

Global Analysis of *ATM* Polymorphism Reveals Significant Functional Constraint

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ATM, the gene that is mutated in ataxia-telangiectasia, is associated with cerebellar degeneration, abnormal proliferation of small blood vessels, and cancer. These clinically important manifestations have stimulated interest in defining the sequence variation in the *ATM* gene. Therefore, we undertook a comprehensive survey of sequence variation in *ATM* in diverse human populations. The protein-encoding exons of the gene (9,168 bp) and the adjacent intron and untranslated sequences (14,661 bp) were analyzed in 93 individuals from seven major human populations. In addition, the coding sequence was analyzed in one chimpanzee, one gorilla, one orangutan, and one Old World monkey. In human *ATM*, 88 variant sites were discovered by denaturing high-performance liquid chromatography, which is 96%–100% sensitive for detection of DNA sequence variation. *ATM* was compared to 14 other autosomal genes for nucleotide diversity. The noncoding regions of *ATM* had diversity values comparable to other genes, but the coding regions had very low diversity, especially in the last 29% of the protein sequence. A test of the neutral evolution hypothesis, through use of the Hudson/Kreitman/Agudé statistic, revealed that this region of the human *ATM* gene was significantly constrained relative to that of the orangutan, the Old World monkey, and the mouse, but not relative to that of the chimpanzee or the gorilla. *ATM* displayed extensive linkage disequilibrium, consistent with suppression of meiotic recombination at this locus. Seven haplotypes were defined. Two haplotypes accounted for 82% of all chromosomes analyzed in all major populations; two others carrying the same D126E missense polymorphism accounted for 33% of chromosomes in Africa but were never observed outside of Africa. The high frequency of this polymorphism may be due either to a population expansion within Africa or to selective pressure.

Introduction

The human *ATM* gene is an important case study for mutation analysis. *ATM* is the gene mutated in the human recessive disease ataxia-telangiectasia (A-T [MIM 208900]) (Gatti 2001). In addition to the characteristic ataxia and oculocutaneous telangiectasias that gave the disease its name, patients with A-T have a 100-fold increased risk for cancer (Morrell et al. 1986). Furthermore, obligate heterozygous carriers may have a sixfold relative risk for cancer, implicating *ATM* as a possible tumor-suppressor gene (Morrell et al. 1990). This has been corroborated by a recent Dutch study showing an increased risk of breast cancer in *ATM* heterozygotes (Broeks et al. 2000). Other breast cancer studies, however, have been at odds with these results (Vorechovsky et al. 1996b; FitzGerald et al. 1997; Bay et al. 1998;

Chen et al. 1998; Bebb et al. 1999; Janin et al. 1999; Olsen et al. 2001).

The conflicting estimates of *ATM* mutation frequencies in patients with breast cancer may be due to the different patient populations that have been studied or to the insensitivity of available mutation detection methods. Indeed, there are many technical challenges involved in analysis of the *ATM* gene. The 13-kb mRNA is assembled from 66 exons distributed across a genomic region of 150 kb. The coding sequence alone encompasses 9,168 bp (Uziel et al. 1996; Platzer et al. 1997). Gel-based strategies for finding sequence variation in this gene—such as mismatch cleavage analysis, dideoxy sequencing, the protein truncation test, or single-strand conformation polymorphism analysis—are cumbersome and/or expensive. As a result, analyses of samples from patients with A-T detected only 60%–80% of the expected alleles (Gilad et al. 1996; Telatar et al. 1996; Vorechovsky et al. 1996a; Concannon and Gatti 1997; Broeks et al. 1998; Ejima and Sasaki 1998; Sasaki et al. 1998; Castellví-Bel et al. 1999; Gatti et al. 1999; Sandoval et al. 1999; Teraoka et al. 1999).

Denaturing high-performance liquid chromatography (DHPLC) is a novel, non-gel-based method that is very

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sensitive for detection of DNA sequence variation. Detection of sequence variation by DHPLC is based on differences in retention of perfectly matched homoduplexes and heteroduplexes containing one or more mismatched base pairs (Oefner and Underhill 1995, 1998). The choice of temperature during DHPLC is critical for achieving maximum detection sensitivity, which is 96%–100%. Blinded analyses have shown that DHPLC is superior to conventional methods (O'Donovan et al. 1998; Choy et al. 1999; Jones et al. 1999; Wagner et al. 1999b).

This article presents the results of the application of DHPLC to an analysis of global genetic variation in *ATM*. The sequence diversity of human *ATM* is compared with orthologs in four primate species, as well as with 14 other human autosomal genes. The implications of these findings for the identification of neutral sequence variation are discussed.

Subjects, Material, and Methods

Subjects and DNA Samples

DNA was obtained from chimpanzee, gorilla, orangutan, and macaque (Old World monkey) blood samples, and from 93 human lymphoblastoid cell lines derived from individuals enrolled according to approved human subject protocols. These individuals were believed to have no obvious genetic disease, although no medical records are available to confirm this. More than 60% of the samples came from males. In detail, the individuals included 18 from Africa (4 Biaka pygmies, 3 Mbuti Zaire pygmies, 4 Lisongo, 1 Omega San, 1 Namibian San, 1 Tsumkwe San, 1 Mandenka, 2 Ethiopian Jews, and 1 Sudanese), 9 from the Middle East (2 Druze, 2 Bedouin, 2 Palestinian, 2 Sephardim, and 1 Iranian), 12 from the Indian peninsula (1 Pathan, 2 Sindhi, 2 Brushaski, 2 Baluchi, 1 Brahui, 1 Makran, 1 Hazara, 1 Kalash, and 1 Tamil), 20 from Asia (3 Cambodians, 1 Hmong, 1 Atayal, 1 Ami, 8 Han Chinese, 4 Japanese, 1 Korean, and 1 Yakut), 16 from Europe (2 French, 2 European Americans from Utah, 1 Amish, 2 Germans, 2 Italian, 1 Dane, 2 Ashkenazi, 1 Adygei, 1 Georgian, 1 Caucasian, and 1 Russian), 8 from Oceania (2 New Guinean, 2 Melanesian, 2 Australian Aborigines, 1 Micronesian, and 1 Samoan), and 10 American Indians (1 Karitiana, 1 Surui, 2 Mayans, 2 Colombian Indians, 1 Quechua, 1 Muskogee, 1 Pima, and 1 Navaho).

PCR primers designed from the human *ATM* sequence were used to amplify the homologous regions of *ATM* for sequencing in four primate species: chimpanzee, gorilla, orangutan, and macaque monkey. The orangutan and macaque samples were obtained from Coriell Cell Repositories. Some exons from the primate species did

not readily amplify with the human primers. The proportion of the *ATM* coding sequence amplified in each species is listed in the Results section. The chimpanzee sample was also analyzed by DHPLC for all *ATM* exon regions except exons 14 and 35. The PCR products from the chimpanzee template were sequenced even when the DHPLC profile was homozygous.

DNA Extraction

Total genomic DNA was prepared through use of a QIAamp DNA Mini Kit (Qiagen). DNA samples were diluted with TE buffer (10 mM Tris, 1 mM EDTA) to a working concentration of 30–50 ng/ μ l and were stored in an 96-well microtiter plate format. For PCR, 2 μ l of the DNA stocks were dispensed into 96-well microtiter plates by a Hydra96 robot (Robbins Scientific) and were dried for 10–20 min by a SpeedVac Concentrator (Model SC210A or AES1010, Savant Instruments).

PCR Conditions

All 62 coding exons (9,168 bp) of *ATM*, as well as 14,661 bp of noncoding exon sequence (9,110 bp of intron sequence adjacent to coding exons and 5,551 bp of 5' and 3' noncoding exon sequence), were PCR amplified from genomic DNA through use of the 71 primer pairs listed in table 1. All primers were complementary to intron sequences near the exon boundaries except those in the 5' and 3' untranslated sequence that were amplified in overlapping segments. The exons were numbered according to established convention (Platzer et al. 1997). PCR primers used for amplification of regions containing *ATM* exons 10, 12, 19, 20, 23–37, 40–44, 55, 56, 57, 58, and 63 have been published elsewhere (Hacia et al. 1998). Primers for the remaining exon regions were selected from the published genomic sequence for *ATM* (GenBank accession number HSU82828), using the computer program Oligo 4.0 or Oligo 6.4 (Molecular Biology Insights). Amplicons were optimized for DHPLC by the choice of primer pairs that minimized the temperature difference in melting domains across the region and that maximized the length screened, to as many as 550 bp. The exons were amplified individually, except in four cases, in which two nearby exons could be amplified together.

PCR amplification was performed with AmpliTaq Gold (PE Biosystems) in 30–50- μ l reactions, using a Touchdown PCR protocol that made it possible to use the same conditions for every amplicon. The samples were then taken directly from PCR to a denature/reanneal protocol, which involves heating to 95°C then slowly cooling to 65°C over 30 min, using the PCR System 9700 thermocycler (PE Biosystems). Touchdown PCR conditions were 1 cycle of 95°C for 10 min; followed by 14 cycles of 95°C

Table 1

Primers and DHPLC Conditions for Mutational Analysis of Human ATM

ATM EXON	PRIMER		LENGTH OF SEQUENCE (bp)			DHPLC CONDITIONS	
	Forward (5'→3')	Reverse (5'→3')	Coding	Non- coding ^a	Total	Temper- ature (°C)	Gradient (% of Buffer B)
Promotor	GCCCAGAACCTCCGAATGACG	CGACTTAGCGTTTGCGGGCTCG	0	493	535	63	59–64
1A	AATGTTTTGGGGCAGTGTTT	AGGAAAGATGGAGTGAGGAGAG	0	370	412	63	58–63
1B	GACTCCTCCCTCTCCTCACTC	CCATCTGGAAGGCTTCTACC	0	515	556	60	60–65
1B, 2	TGCAAACCTCAGCCTGAGACT	CATGCCATTCTTTTCTAGTGC	0	491	532	59	54–60
3	TGAACCTTGAGTGGAACCTA	CTCTGAGGAAAACAAAAACACA	0	294	335	57	53–58
3	TTGGCACCAGTTAGTTCAGA	CAGAAGATGCTCATTCACTGA	0	260	300	54	55–60
4, 5	TACACATTTTTTCACACCTCTTTC	AGGCATAATGATATATAGGAAGCA	185	263	496	50, 55	60–66, 58–64
6	ATTGGTCTTGAGGAGTTAGGC	AAAAACTCACGCGACAGTAATC	146	202	392	54	58–64
7	TTGCCAATTTCTTCTCTACAAAAG	TTAAGGGTCAGTTCGATAACCATA	165	241	454	55	54–60
8	CTTTTTCTGTATGGGATTATGGA	TTCTGTTATGATGGATCAATGTTT	166	177	390	50, 55	57–63, 51–56
9	CAGCATAACCACTTCATAACTG	TCATATCCTCCTAAAGAACAC	239	131	412	54	56–61
10	CTAGCAGTGAAACAGAGTA	ATAGGCTTTTTGTGAGAACA	164	121	325	54	55–60
11	GCAACAACAGCGAAAACCTCTG	GAATGAGAAAATGGTAACTCTT	170	139	350	53, 56	56–61, 53–58
12	TGTGATGGAATAGTTTTCAA	AGTAACAAACTATGAAAATGA	372	98	511	57	56–62
13	CAATAGCTTGCTTTTCACAAT	TGGCATCAAATAAGTGGAGAG	195	92	335	57	54–59
14	GATGAAAGCAATTTTAATCTAGGA	TCAGTTTTTCTCATTGGCACTT	96	340	482	54	56–62
15	CATATAAGGCAAAGCATTAG	AGTTTACCAAAGTTGAATCATA	226	72	340	55	53–59
16	GTTGTTTTAGAGCTATCCAGGA	CTGCATCATGTACCCCAAGAAC	126	332	502	53, 57	58–63, 55–61
17	CGTGGAACCTTCAAAAACATTTT	CAAAAACAGTAACACCAACCAGT	126	346	517	54, 59	59–65, 54–59
18	AGCTCACTTATCTTTAGGGTCAA	GGCCTTAATTTCCACATTTGT	90	329	463	54	57–62
19	CTCCTGCAAGAAGCCATCT	AAGAAATCCCAAGTAGTAAAT	172	38	250	57	53–58
20	CTTTTTTTGTGAAGAGGAGGA	TTTCAATTTCTCAAAGACACCA	200	156	400	51, 58	58–64, 52–58
21	TTTTTCCTCCTACCATCTT	CTTAACAGAACACATCAGTTATT	83	78	173	55	50–55
22	TAAAATAACTGATGTGTTCTGTT	CAAAACTTGCAATTCGTATC	156	150	286	56	54–60
23, 24	TAGCACAGAAAAGACATATTGGAAG	TGTAAGACATTTCTACTGCCATCTG	207	236	491	55	56–61
25	AGTGCTGGTCTGAACCTCTTTA	TTGCTATGATTTGACCCATTGTG	118	324	488	54, 57	56–60, 51–57
26	TGGAGTTCAGTTGGGATTTTA	TTCCAGTGCAGCTAAGGAAGC	174	87	303	51, 55	58–64, 56–61
27	CTTAACACATTGACTTTTTGG	GTATGTGTGTTGCTGGTGAG	170	78	288	54	54–59
28	TGCTGATGGTATTAACAGTTT	GGTTGGCTATGCTAGATAATGAT	247	192	485	51, 56	58–64, 54–60
29	GAGCTGTCTTGACGTTACACAG	TTAAAAAGAGTGATGTCTATAA	116	131	290	53, 57	56–61, 51–57
30	TAAAAACGATGACTGTATT	GAAGGAATGTTCTATTATTA	127	40	207	56	51–56
31	CTGAAAATTAATAAATFGGCAAT	AAAACAGGAAGAACAGGATAGAAA	200	227	475	54	56–61
32	CTTACTGGTGTGTTGTTGTTTT	CCATTTTGAAGATGAGTCAG	175	26	241	57	52–58
33	GTTTTGTTGGCTTACTTTA	GAGCATTACAGATTTTTGAA	165	99	304	53	53–59
34	GTGTTAAAAGCAAGTTACATT	AAGAAACAGGTAGAAATAGC	133	33	207	56	50–55
35	GCAATTATAACAAAAAGTGT	TATATGTGATCCGCAGTTGAC	96	78	215	57	53–58
36	CAGCATTATAGTTTTGAAAT	GTGTGAAGTATCATTCTCCA	172	114	326	55	54–60
37	TGGTGTACTTGATAGGCATT	GACCCACAGCAAACAGAACTG	142	63	245	57	52–57
38	AACCTAATTTTTCTGCTGCCATA	GAGTGGGGGTGATATTATGTGA	177	279	501	55	58–64
39	GCAGTATGTTGAGTTTATGGCA	GCAACTGTTGGCAACTTTTTAT	178	260	481	53, 57	58–64, 54–60
40	ATAACAAGAAGGAAGAAGGT	ACGTAAGAAGCAACACTCATT	88	56	184	58	51–56
41	CAACATGCTTTTATTTTGATA	TATATACCCTTATTGAGACAA	156	90	288	55	53–59
42	TCTCATTAAGAGAGGTGTTCT	TGAGATAAATACTGTCATAAA	88	34	164	56	(49) 51–57
43, 44	AAATTTGCTAAATTTATAGCCGA	AGTGATGGCTTTACCAAATCTGG	192	152	391	57	55–60
45	TTTGCTGTTTTTTCTCTGGT	CAGTTGTTGTTTGAATGAGGAGA	149	91	285	56	53–59
46	ATTTTGTCTTTGGTGAAGCTA	CAAGTTTTTCAAAAAGAAGCCA	105	109	258	53	55–60
47	GCAAAGCCTATGATGAGAACTC	CAGAAAAGCTGCACCTTAGGAT	120	103	267	53, 57	55–61, 50–55
48	TCTTGTCACTACAAAAGTTCCTTT	TCTTTTTCCCTCAGGCTTTC	235	165	444	51, 56	61–67, 56–61
49	CCTCAATGAATGGTAGTTGCT	GTAACAACTAATCCAGCCAATA	168	87	299	53, 58	57–63, 51–56
50	CCAAAGCAGATGAGGAAAAC	TCTTGATGAAAAGATGAAGCATAT	114	165	325	56	54–59
51	GTGTATTACCTTAATTTGAGTG	CCAAAAGACCAAGATAATCT	218	191	451	55	61–67
52	TCCTTAGAAGTTTGCTTTTTTC	CTGGACCAAGTGCTAGGAATA	208	199	450	57	57–62
53	CTAGAGTACCCATTAGAAAGACCT	GTGTATGCCTGCATGTGTGA	114	346	504	50, 55	64–69, 59–64

(continued)

Table 1 (continued)

Primers and DHPLC Conditions for Mutational Analysis of Human ATM

ATM EXON	PRIMER		LENGTH OF SEQUENCE (bp)			DHPLC CONDITIONS	
	Forward (5'→3')	Reverse (5'→3')	Coding	Non- coding ^a	Total	Temper- ature (°C)	Gradient (% of Buffer B)
54	CTCTGCCTTTTCTCACACAT	CCTTGAACCGATTTTAGATGG	159	218	419	56	54–60
55	GGGTAGTTCCTTATGTAATGT	GTAACACAGCAAGAAAGTAACGT	139	42	225	56	50–56
56	GACCTTCAATGCTGTTCCCTCAGT	AGGTTGAAACATATGAAATTTGCC	83	135	265	54	52–58
57	ACCCGGCCTAAAGTTGTAGT	AATGGAGAAAAGCCTGGTTC	141	278	459	57	53–59
58	TTTGCTATTCTCAGATGACTCT	ATGTTTGGTGAACACTAACAGAAG	117	69	232	56	51–56
59	GCTGAATGATCATCAAATGCTCT	ATAATATCTGACAGCTGTCAGCT	150	99	295	52, 57	60–66, 54–60
60	TTTATTGCCCTATATCTGTGCAT	AAAAAGTGCTGAATCAAACAAA	166	134	345	55	56–61
61	CAACATGGCCGGTTATGC	CACTCAGTACCCAGGCAGA	87	305	430	54	57–63
62	GTGGTTTCTTGCCCTTTGTAAAGTT	AATCCTCCCCTTCAGCCTCTT	115	162	323	58	58–63
63	TAGGCTCAGCATACTACACAT	GACGAGATAACAGTCTACCT	64	117	223	55	51–56
64, 65	GGCTATTTGTATGATACTGGTTC	CTAAAGGCTGAATGAAAGGGTA	318	191	555	53, 58	60–65, 55–61
65	TACCCITTCATTCAGCCTTTAG	TTTTTTTTTTGAGATGGAGTTTC	0	470	515	56, 61	64–69, 59–64
65	TCTCAAAAAAAAAAAAAAAAAAACA	TGGGAATATGACATAAACAGACA	0	538	586	53	60–65
65	AGGCTTTATCTATGGGAATCTT	AGAGGTGAATATGTGAGCTGAT	0	370	414	59	56–61
65	CTCATTTTTGACCGTAAGGA	AAGTTCTGGAGATTGTTTATAG	0	411	453	56	59–64
65	CCTCCCCTAAAACCAATCT	AGTTATTTCTCCTAGGCTTGTG	0	417	459	54	58–63
65	ATGGCTTTGAAAAGTTTATCA	TAGGGTGGGAAAGCTATTATC	0	579	621	56	56–61
65	ATGAAAACCAATAGTGAAGC	TGGCACACAGAACACACAA	0	467	508	55	59–64

^a Noncoding length does not include primer sequence.

for 20 s, 63°C for 1 min (decreasing by 0.5°C/cycle), and 72°C for 1 min; 19 cycles of 95°C for 20 s, 56°C for 45 s, and 72°C for 45 s; and 1 cycle of 72°C for 7 min. PCR was carried out in a separate room, and only filtered pipette tips were used. To monitor for the presence of contamination, every plate had a negative control containing no added DNA.

DHPLC

The optimum temperature of analysis was determined, for each amplicon, by the DHPLC Melt program (Jones et al. 1999), available at the DNA Variation Group Web site. All ATM amplicons were run within 1°C of the recommended temperature, as indicated in table 1. If the program recommended two temperatures, then both temperatures were used, except in nine cases (exons 12, 15, 35, 41, 42, 43/44, 51, 58, and 60), for which only the highest temperature was used.

The chromatographic profiles of all but two ATM polymorphisms were clearly distinct from that of a homozygous control. Two sequence variants of ATM produced only a subtly different chromatographic profile when analyzed at the recommended DHPLC conditions. For the first one, 5185C→G, the normal allele had one leading shoulder, and the heterozygous allele had two leading shoulders. For the second one, IVS62-55T→C, the normal allele had a slightly broadened peak, and the heterozygous allele had a leading shoulder on that peak.

Microtiter plates containing completed PCR reactions

were loaded into an autosampler for automated DHPLC, using either the Transgenomic WAVE System or the Varian Helix System. Injection volume was 10–12 µl. In both systems, the DNASep column was used. The samples were run using the temperature and gradient conditions listed in table 1. The gradient was generated by increasing the concentration of buffer B (0.1M triethylamine acetate, 25% acetonitrile) relative to buffer A (0.1M triethylamine acetate). The numbers (X–Y) listed in the “DHPLC Gradient” column in table 1 represent shorthand notation for the gradient (expressed as a percentage of buffer b): 50%–X% in 0.5 min; X%–Y% in 3.0 min; Y%–95% in 0.1 min; 95% for 0.5 min; 95%–50% in 0.1 min; 50% for 0.8 min. The acetonitrile gradient was adjusted so that the homoduplex signal from the reference sample eluted from the column at a retention time of 2.8–3.4 min. These conditions were found empirically to maximize the resolution of heteroduplex and homoduplex signals. Each sample run took 6 min.

All samples were completely analyzed for the entire region sampled, except those from two Africans: a Mandenka, for whom insufficient amounts of DNA were available, and a Sudanese, who replaced another African after the study was already underway. Sequence variants observed in both samples are listed in the Results section, but the Mandenka could not be genotyped and therefore was not included in the haplotype analysis.

Genotypes of the 17 most frequent polymorphisms

were determined by DHPLC. Samples that were homozygous for either allele had only one peak and would be indistinguishable from one another without a reference. Therefore, the amplicons from the homozygotes were mixed with a sample of known genotype, through use of a protocol originally established for the Y chromosome (Underhill et al. 1997).

Direct DNA Sequencing

The chemical nature and location of the mismatches underlying the different heteroduplex profiles detected were determined by direct DNA sequencing. For this purpose, excess oligonucleotide primers and dinucleotide triphosphates were removed by treating 10 μ l of each PCR reaction with 1 unit each of exonuclease I and shrimp alkaline phosphatase (Amersham/Life Technologies) for 30 min at 37°C and for 15 min at 80°C. The PCR products were then sequenced with the BigDye Deoxy Terminator cycle sequencing kit (PE Biosystems), according to the manufacturer's instructions. After solid-phase extraction with Sephadex G-50 (Amersham Pharmacia), the sequencing reactions were analyzed with a PE Biosystems 377A sequencer.

Statistical Analysis

Nucleotide diversity was calculated as estimated nucleotide diversity (π), if complete genotypes were available (*AMPD1*, *ATM*, *BRCA1*, *DDFRY*, *MMP1*, *MMP3*, *MMP12*, *SMCY*, and *UTY*), or as average heterozygosity (θ), if only heterozygotes were known (*ABCB1*, *BRCA2*, *CACNA1A*, *COX2*, *FBN1*, *IL4*, *RB1*, *WRN*, and *XRCC1*). The value of θ is very close to that of π if Hardy-Weinberg equilibrium is satisfied. In a sample of n chromosomes, π was calculated from the equation $\pi = \sum_{i < j} \pi_{ij} / n_c$, where π_{ij} is the number of nucleotide differences between the i th and j th DNA sequences and $n_c = n(n - 1)/2$ (Nei 1987). Average heterozygosity per site was calculated by dividing the sum of the relative frequencies of heterozygotes per polymorphic site by the total number of base pairs screened. Tajima's D statistic (Tajima 1989b) was calculated by the equation

$$D = \frac{d}{\sqrt{\hat{V}(d)}},$$

where $d = \pi - S / \sum_{i=1}^{n-1} 1/i$, S is the number of segregating nucleotides and $\hat{V}(d)$ is an estimator of the variance of d . The value of D is expected to be 0 for selectively neutral variants and infinite sites in a constant population. A greater-than-expected number of rare variants would result in a negative value of D , indicating either purifying selection or population expansion (Tajima 1989a). The Hudson/Kreitman/Aguadé (HKA) test

(Hudson et al. 1987) was applied, using a computer program obtained from M. Nachman, to further investigate the possibility of selection acting on the *ATM* gene. The HKA test compares levels of intraspecific polymorphisms at different loci and interspecific sequence differences at these loci, with expectations—under a neutral evolution model—of an infinite number of sites. A neutral model predicts that the ratio between levels of intraspecific polymorphism and interspecies divergence should be the same for different genes, since both are a function of the neutral mutation rate. Selection, in contrast, can lead to an uncoupling of levels of polymorphism and divergence.

Inference of Haplotypes from Simple Sequence Polymorphisms (SSPs)

Haplotypes were inferred by a maximum-parsimony approach, as described elsewhere (Jin et al. 1999), for each of the 91 individuals for whom complete genotyping data had been obtained at the 17 sites that were heterozygous in >3 individuals (fig. 3). Polymorphic sites from a group of haplotypes or sequences were considered congruent if they could be accommodated by the same phylogenetic topology. Polymorphic sites were considered recurrent if linkage to flanking markers could not be explained by a single recombination event. In the construction of the tree by maximum parsimony, haplotypes of each individual with multiple polymorphisms were inferred, assuming the smallest number of mutational steps and that any incongruence between loci indicates recombination or recurrent mutation.

Of the 17 common polymorphic sites, 10 could be accommodated by the same phylogenetic topology, whereas 5 sites were found to be incongruent because of recurrent mutation, or reversion. Site IVS4+37insAA was recurrent in samples from all the population groups. Site IVS22-77T→C was recurrent in three samples, one from America and two from Asia; site IVS25-12insA was recurrent in Africa only. Site IVS48-69insATT was found to be recurrent in one African sample and in two American samples, and site IVS61+104C→T (part of a CpG motif) was recurrent in two samples, one from Africa and one from the Middle East. All recurrent sites can be explained by common mutation mechanisms.

Comparison of ATM with Other Genes

DHPLC analysis of 14 autosomal and 3 Y-chromosome genes was performed in a way similar to that described for *ATM*, using gene-specific PCR products spanning the coding and flanking intron sequences for each gene. The human gene names are standard for the online resource LocusLink. The GenBank accession numbers are as follows—*ABCB1* (also called "MDR1"): AC002457; *AMPD1*: M60092; *BRCA1*: U14680;

BRCA2: U43746; *CACNA1A* (also called "EA2"): AF004884; *COX2* (also called "PTGS2"): U04636; *FBN1*: L13923; *IL4*: M23442; *MMP1* (also called "MTE"), *MMP3* (collagenase), and *MMP12* (stromelysin): U78045; *RB1*: M15400; *WRN*: AF091214; and *XRCC1*: M36089. The mRNA and amino acid sequences of mouse *Atm* was obtained from GenBank (accession number MMU43678).

Results

SSPs

Variation in the human *ATM* gene was analyzed by DHPLC, which detects DNA sequence variation with a sensitivity of 96%–100% (Choy et al. 1999; Jones et al. 1999; Wagner et al. 1999b). The sensitivity of DHPLC in this study was confirmed in our laboratory by a blinded analysis of 73 known A-T patient samples, in which 99 of 100 previously identified variants in *ATM* were detected (data not shown).

Table 2 lists the 88 variant sites found in 93 human representatives from seven continental regions. Transitions accounted for 59% of all sequence variants. Transversions, deletions, and insertions accounted for 32%, 3.4%, and 5.7% of sequence variants, respectively. Sequence variation occurred in 26 of 9,168 nucleotides (1 in 353) in the coding regions, and in 62 of 14,661 nucleotides (1 in 236) in the noncoding regions. Of the 26 polymorphisms located in exons, 8 were silent, and 18 were missense polymorphisms. Of the 18 missense polymorphisms, 9 resulted in nonconservative amino acid changes, but their functional significance remains uncertain. With two exceptions, namely the conservative amino acid changes D126E and D1853N, all missense polymorphisms were observed only once or twice in the 93 individuals tested. The global distribution of D126E was unusually high in Africa.

Of the 88 polymorphisms listed in table 2, 53 (60%) were observed only once, and they were found in both the noncoding and coding regions. The frequency of singletons is very similar to that observed in *BRCA2*, where they constituted 59% of all sites (Wagner et al. 1999b). However, it was quite different from the Werner syndrome gene (Passarino et al. 2001), in which only 33% of the 58 polymorphisms identified in an identical set of individuals were singletons. Another 18 polymorphic sites in *ATM* were observed two or three times in the screening set. The remaining 17 polymorphisms were observed in four or more individuals.

Consistent with the oldest human populations existing in Africa (Stringer and Andrews 1988; Tishkoff et al. 1998; Underhill et al. 2000), 61% (54/88) of the polymorphisms were found there. Not surprisingly, 17 of those polymorphisms were also detected in other con-

tinents. (The derived allele of IVS17-114C→G was found a second time, in Oceania, as a homozygote.)

Haplotype Analysis

Haplotypes for each individual were inferred by a maximum-parsimony approach, using the genotype data of 17 polymorphic sites that had been observed to be heterozygous in four or more individuals. The genotypes of each individual are diagrammed in figure 1. Ten of the sites were in complete linkage disequilibrium over >133 kb.

Seven haplotypes, H1–H7, could be inferred, and their phylogenetic relationship is depicted in figure 2. Two clusters of haplotypes, H2–H3 and H4–H7, could be distinguished. H1 was hypothesized to be the oldest haplotype in the phylogeny, since it was identical to the chimpanzee haplotype. Of 10 sites defining the haplotypes, only two single-base-pair changes resulted in amino acid changes, which are indicated in parentheses. Arrows indicate the number and direction of sequence changes. Several intermediate haplotypes between H2 and H3 and between H4 and H5 were not observed in the present study, because of either the relatively small size of the screening set or their disappearance due to random genetic drift or selection.

The color coding in figure 2 indicates the geographic distribution, and the areas of the circles are proportional to the frequencies of the seven haplotypes. Strikingly, two haplotypes, H2 and H4, were found in every region of the world, accounting for 82% of the chromosomes observed.

Like nucleotide diversity, haplotype diversity was greatest in Africa, where five out of seven haplotypes were found. This is consistent with many other observations leading to the hypothesis of an African origin of modern humans. Of the two haplotypes not found in Africa, one is a singleton (H5), whereas the other (H3) was observed at relatively low frequencies on all continents. H1 was only observed in Africa and Oceania.

The African haplotypes H6 and H7, which share the missense polymorphism D126E, were particularly intriguing. These two haplotypes were very common in Africa but were not found elsewhere in the world. H6 was only found in the rain forests of central Africa, but H7 was found in climatically diverse regions all across Africa. H5 also shared D126E and was found only once, in an individual from the Makran coast of Pakistan; this haplotype may be associated with a relatively recent introduction from Africa, through trade relationships.

The geographic distribution of D126E was unusual when compared to distributions of missense polymorphisms in the 14 other autosomal genes reviewed in this study. All except one of the missense polymorphisms in these genes were randomly distributed, with equal per-

Table 2

Sequence Variants Found in ATM, Their Geographic Location, and DHPLC Detection Temperature

GENOMIC POSITION ^a (LOCATION WITHIN GENE)	POLYMORPHISM	AMINO ACID CHANGE	DHPLC TEMPERATURE (°C)	NO. OF HETEROZYGOUS INDIVIDUALS IN							Total (n = 93)	REFERENCE ^b
				Africa (n = 18)	Middle East (n = 9)	Indian Peninsula (n = 12)	Oceania (n = 8)	Europe (n = 16)	Asia (n = 20)	Americas (n = 10)		
10152 (promotor)	10152 G→C		63	1							1	
10182 (promotor)	10182 T→A		63	8	4	1	2	10	7	5	37	9
10807 (5' UTR)	-787 A→G		63	1							1	
10948 (intron 1a)	IVS1a+61 A→G		63	1							1	
11251 (5' UTR)	-615 A→G		59						1		1	
11512 (5' UTR)	-354 G→A		59						1		1	
12194 (intron 2)	IVS2-291 G→A		56	8	4	1	2	10	7	5	37	
12203 (intron 2)	IVS2-282 A→G		56	2				1			2	
12220 (intron 2)	IVS2-265 C→T		56								1	
12378 (intron 2)	IVS2-107 G→C		56	1							1	
15247 (intron 3)	IVS3-49 A→G		50						1		1	
15252 (intron 3)	IVS3-44 T→C		50	1							1	
15403 (intron 4)	IVS4+6 A→G		55				1				1	
15434 (intron 4)	IVS4+37 insAA		50, 55	9	7	3	2	5	12	7	45	3, 6
15548 (exon 5)	146 C→G	S49C	55				1				2	3
23296 (intron 6)	IVS6-71 A→G		55					2			2	
23413 (exon 7)	378 T→A	D126E	55	10		1					11	
23440 (exon 7)	405 T→C	A135A	55			2					2	
23615 (intron 7)	IVS7+84 A→G		55						1		1	
31591 (intron 7)	IVS7-48 T→G		50	2							2	
31788 (exon 8)	646 G→T	A216S	55	1							1	
31799 (exon 8)	657 T→C	C219C	55	4							4	
31842 (intron 8)	IVS8+38 T→C		55	6							6	
32736 (intron 9)	IVS9+25 T→G		54, 55	10		1					11	
36728 (exon 11)	1176 C→G	G392G	56	1							1	
38688 (exon 12)	1541 G→A	G514D ^e	57	1							1	
39655 (exon 13)	1744 T→C	F582L ^e	57	1	1						2	
40414 (intron 13)	IVS13-85 A→G		54	1							1	
43827 (intron 15)	IVS15-69 C→G		53	1			1				2	
43828 (intron 15)	IVS15-68 T→C		53	1				2			2	
44096 (intron 16)	IVS16+75 T→C		57	1							1	
44099 (intron 16)	IVS16+78 G→A		53					1			1	
45192 (exon 17)	2281 A→T	T761S	54	1							1	
46553 (intron 17)	IVS17-114 C→G		54	1							1	
46611 (intron 17)	IVS17-56 G→A ^d		54	6	3	3	3	9	8	5	37	3
54956 (exon 19)	2572 T→C	F858L ^e	58					1			1	
56073 (intron 19)	IVS19-17 G→T		58	2							2	
56317 (intron 20)	IVS20+28 insA		58	1							1	3, 5, 6
60136 (intron 22)	IVS22-77 T→C		56	1	3	4	3	9	10	4	34	5, 9
60253 (exon 23)	3118 A→G	M1040V	55, 56	1							1	2
60273 (exon 23)	3138 T→G	L1046L	55, 56					1			1	
60285 (exon 23)	3150 T→C ^d	L1050L	55, 56			1					1	
60410 (exon 24)	3161 C→G	P1054R ^e	55, 56				1				1	1, 3, 8

67162 (intron 24)	IVS24-9 delT	56	3	2	1	2	10	5, 6
67305 (intron 25)	IVS25+17 T→C ^d	56	2				2	
68663 (intron 25)	IVS25-12 insA	50, 51	4	2	7	11	4	6
68876 (intron 26)	IVS26+28 A→C	51, 55	1				1	
71872 (intron 27)	IVS27-34 A→G	51	1				1	
72096 (exon 28)	3937 G→C	51, 56	1				1	
72157 (intron 28)	IVS28+5 G→T	51, 56	2				2	
76682 (exon 30)	4138 C→T	56	2	1	1	1	2	3
80435 (exon 32)	4578 C→T	57	1				2	
80956 (intron 32)	IVS32-32 del3	53	1				1	
80999 (exon 33)	4623 G→T	53	1		1		1	
82583 (intron 33)	IVS33-20 A→G ^d	55	1				1	
82628 (exon 34)	4802 G→A	55, 56	1				1	
82697 (exon 34)	4871 A→G ^d	56	1				1	
84955 (intron 34)	IVS34-7 T→C	52	1				1	
87320 (intron 35)	IVS35-68 T→G	54	10	1			11	
89328 (exon 37)	5185 G→C	57	1				1	
90446 (intron 37)	IVS37-80 T→G	55		1			1	
90464 (intron 37)	IVS37-62 G→T	55		1			1	
92265 (intron 38)	IVS38-83 G→A ^d	53		2			1	
92333 (intron 38)	IVS38-15 G→C	53, 57		1			1	
92340 (intron 38)	IVS38-8 T→C	57		1			1	3, 5, 6
92408 (exon 39)	5557 G→A	53, 57	3	2	1	2	10	3, 5, 7, 8
92409 (exon 39)	5558 A→T	53, 57	1	1			2	8
97863 (exon 41)	5793 T→C	55	1				1	3, 5
98004 (intron 41)	IVS41+16 A→G	55	1				1	
103693 (exon 44)	6108 T→C ^d	57			1		1	
113654 (intron 48)	IVS48-69 insATT	53	8	3	9	8	37	5
115239 (intron 49)	IVS49-71 C→T ^d	56	2				2	
115338 (exon 50)	7004 C→A	56	1				1	
118131 (intron 52)	IVS52+45 delTT	57		1			1	
119423 (intron 53)	IVS53-121 insGGCA	55			2		2	
135133 (intron 61)	IVS61+104 C→T ^d	54	2	4	6	9	33	4
142611 (intron 62)	IVS62-55 T→C ^d	54, 55	7	3	8	8	37	5, 9
153599 (3' UTR)	9407 C→T	56, 61	1	1			1	
153734 (3' UTR)	9542 A→G	56, 61	1				1	
154046 (3' UTR)	9854 T→G	53	2	1			3	
154789 (3' UTR)	10597 T→C	59	1				1	
155442 (3' UTR)	11250 C→T	56	1				1	
155651 (3' UTR)	11459 T→C	54	1				1	
155696 (3' UTR)	11504 C→T	54	1				1	
156434 (3' UTR)	12242 C→T	56	2				2	
156498 (3' UTR)	12306 A→G	56			1		1	
156592 (3' UTR)	12400 C→T	55	1				1	
156755 (3' UTR)	12563 T→G	55	7	3	8	8	37	

^a Genomic position in GenBank (accession number U82828).

^b 1, Vorechovsky et al. (1996a); 2, Vorechovsky et al. (1997); 3, Shayeghi et al. (1998); 4, Bay et al. (1999); 5, Castellvi-Bel et al. (1999); 6, Li et al. (1999); 7, Maillat et al. (1999); 8, Sandoval et al. (1999); 9, Bonnen et al. (2000).

^c Nonconservative amino acid change.

^d DNA variant at CpG or CpNG site.

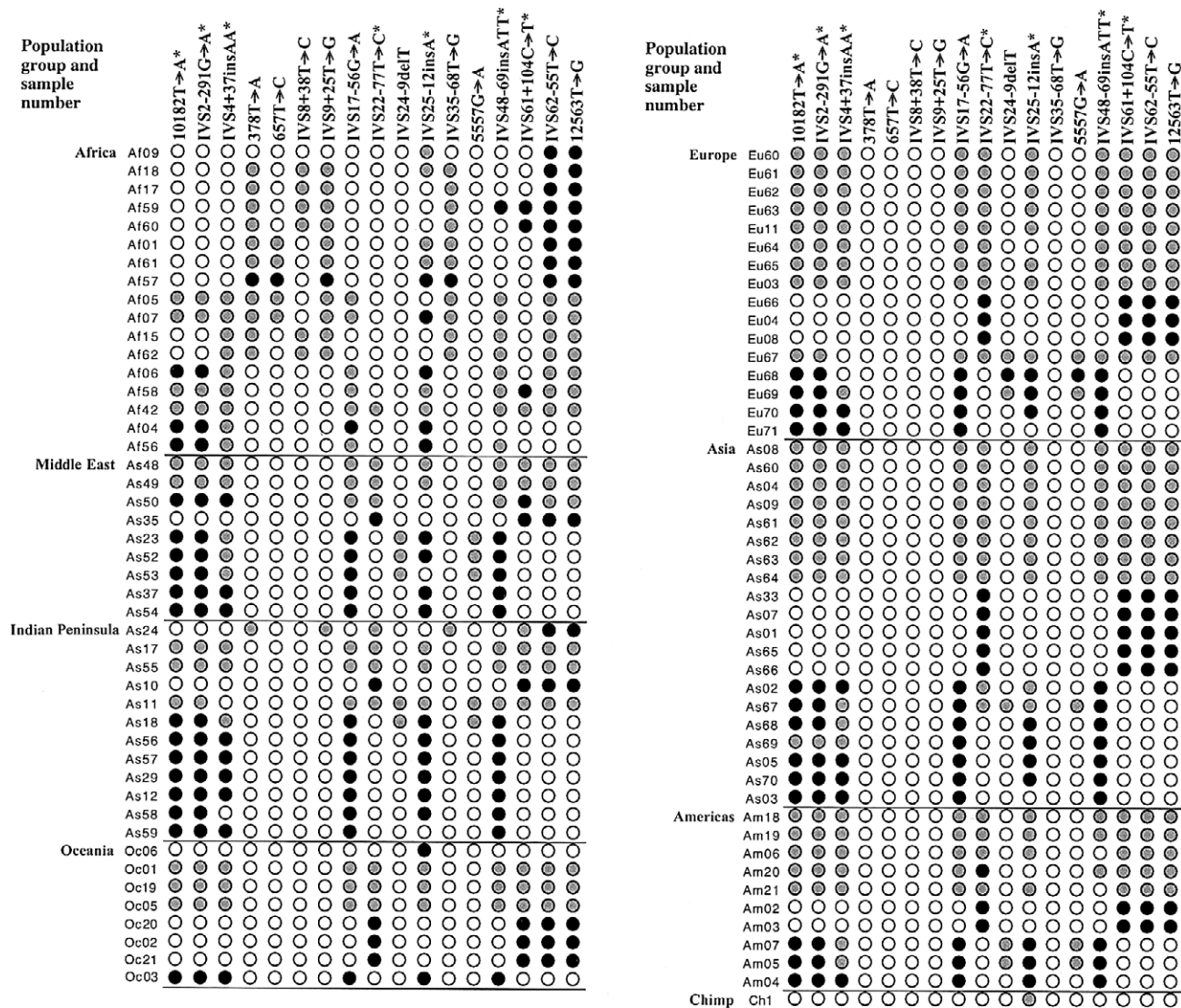


Figure 1 Genotype data for 17 polymorphic sites in *ATM*, obtained for 91 representatives from seven major human populations. An asterisk (*) indicates that the polymorphism was not included in the haplotype analysis, because of recombination or recurrent mutation. White circles represent the homozygous ancestral allele, black circles the homozygous derived allele, and gray circles the heterozygotes. The nucleotide positions of the 17 polymorphic sites, in relation to the cDNA sequence (GenBank accession number U82828), are given at the top.

centages in African and non-African populations. The exception was a missense polymorphism in *MDR1* (A259S) that was heterozygous in 49% of non-Africans but was never seen in Africans.

The non-African haplotype, H3, was distinguished by the missense polymorphism D1853N. H3 was found on an average of 8% of chromosomes everywhere except in Africa. Its distribution and distinct absence in Africa is similar to that observed for M9 on the Y chromosome (Underhill et al. 1997).

Comparison of *ATM* Orthologs

Figure 3 shows a comparison of the *ATM* coding sequence in human and chimpanzee. Figure 3A shows the distribution of differences, along the *ATM* protein, between human and chimpanzee, as well as polymorphisms within the single chimpanzee individual. There were 32 coding-sequence differences between human and chimpanzee. Of the single-base-pair changes, 9 were polymorphic in the single chimpanzee sample, and the

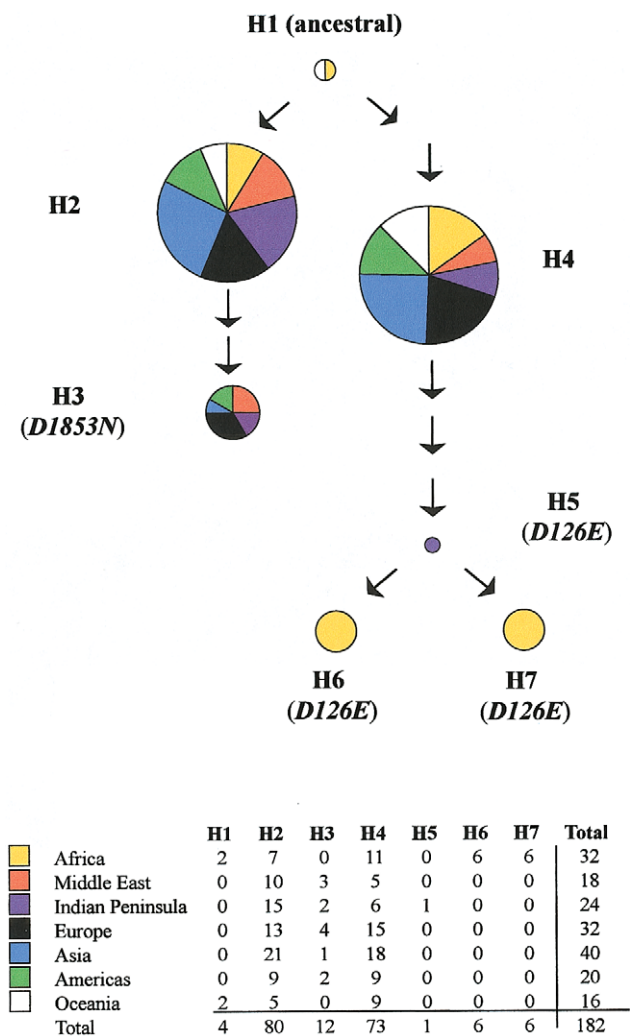


Figure 2 Phylogenetic relationship among seven ATM haplotypes. A chimpanzee sequence was used to determine the root of the phylogeny (H1). The circles each represent one haplotype, the area of the circle is proportional to the number of chromosomes observed with that haplotype, and the colors represent seven distinct geographic regions. The number of arrows indicates the number of changes required to generate the next related haplotype. Missense polymorphisms are indicated in parentheses. The number of observations are summarized in the table at the bottom of the figure. The haplotypes were defined by the nine congruent sites observed in ATM, including eight single-base-pair changes and one deletion. The nucleotide positions and the base pair changes defining the haplotypes are 378T→A, 657T→C, IVS8+38T→C, IVS9+25T→G, IVS17-56G→A, IVS24-9delT, IVS35-68T→G, 5557G→A, IVS62-55T→C, and 12563T→G where variation corresponding to amino acid changes is underlined. There are 133,342 bp between the first and the last markers. Haplotypes are defined as follows (the base pair change defining a new haplotype is underlined)—H1: TTTTATTGTT; H2: TTTGTGTT; H3: TTTG(delT)TATT; H4: TTTTATTGCG; H5: ATTGATGCG; H6: ACTGATGCG; H7: ATCGATGCG.

other 23 were homozygous for different base pairs in human and chimpanzee. Twelve variants resulted in an amino acid change, and 20 were silent. Figure 3B shows the distribution and frequency of coding-sequence polymorphisms within humans. In figures 3A and 3B, sequence differences that resulted in an amino acid change are shown as black symbols, and silent base-pair changes are shown as white symbols.

Two regions of the protein with known functional motifs encoding the leucine zipper and kinase domains, as well as one region with homology to the distantly related yeast (*Saccharomyces cerevisiae*) Tel1p protein are indicated by solid shading. The shaded regions represent ~29% of the amino acid coding sequence. Of the 58 polymorphisms found in human or chimpanzee, only 3 map to the conserved regions of the protein. If polymorphisms are assumed to be distributed uniformly and at random, the probability of seeing three or fewer in the conserved region is <.01.

Nucleotide Diversity

Figure 4 shows the nucleotide diversity of 15 autosomal and 3 Y-chromosome genes (Shen et al. 2000) that have been analyzed by DHPLC. Nucleotide diversity was calculated from the number of differences between any two randomly chosen sequences. Given the number of segregating sites, the nucleotide diversity of the coding region of ATM was very low. For the 9,168-bp coding region, the value was $0.71 \pm 0.61 \times 10^{-4}$. That is 4.5-fold less sequence diversity than the average in 64,676 coding base pairs in 15 other autosomal genes analyzed by DHPLC (Wagner et al. 1999a; Shen et al. 2000; Passarino et al. 2001; dbSNP Home Page; D. Cox, C. Franco, R. Ghali, P.J. Oefner, A. Roxas, P. Shen, T.A. Sivakumaran, R. Sung, T. Tang, F. Wong, W.-T. Yang, unpublished data), and 7-fold less than that reported in 135,823 coding base pairs in 106 human genes (Cargill et al. 1999).

There was a large difference between the nucleotide diversities of ATM in the coding and noncoding regions. Whereas most genes in the study had similar nucleotide-diversity estimates in the protein coding and noncoding regions, with ratios ranging from 1:2.5 to 1:1, in ATM the ratio was 1:7.5. Since the sequence diversity was normal in the noncoding regions compared to that in the other genes, it is clear that there was not a generally lower mutation rate in the chromosomal region containing ATM. More likely, the lower sequence diversity in the coding region is due to selective pressure for maintaining the protein sequence.

Only three genes—two on the Y chromosome (*SMCY* and *DFFRY*) and one small autosomal gene with 2,650 bp of coding sequence (the retinoblastoma gene,

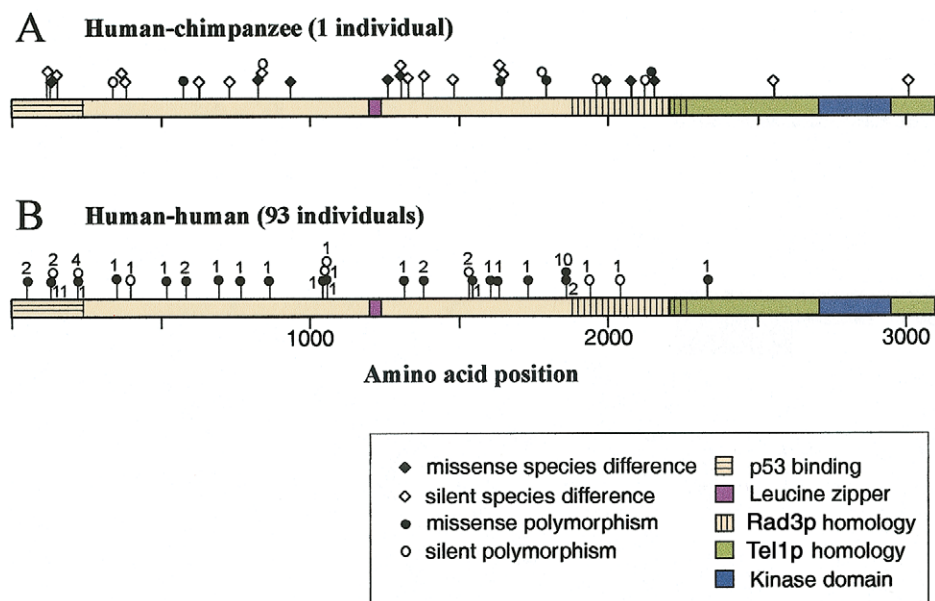


Figure 3 Distribution of coding-sequence polymorphisms in *ATM* and differences between chimpanzee and human. *A*, Location of polymorphisms and coding-sequence differences in chimpanzee compared to human. *B*, Location and frequency of polymorphisms observed in human *ATM*. The horizontal bar represents amino acid sequence of *ATM* from 1 to 3056. Colored and shaded regions of the amino acid sequence represent possible functional domains of the molecule: p53 binding (Khanna et al. 1998), leucine zipper (Morgan et al. 1997), homology to *S. pombe* Rad3p (Bentley et al. 1996) and *S. cerevisiae* Tel1p (Greenwell et al. 1995; Morrow et al. 1995), and the serine kinase domain (Zakian 1995). Ball-and-stick figures along the amino acid sequence represent amino acid positions. Circles are mapped at positions that are polymorphic either within the 93 human individuals (with the number of individuals adjacent to each circle) or within the single chimpanzee individual; diamonds represent homozygous differences between human and chimpanzee. Black circles or diamonds represent missense polymorphisms, and white circles or diamonds represent silent changes.

RB1)—had less coding diversity than *ATM*. When *ATM* and *RB1* were compared more closely, it is interesting that the last 2,650 bp (29%) of the *ATM* coding region had even less sequence diversity than *RB1* (π was 0.0415×10^{-4} and 0.076×10^{-4} , respectively.) Even when the remaining 6,518 bp of *ATM* were considered separately, the sequence diversity was 0.965×10^{-4} , suggesting considerable constraint on the evolution of this gene compared to other autosomal genes. Loss of some neutral sequence diversity across the gene might be expected during background selection, because deleterious mutations will eliminate variants that are linked on the same haplotype.

When nucleotide diversity was calculated for African and non-African populations separately, most genes showed little difference. However, in *ATM*, the non-African population had four times less sequence diversity (0.437×10^{-4}) than did the African population (1.75×10^{-4}).

Statistical Analysis for the Hypothesis of Selection at *ATM*

Calculation of the Tajima's *D* statistic also suggested that selection has operated on *ATM*. In the Tajima's *D*

test, $D = 0$ for selectively neutral mutations in a constant-population infinite-sites model, whereas $D < 0$ in the case of purifying selection or in an expanding population (Tajima 1989a, 1989b). In an expanding-population model (Sherry et al. 1994; Kimmel et al. 1998; Pritchard et al. 1999; Shen et al. 2000; Zhivotovsky et al. 2000), all genes would be expected to behave similarly. However, Tajima's *D* value was statistically negative for only four of the autosomal genes reviewed in the present study, including *ATM*. For example, for *ATM*, $D = -1.98$, which was statistically significant at $P < .05$, reflecting the overabundance of rare alleles.

The HKA test (Hudson et al. 1987) compares the number of intraspecies (within-human) polymorphisms and interspecies sequence differences at different loci, with the expectation of a model of neutral evolution. First, the human and chimpanzee orthologs were compared. The coding region of *ATM* had 26 polymorphisms in humans over 9,168 bp and had 32 differences between humans and chimpanzee over 9,029 bp. The combined coding regions of 11 other autosomal genes (*AMPD1*, *CSTB*, *MMP1*, *MMP3*, *MMP12*, *ABCB1*, *BRCA2*, *XRCC1*, *FBN1*, *COX2*, and *IL-4*) had 123 polymorphic sites in human over 30,996 bp and 79 dif-

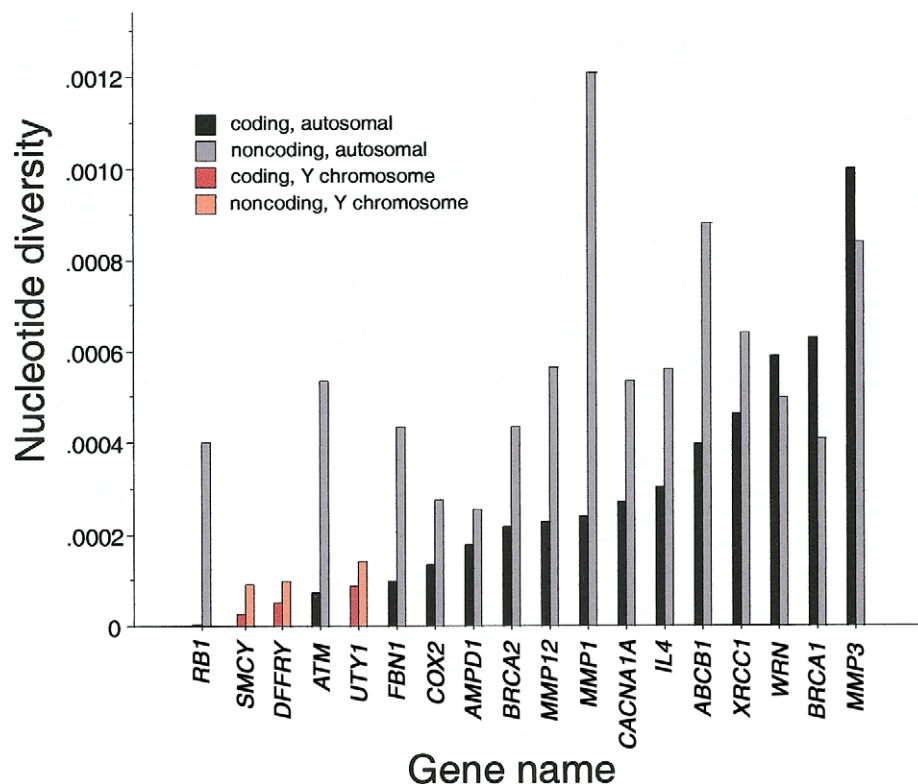


Figure 4 Nucleotide diversity in coding and noncoding regions of 15 autosomal and 3 Y-chromosome genes. Nucleotide diversity, or heterozygosity, was calculated as described in the Subjects, Material, and Methods section. Autosomal genes are shown in black and gray, and Y-chromosome genes are shown in red and pink.

ferences between human and chimpanzee over 22,343 bp. The HKA statistic for reduced variability in human *ATM* compared to chimpanzee was not statistically significant ($\chi^2_{[1]} = 0.47$, $P = .49$).

However, the HKA test would fail to detect selection if the same selective pressures were operating in both human and chimpanzee. To test the possibility that the reduced variability of the last 29% of the *ATM* coding sequence was due to selective pressure in both chimpanzee and human, five cross-species comparisons were performed (table 3). In contrast to human and chimpanzee, there was little reduced variability in that region in gorilla ($\chi^2_{[1]} = 3.58$, $P = .059$) and none in orangutan, Old World monkey, or mouse ($\chi^2_{[1]} > 4.7$, $P < .02$). Thus, selective pressure appears to be operating in the last 29% of the *ATM* coding region in humans, chimpanzees, and possibly in gorilla, but not in orangutan, Old World monkey, or mouse.

Discussion

The present study represents the first comprehensive survey of neutral variation in the *ATM* gene in diverse hu-

man populations. *ATM* is important for the regulation of cellular responses to DNA damage, for oxidative stress, and for the control of cell cycle checkpoints. It is a protein kinase that phosphorylates many substrates, including p53 tumor suppressor protein.

All of the protein-encoding exons of the gene (9,168 bp), as well as adjacent intron and untranslated sequences (14,661 bp), were analyzed in 1 chimpanzee and 93 human samples. The sequences analyzed were those that would most likely affect protein function, either by altering amino acids in functional domains or by affecting intron splicing. A diverse collection of 93 human genomic DNAs were chosen for analysis. To include as much genetic diversity as possible, African and Oceanian populations were overrepresented relative to others.

The analysis method, DHPLC, was shown to be 99% sensitive for detection of sequence variation in the *ATM* gene (data not shown.) Important technical details, such as use of a temperature-prediction algorithm and examples of subtle chromatographic shifts, have been included here so that others can reproduce the sensitivity reported.

Table 3**Comparisons of Two ATM Gene Regions with Orthologs in Five Other Species, Using the HKA Statistic**

SPECIES	NO. OF DIFFERENCES (NO. OF BASE PAIRS ANALYZED) IN		χ^2	P
	First 71% of ATM	Last 29% of ATM		
Chimpanzee	21 (6518)	2 (2650)	.157	.692
Gorilla	28 (5341)	7 (1855)	3.58	.059
Orangutan	42 (4795)	19 (2308)	5.02	.025 ^a
Old World Monkey	68 (3364)	28 (1406)	5.38	.020 ^a
Mouse	970 (6518)	349 (2650)	4.72	.030 ^a

^a Statistically significant.

Sequence Diversity in ATM

A total of 88 different polymorphic sites were discovered in human *ATM*, and 23 homozygous differences were found between human and chimpanzee in the coding region. The chimpanzee was heterozygous (polymorphic) at nine additional sites. Only one human sample, from an African, had as many heterozygous sites, consistent with a report elsewhere that chimpanzee populations have greater genetic diversity than do human populations (Kaessmann et al. 1999).

Most of the *ATM* polymorphisms were relatively rare, leading to a low overall sequence diversity. The high number of rare variants contributed to the generation of a significantly negative value for Tajima's *D* statistic. Such an effect can occur for a rapidly expanding population. However, the number of rare variants in *ATM* was higher than the average seen in 14 other autosomal genes, suggesting that other forces were operating. For example, purifying selection would cause this effect by eliminating variation linked to deleterious mutations.

The low sequence diversity in the coding region of *ATM* was noteworthy, because it encodes a very large (350 kDa) protein that may be able to tolerate many amino acid changes. However, *ATM* was the second-least variable of the autosomal genes analyzed. The only autosomal gene with less coding-sequence diversity was *RB1*. Interestingly, both *ATM* and *RB1* have functions in cell-cycle control (Mulligan and Jacks 1998; Lavin 1999) and therefore may have similar constraints on their evolution.

The overall diversity of *ATM* was comparable to that of three genes on the Y chromosome. The Y chromosome has previously been shown to have less diversity than autosomal genes, mostly because of its fourfold smaller effective population size (Jobling and Tyler-Smith 1995; Nachman 1998), but also because of the possible action of sexual selection (Wyckoff et al. 2000) and demographic factors, such as polygamy (Shen et al. 2000).

Haplotype Analysis

Of 17 common markers in *ATM*, 10 showed no evidence of recurrent mutation and were in complete linkage disequilibrium with each other over >133 kb. Previous reports have also demonstrated extensive linkage disequilibrium at *ATM* (Gatti 1998; Li et al. 1999; Bonnen et al. 2000), and in other regions of the genome (Collins et al. 1999; Huttley et al. 1999; Gordon et al. 2000; Taillon-Miller et al. 2000). Interestingly, the rate of recombination appears to be the same in patients with A-T and in unaffected individuals (Lange et al. 1995).

Through use of haplotypes defined by the 10 markers that were completely linked, it was possible to construct a parsimonious phylogeny (fig. 4). Because the mutation rate of single-nucleotide changes is much lower than that of nucleotide repeats, the resulting phylogeny is older than one derived from microsatellite markers.

A previous study (Bonnen et al. 2000) identified haplotypes at *ATM*, using SNP markers that were identified only in noncoding sequence. Different regions of the *ATM* gene were analyzed in the two studies, with ~25% overlap in sequence. Consequently, only two markers, IVS22-77T→C and IVS62-55T→C, were found by both groups. In the present study, IVS22-77T→C was not used in the definition of haplotypes, because it was recurrent in three samples. The genotypes of a third marker that was common in the population, 10182T→A, were determined in this set of samples.

The observed number and global distribution of haplotypes in *ATM* were comparable to those reported earlier (Bonnen et al. 2000). Both studies observed that a small number of haplotypes represented the vast majority of chromosomes analyzed, with 2 of 7 haplotypes representing 82% of chromosomes (present study) and 6 of 22 haplotypes representing 89% of chromosomes (Bonnen et al. 2000). Some of the haplotypes in the two studies may be identical. For example, three missense polymorphisms were associated with unique haplotypes in the two studies: S49C was found on haplotype 2 (Bonnen et al. 2000) and on H4 (this study), P1054R was

found on haplotype 17 and on H2, and D1853N was found on haplotype 15 and on H3.

Implications for Identification of Neutral Variation

Our observations of DNA sequence variation in the human *ATM* gene have important implications for distinguishing between neutral variants and functional mutations. For example, all of the 88 variants reported here are likely to be neutral, unless one or two individuals are among the 1%–2% of the population that are carriers of *ATM* mutations (Gatti et al. 1999; Li and Swift 2000). Functional mutations in carriers may exist either in protein-coding DNA or in noncoding DNA associated with splicing. Four intron variants near splice-donor or -acceptor sites were compared with splice consensus sequences, using an algorithm available at the Berkeley Drosophila Genome Project Web site. None of them significantly altered the splice consensus score, although analysis of RNA may be necessary to further clarify this issue. One variant associated with breast cancer, IVS10-6T→G (Broeks et al. 2000), and one missense polymorphism common in the German population, 2119T→C (“S707R” in the report by Dörk et al. [1997]), were not detected in our cohort.

Additional general conclusions about neutral variation in *ATM* can be drawn. The significantly negative value of Tajima’s *D* statistic, as well as the low nucleotide diversity in the protein-coding region, suggest that *ATM* is under an unusual degree of evolutionary constraint. Whereas the diversity in the coding sequence was very low, the diversity of noncoding sequence was comparable to that in other genes, indicating that the lack of diversity was not caused by a generally lower mutation rate at the *ATM* locus.

Not surprisingly, the smallest amount of sequence diversity was found in conserved regions that have putative functional domains. For example, there was only a single sample with a single variant in the entire carboxy-terminal 29% of the amino acid sequence, corresponding to the kinase and Tel1p homology domains. This region of *ATM* was significantly less diverse in human and chimpanzee than it was in orangutan, Old World monkey, and mouse. Consequently, either a selective pressure operates only in the former group or the selective pressures in the two groups are different because of divergent roles for the *ATM* protein in the different species.

Intriguingly, the functional constraint in *ATM* may not be restricted to the amino acid sequence. The reduced number of silent mutations in the 3′ noncoding region of the gene suggests that this region may contain sequences that regulate mRNA stability or splicing. For example, the smallest exon in the gene, exon 63, is <100 bp in length and has a splice-acceptor site with a very weak homology to known splice donor consensus se-

quences. Efficient splicing at such exons is likely to require splicing enhancers (Carlo et al. 1996; Cooper and Mattox 1997).

Differences in ATM between African and Non-African Populations

In addition to the low overall sequence diversity in *ATM* compared to other human genes, there were striking differences between African and non-African populations. For example, the sequence diversity of *ATM* in Africa was fourfold greater than it was outside of Africa. One reason for this difference was the presence of three frequent polymorphisms that defined the African-specific haplotypes H6 and H7. H6 was concentrated in central Africa, but H7 was found all across the continent.

Only two common amino acid substitutions were observed in the global population, and they were both relatively conservative changes (D→N and D→E). The D1856N variant was relatively common in non-Africans and was not found in Africans. In contrast, the D126E variant was very common in Africans but was extremely rare in non-Africans. Because the divergent *ATM* proteins were geographically isolated from one another, it is possible that the polymorphisms arose and were propagated by random genetic drift after the migration of humans out of Africa. The D126E variant may have been propagated with haplotype H7 in the Bantu expansion within Africa (Cavalli-Sforza 1994), in a situation analogous to that of markers M40 and M96 in the published Y-chromosome phylogeny (Underhill et al. 2000).

It is also possible, however, that the high allele frequency of D126E in Africa and its absence elsewhere is due to selective pressure. The presence of an allele that has reached equilibrium in one human population yet is not found elsewhere in the world is very unusual (Halushka et al. 1999); the overwhelming majority of alleles that are common in Africa are also common elsewhere (Zietkiewicz et al. 1997; Tishkoff et al. 1998). High heterozygosity for a locus might be caused by balancing selection in an area where the presence of two different alleles is advantageous, as is the case with sickle-cell anemia (MIM 603903). Although the proportion of individuals with the genotypes D/D, D/E, and E/E was consistent with Hardy-Weinberg expectations, the number of individuals analyzed here was too small to rule out selective pressure.

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Electronic-Database Information

Accession numbers and URLs for data in this article are as follows:

Berkeley Drosophila Genome Project, http://www.fruitfly.org/seq_tools/splice.html (for splice site prediction algorithm)
dbSNP Home Page, <http://www.ncbi.nlm.nih.gov/SNP/> (for polymorphisms for genes)

DNA Variation Group, <http://insertion.stanford.edu/melt.html> (for DHPLC Melt program for prediction of DHPLC analysis temperature)

GenBank, <http://www.ncbi.nlm.nih.gov/Genbank/> (for genomic sequences of *ATM* [accession number HSU82828]; *ABCB1* [accession number AC002457]; *AMPD1* [accession number M60092]; *BRCA1* [accession number U14680]; *BRCA2* [accession number U43746]; *CACNA1A* [accession number AF004884]; *COX2* [accession number U04636]; *FBN1* [accession number L13923]; *IL4* [accession number M23442]; *MMP1*, *MMP3*, and *MMP12* [accession number U78045]; *RB1* [accession number M15400]; *WRN* [accession number AF091214]; *XRCC1* [accession number M36089]; and for the mRNA and amino acid sequences of mouse *Atm* [accession number MMU43678])

LocusLink, <http://www.ncbi.nlm.nih.gov/LocusLink/> (for gene sequences)

Online Mendelian Inheritance in Man (OMIM), <http://www.ncbi.nlm.nih.gov/Omim/> (for A-T [MIM 208900])

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