



LETTER

Characterization of Short Tandem Repeats from Thirty-One Human Telomeres

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Completion of genetic and physical maps requires markers from the ends (telomeres) of every human chromosome. We have searched for short tandem repeats (microsatellites) in cosmid and P1 clones and generated 661 sequence-tagged sites (STS) from the terminal 300 kb of 31 human chromosome ends. PCR assays were successfully designed for 58 microsatellites and mapped both genetically and on radiation hybrids (RHs) to confirm their telomeric location. Sequence analysis revealed marked variation in sequence composition, consistent with the hypothesis that even very highly GC-rich chromosome bands (the T bands) are not homogenous. The STSs that we have generated will be a necessary resource for the construction of physical maps of these complex regions of the genome.

[Information about the microsatellites is available electronically at <http://www.cshl.org/gr> and sequence has been deposited in the Genome Database (GDB).]

Polymorphic markers from the ends of human chromosomes are valuable for a number of reasons. Without them, genetic maps are not complete, leading to the possibility of a disease gene being missed in the course of a mapping experiment. So far, polymorphic markers have been reported for 15 chromosome ends (Blouin et al. 1995; Browne et al. 1995; De Lange et al. 1990; Freije et al. 1992; Hing et al. 1993; Vocero-Akbani et al. 1996; Wintle et al. 1997), but for some clinical applications multiple markers will be needed at every chromosome end. For instance, subtelomeric rearrangements have been found in ~7% of cases of idiopathic mental retardation (Flint et al. 1995), but single markers do not have sufficiently high heterozygosity to detect all cases of monosomy and trisomy (Wilkie 1993). Terminal markers will also be required for high resolution analysis and physical characterization of regions that are involved in a number of human genetic diseases (Ledbetter 1992). Molecular probes from the terminal regions are already proving to be

useful diagnostic tools for a number of disorders involving the telomeric regions (NIH/IMM Collaboration 1996).

Unfortunately, characterization of the ends of human chromosomes is complicated by the presence of subtelomeric repetitive sequences. These sequences lie immediately adjacent to the telomere proper, which consists of a tandemly repeated 6-mer (TTAGGG) that protects chromosomes from degradation and fusion (for review, see Blackburn and Greider 1995; Kipling 1995). Subtelomeric sequences contain a wide variety of repetitive DNA, ranging from interspersed repeats, where one or a few copies are found on a restricted number of chromosome ends, to highly repetitive sequences present in many subtelomeric regions (Brown et al. 1990; Cross et al. 1990; De Lange et al. 1990; Wilkie et al. 1991; Royle et al. 1992; Youngman et al. 1992). The repetitive nature of subtelomeric regions has made it difficult to clone these regions using conventional approaches. However, the discovery that human telomeric sequences can function in yeast made it possible to clone human telomeres as yeast artificial chromosomes (half-YACs; Brown 1989; Ri-

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ethman et al. 1989). Previous work has demonstrated that the DNA cloned in half-YACs can faithfully represent human subtelomeric structure (Brown et al. 1990; Riethman et al. 1993; Macina et al. 1994; Negorev et al. 1994; Martin-Gallardo et al. 1995).

In this present study a variety of strategies were used to screen half-YAC DNA for polymorphic di-, tri-, and tetranucleotide repeats. In addition, a random collection of sequence was obtained to investigate sequence composition and sequence similarities between telomeres. Markers were genetically mapped on Centre d'Etude du Polymorphisme Humain (CEPH) panels and physically mapped using a set of radiation hybrids (RHs).

RESULTS AND DISCUSSION

We have developed PCR assays for 58 newly characterized markers from 28 half-YACs, 7 cosmids, and 5 P1 clones, representing 31 human telomeres. Thirty-eight of these markers are polymorphic. Table 1 shows the markers developed in this study, as well as those identified by others that we have found to be present in the clones we characterized. For completeness, telomeric markers reported by other workers are given. Table 1 shows that there are now unique sequence-tagged sites (STSs) for 28 human telomeres.

Short tandem repeat (STR) (microsatellite) markers were derived from three sources. First, we had complete sequence from the 16p (286 kb) (Flint et al. 1997a) and 4p (118 kb) (Youngman et al. 1992; Flint et al. 1997b) telomeres and knew which parts of the sequence were not repetitive. PCR assays could therefore be designed for microsatellites lying in unique DNA within 200 kb of the chromosome terminus. Second, hybridization screening with oligonucleotides and *Alu*-PCR identified sequence from half-YACs that contained microsatellites (see Methods). Third, we subcloned P1s and cosmids that had been isolated using half-YAC vector-insert junction sequence (for 2q, 13q, 6q) or were known from other data to contain subtelomeric sequence (19p, 19q, 22q, 20p) (NIH/IMM Collaboration 1996; Ning et al. 1996).

By combining these resources, we detected 167 dinucleotide microsatellites with more than 6 repeats and 20 tri- or tetramicrosatellites with more than 4 repeats. Eleven microsatellites had been or were reported during the course of this study. To design PCR assays for the remainder, we first excluded repetitive sequences. In particular, no primers were designed for microsatellites lying within

sequence that showed a similarity of >95% either to other sequence from the half-YACs or to known subtelomeric repeats. However, of the remaining 89 microsatellites, only 69 amplified a single chromosome from a monochromosomal hybrid panel.

The majority of the polymorphic markers were mapped on at least eight CEPH families. With the exception of the 2q markers, the best ordering of the new markers placed them in the most distal bin of each chromosome arm. The 2q markers mapped proximally to the most distal framework marker *D2S125*. However, *D2S125* did not amplify the 2q half-YAC or P1 clones, suggesting that there is insufficient genotyping data to order these markers correctly. Thirty-nine markers were placed with lod scores of 15 or greater on an RH panel, extending the map at 11 telomeres. At least one marker from every telomere was given a placement on the RH map. RH mapping put microsatellites from 6q, 8q, and 11q five centriRays (cR) or less centromeric of the existing distal markers, whereas the 18p marker mapped 10.5 cR centromeric and the 18q marker mapped 6.9 cR centromeric. However, existing distal markers did not amplify the corresponding telomere containing half-YACs. Because RecA-assisted restriction endonuclease (RARE) mapping has confirmed the fidelity of 6q, 8q, and 18q half-YACs, the RH map order may be incorrect. The RH mapping data are available electronically at <http://www-genome.wi.mit.edu> and a summary of RH and genetic mapping is available at <http://www.cshl.org/gr>.

The availability of complete sequence data for two telomeres (16p and 4p) allows us to assess the results of the mapping data. In line with other reports (Blouin et al. 1995; Donis-Keller et al. 1987) we find that genetic distance is inflated at the telomeres: Although the 16p markers are separated by 86,283 bp the genetic distance is >3 cM. However, neither genetic nor RH mapping data returned the correct order for the markers at 4p or 16p.

One marker showed an anomalous pattern of inheritance. Although detecting a single chromosome on the somatic cell panel and mapping by RH panel analysis to 2q, the marker *2QTEL44* was hemizygous in some CEPH families. This is consistent with the observation that there is a 50-kb chromosome length polymorphism at 2q (Macina et al. 1994) and predicts that *2QTEL44* lies within the polymorphic region. Because of this polymorphism, *2QTEL44* is not useful in all families for genetic analyses.

We investigated the sequence composition of subtelomeric regions. There is evidence that these

Table 1. STSs for 31 Human Telomeres

Name ^a	Het.	Size	Primer F	Primer R	Reference ^b
1QTEL10	0.00	119	GATCCATTCCTGTATGATGG	ACTCATTCTACGAAGTCAGC	
1QTEL19	0.75	156-189	GGAGTTAAGGTTGAAGAGCC	TTCACGTACAACAGTATCTC	
1QTEL36	0.00	146	CAAATACACTGTTGGGCATG	GTGCCTTCCAGAGATATGTC	
2PTEL12	0.79	134-148	CTGTGCTTCTGCAGGTTAGA	TACCTAGGTGAGAGTTATCC	
2PTEL23	0.56	164-200	GCCCTTCCCTACTTATTCTT	CCTATAGCAGTGGGATCCTA	
2PTEL27	0.53	230-242	TATATACATTAGGAATAATGAGAGT	GTCCCTCTCCATGTATAGA	
2PTEL31	0.27	167-176	TCCAGAACATGTGCTCCTGT	AGCTGAGATCGCACAAITTC	
2P*	0.82	119-135	CTCCACTTAAGCTTGCTTTACA	CCCTAAAAGCCTCACTACATG	1
2QTEL37	0.23	179-184	ATCCCGGCCATCTGCCTAC	CACCAGTCTTGATGGTAAC	
2QTEL44	0.56	175-185	AGCCTGGGGTGACAAAATCT	AGACGTCTCCAAAGCCAGTT	
2QTEL47	0.70	146-162	GTGAGGTGAGGAAACGCTAAG	CTGTATCGCTATGAGCCAG	
2QTEL86	0.59	226-258	AAACGTGGCAGGAGCTATGG	CATTGTTAGTTTTGCATCGC	
2QTEL98	0.00	169	CCTTTCTCCACATCCCTCAA	TCCCAGACGTTTTGTTAGGG	
3PTEL01	0.52	186-230	AGAGTTCCTAGAGGGACAG	TTGCCTGCAGTCTTCTGCC	
3PTEL02	0.00	179	TGAACTGTGGATAACTGAG	GGAAGCTGAAAAGCCAAACA	
3PTEL25	0.63	182-190	GCTAGCATGAGAATGTATAG	TACGCCTAATGAGATAACAG	
3QTEL05	0.79	150-164	TCACAGTGGCCAAAGATATCA	TCCATGTTGCTGCAAATGAC	
3QTEL06	0.78	262-276	TCACAAGGGAAAATAACTGTTTTAC	TTCTGTAAACCTCCAAAAT	2
3QTEL07	0.75	134-152	GGAAGTTTCAGCCAACG	TTAGTCCCACTGATGTTACATTT	2
4PTEL01	0.00	179	TATTGCTCTCTATGTCTTGC	GCTCATAAGAGACAAAAGAAG	
4PTEL02	0.74	153-169	ACAGCTAAAGCAGGTAATGG	GAGCGAGACTCAGTCTCAA	
4PTEL04	0.67	166-182	CTAGCTTTGATTCTATTGACC	GGTCTAAATCAATGACCTAAGC	
4PTEL05	0.00	140	CCATGTCTCATGCTAAGGCT	AACCGCCCACTACTACTCAG	
5QTEL70	0.00	191	CTATTTTTATTTCAGTTGGCTGTTT	AAGGAAACGTTTCTCTAAGTTATTA	
6QTEL53	0.74	103	GGCTAATAAATGCTTAGAGCC	GGGCTTAGTTGTTTTCCATTAG	1
6QTEL54	0.50	206-210	CAGAACAGATTAAGACTCAG	GCATTTATCAACTTGTGTCC	
6QTEL57	0.00	169	TGTGTTGCTCATCCACATGG	CATGCATTAACCTGCAG	
7Q*	0.84	217-235	GCCCAGCCTGTGTATGGTTA	CTAAAGGAAGTTCTACAGG	3
8PTEL91	0.00	144	CCCAGCATCTGACATGAGAA	TTATCGCTCAAGAAGTAGAC	
8QTEL11	0.72	94-112	TGAGATCTGTCTCTATACAC	CTACAGGTGTGTGCTACCAT	
8QTEL25	0.61	150-164	GGGCTTATTAACCTATGAGCAC	GAGTTTTACCTATCTCATTGC	
8QTEL54	0.79	159-177	GTTCTCTGAACCCTAATGCA	GTTTCCAGCATAGCACATCT	
9QTEL33	0.17	122-130	ATCTGTGTTGGATTCTTGGC	ACTGAACACACCTGTACAGG	
10PTEL35	0.76	134-150	CAGAGACTGGCATTCCCAA	GCTTTGAAAGTCACCAAGTCC	
10PTEL45	0.58	186-198	TGGGTAACAGAGTGAGACTGTCTC	AGTACACTGATGATTTTCATTTCCCT	
10PTEL62	0.69	116-130	GAAAGAAATGTCAATTCTGCA	TAGGGATCCCCTCTCCTGTT	
10P*	0.81	151-185	GGCTTAAAAGTAGGTAATTAC	CGCTTGGAACTTTTCAAGAT	1
10QTEL23	0.37	138-164	AGCAGAAGTCCAGTGTCAAGT	TCCATAAGTGCATGAGCCAA	1
10QTEL24	0.00	163	CTCCAAGGGTAACATTGAAC	CGTAAACGTTGTGAGATGGT	
11PTEL03	0.85	168-202	AGGGCAATGAGGACATGAAC	ATGTGGCTGGTCCACCTG	4
11QTEL38	0.00	158	AGGGTCTAAGCTACCCAAAG	TATGCAGGTTACAGTCAAG	
12QTEL04	0.81	177-203	AGGTGCGAGTGAGCCAAAGATT	TTCTTGGGTCTCAAGAGATC	
12QTEL07	0.00	197	GGAAACCAGCGATGAACAGA	GGACATCCTCAGATGTAGAC	
12QTEL36	0.47	230-234	AGCTAAAATCATGGGATCTCTACTA	CCAGATTATTTCTCATCTGTTTTAT	
12QTEL82	0.75	208-258	GTTCCAAGGGGAGAGTTTCAT	TAAAATGATAGTTGCACAATAATGG	
12QTEL87	0.49	170-174	TGAGACTGCAGTGAACCATG	TCTTTCTTGAAGAGGAAGCC	
13QTEL10	0.36	100-150	TACAAAGCACTGTGAGAAAATGG	ATGCTGGAGCAAGCTAGGAC	1
13QTEL56	0.30	162-166	TTGCAGTGAGCTGATATCGC	TAAACAGGATCTCTGAAGCG	
14QTEL01	0.64	174-182	GTGCCTGTAGGTATCTATGC	GCTCCCTATTTGCAAGATAC	5
14QTEL04	0.74	145-161	TGCTGTTGGACTCAGGTAGCTA	TCTCTAAAGCTACTATAACCCAG	1
14QTEL23	0.14	194-196	GATCACGCCAAATAGTATGT	TGAGATCTGTCTTGGAAACC	
16PTEL02	0.75	156-172	GAGCGAGACTCCGTCTAAA	CAGCAGCCTCAGGGTT	2
16PTEL03	0.81	174-186	ACCTAGATCCCTCCAGGTTT	GGGCCATTATTCAGCCAATC	
16PTEL05	0.76	170-182	AGCTGAGATCACGCCATTGC	TGTGAGGAGACAGGAAAGAG	
16PTEL06	0.84	149-185	GAACAGGACATGGCTGTCAT	TCTACATGTGCTTGAAGAGC	
16PTEL07	0.00	158	GGTGGACAAATGTACGAAGC	CTGAGATCGTGTCTTGCAC	
17PTEL37	0.00	196	CTGCCTTAGTGTCTCTGAGT	CACAGGGACGCACATGCTTT	
17PTEL49	0.00	261	AGTAGGTTTCAGTTGCCTTTTC	AGAGACACACAAATGACAATTAG	
17PTEL80	0.00	190	ACGCACATGCTTTCACGAAC	CCTGCCTTAGTGTCTCTGAG	
17QTEL13	0.50	233-235	CGTGCCACTCAAATATAAAC	CAAAAATAAAACTGCAAGCAATATA	

(Table 1 continued on following page.)

Table 1. (Continued)

Name ^a	Het.	Size	Primer F	Primer R	Reference ^b
18PTEL02	0.00	220	TCATTTATATGAAATTTCAAGGGAT	AAAAATAAAGCAATTGCTCATAGAA	
18P*	0.80	225-237	GCCTCATTTTCATGGAGGTGG	CTCATTTTTCAGTCCATCTGCAAG	1
18QTEL11	0.76	150-172	CCTATTTAAGTTTCTGTAAGG	ATGGTGTAGACCCTGTGGAA	
18QTEL69	0.84	118-144	ATTGCCATTCAAGGCTGAAC	GTTTTGGGAATGTCAAGAAGTACC	2
20PTEL04	0.84	152-194	GAATTCAGACTTGAGCTGG	GCTCAGTAATCTATCACTTC	
20PEND	0.70	149-173	CCCAATCTCCATAGTTCTGG	AGCTCTTCATTAATTTCTAGG	
20PTEL18	0.50	139-141	GATAGTCACTTCAACAGATGG	GTTTGCCAGGCTCACATTTA	
20PTHY33	0.81	245-261	GGTTCAATGCTACTCAATGGC	AACCACACTGACATCGTAGTGG	
21QTEL07	0.78	311-343	GAACCCATCTCACATGCAG	GAAGTGCTCTAAGAACTTGC	6
21QTEL08	0.00	190	TCAAATCTTTGTCAGAGGCG	GGAATGGGCAAATATTTCTGTG	
21QTEL14	0.39	182-194	CTAAGGACACATGCCCAATG	ACAGAGAAGGTGGGAGATTG	
22QTEL31	0.00	183	TGCATTAGGTAGATGCTGGG	TACACTAGACCAGGTGAAG	
22QTEL32	0.00	189	GACTGAGCCAAGCATGATGG	GCGTTATCCGCTCACCCATG	
22Q*	0.76	194-210	TTGCAGACAGCAGACTACAGG	TTCAGTCTGTGGCTGTCCAG	1
XQYQ*	0.70	220-244	GGCCTGAATTCATTTATTATTCTAATAG	GAACAGGCAAAGATGCCCACTCTC	7

^aListed are markers that have been mapped to human telomeres. These markers are identified by an asterisk (*).

^bMarkers identified during this project have been reported by other workers. (1) Vocero-Akbani et al. (1996); (2) Gyapay et al. (1994); Dib et al. (1996); (3) Hing et al. (1993); (4) Browne et al. (1995); (5) Blouin et al. (1995); (6) Wintle et al. (1997); (7) Freije et al. (1992).

regions are enriched for *Alu* repetitive sequences, GC content, and genes (Bickmore and Sumner 1989; Holmquist 1992), but the data are derived from low resolution methods. Our sequence data provide a more detailed picture, indicating considerable variation in these parameters among telomeres.

This study generated 267,549-bp sequence data. On average, 6% of each half-YAC was sequenced (range 2%–15%); approximately half derived from subclones that hybridized to oligonucleotide repeat probes, and the other half was a random sample. A summary of the sequence composition is given in Figure 1 and on-line at <http://www.cshl.org/gr>. We found that ~30% of the sequence was present on more than one chromosome end (this figure excludes *Alu*, L1, and other repetitive sequences dispersed throughout the genome), as judged by sequence comparison and PCR analysis of a monochromosomal somatic cell hybrid panel. Thus, ~30% of our sequence contains subterminal repeats. With the exception of *2QTEL44*, we believe that all of the microsatellites that we mapped lie centromeric to these subterminal repeats.

Analysis of sequence composition showed that the GC content for all sequence was 0.45; however, there was marked variation among telomeres: The GC content of 3p was 37% compared to a GC content of 52% for 17p. These differences were maintained when microsatellite sequences and other repeats were excluded from the analysis. The interchromosomal differences were also independent of

the total amount of sequence and the number of individual sequences obtained.

All sequence was screened for *Alu* and non-*Alu* repetitive DNA. Again, there was variation in the

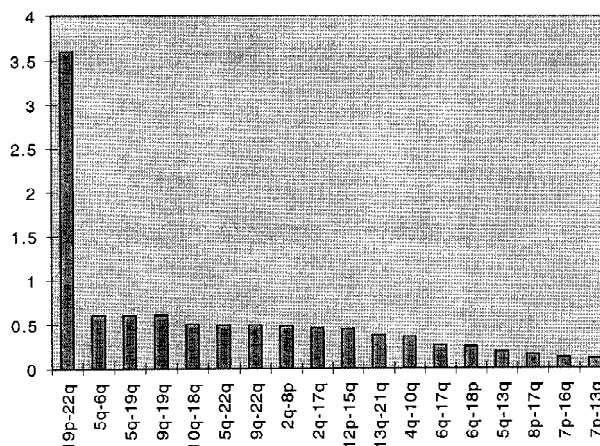


Figure 1 Intertelomeric sequence comparisons were performed with MSPcrunch. Intersequence comparisons were regarded as significant for BLASTN scores >150. The similarity score (y-axis) was then calculated by dividing the number of matches between two arms by the product of the number of clones sequenced for each arm and then multiplied by 100. The high 19q-22q similarity score is attributed to the fact that there were four matches among sequences from these arms and relatively few clones sequenced (7 for 19q and 17 for 22q).

Alu frequency at each telomere, but there was no correlation between the two types of repeat. Regression analysis of GC content on non-*Alu* repeats was marginally significant ($P < 0.018$, $F = 6.275$ with 32 df, correlation coefficient -0.4), indicating that GC content was partly determined (inversely related) by the presence of non-*Alu* repeats.

Our analyses confirmed the expected sequence similarity among subtelomeric repeats on different chromosomes. For example, a large proportion of sequence from 2q was found to be >95% identical with sequence from 8p (Macina et al. 1994). We also detected extensive similarities between 4p and 4q; 4q and 10q; 16p and 10p, 18p, 9q (Wilkie et al. 1991); 5q and 6q; and 10q and 18q.

In conclusion, we have characterized 58 microsatellites from 31 human telomeres; 38 of these are polymorphic. The telomeric localization of these markers is attested to by data from three sources. First, molecular characterization of some half-YACs has demonstrated that they contain faithful representations of human telomeres. RARE site-specific cleavage has confirmed that half-YACs contain human telomeric and subtelomeric DNA for chromosomes 1q, 2p, 2q, 6q, 8q, 12q, 13q, 14q, 18p, 18q, and 21q (NIH/IMM Collaboration 1996). Cloned contigs of the 16p, 4p, and 22q telomeres have been compared with genomic data and, in the case of the 16p and 4p telomeres, have been completely sequenced (Flint et al. 1997a,b). Second, sequence analysis presented here and fluorescent in situ hybridization data from cosmid subclones derived from the half-YACs are consistent with the telomeric origin of a further 15 half-YACs (3p, 3q, 4q, 5q, 7p, 8p, 9q, 10p, 10q, 11p, 11q, 16q, 17p, 17q, 20p) (NIH/IMM Collaboration 1996). Finally, we present genetic and RH mapping data demonstrating a telomeric location for the markers (available electronically at <http://www.cshl.org/gr>).

Our data also allow us to draw some conclusions about the sequence organization and composition of the terminal regions of human chromosomes. The variation in sequence composition at human telomeres that we have observed is consistent with the hypothesis that even very highly GC-rich chromosome bands (the T bands) are not homogenous (Holmquist 1992). We conclude that these bands contain regions with markedly different base composition and repeat content. It remains to be shown how this relates to larger scale chromosome structural features. Nevertheless, the sequence analyses described here and the markers that have been developed provide a rich resource for physical and genetic mapping of the human genome.

METHODS

Acquisition of Sequence from Half-YACs

The complete sequence of two telomeres (285 kb from 16p and 118 kb from 4p) was obtained (Flint et al. 1997a,b), permitting the recognition of di- and trinucleotide repeats by computer analysis. To obtain sequence from half-YACs, cosmid libraries were constructed from *Mbo*I partial digests of yeast DNA in agarose plugs (NIH/IMM Collaboration 1996). Each cosmid was fingerprinted by digestion to completion with *Bam*HI endonuclease, and 6–12 cosmids with minimal overlap were chosen for sequence analysis. Cosmid DNA from each half-YAC was pooled, sonicated, and a 1- to 2-kb fraction cloned into M13. M13 libraries were plated out and plaques transferred to Hybond N (Amersham International) nylon membranes. Filters were screened by hybridization to oligonucleotides for all combinations of di- and trinucleotide repeats and to GGAA(3) and GAAA(3) oligonucleotides. In addition, 96 randomly selected M13 clones were sequenced from each half-YAC library. M13 clones were sequenced using an ABI model 373 sequencer.

Seven markers were developed from sequences obtained by two alternate methods. *Alu*-CA PCR (Mutirangura et al. 1993) was used to isolate CA repeats and the unique sequence flanking one side of markers *2PTEL12*, *2QTEL44*, *8QTEL11*, *8QTEL25*, and *12QTEL04*. Using a primer selected from the *Alu*-CA PCR sequence and a primer from the vectorette sequence, vectorette PCR (Riley et al. 1990) was used to isolate the entire microsatellite sequence of each marker. 20PA36, 20PEND, and 20PTHY33 were isolated from 20p telomeric cosmids by standard subcloning methods. Fragments hybridizing to di- or tetranucleotide repeat oligonucleotides were subcloned into plasmid vectors and sequenced.

Identification of Specific and Polymorphic Repeats

Amplifications were performed in 96-well polycarbonate using a PTC-100 thermocycler (MJ Research, Watertown, MA). DNA was amplified in a 15- μ l reaction containing the following: 10 mM Tris-HCl (pH 8.3), 50 mM KCl; 1.5 mM MgCl₂; 0.01% gelatin; 0.2 mM dATP; 0.2 mM dGTP, 0.2 mM dTTP; 0.0024 mM dCTP; 1 μ Ci of [α -³²P]dCTP (3000 Ci/mmol, Amersham Corp. Arlington Heights, IL); 0.45 units of *Taq* polymerase (Perkin Elmer, Foster City, CA); 20 ng of DNA; and 0.67 μ M of each primer. After initial denaturation at 95°C for 3 min, amplification was performed for 30 cycles at 95°C for 1 min, 55°C for 1 min, and 72°C for 1 min. A final extension step of 10 min at 72°C was also performed. Products were separated by electrophoresis at 80 W through gels containing 6% polyacrylamide and 8 M urea (Sequagel-6, National Diagnostics, Atlanta, GA). The gels were exposed directly to autoradiography film at -80°C without drying.

Markers were tested for heterozygosity and specificity using a single gel format containing the products of amplification from 20 unrelated CEPH parents and either National Institute of General Medical Sciences (NIGMS) human/rodent mapping panel 2 (Coriell Cell Repositories, Camden, NJ) or a monochromosomal somatic cell hybrid panel acquired from the UK Human Genome Mapping Project (HGMP) Resource Center. Those markers that were specific for the expected chromosome and had multiple alleles were used to amplify DNA from 8–18 CEPH families to perform linkage analysis. Heterozygosity scores and allele frequencies were determined

using genotypes from unrelated individuals from either the initial screening gels (40 chromosomes) or from the mapping gels (70–128 chromosomes).

Genetic and RH Mapping

CRI-MAP (version 2.4; P. Green, unpubl.) was used to construct small linkage maps for several telomeres. Genotypes for distal markers were obtained from the Genotype CEPH database (<http://www.cephb.fr/cephdb/>). Markers were chosen primarily from the Cooperative Human Linkage Center (CHLC) maps (Murray et al. 1994), although other known telomeric markers were sometimes included in the analysis. Orders were generated by starting with the reference markers from the CHLC framework maps. These were entered as fixed markers in the CRI-MAP program. Additional markers were inserted one to two at a time and accepted in the order if they gave 1000:1 odds of being correct. They were then fixed in order, and the next markers were added. After all markers were ordered, the CRI-MAP fixed program was used to determine map position. For most telomeres, the order of those markers present within the half-YAC could not be determined with 1000:1 odds. Several of the most distal reference markers could not be placed with 1000:1 odds either. In those cases, the best order was used for determining map position. RH mapping was carried out using established protocols (Hudson, et al. 1995).

Data Analysis and Primer Design

After excluding *Alu* and other repetitive DNA, sequences were screened against dbEST and EMBL with BLASTN and against a nonredundant compilation of SWISS-PROT, PIR, and WORM-REP (*Caenorhabditis elegans* genes) with BLASTX. BLAST output was filtered using MSPcrunch (Sonnhammer and Durbin 1994), requiring a minimum of 90% identity for dbEST and EMBL matches. Sequence was viewed from within an ACEDB database. BLASTN/MSPcrunch was also used to identify sequence matches between telomeres. Sequences were then processed automatically for analysis by the PRIMER program (vs. 3) using scripts developed in the course of this project (available on request from jf@worf.molbiol.ox.ac.uk).

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