 2004 / Accepted: 25 January 2005 / Published online: 2 April 2005

Abstract Asthma is a phenotypically heterogeneous disorder with many etiologic factors and clinical characteristics. T-bet, a Th1-specific transcription factor of T-box family, has been found to control interferon-γ (IFN-γ) expression in T cells. Mice lacking the T-bet gene (*tbx21*) demonstrate multiple physiological and inflammatory features reminiscent of human asthma. In order to examine whether polymorphisms in the candidate gene, *TBX21*, located on chromosome 17q21.32, are related to the risk of human asthma phenotypes, we have searched for genetic variations in the human *TBX21* gene and identified 24 single nucleotide polymorphisms (SNPs), including five novel SNPs, by direct sequencing in Japanese subjects. Among asthma phenotypes, a promoter −1993T → C SNP, which is in linkage disequilibrium with a synonymous coding 390A → G SNP in exon 1, is significantly associated with a risk of aspirin-induced asthma (AIA; $P=0.004$, $P_c=0.016$). This association has also been confirmed in additional independent samples of asthma with nasal polyposis ($P=0.008$), regardless of aspirin hypersensitivity. Furthermore, our data indicate that the −1993T → C substitution increases the affinity of a particular nuclear protein to the binding site of *TBX21* covering the −1993 position, resulting in increased transcriptional activity of the *TBX21* gene. Thus, in addition to the antigen-driven excess Th2 response, increased T-bet (and subsequent IFN-γ)

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production in human airways of individuals with the −1993T → C polymorphism could contribute to the development of certain asthma-related phenotypes, such as AIA.

Introduction

Asthma is defined as a chronic inflammatory lung disease that is characterized by airway hyperreactivity, eosinophil inflammation, and mucus hypersecretion resulting in intermittent airway obstruction (Busse and Lemanske 2001). A considerable increase has been noted in the incidence of allergic diseases including asthma in industrialized societies over the past three decades (Bach 2002; Woolcock and Peat 1997). The etiology of asthma is complex and multifactorial; development of the disease is controlled by both host genetic factors and a variety of environmental exposures. Although environmental influences, particularly a decrease in infections because of improved hygiene, might have increased allergic diseases, at least a dozen polymorphic genes have been calculated to regulate asthma, by controlling the inflammatory response, immunoglobulin E (IgE), cytokine, and chemokine production, and airway remodeling (Cookson 1999; Fahy et al. 2000; Umetsu et al. 2002).

Asthma is thought to arise from an imbalance in T helper type 1 (Th1)-Th2 immune regulation, resulting in the driving of the development of Th2-biased immune responses and the overproduction of cytokines such as interleukin 4 (IL-4), IL-5, IL-9, and IL-13, which mediate allergic inflammation (Renauld 2001; Umetsu et al. 2002). In contrast, Th1-type cytokine interferon-γ (IFN-γ) is essential for macrophage activation in cellular defense mechanisms, and IFN-γ-producing Th1 cells have been suggested to protect against allergic responses by dampening the activity of Th2 effector cells (Renauld 2001). However, the evidence from other in vivo studies of asthma conflicts with this hypothesis, suggesting a contribution of IFN-γ to asthmatic airway inflammation (Busse and Lemanske 2001; Salvi et al. 2001).

T-bet is a member of the T-box family of transcription factors that has been found to be expressed in IFN-γ-producing Th1, but not in Th2, cells. T-bet is a transcriptional regulator essential for the lineage commitment of Th1 cells by directly activating Th1-associated genetic programs and repressing Th2 cytokine production (Szabo et al. 2000). Recently, evidence has shown decreased numbers of $CD4^+$ T cells expressing T-bet in the airways of patients with allergic asthma, relative to control subjects (Finotto et al. 2002). Furthermore, deletion of the T-bet gene, *tbx21*, in mice results in airway eosinophilia, Th2 cytokine production, airway hyperresponsiveness (AHR), and changes of airway remodeling without allergen sensitization and challenge. Thus, T-bet-deficient mice demonstrate multiple physiological and inflammatory features reminiscent of human asthma (Finotto et al. 2002).

The human T-bet gene (*TBX21*) is located on chromosome 17q21.32, a region near to that linked with asthma in a genome screen for asthma and skin tests (Dizier et al. 2000; Zhang et al. 1999). Moreover, the region on mouse chromosome 11 that is syntenic to human chromosome 17q12-q22 has been linked to AHR (Zhang et al. 1999). So far, to our knowledge, there have been no reports showing disease-related polymorphism(s) in the *TBX21* gene. Based on these observations, we propose that genetic polymorphism contributes to susceptibility to human asthma and/or related phenotypes. To test this hypothesis, we have searched for polymorphisms in *TBX21* and then conducted a genetic association study in the Japanese population. Finally, we have investigated the functional consequences of disease-related polymorphisms.

Materials and methods

Subjects

We recruited 361 patients with childhood asthma (mean age 9.7 years, range 4–15 years, mean total serum IgE level, 1021 U/ml; 92% of whom were atopic), 313 adult patients with atopic asthma (mean age 49 years, range 20–81 years; mean total IgE, 775.7 U/ml), and 88 adult patients with non-atopic asthma (mean age 59 years, range 42–75 years; mean total IgE, 174.8 U/ml) from the Osaka Prefectural Habikino Hospital and the Miyatake Asthma Clinic. Patients with aspirin-induced asthma (AIA; mean age 53 years, range 24–73 years; 54% of whom were atopic; ≥50% had nasal polyposis) were recruited from the National Sagamihara Hospital. All patients with asthma were diagnosed according to the criteria of the National Institutes of Health, with minor modifications (National Heart, Lung, and Blood Institute, National Institutes of Health, 1997, http://www.nhlbi.nih.gov/guidelines/asthma/asthgdln.htm). The diagnosis of atopic asthma was based on the positive immunoassay test to common allergens (at least one of the following: *Dermatophagoides pteronyssinus*, *Dermatophagoides farinae*, and *Aspergillus fumigatus*) or a higher total serum IgE of ≥400 kU/l, as used in our previous study (Mao et al. 1996). The criteria for a diagnosis of non-atopic asthma was a total serum IgE of < 400 kU/l and the absence of allergen-specific IgE (≤ 0.35 kU/l). All patients with AIA were documented to have histories of asthmatic attacks, such as severe bronchoconstriction and nasal symptoms, following the ingestion of more than two different kinds of non-steroidal anti-inflammatory drugs (NSAIDs) or to have had a positive reaction to aspirin systemic challenge. Of 72 AIA patients (58%), 42 were diagnosed on the basis of the aspirin challenge test, as previously described (Kawagishi et al. 2002; Mita et al. 2001). We also

independently recruited 42 asthmatic patients with nasal polyposis (AS/NP; mean age 54 years, range 23–75 years; 73% of whom were atopic). The NP was diagnosed on the basis of history, including nasal symptoms, clinical examination, nasal endoscopy, and sinus computerized tomography scanning. All adult asthmatics, except AIA patients, had no past history of aspirin hypersensitivity. Controls were 640 randomly selected healthy individuals with an age range 18–83 years from the same geographic areas who had neither respiratory symptoms nor history of asthma-related diseases and aspirin hypersensitivity. All subjects in this study were ethnically Japanese and gave written informed consent to participate in the study (or, for individuals less than 16 years old, their parents gave consent), according to the process approved by the Ethical Committee at the SNP Research Center, The Institute of Physical and Chemical Research (RIKEN), Yokohama.

Screening for polymorphisms and genotyping

To identify single-nucleotide polymorphisms (SNPs) in the human *TBX21* gene, we sequenced all six exons, including a minimum of 200 bases of flanking intronic sequence, 2.2 kb of the 5′ flanking region, and 2.5 kb continuous to the 3′ flanking region of the sixth exon from 24 asthmatic subjects (12 unrelated children and 12 adults). Eighteen primer sets were designed on the basis of the *TBX21* genomic sequence from the GenBank database (accession number AC003665; Table 1). For each polymerase chain reaction (PCR), 5 ng genomic DNA was amplified in a total reaction volume of 10 μl containing 12.5 pmol each primer, 3.9 mM $MgCl_2$, 1.25 mM each dNTP, 0.5 U *Taq* polymerase. Cycling conditions were an initial 95°C for 2 min, followed by 37 cycles at 94°C for 30 s, 58°C or 60°C for 30 s, and 72°C for 3 min, with a final extension of 7 min at 72°C. Each fragment amplified by PCR was sequenced by using the BigDye Terminator (Applied Biosystems, Foster City, Calif., USA) on an ABI Prism 3700 Genetic Analyzer (Applied Biosystems). The sequences were analyzed, and polymorphisms were identified by using the SEQUENCHER program (Gene Codes Corporation, Ann Arbor, Mich., USA). Four selected SNPs, viz., −1993T → C, 99C → G, 1298T → C, and 7725T → C, were genotyped by three methods: PCR-RFLP (PCR-restriction fragment lenght polymorphism; for −1993T → C and 1298T → C), Invader assay (for 99C → G), and direct sequencing (for 7725T → C). For PCR-RFLP analysis, we used mismatched primers for the −1993T → C SNP (5′-GGTCTTACTGAAAGCTCTCA-3′ and 5′- TCTCCTCCCCAACACCTTACGC-3′) and for the 1298T → C SNP (5′-GGCTAGTGCAGTAAAGCTTG-3′ and 5′-GGTTTTCACTGGACCAGCCGC-3′) where the changed nucleotides are underlined. The amplified products were digested with *Hha*I (−1993T → C) or *BstU*I (1298T → C) restriction enzymes (New England Biolabs, Bevery, Mass., USA) according to the manufacturer's instructions and were separated by electrophoresis on 4% agarose gels. Based on information available from the public JSNP database (http://snp.ims.u-tokyo.ac.jp), we generated the 99C → G SNP (IMS-JST000934) genotypes by using the Invader assay as previously described (Ohnishi et al. 2001). For the 7725T → C SNP, we performed direct sequencing with primers 5′-TTATCCAGGGTCATAGGGTAG-3′ and 5′-CCTCAGCCTTTAGAGAAGTTG-3′.

Luciferase assay

We generated luciferase reporter constructs, pGL3/−1993T and pGL3/−1993C, by cloning three concatenated copies of a 20-bp fragment of the *TBX21* gene into pGL3-Basic vector (Promega, Madison, Wis., USA) in the *Nhe*I site. The 20-bp primer sets carrying −1993T or −1993C alleles were 5′- CTAGCGGAGAAATGGTGGGTAAGGT T-3′ (forward) and 3′- GCCTCTTTACCACCCATTCCA AGATC-5′ (reverse) or 5′- CTAGC

Table 1 Primer sequences used in screening for SNPs of the human *TBX21* gene

F1	5′-TTTCCAGTAATAGCCGCTCCT-3′	R1	5′-CACAGCCTAGACACTGGTTC-3′
F2	5′-TTGCATAGTTACCATCCACCG-3′	R2	5′-GACCTTGGGATCCTTCACTAC-3′
F3	5′-AAGACTCCATTTGATCTTCAAC-3′	R3	5′-TTCACTCCACAAGGTGTCATG-3′
F4	5′-GTCAGGCTGGGACAGAAATG-3′	R4	5′-TGAGTTGGCTGCATCTTGTAG-3′
F5	5′-CTGGCTGCTGCTGATGCAG-3′	R5	5′-TGTCACTAGAGTCGCAGCGC-3′
F6	5′-AGTACTCGCCAAGAGCGTAG-3′	R6	5′-AAAAACAGACGAGACGTTCTTG-3′
F7	5′-TCGCGCTCAACAACCACCTG-3′	R7	5′-CTCAAAGTAAGACCGGAAAGG-3′
F8	5′-GGCTAGTGCAGTAAAGCTTG-3′	R8	5′-GACCAGAAGCTTGGGCTGTG-3′
F9	5′-CTCTGTTGTGTGGTCAGGAG −3′	R9	5′-TGAGAAGGTATGGAGGTAACC-3′
F10	5′-TTGAAGGAGGCAGTGGCTC-3′	R10	5′-AACACAGCTACCCAAAGTTATC-3′
F11	5′-TTATCCAGGGTCATAGGGTAG-3′	R11	5′-CCTCAGCCTTTAGAGAAGTTG-3′
F12	5′-TAACTTCCTCTACTTTTCCTGG-3′	R12	5′-AAACATCCTGTAGTGGCTGG-3′
F13	5′-TGCCTGGGCACTGTTGCAG-3′	R13	5′-GAAAAACGAACCTTCCTTCCTG-3′
F14	5′-CAACAATGTGACCCAGGTAG-3′	R14	5′-CAAGCTTTCCAACTCCAGTG-3′
F15	5′-GCCCTGTTTGTGCTGATACC-3′	R15	5′-CACAAGCAGAACCAGTCACC-3′
F16	5′-TGGGTTCAACTCAGCTTTGGT −3′	R16	5′-CTTTCATCATGTCATCTGCTC-3′
F17	5′-GCGAAGGAGACTCTAAGAGG-3′	R17	5′-TCTTGCTTCTTGAGATGTGGG-3′
F18	5′-CACGTATGTTATAACCATCAGC-3′	R18	5′-AGAGATAAAGGTGGAGGGCTG-3′