TABLE 4

Kindred 2082 Recombinants

Family	ID	M/P	Mfd15	Mfd191	Mfd188	SCG40	6C1	42D6
75		M	0	1	1	1	-	-
63		M	0	0	1	1	-	1
125		M	1	1	1	0	-	0
40		M	1	1	0	0	-	0

Analysis of markers Mfd15, Mfd188, Mfd191, and THRA1 in our recombinant families.

Mfd15, Mfd188, Mfd191 and THRA1 were typed in our recombinant families and examined for additional information to localize the BRCA1 locus. In kindred 1901, the Mfd15 recombinant was recombinant for THRA1 but uninformative for Mfd191, thus placing BRCA1 distal to THRA1. In K2082, the recombinant with Mfd15 also was recombinant with Mfd191, thus placing the BRCA1 locus distal to Mfdl91 (Goldgar *et al.*, 1994). Examination of THRA1 and Mfd191 in kindred K2035 yielded no further localization information as the two branches were concordant for both markers. However, SCG40 and 6C1 both displayed the same pattern as Mfd188, thus increasing our confidence in the localization information provided by the Mfd188 recombinant in this family. The BRCA1 locus, or at least a portion of it, therefore lies within an interval bounded by Mfd191 on the proximal side and Mfd188 on the distal side.

EXAMPLE 4

Development of Genetic and Physical Resources in the Region of Interest

To increase the number of highly polymorphic loci in the Mfd191-Mfd188 region, we developed a number of STR markers in our laboratory from cosmids and YACs which physically map to the region. These markers allowed us to further refine the region.

STSs were identified from genes known to be in the desired region to identify YACs which contained these loci, which were then used to identify subclones in cosmids, P1s or BACs. These subclones were then screened for the presence of a CA tandem repeat using a $(CA)_n$ oligonucleotide (Pharmacia). Clones with a strong signal were selected preferentially, since they were more likely to represent CA-repeats which have a large number of repeats and/or are of near-perfect fidelity to the $(CA)_n$ pattern. Both of these characteristics are known to increase the probability of polymorphism (Weber, 1990). These clones were sequenced directly from the vector to locate the repeat. We obtained a unique sequence on one side of the CA-repeat by using one of a set of possible primers complementary to the end of a CA-repeat, such as $(GT)_{10}T$. Based on this unique sequence, a primer was made to sequence back across the repeat in the other direction, yielding a unique sequence for design of a second primer flanking the CA-repeat. STRs were then screened for polymorphism on a small group of unrelated individuals and tested against the hybrid panel to confirm their physical localization. New markers which satisfied these criteria were then typed in a set of 40 unrelated individuals from the Utah and CEPH families to obtain allele frequencies appropriate for the study population. Many of the other markers reported in this study were tested in a smaller group of CEPH unrelated individuals to obtain similarly appropriate allele frequencies.

Using the procedure described above, a total of eight polymorphic STRs was found from these YACS. Of the loci identified in this manner, four were both polymorphic and localized to the BRCA1 region. Four markers did not localize to chromosome 17, reflecting the chimeric nature of the YACs used. The four markers which were in the region were denoted AA1, ED2, 4-7, and YM29. AA1 and ED2 were developed from YACs positive for the RNU2 gene, 4-7 from an EPB3 YAC and YM29 from a cosmid which localized to the region by the hybrid panel. A description of the number of alleles, heterozygosity and source of these four and all other STR polymorphisms analyzed in the breast cancer kindreds is given below in Table 5.

TABLE 5

Polymorphic Short Tandem Repeat Markers Used for Fine Structure Mapping of the BRCA1 Locus

Clone	Gene	Na**	Hetero-zygosity	Allele* Frequency (%) 1	2	3	4	5	6
Mfd15	D17S250	10	0.82	26	22	15	7	7	23
THRA1	THRA1	5							
Mfd191	D17S776	7	0.55	48	20	11	7	7	7
ED2	D17S1327	12	0.55	62	9	8	5	5	11
AA1	D17S1326	7	0.83	28	28	25	8	6	5
CA375	D17S184	10	0.75	26	15	11	9	9	20
4-7	D17S1183	9	0.50	63	15	8	6	4	4
YM29	--	9	0.62	42	24	12	7	7	8
Mfd188	D17S579	12	0.92	33	18	8	8	8	25
SCG40	D17S181	14	0.90	20	18	18	10	8	35
42D6	D17S588	11	0.86	21	17	11	10	9	32
6C1	D17S293	7	0.75	30	30	11	11	9	9
Z109	D17S750	9	0.70	33	27	7	7	7	19
tdj1475	D17S1321	13	0.84	21	16	11	11	8	33
CF4	D17S1320	6	0.63	50	27	9	7	4	3
tdj1239	D17S1328	10	0.80	86	10	9	7	4	14
U5	D17S1325	13	0.83	19	16	12	10	9	34

* Allele codes 1-5 are listed in decreasing frequency; allele numbers do not correspond to fragment sizes. Allele 6 frequency is the joint frequency of all other alleles for each locus.

** Number of alleles seen in the genetically independent DNA samples used for calculating allele frequencies.

The four STR polymorphisms which mapped physically to the region (4-7, ED2, AA1, YM29) were analyzed in the meiotic, breakpoint panel shown initially in Tables 3 and 4. Tables 6 and 7 contain the relevant CEPH data and Kindred 2082 data for localization of these four markers. In the tables, M/P indicates a maternal or paternal recombinant. A "1" indicates inherited allele is of grandpaternal origin, while a "0" indicates grandmaternal origin, and "-" indicates that the locus was untyped or uninformative.

TABLE 6

Key Recombinants Used for Genetic Ordering of New STR Loci Developed in Our Laboratory Within the BRCA1 Region of 17q

CEPH Family	ID	M/P	Mfd15	THRA1	Mfd191	ED2	AA1	Z109	4-7	YM29	Mfd188	SCG40	42D6
13292	4	M	1	1	1	1	1	0	0	0	0	0	0
13294	4	M	1	0	0	-	0	-	-	-	0	-	-
13294	6	M	0	0	1	-	1	-	-	-	1	-	-
1333	4	M	1	1	1	-	0	-	-	0	0	-	0
1333	6	M	0	0	1	-	1	-	-	1	1	-	1
1333	3	M	0	0	1	-	-	-	1	1	1	-	1

TABLE 7

Kindred 2082 Recombinants

ID	M/P	Mfd15	Mfd191	ED2	AA1	4-7	YM29	Mfd188	SCG40	42D6
63	M	0	0	1	-	1	1	1	1	1
125	M	1	1	1	-	1	1	1	0	0
40	M	1	1	0	-	0	-	0	0	0
22	P	0	0	1	1	1	1	1	1	1

From CEPH 1333-04, we see that AA1 and YM29 must lie distal to Mfdl91. From 13292, it can be inferred that both AA1 and ED2 are proximal to 4-7, YM29, and Mfd188. The recombinants found in K2082 provide some additional ordering information. Three independent observations (individual numbers 22, 40, & 63) place AA1, ED2, 4-7, and YM29, and Mfd188 distal to Mfd191, while ID 125 places 4-7, YM29, and Mfd188 proximal to SCG40. No genetic information on the relative ordering within the two clusters of markers AA1/ED2 and 4-7/YM29/Mfd188 was obtained from the genetic recombinant analysis. Although ordering loci with respect to hybrids which are known to contain "holes" in which small pieces of interstitial human DNA may be missing is problematic, the hybrid patterns indicate that 4-7 lies above both

YM29 and Mfd188.

EXAMPLE 5

Genetic Analyses of Breast Cancer Kindreds with Markers AA1, 4-7, ED2, and YM29

In addition to the three kindreds containing key recombinants which have been discussed previously, kindred K2039 was shown through analysis of the newly developed STR markers to be linked to the region and to contain a useful recombinant.

Table 8 defines the haplotypes (shown in coded form) of the kindreds in terms of specific marker alleles at each locus and their respective frequencies. In Table 8, alleles are listed in descending order of frequency; frequencies of alleles 1-5 for each locus are given in Table 5. Haplotypes coded H are BRCA1 associated haplotypes, P designates a partial H haplotype, and an R indicates an observable recombinant haplotype. As evident in Table 8, not all kindreds were typed for all markers; moreover, not all individuals within a kindred were typed for an identical set of markers, especially in K2082. With one exception, only haplotypes inherited from affected or at-risk kindred members are shown; haplotypes from spouses marrying into the kindred are not described. Thus in a given sibship, the appearance of haplotypes X and Y indicates that both haplotypes from the affected/at-risk individual were seen and neither was a breast cancer associated haplotype.

TABLE 8

Breast Cancer Linked Haplotypes Found in the Three Kindreds

Kin.	HAP	Mfd 15	THRA1	Mfd 191	tdj 1475	ED2	AA1	Z109	CA375	4-7	YM29	Mfd 188	SCG40	6C1	42D6
1901	H1	1	5	5	3	1	4	NI	NI	1	1	3	NI	NI	1
	R2	9	2	5	6	1	4	NI	NI	1	1	3	NI	NI	1
2082	H1	3	NI	4	6	6	1	NI	NI	2	1	4	2	NI	1
	P1	3	NI	4	NI	NI	NI	NI	NI	NI	NI	4	2	NI	1
	P2	3	NI	NI	NI	NI	NI	NI	NI	NI	NI	4	NI	NI	NI
	R1	6	NI	1	5	6	1	NI	NI	2	1	4	2	NI	1
	R2	6	NI	4	6	6	1	NI	NI	2	1	4	2	NI	1
	R3	3	NI	4	NI	6	1	NI	NI	2	1	4	1	NI	7
	R4	7	NI	1	NI	1	5	NI	NI	4	6	1	2	NI	1
	R5	3	NI	4	NI	NI	NI	NI	NI	NI	2	1	NI	NI	NI
	R6	3	NI	4	3	1	2	NI	NI	1	2	2	6	NI	6
	R7	3	NI	4	3	7	1	NI	NI	1	1	3	7	NI	4
2035	HI	8	2	1	NI	5	1	1	4	3	1	6	8	2	4
	H2	8	2	1	NI	5	1	1	2	1	1	2	3	1	4
	R2	8	2	1	NI	5	1	1	2	1	1	2	3	6	1

In kindred K1901, the new markers showed no observable recombination with breast cancer susceptibility, indicating that the recombination event in this kindred most likely took place between THRA1 and ED2. Thus, no new BRCA1 localization information was obtained based upon studying the four new markers in this kindred. In kindred 2082 the key recombinant individual has inherited the linked alleles for ED2, 4-7, AA1, and YM29, and was recombinant for tdj1474 indicating that the recombination event occurred in this individual between tdj 1474 and ED2/AA1.

There are three haplotypes of interest in kindred K2035, H1, H2, and R2 shown in Table 8. H1 is present in the four cases and one obligate male carrier descendant from individual 17 while H2 is present or inferred in two cases and two obligate male carriers in descendants of individual 10. R2 is identical to H2 for loci between and including Mfd15 and SCG40, but has recombined between SCG40 and 42D6. Since we have established that BRCA1 is proximal to 42D6, this H2/R2 difference adds no further localization information. H1 and R2 share an identical allele at Mfd15, THRA1, AA1, and ED2 but differ for loci presumed distal to ED2, i.e., 4-7, Mfd188, SCG40, and 6C1. Although the two haplotypes are concordant for the 5th allele for marker YM29, a marker which maps physically between 4-7 and Mfd188, it is likely that the alleles are shared identical by state rather than identical by descent since this allele is the most common allele at this locus with a frequency estimated in CEPH parents of 0.42. By contrast, the linked alleles shared at the Mfd15 and ED2 loci have frequencies of 0.04 and 0.09, respectively. They also share more common alleles at Mfd191 (frequency = 0.52), THRA1, and AA1 (frequency = 0.28). This is the key recombinant in the set as it is the sole recombinant in which breast cancer segregated with the proximal portion of the haplotype, thus setting the distal boundary. The evidence from this kindred therefore places the BRCA1 locus proximal to 4-7.

The recombination event in kindred 2082 which places BRCA1 distal to tdj 1474 is the only one of the four events described which can be directly inferred; that is, the affected mother's genotype can be inferred from her spouse and offspring, and the recombinant haplotype can be seen in her affected daughter. In this family the odds in favor of affected individuals carrying BRCA1 susceptibility alleles are extremely high; the only possible interpretations of the data are that BRCA1 is distal to Mfd191 or alternatively that the purported recombinant is a sporadic case of ovarian cancer at age 44. Rather than a directly observable or inferred recombinant, interpretation of kindred 2035 depends on the observation of distinct 17q-haplotypes segregating in different and sometimes distantly related branches of the kindred. The observation that portions of these haplotypes have alleles in common for some markers while they differ at other markers places the BRCA1 locus in the shared region. The confidence in this placement depends on several factors: the relationship between the individuals carrying the respective haplotypes, the frequency of the shared allele, the certainty with which the haplotypes can be shown to segregate with the BRCA1 locus, and the density of the markers in the region which define the haplotype. In the case of kindred 2035, the two branches are closely related, and each branch has a number of early onset cases which carry the respective haplotype. While two of the shared alleles are common, (Mfd191, THRA1), the estimated frequencies of the shared alleles at Mfd15, AA1, and ED2 are 0.04, 0.28, and 0.09, respectively. It is therefore highly likely that these alleles are identical by descent (derived from a common ancestor) rather than identical by state (the same allele but derived from the general population).

EXAMPLE 6

Refined Physical Mapping Studies Place the BRCA1 Gene in a Region Flanked by tdj 1474 and U5R

Since its initial localization to chromosome 17q in 1990 (Hall *et al.*, 1990) a great deal of effort has gone into localizing the BRCA1 gene to a region small enough to allow implementation of effective positional cloning strategies to isolate the gene. The BRCA1 locus was first localized to the interval Mfd15 (D17S250) - 42D6 (D17S588) by multipoint linkage analysis (Easton *et al.*, 1993) in the collaborative Breast Cancer Linkage Consortium dataset consisting of 214 families collected worldwide. Subsequent refinements of the localization have been based upon individual recombinant events in specific families. The region THRA1 - D17S183 was defined by Bowcock *et al.*, 1993; and the region THRA1 - D17S78 was defined by Simard *et al.*, 1993.

We further showed that the BRCA1 locus must lie distal to the marker Mfd191 (D17S776) (Goldgar *et al.*, 1994). This marker is known to lie distal to THRA1 and RARA. The smallest published region for the BRCA1 locus is thus between D17S776 and D17S78. This region still contains approximately 1.5 million bases of DNA, making the isolation and testing of all genes in the region a very difficult task. We have therefore undertaken the tasks of constructing a physical map of the region, isolating a set of polymorphic STR markers located in the region, and analyzing these new markers in a set of informative families to refine the location of the BRCA1 gene to a manageable interval.

Four families provide important genetic evidence for localization of BRCA1 to a sufficiently small region for the application of positional cloning strategies. Two families (K2082, K1901) provide data relating to the proximal boundary for BRCA1 and the other two (K2035, K1813) fix the distal boundary. These families are discussed in detail below. A total of 15 Short Tandem Repeat markers assayable by PCR were used to refine this localization in the families studied. These markers include DS17S7654, DS17S975, tdj1474, and tdj1239. Primer sequences for these markers are provided in SEQ ID NO:3 and SEQ ID NO:4 for DS17S754; in SEQ ID NO:5 and SEQ ID NO:6 for DS17S975; in SEQ ID NO:7 and SEQ ID NO:8 for tdj1474; and, in SEQ ID NO:9 and SEQ ID NO:10 for tdj 1239.

Kindred 2082

Kindred 2082 is the largest BRCA1-linked breast/ovarian cancer family studied to date. It has a LOD score of 8.6, providing unequivocal evidence for 17q linkage. This family has been previously described and shown to contain a critical recombinant placing BRCA1 distal to MFD191 (D17S776). This recombinant occurred in a woman diagnosed with ovarian cancer at age 45 whose mother had ovarian cancer at age 63. The affected mother was deceased; however, from her children, she could be inferred to have the linked haplotype present in the 30 other linked cases in the family in the region between Mfd15 and Mfd188. Her affected daughter received the linked allele at the loci ED2, 4-7, and

Mfd188, but received the allele on the non-BRCA1 chromosome at Mfd15 and Mfd191. In order to further localize this recombination breakpoint, we tested the key members of this family for the following markers derived from physical mapping resources: tdj1474, tdj1239, CF4, D17S855. For the markers tdj1474 and CF4, the affected daughter did not receive the linked allele. For the STR locus tdj1239, however, the mother could be inferred to be informative and her daughter did receive the BRCA1-associated allele. D17S855 was not informative in this family. Based on this analysis, the order is 17q centromere - Mfd191 - 17HSD - CF4 - tdj1474 - tdj1239 - D17S855 - ED2 - 4-7 - Mfd188 - 17q telomere. The recombinant described above therefore places BRCA1 distal to tdj1474, and the breakpoint is localized to the interval between tdj1474 and tdj1239. The only alternative explanation for the data in this family other than that of BRCA1 being located distal to tdj 1474, is that the ovarian cancer present in the recombinant individual is caused by reasons independent of the BRCA1 gene. Given that ovarian cancer diagnosed before age 50 is rare, this alternate explanation is exceedingly unlikely.

Kindred 1901

Kindred 1901 is an early-onset breast cancer family with 7 cases of breast cancer diagnosed before 50, 4 of which were diagnosed before age 40. In addition, there were three cases of breast cancer diagnosed between the ages of 50 and 70. One case of breast cancer also had ovarian cancer at age 61. This family currently has a LOD score of 1.5 with D17S855. Given this linkage evidence and the presence of at lease one ovarian cancer case, this family has a posterior probability of being due to BRCA1 of over 0.99. In this family, the recombination comes from the fact that an individual who is the brother of the ovarian cancer case from which the majority of the other cases descend, only shares a portion of the haplotype which is cosegregating with the other cases in the family. However, he passed this partial haplotype to his daughter who developed breast cancer at age 44. If this case is due to the BRCA1 gene, then only the part of the haplotype shared between this brother and his sister can contain the BRCA1 gene. The difficulty in interpretation of this kind of information is that while one can be sure of the markers which are not shared and therefore recombinant, markers which are concordant can either be shared because they are non-recombinant, or because their parent was homozygous. Without the parental genotypic data it is impossible to discriminate between these alternatives. Inspection of the haplotype in K1901, shows that he does not share the linked allele at Mfd15 (D17S250), THRA1, CF4 (D17S1320), and tdj1474 (17DS1321). He does share the linked allele at Mfd191 (D17S776), ED2 (D17S1327), tdj1239 (D17S1328), and Mfd188 (D17S579). Although the allele shared at Mfd191 is relatively rare (0.07), we would presume that the parent was homozygous since they are recombinant with markers located nearby on either side, and a double recombination event in this region would be extremely unlikely. Thus the evidence in this family would also place the BRCA1 locus distal to tdj1474. However, the lower limit of this breakpoint is impossible to determine without parental genotype information. It is intriguing that the key recombinant breakpoint in this family confirms the result in Kindred 2082. As before, the localization information in this family is only meaningful if the breast cancer was due to the BRCA1 gene. However, her relatively early age at diagnosis (44) makes this seem very likely since the risk of breast cancer before age 45 in the general population is low (approximately 1%).

Kindred 2035

This family is similar to K1901 in that the information on the critical recombinant events is not directly observed but is inferred from the observation that the two haplotypes which are cosegregating with the early onset breast cancer in the two branches of the family appear identical for markers located in the proximal portion of the 17q BRCA1 region but differ at more distal loci. Each of these two haplotypes occurs in at least four cases of early-onset or bilateral breast cancer. The overall LOD score with ED2 in this family is 2.2, and considering that there is a case of ovarian cancer in the family (indicating a prior probability of BRCA1 linkage of 80%), the resulting posterior probability that this family is linked to BRCA1 is 0.998. The haplotypes are identical for the markers Mfd15, THRA1, Mfd191, ED2, AA1, D17S858 and D17S902. The common allele at Mfd15 and ED2 are both quite rare, indicating that this haplotype is shared identical by descent. The haplotypes are discordant, however, for CA375, 4-7, and Mfd188, and several more distal markers. This indicates that the BRCA1 locus must lie above the marker CA-375. This marker is located approximately 50 kb below D17S78, so it serves primarily as additional confirmation of this previous lower boundary as reported in Simard *et al.* (1993).

Kindred 1813

Kindred 1813 is a small family with four cases of breast cancer diagnosed under the age of 40 whose mother had breast cancer diagnosed at age 45 and ovarian cancer at age 61. This situation is somewhat complicated by the fact the four cases appear to have three different fathers, only one of whom has been genotyped. However, by typing a number of different markers in the BRCA1 region as well as highly polymorphic markers elsewhere in the genome, the paternity of all children in the family has been determined with a high degree of certainty. This family yields a maximum multipoint LOD score of 0.60 with 17q markers and, given that there is at least one case of ovarian cancer, results in a posterior probability of being a BRCA1 linked family of 0.93. This family contains a directly observable recombination event in individual 18 (see Figure 5 in Simard *et al.*, *Human Mol. Genet.* **2**:1193-1199 (1993)), who developed breast cancer at age 34. The genotype of her affected mother at the relevant 17q loci can be inferred from her genotypes, her affected sister's genotypes, and the genotypes of three other unaffected siblings. Individual 18 inherits the BRCA1-linked alleles for the following loci: Mfd15, THRA1, D17S800, D17S855, AA1, and D17S931. However, for markers below D17S931, i.e., U5R, vrs31, D17S858, and D17S579, she has inherited the alleles located on the non-disease bearing chromosome. The evidence from this family therefore would place the BRCA1 locus proximal to the marker U5R. Because of her early age at diagnosis (34) it is extremely unlikely that the recombinant individual's cancer is not due to the gene responsible for the other cases of breast/ovarian cancer in this family; the uncertainty in this family comes from our somewhat smaller amount of evidence that breast cancer in this family is due to BRCA1 rather than a second, as yet unmapped, breast cancer susceptibility locus.

Size of the region containing BRCA1

Based on the genetic data described in detail above, the BRCA1 locus must lie in the interval between the markers tdj1474 and U5R, both of which were isolated in our laboratory. Based upon the physical maps shown in Figures 2 and 3, we can try to estimate the physical distance between these two loci. It takes approximately 14 P1 clones with an average insert size of approximately 80 kb to span the region. However, because all of these P1s overlap to some unknown degree, the physical region is most likely much smaller than 14 times 80 kb. Based on restriction maps of the clones covering the region, we estimate the size of the region containing BRCA1 to be approximately 650 kb.

EXAMPLE 7

Identification of Candidate cDNA Clones for the BRCA1 Locus by Genomic Analysis of the Contig Region

Complete screen of the plausible region.

The first method to identify candidate cDNAs, although labor intensive, used known techniques. The method comprised the screening of cosmids and P1 and BAC clones in the contig to identify putative coding sequences. The clones containing putative coding sequences were then used as probes on filters of cDNA libraries to identify candidate cDNA clones for future analysis. The clones were screened for putative coding sequences by either of two methods.

Zoo blots.

The first method for identifying putative coding sequences was by screening the cosmid and P1 clones for sequences conserved through evolution across several species. This technique is referred to as "zoo blot analysis" and is described by Monaco, 1986. Specifically, DNAs from cow, chicken, pig, mouse and rat were digested with the restriction enzymes EcoRI and HindIII (8 μg of DNA per enzyme). The digested DNAs were separated overnight on an 0.7% gel at 20 volts for 16 hours (14 cm gel), and the DNA transferred to Nylon membranes using standard Southern blot techniques. For example, the zoo blot filter was treated at 65°C in 0.1 x SSC, 0.5% SDS, and 0.2M Tris, pH 8.0, for 30 minutes and then blocked overnight at 42°C in 5x SSC, 10% PEG 8000, 20 mM $NaPO_4$ pH 6.8, 100 μg/ml Salmon Sperm DNA, Ix Denhardt's, 50% formamide, 0.1% SDS, and 2 μg/ml C_0t-1 DNA.

The cosmid and P1 clones to be analyzed were digested with a restriction enzyme to release the human DNA from the vector DNA. The DNA was separated on a 14 cm, 0.5% agarose gel run overnight at 20 volts for 16 hours. The human DNA bands were cut out of the gel and electroeluted from the gel wedge at 100 volts for at least two hours in 0.5x Tris Acetate buffer (Maniatis *et al.*, 1982). The eluted Not I digested DNA (~15 kb to 25 kb) was then digested with EcoRI restriction enzyme to give smaller fragments (~0.5 kb to 5.0 kb) which melt apart more easily for the next step of labeling the DNA with radionucleotides. The DNA fragments were labeled by means of the hexamer random prime labeling method (Boehringer-Mannheim, Cat. #1004760). The labeled DNA was spermine precipitated (add 100 μl TE, 5 μl 0.1 M spermine, and 5 μl of 10 mg/ml salmon sperm DNA) to remove unincorporated radionucleotides. The labeled DNA was then resuspended in 100 μl TE, 0.5 M NaCl at 65°C for 5 minutes and then blocked with Human C_0t-1 DNA for 2-4 hrs. as per the manufacturer's instructions (Gibco/BRL, Cat. #5279SA). The C_0t-1 blocked probe was incubated on the zoo blot filters in the blocking solution overnight at 42°C. The filters were washed for 30 minutes at room temperature in 2 x SSC, 0.1% SDS, and then in the same buffer for 30 minutes at 55°C. T_he filters were then exposed 1 to 3 days at -70°C to Kodak XAR-5 film with an intensifying screen. Thus, the zoo blots were hybridized with either the pool of Eco-R1 fragments from the insert, or each of the fragments individually.

HTF island analysis.

The second method for identifying cosmids to use as probes on the cDNA libraries was HTF island analysis. Since the pulsed-field map can reveal HTF islands, cosmids that map to these HTF island regions were analyzed with priority. HTF islands are segments of DNA which contain a very high frequency of unmethylated CpG dinucleotides (Tonolio *et al.*, 1990) and are revealed by the clustering of restriction sites of enzymes whose recognition sequences include CpG dinucleotides. Enzymes known to be useful in HTF-island analysis are AscI, NotI, BssHII, EagI, SacII, NaeI, NarI, SmaI, and MluI (Anand, 1992). A pulsed-field map was created using the enzymes NotI, NruI, EagI, SacII, and SalI, and two HTF islands were found. These islands are located in the distal end of the region, one being distal to the GP2B locus, and the other being proximal to the same locus, both outside the BRCA1 region. The cosmids derived from the YACs that cover these two locations were analyzed to identify those that contain these restriction sites, and thus the HTF islands.

cDNA screening.

Those clones that contain HTF islands or show hybridization to other species DNA besides human are likely to contain coding sequences. The human DNA from these clones was isolated as whole insert or as EcoRI fragments and labeled as described above. The labeled DNA was used to screen filters of various cDNA libraries under the same conditions as the zoo blots except that the cDNA filters undergo a more stringent wash of 0.1 x SSC, 0.1% SDS at 65°C for 30 minutes twice.

Most of the cDNA libraries used to date in our studies (libraries from normal breast tissue, breast tissue from a woman in her eighth month of pregnancy and a breast malignancy) were prepared at Clonetech, Inc. The cDNA library generated from breast tissue of an 8 month pregnant woman is available from Clonetech (Cat. #HL1037a) in the Lambda gt-10 vector, and is grown in C600Hfl bacterial host cells. Normal breast tissue and malignant breast tissue samples were isolated from a 37 year old Caucasian female and one-gram of each tissue was sent to Clonetech for mRNA processing and cDNA library construction. The latter two libraries were generated using both random and oligo-dT priming, with size selection of the final products which were then cloned into the Lambda Zap II vector, and grown in XL1-blue strain of bacteria as described by the manufacturer. Additional tissue-specific cDNA libraries include human fetal brain (Stratagene, Cat. 936206), human testis (Clonetech Cat. HL3024), human thymus (Clonetech Cat. HL1127n), human brain (Clonetech Cat. HL11810), human placenta (Clonetech Cat 1075b), and human skeletal muscle (Clonetech Cat. HL1124b).

The cDNA libraries were plated with their host cells on NZCYM plates, and filter lifts are made in duplicate from each plate as per Maniatis *et al.* (1982). Insert (human) DNA from the candidate genomic clones was purified and radioactively labeled to high specific activity. The radioactive DNA was then hybridized to the cDNA filters to identify those cDNAs which correspond to genes located within the candidate cosmid clone. cDNAs identified by this method were picked, replated, and screened again with the labeled clone insert or its derived EcoRI fragment DNA to verify their positive status. Clones that were positive after this second round of screening were then grown up and their DNA purified for Southern blot analysis and sequencing. Clones were either purified as plasmid through *in vivo* excision of the plasmid from the Lambda vector as described in the protocols from the manufacturers, or isolated from the Lambda vector as a restriction fragment and subcloned into plasmid vector.

The Southern blot analysis was performed in duplicate, one using the original genomic insert DNA as a probe to verify that cDNA insert contains hybridizing sequences. The second blot was hybridized with cDNA insert DNA from the largest cDNA clone to identify which clones represent the same gene. All cDNAs which hybridize with the genomic clone and are unique were sequenced and the DNA analyzed to determine if the sequences represent known or unique genes. All cDNA clones which appear to be unique were further analyzed as candidate BRCA1 loci. Specifically, the clones are hybridized to Northern blots to look for breast specific expression and differential expression in normal versus breast tumor RNAs. They are also analyzed by PCR on clones in the BRCA1 region to verify their location. To map the extent of the locus, full length cDNAs are isolated and their sequences used as PCR probes on the YACs and the clones surrounding and including the original identifying clones. Intron-exon boundaries are then further defined through sequence analysis.

We have screened the normal breast, 8 month pregnant breast and fetal brain cDNA libraries with zoo blot-positive Eco R1 fragments from cosmid BAC and P1 clones in the region. Potential BRCA1 cDNA clones were identified among the three libraries. Clones were picked, replated, and screened again with the original probe to verify that they were positive.

Analysis of hybrid-selected cDNA.

cDNA fragments obtained from direct selection were checked by Southern blot hybridization against the probe DNA to verify that they originated from the contig. Those that passed this test were sequenced in their entirety. The set of DNA sequences obtained in this way were then checked against each other to find independent clones that overlapped. For example, the clones 694-65, 1240-1 and 1240-33 were obtained independently and subsequently shown to derive from the same contiguous cDNA sequence which has been named EST:489:1.

Analysis of candidate clones.

One or more of the candidate genes generated from above were sequenced and the information used for identification and classification of each expressed gene. The DNA sequences were compared to known genes by nucleotide sequence comparisons and by translation in all frames followed by a comparison with known amino acid sequences. This was accomplished using Genetic Data Environment (GDE) version 2.2 software and the Basic Local Alignment Search Tool (Blast) series of client/server software packages (e.g., BLASTN 1.3.13MP), for sequence comparison against both local and remote sequence databases (e.g., GenBank), running on Sun SPARC workstations. Sequences reconstructed from collections of cDNA clones identified with the cosmids and P1s have been generated. All candidate genes that represented new sequences were analyzed further to test their candidacy for the putative BRCA1 locus.

Mutation screening.

To screen for mutations in the affected pedigrees, two different approaches were followed. First, genomic DNA isolated from family members known to carry the susceptibility allele of BRCA1 was used as a template for amplification of candidate gene sequences by PCR. If the PCR primers flank or overlap an intron/exon boundary, the amplified fragment will be larger than predicted from the cDNA sequence or will not be present in the amplified mixture. By a combination of such amplification experiments and sequencing of P1, BAC or cosmid clones using the set of designed primers it is possible to establish the intron/exon structure and ultimately obtain the DNA sequences of genomic DNA from the pedigrees.

A second approach that is much more rapid if the intron/exon structure of the candidate gene is complex involves sequencing fragments amplified from pedigree lymphocyte cDNA. cDNA synthesized from lymphocyte mRNA extracted from pedigree blood was used as a substrate for PCR amplification using the set of designed primers. If the candidate gene is expressed to a significant extent in lymphocytes, such experiments usually produce amplified fragments that can be sequenced directly without knowledge of intron/exon junctions.

The products of such sequencing reactions were analyzed by gel electrophoresis to determine positions in the sequence that contain either mutations such as deletions or insertions, or base pair substitutions that cause amino acid changes or other detrimental effects.

Any sequence within the BRCA1 region that is expressed in breast is considered to be a candidate gene for BRCA1. Compelling evidence that a given candidate gene corresponds to BRCA11 comes from a demonstration that pedigree families contain defective alleles of the candidate.

EXAMPLE 8

Identification of BRCA1

Identification of BRCA1.

Using several strategies, a detailed map of transcripts was developed for the 600 kb region of 17q21 between D17S1321 and D1751324. Candidate expressed sequences were defined as DNA sequences obtained from: 1) direct screening of breast, fetal brain, or lymphocyte cDNA libraries, 2) hybrid selection of breast, lymphocyte or ovary cDNAs, or 3) random sequencing of genomic DNA and prediction of coding exons by XPOUND (Thomas and Skolnick, 1994). These expressed sequences in many cases were assembled into contigs composed of several independently identified sequences. Candidate genes may comprise more than one of these candidate expressed sequences. Sixty-five candidate expressed sequences within this region were identified by hybrid selection, by direct screening of cDNA libraries, and by random sequencing of P1 subclones. Expressed sequences were characterized by transcript size, DNA sequence, database comparison, expression pattern, genomic structure, and, most importantly, DNA sequence analysis in individuals from kindreds segregating 17q-linked breast and ovarian cancer susceptibility.

Three independent contigs of expressed sequence, 1141:1 (649 bp), 694:5 (213 bp) and 754:2 (1079 bp) were isolated and eventually shown to represent portions of BRCA1. When ESTs for these contigs were used as hybridization probes for Northern analysis, a single transcript of approximately 7.8 kb was observed in normal breast mRNA, suggesting that they encode different portions of a single gene. Screens of breast, fetal brain, thymus, testes, lymphocyte and placental cDNA libraries and PCR experiments with breast mRNA linked the 1141:1, 694:5 and 754:2 contigs. 5'

RACE experiments with thymus, testes, and breast mRNA extended the contig to the putative 5' end, yielding a composite full length sequence. PCR and direct sequencing of P1s and BACs in the region were used to identify the location of introns and allowed the determination of splice donor and acceptor sites. These three expressed sequences were merged into a single transcription unit that proved in the final analysis to be BRCA1. This transcription unit is located adjacent to D17S855 in the center of the 600 kb region (Fig. 4).

Combination of sequences obtained from cDNA clones, hybrid selection sequences, and amplified PCR products allowed construction of a composite full length BRCA1 cDNA (SEQ ID NO:1). The sequence of the BRCA1 cDNA (up through the stop codon) has also been deposited with GenBank and assigned accession number U-14680. This deposited sequence is incorporated herein by reference. The cDNA clone extending farthest in the 3' direction contains a poly (A) tract preceded by a polyadenylation signal. Conceptual translation of the cDNA revealed a single long open reading frame of 208 kilodaltons (amino acid sequence: SEQ ID NO:2) with a potential initiation codon flanked by sequences resembling the Kozak consensus sequence (Kozak, 1987). Smith-Waterman (Smith and Waterman, 1981) and BLAST (Altschul *et al.*, 1990) searches identified a sequence near the amino terminus with considerable homology to zinc-finger domains (Fig. 5). This sequence contains cysteine and histidine residues present in the consensus C3HC4 zinc-finger motif and shares multiple other residues with zinc-finger proteins in the databases. The BRCA1 gene is composed of 23 coding exons arrayed over more than 100 kb of genomic DNA (Fig. 6). Northern blots using fragments of the BRCA1 cDNA as probes identified a single transcript of about 7.8 kb, present most abundantly in breast, thymus and testis, and also present in ovary (Fig. 7). Four alternatively spliced products were observed as independent cDNA clones; 3 of these were detected in breast and 2 in ovary mRNA (Fig. 6). A PCR survey from tissue cDNAs further supports the idea that there is considerable heterogeneity near the 5' end of transcripts from this gene; the molecular basis for the heterogeneity involves differential choice of the first splice donor site, and the changes detected all alter the transcript in the region 5' of the identified start codon. We have detected six potential alternate splice donors in this 5' untranslated region, with the longest deletion being 1,155 bp. The predominant form of the BRCA1 protein in breast and ovary lacks exon 4. The nucleotide sequence for BRCA1 exon 4 is shown in SEQ ID NO:11, with the predicted amino acid sequence shown in SEQ ID NO:12.

Additional 5' sequence of BRCA1 genomic DNA is set forth in SEQ ID NO:13. The G at position 1 represents the potential start site in testis. The A in position 140 represents the potential start site in somatic tissue. There are six alternative splice forms of this 5' sequence as shown in Figure 8. The G at position 356 represents the canonical first splice donor site. The G at position 444 represents the first splice donor site in two clones (testis 1 and testis 2). The G at position 889 represents the first splice donor site in thymus 3. A fourth splice donor site is the G at position 1230. The T at position 1513 represents the splice acceptor site for all of the above splice donors. A fifth alternate splice form has a first splice donor site at position 349 with a first acceptor site at position 591 and a second splice donor site at position 889 and a second acceptor site at position 1513. A sixth alternate form is unspliced in this 5' region. The A at position 1532 is the canonical start site, which appears at position 120 of SEQ ID NO:1. Partial genomic DNA sequences determined for BRCA1 are set forth in Figures 10A-10H and SEQ ID Numbers:14-34. The lower case letters (in figures 10A-10H) denote intron sequence while the upper case letters denote exon sequence. Indefinite intervals within introns are designated with vvvvvvvvvvvvv in Figures 10A-10H. The intron/exon junctions are shown in Table 9. The CAG found at the 5' end of exons 8 and 14 is found in some cDNAs but not in others. Known polymorphic sites are shown in Figures 10A-10H in boldface type and are underlined.

TABLE 9

Exon No.	Base Position* 5'	Base Position* 3'	Length	Intron Borders 5'	Intron Borders 3'
e1	1	100	100	GATAAATTAAAACTGCGACTGCGCGGCGTG[35*]	GTAGTAGAGTCCCGGGAAAGGGACAGGGGG[36]
e2	101	199	99	ATATATATATGTTTTTCTAATGTGTTAAAG[37]	GTAAGTCAGCACAAGAGTGTATTAATTTGG[38]
e3	200	253	54	TTTCTTTTTCTCCCCCCCCTACCCTGCTAG[39]	GTAAGTTTGAATGTGTTATGTGGCTCCATT[40]
e4	***	***	111	AGCTACTTTTTTTTTTTTTTTTTGAGACAG[41]	GTAAGTGCACACCACCATATCCAGCTAAAT[42]
e5	254	331	78	AATTGTTCTTTCTTTCTTTATAATTTATAG[43]	GTATATAATTTGGTAATGATGCTAGGTTGG[44]
e6	332	420	89	GAGTGTGTTTCTCAAACAATTTAATTTCAG[45]	GTAAGTGTTGAATATCCCAAGAATGACACT[46]
e7	421	560	140	AAACATAATGTTTTCCCTTGTATTTTACAG[47]	GTAAAACCATTTGTTTTCTTCTTCTTCTTC[48]
e8	561	666	106	TGCTTGACTGTTCTTTACCATACTGTTTAG[49]	GTAAGGGTCTCAGGTTTTTTAAGTATTTAA[50]
e9	667	712	46	TGATTTATTTTTTGGGGGGAAATTTTTTAG[51]	GTGAGTCAAAGAGAACCTTTGTCTATGAAG[52]
e10	713	789	77	TCTTATTAGGACTCTGTCTTTTCCCTATAG[53]	GTAATGGCAAAGTTTGCCAACTTAACAGGC[54]
e11	790	4215	3426	GAGTACCTTGTTATTTTTGTATATTTTCAG[55]	GTATTGGAACCAGGTTTTTGTGTTTGCCCC[56]
e12	4216	4302	87	ACATCTGAACCTCTGTTTTTGTTATTTAAG[57]	AGGTAAAAAGCGTGTGTGTGTGTGCACATG[58]
e13	4303	4476	174	CATTTTCTTGGTACCATTTATCGTTTTTGA[59]	GTGTGTATTGTTGGCCAAACACTGATATCT[60]
e14	4477	4603	127	AGTAGATTTGTTTTCTCATTCCATTTAAAG[61]	GTAAGAAACATCAATGTAAAGATGCTGTGG[62]

* Base numbers in SEQ ID NO:1.
** Numbers in superscript refer to SEQ ID NOS.
*** e4 from SEQ ID NO:11.

TABLE 9 (cont'd)

Exon No.	Base Position* 5'	Base Position* 3'	Length	Intron Borders 5'	Intron Borders 3'
e15	4604	4794	191	ATGGTTTTCTCCTTCCATTTATCTTTCTAG[63]**	GTAATATTTCATCTGCTGTATTGGAACAAA[64]
e16	4795	5105	311	TGTAAATTAAACTTCTCCCATTCCTTTCAG[65]	GTGAGTGTATCCATATGTATCTCCCTAATG[66]
e17	5106	5193	88	ATGATAATGGAATATTTGATTTAATTTCAG[67]	GTATACCAAGAACCTTTACAGAATACCTTG[68]
e18	5194	5271	78	CTAATCCTTTGAGTGTTTTTCATTCTGCAG[69]	GTAAGTATAATACTATTTCTCCCCTCCTCC[70]
e19	5272	5312	41	TGTAACCTGTCTTTTCTATGATCTCTTTAG[71]	GTAAGTACTTGATGTTACAAACTAACCAGA[72]
e20	5313	5396	84	TCCTGATGGGTTGTGTTTGGTTTCTTTCAG[73]	GTAAAGCTCCCTCCCTCAAGTTGACAAAAA[74]
e21	5397	5451	55	CTGTCCCTCTCTCTTCCTCTCTTCTTCCAG[75]	GTAAGAGCCTGGGAGAACCCCAGAGTTCCA[76]
e22	5452	5525	74	AGTGATTTTACATGTAAATGTCCATTTTAG[77]	GTAAGTATTGGGTGCCCTGTCAGTGTGGGA[78]
e23	5526	5586	61	TTGAATGCTCTTTCCTTCCTGGGGATCCAG[79]	GTAAGGTGCCTCGCATGTACCTGTGCTATT[80]
e24	5587	5914	328	CTAATCTCTGCTTGTGTTCTCTGTCTCCAG[81]	

* Base numbers in SEQ ID NO:1.
** Numbers in superscript refer to SEQ ID NOS.

Low stringency blots in which genomic DNA from organisms of diverse phylogenetic background were probed with BRCA1 sequences that lack the zinc-finger region revealed strongly hybridizing fragments in human, monkey, sheep and pig, and very weak hybridization signals in rodents. This result indicates that, apart from the zinc-finger domain, BRCA1 is conserved only at a moderate level through evolution.

Germline BRCA1 mutations in 17q-linked kindreds.

The most rigorous test for BRCA1 candidate genes is to search for potentially disruptive mutations in carrier individuals from kindreds that segregate 17q-linked susceptibility to breast and ovarian cancer. Such individuals must contain BRCA1 alleles that differ from the wildtype sequence. The set of DNA samples used in this analysis consisted of DNA from individuals representing 8 different BRCA1 kindreds (Table 10).

TABLE 10

KINDRED DESCRIPTIONS AND ASSOCIATED LOD SCORES

Kindred	Cases (n)			Sporadic Cases[1] (n)	LOD Score	Marker(s)
	Br	Br<50	Ov			
2082	31	20	22	7	9.49	D17S1327
2099	22	14	2*	0	2.36	D17S800/D17S855[2]
2035	10	8	1*	0	2.25	D17S1327
1901	10	7	1*	0	1.50	D17S855
1925	4	3	0	0	0.55	D17S579
1910	5	4	0	0	0.36	D17S579/D17S250[2]
1927	5	4	0	1	-0.44	D17S250
1911	8	5	0	2	-0.20	D17S250

[1] Number of women with breast cancer (diagnosed under age 50) or ovarian cancer (diagnosed at any age) who do not share the BRCA1-linked haplotype segregating in the remainder of the cases in the kindred.

[2] Multipoint LOD score calculated using both markers

* kindred contains one individual who had both breast and ovarian cancer; this individual is counted as a breast cancer case and as an ovarian cancer case.

The logarithm of the odds (LOD) scores in these kindreds range from 9.49 to -0.44 for a set of markers in 17q21. Four of the families have convincing LOD scores for linkage, and 4 have low positive or negative LOD scores. The latter kindreds were included because they demonstrate haplotype sharing at chromosome 17q21 for at least 3 affected members. Furthermore, all kindreds in the set display early age of breast cancer onset and 4 of the kindreds include at least one case of ovarian cancer, both hallmarks of BRCA1 kindreds. One kindred, 2082, has nearly equal incidence of breast and ovarian cancer, an unusual occurrence given the relative rarity of ovarian cancer in the population. All of the kindreds except two were ascertained in Utah. K2035 is from the midwest. K2099 is an African-American kindred from the southern USA.

In the initial screen for predisposing mutations in BRCA1, DNA from one individual who carries the predisposing haplotype in each kindred was tested. The 23 coding exons and associated splice junctions were amplified either from genomic DNA samples or from cDNA prepared from lymphocyte mRNA. When the amplified DNA sequences were compared to the wildtype sequence, 4 of the 8 kindred samples were found to contain sequence variants (Table 11).

TABLE 11

PREDISPOSING MUTATIONS

Kindred Number	Mutation	Coding Effect	Location*
2082	C→T	Gln→Stop	4056
1910	extra C	frameshift	5385
2099	T→G	Met→Arg	5443
2035	?	loss of transcript	
1901	11 bp deletion	frameshift	189

* In Sequence ID NO:1

All four sequence variants are heterozygous and each appears in only one of the kindreds. Kindred 2082 contains a nonsense mutation in exon 11 (Fig. 9A), Kindred 1910 contains a single nucleotide insertion in exon 20 (Fig. 9B), and Kindred 2099 contains a missense mutation in exon 21, resulting in a Met→Arg substitution. The frameshift and nonsense mutations are likely disruptive to the function of the BRCA1 product. The peptide encoded by the frameshift allele in Kindred 1910 would contain an altered amino acid sequence beginning 108 residues from the wildtype C-terminus. The peptide encoded by the frameshift allele in Kindred 1901 would contain an altered amino acid sequence beginning with the 24th residue from the wildtype N-terminus. The mutant allele in Kindred 2082 would encode a protein missing 551 residues from the C-terminus. The missense substitution observed in Kindred 2099 is potentially disruptive as it causes the replacement of a small hydrophobic amino acid (Met), by a large charged residue (Arg). Eleven common polymorphisms were also identified, 8 in coding sequence and 3 in introns.

The individual studied in Kindred 2035 evidently contains a regulatory mutation in BRCA1. In her cDNA, a polymorphic site (A→G at base 3667) appeared homozygous, whereas her genomic DNA revealed heterozygosity at this position (Fig. 9C). A possible explanation for this observation is that mRNA from her mutated BRCA1 allele is absent due to a mutation that affects its production or stability. This possibility was explored further by examining 5 polymorphic sites in the BRCA1 coding region, which are separated by as much as 3.5 kb in the BRCA1 transcript. In all cases where her genomic DNA appeared heterozygous for a polymorphism, cDNA appeared homozygous. In individuals from other kindreds and in non-haplotype carriers in Kindred 2035, these polymorphic sites could be observed as heterozygous in cDNA, implying that amplification from cDNA was not biased in favor of one allele. This analysis indicates that a BRCA1 mutation in Kindred 2035 either prevents transcription or causes instability or aberrant splicing of the BRCA1 transcript.

Cosegregation of BRCA1 mutations with BRCA1 haplotypes and population frequency analysis.

In addition to potentially disrupting protein function, two criteria must be met for a sequence variant to qualify as a candidate predisposing mutation. The variant must: 1) be present in individuals from the kindred who carry the predisposing BRCA1 haplotype and absent in other members of the kindred, and 2) be rare in the general population.

Each mutation was tested for cosegregation with BRCA1. For the frameshift mutation in Kindred 1910, two other haplotype carriers and one non-carrier were sequenced (Fig.9B). Only the carriers exhibited the frameshift mutation. The C to T change in Kindred 2082 created a new AvrII restriction site. Other carriers and non-carriers in the kindred were tested for the presence of the restriction site (Fig. 9A). An allele-specific oligonucleotide (ASO) was designed to detect the presence of the sequence variant in Kindred 2099. Several individuals from the kindred, some known to carry the haplotype associated with the predisposing allele, and others known not to carry the associated haplotype, were screened by ASO for the mutation previously detected in the kindred. In each kindred, the corresponding mutant allele was detected in individuals carrying the BRCA1-associated haplotype, and was not detected in noncarriers. In the case of the potential regulatory mutation observed in the individual from Kindred 2035, cDNA and genomic DNA from carriers in the kindred were compared for heterozygosity at polymorphic sites. In every instance, the extinguished allele in the cDNA sample was shown to lie on the chromosome that carries the BRCA1 predisposing allele (Fig. 9C).

To exclude the possibility that the mutations were simply common polymorphisms in the population, ASOs for each mutation were used to screen a set of normal DNA samples. Gene frequency estimates in Caucasians were based on random samples from the Utah population. Gene frequency estimates in African-Americans were based on 39 samples provided by M. Peracek-Vance which originate from African-Americans used in her linkage studies and 20 newborn

Utah African-Americans. None of the 4 potential predisposing mutations was found in the appropriate control population, indicating that they are rare in the general population. Thus, two important requirements for BRCA1 susceptibility alleles were fulfilled by the candidate predisposing mutations: 1) cosegregation of the mutant allele with disease, and 2) absence of the mutant allele in controls, indicating a low gene frequency in the general population.

Phenotypic Expression of BRCA1 Mutations.

The effect of the mutations on the BRCA1 protein correlated with differences in the observed phenotypic expression in the BRCA1 kindreds. Most BRCA1 kindreds have a moderately increased ovarian cancer risk, and a smaller subset have high risks of ovarian cancer, comparable to those for breast cancer (Easton *et al.*, 1993). Three of the four kindreds in which BRCA1 mutations were detected fall into the former category, while the fourth (K2082) falls into the high ovarian cancer risk group. Since the BRCA1 nonsense mutation found in K2082 lies closer to the amino terminus than the other mutations detected, it might be expected to have a different phenotype. In fact, Kindred K2082 mutation has a high incidence of ovarian cancer, and a later mean age at diagnosis of breast cancer cases than the other kindreds (Goldgar *et al.*, 1994). This difference in age of onset could be due to an ascertainment bias in the smaller, more highly penetrant families, or it could reflect tissue-specific differences in the behavior of BRCA1 mutations. The other 3 kindreds that segregate known BRCA1 mutations have, on average, one ovarian cancer for every 10 cases of breast cancer, but have a high proportion of breast cancer cases diagnosed in their late 20's or early 30's. Kindred 1910, which has a frameshift mutation, is noteworthy because three of the four affected individuals had bilateral breast cancer, and in each case the second tumor was diagnosed within a year of the first occurrence. Kindred 2035, which segregates a potential regulatory BRCA1 mutation, might also be expected to have a dramatic phenotype. Eighty percent of breast cancer cases in this kindred occur under age 50. This figure is as high as any in the set, suggesting a BRCA1 mutant allele of high penetrance (Table 10).

Although the mutations described above clearly are deleterious, causing breast cancer in women at very young ages, each of the four kindreds with mutations includes at least one woman who carries the mutation who lived until age 80 without developing a malignancy. It will be of utmost importance in the studies that follow to identify other genetic or environmental factors that may ameliorate the effects of BRCA1 mutations.

In four of the eight putative BRCA1-linked kindreds, potential predisposing mutations were not found. Three of these four have LOD scores for BRCA1-linked markers of less than 0.55. Thus, these kindreds may not in reality segregate BRCA1 predisposing alleles. Alternatively, the mutations in these four kindreds may lie in regions of BRCA1 that, for example, affect the level of transcript and therefore have thus far escaped detection.

Role of BRCA1 in Cancer.

Most tumor suppressor genes identified to date give rise to protein products that are absent, nonfunctional, or reduced in function. The majority of TP53 mutations are missense; some of these have been shown to produce abnormal p53 molecules that interfere with the function of the wildtype product (Shaulian *et al.*, 1992; Srivastava *et al.*, 1993). A similar dominant negative mechanism of action has been proposed for some adenomatous polyposis coli (APC) alleles that produce truncated molecules (Su *et al.*, 1993), and for point mutations in the Wilms' tumor gene (WT1) that alter DNA binding of the protein (Little *et al.*, 1993). The nature of the mutations observed in the BRCA1 coding sequence is consistent with production of either dominant negative proteins or nonfunctional proteins. The regulatory mutation inferred in Kindred 2035 cannot be a dominant negative; rather, this mutation likely causes reduction or complete loss of BRCA1 expression from the affected allele.

The BRCA1 protein contains a C_3HC_4 zinc-finger domain, similar to those found in numerous DNA binding proteins and implicated in zinc-dependent binding to nucleic acids. The first 180 amino acids of BRCA1 contain five more basic residues than acidic residues. In contrast, the remainder of the molecule is very acidic, with a net excess of 70 acidic residues. The excess negative charge is particularly concentrated near the C-terminus. Thus, one possibility is that BRCA1 encodes a transcription factor with an N-terminal DNA binding domain and a C-terminal transactivational "acidic blob" domain. Interestingly, another familial tumor suppressor gene, WT1, also contains a zinc-finger motif (Haber *et al.*, 1990). Many cancer predisposing mutations in WT1 alter zinc-finger domains (Little *et al.*, 1993; Haber *et al.*, 1990; Little *et al.*, 1992). WT1 encodes a transcription factor, and alternative splicing of exons that encode parts of the zinc-finger domain alter the DNA binding properties of WT1 (Bickmore *et al.*, 1992). Some alternatively spliced forms of WT1 mRNA generate molecules that act as transcriptional repressors (Drummond *et al.*, 1994). Some BRCA1 splicing variants may alter the zinc-finger motif, raising the possibility that a regulatory mechanism similar to that which occurs in WT1 may apply to BRCA1.

EXAMPLE 9

Analysis of Tumors for BRCA1 Mutations

To focus the analysis on tumors most likely to contain BRCA1 mutations, primary breast and ovarian carcinomas were typed for LOH in the BRCA1 region. Three highly polymorphic, simple tandem repeat markers were used to assess LOH: D17S1323 and D17S855, which are intragenic to BRCA1, and D17S1327, which lies approximately 100 kb distal to BRCA1. The combined LOH frequency in informative cases (i.e., where the germline was heterozygous) was 32/72 (44%) for the breast carcinomas and 12/21 (57%) for the ovarian carcinomas, consistent with previous measurements of LOH in the region (Futreal *et al.*, 1992b; Jacobs *et al.*, 1993; Sato *et al.*, 1990; Eccles et al., 1990; Cropp *et al.*, 1994). The analysis thus defined a panel of 32 breast tumors and 12 ovarian tumors of mixed race and age of onset to be examined for BRCA mutations. The complete 5,589 bp coding region and intron/exon boundary sequences of the gene were screened in this tumor set by direct sequencing alone or by a combination of single-strand conformation analysis (SSCA) and direct sequencing.

A total of six mutations (of which two are identical) was found, one in an ovarian tumor, four in breast tumors and one in a male unaffected haplotype carrier (Table 12). One mutation, Glu1541Ter, introduced a stop codon that would create a truncated protein missing 323 amino acids at the carboxy terminus. In addition, two missense mutations were identified. These are Ala1708Glu and Met1775Arg and involve substitutions of small, hydrophobic residues by charged residues. Patients 17764 and 19964 are from the same family. In patient OV24 nucleotide 2575 is deleted and in patients 17764 and 19964 nucleotides 2993-2996 are deleted.

TABLE 12

Predisposing Mutations

Patient	Codon	Nucleotide Change	Amino Acid Change	Age of Onset	Family History
BT098	1541	GAG → TAG	Glu → Stop	39	-
OV24	819	1 bp deletion	frameshift	44	-
BT106	1708	GCG → GAG	Ala → Glu	24	+
MC44	1775	ATG → AGG	Met → Arg	42	+
17764	958	4 bp deletion	frameshift	31	+
19964	958	4 bp deletion	frameshift		+*

* Unaffected haplotype carrier, male

Several lines of evidence suggest that all five mutations represent BRCA1 susceptibility alleles:

(i) all mutations are present in the germline;

(ii) all are absent in appropriate control populations, suggesting they are not common polymorphisms;

(iii) each mutant allele is retained in the tumor, as is the case in tumors from patients belonging to kindreds that segregate BRCA1 susceptibility alleles (Smith *et al.*, 1992; Kelsell *et al.*, 1993) (if the mutations represented neutral polymorphisms, they should be retained in only 50% of the cases);

(iv) the age of onset in the four breast cancer cases with mutations varied between 24 and 42 years of age, consistent with the early age of onset of breast cancer in individuals with BRCA1 susceptibility; similarly, the ovarian cancer case was diagnosed at 44, an age that falls in the youngest 13% of all ovarian cancer cases; and finally,

(v) three of the five cases have positive family histories of breast or ovarian cancer found retrospectively in their medical records, although the tumor set was not selected with regard to this criterion.

BT106 was diagnosed at age 24 with breast cancer. Her mother had ovarian cancer, her father had melanoma, and her paternal grandmother also had breast cancer. Patient MC44, an African-American, had bilateral breast cancer at age 42. This patient had a sister who died of breast cancer at age 34, another sister who died of lymphoma, and a brother who died of lung cancer. Her mutation (Met1775Arg) had been detected previously in Kindred 2099, an African-American family that segregates a BRCA1 susceptibility allele, and was absent in African-American and Caucasian controls. Patient MC44, to our knowledge, is unrelated to Kindred 2099. The detection of a rare mutant allele, once in a BRCA1 kindred and once in the germline of an apparently unrelated early-onset breast cancer case, suggests that the Met1775Arg change may be a common predisposing mutation in African-Americans. Collectively, these observations indicate that all four BRCA1 mutations in tumors represent susceptibility alleles; no somatic mutations were detected in the samples analyzed.

The paucity of somatic BRCA1 mutations is unexpected, given the frequency of LOH on 17q, and the usual role of susceptibility genes as tumor suppressors in cancer progression. There are three possible explanations for this result: (i) some BRCA1 mutations in coding sequences were missed by our screening procedure; (ii) BRCA1 somatic mutations fall primarily outside the coding exons; and (iii) LOH events in 17q do not reflect BRCA1 somatic mutations.

If somatic BRCA1 mutations truly are rare in breast and ovary carcinomas, this would have strong implications for the biology of BRCA1. The apparent lack of somatic BRCA1 mutations implies that there may be some fundamental difference in the genesis of tumors in genetically predisposed BRCA1 carriers, compared with tumors in the general population. For example, mutations in BRCA1 may have an effect only on tumor formation at a specific stage early in breast and ovarian development. This possibility is consistent with a primary function for BRCA1 in premenopausal breast cancer. Such a model for the role of BRCA1 in breast and ovarian cancer predicts an interaction between reproductive hormones and BRCA1 function. However, no clinical or pathological differences in familial versus sporadic breast and ovary tumors, other than age of onset, have been described (Lynch *et al.*, 1990). On the other hand, the recent finding of increased TP53 mutation and microsatellite instability in breast tumors from patients with a family history of breast cancer (Glebov *et al.*, 1994) may reflect some difference in tumors that arise in genetically predisposed persons. The involvement of BRCA1 in this phenomenon can now be addressed directly. Alternatively, the lack of somatic BRCA1 mutations may result from the existence of multiple genes that function in the same pathway of tumor suppression as BRCA1, but which collectively represent a more favored target for mutation in sporadic tumors. Since mutation of a single element in a genetic pathway is generally sufficient to disrupt the pathway, BRCA1 might mutate at a rate that is far lower than the sum of the mutational rates of the other elements.

EXAMPLE 10

Analysis of the BRCA1 Gene

The structure and function of BRCA 1 gene are determined according to the following methods.

Biological Studies.

Mammalian expression vectors containing BRCA1 cDNA are constructed and transfected into appropriate breast carcinoma cells with lesions in the gene. Wild-type BRCA1 cDNA as well as altered BRCA1 cDNA are utilized. The altered BRCA1 cDNA can be obtained from altered BRCA1 alleles or produced as described below. Phenotypic reversion in cultures (e.g., cell morphology, doubling time, anchorage-independent growth) and in animals (e.g., tumorigenicity) is examined. The studies will employ both wild-type and mutant forms (Section B) of the gene.

Molecular Genetics Studies.

In vitro mutagenesis is performed to construct deletion mutants and missense mutants (by single base-pair substitutions in individual codons and cluster charged → alanine scanning mutagenesis). The mutants are used in biological, biochemical and biophysical studies.

Mechanism Studies.

The ability of BRCA1 protein to bind to known and unknown DNA sequences is examined. Its ability to transactivate promoters is analyzed by transient reporter expression systems in mammalian cells. Conventional procedures such as particle-capture and yeast two-hybrid system are used to discover and identify any functional partners. The nature and functions of the partners are characterized. These partners in turn are targets for drug discovery.

Structural Studies. Recombinant proteins are produced in *E. coli*, yeast, insect and/or mammalian cells and are used in crystallographical and NMR studies. Molecular modeling of the proteins is also employed. These studies facilitate structure-driven drug design.

EXAMPLE 11

Two Step Assay to Detect the Presence of BRCA1 in a Sample

Patient sample is processed according to the method disclosed by Antonarakis *et al.* (1985), separated through a 1% agarose gel and transferred to nylon membrane for Southern blot analysis. Membranes are UV cross linked at 150 mJ using a GS Gene Linker (Bio-Rad). BRCA1 probe corresponding to nucleotide positions 3631-3930 of SEQ ID NO:1 is subcloned into pTZ18U. The phagemids are transformed into *E. coli* MV1190 infected with M13K07 helper phage (Bio-Rad, Richmond, CA). Single stranded DNA is isolated according to standard procedures (see Sambrook *et al.*, 1989).

Blots are prehybridized for 15-30 min at 65°C in 7% sodium dodecyl sulfate (SDS) in 0.5 M $NaPO_4$. The methods follow those described by Nguyen *et al.*, 1992. The blots are hybridized overnight at 65°C in 7% SDS, 0.5 M $NaPO_4$ with 25-50 ng/ml single stranded probe DNA. Post-hybridization washes consist of two 30 min washes in 5% SDS, 40 mM $NaPO_4$ at 65°C, followed by two 30 min washes in 1% SDS,40 mM $NaPO_4$ at 65°C.

Next the blots are rinsed with phosphate buffered saline (pH 6.8) for 5 min at room temperature and incubated with 0.2% casein in PBS for 30-60 min at room temperature and rinsed in PBS for 5 min. The blots are then preincubated for 5-10 minutes in a shaking water bath at 45°C with hybridization buffer consisting of 6 M urea, 0.3 M NaCl, and 5X Denhardt's solution (see Sambrook, *et al.*, 1989). The buffer is removed and replaced with 50-75 µl/cm^2 fresh hybridization buffer plus 2.5 nM of the covalently cross-linked oligonucleotide-alkaline phosphatase conjugate with the nucleotide sequence complementary to the universal primer site (UP-AP, Bio-Rad). The blots are hybridized for 20-30 min at 45°C and post hybridization washes are incubated at 45°C as two 10 min washes in 6 M urea, 1x standard saline citrate (SSC), 0.1% SDS and one 10 min wash in lx SSC, 0.1% Triton®X-100. The blots are rinsed for 10 min at room temperature with lx SSC.

Blots are incubated for 10 min at room temperature with shaking in the substrate buffer consisting of 0.1 M diethanolamine, 1 mM $MgCl_2$, 0.02% sodium azide, pH 10.0. Individual blots are placed in heat sealable bags with substrate buffer and 0.2 mM AMPPD (3-(2'-spiroadamantane)-4-methoxy4-(3'-phosphoryloxy)phenyl-1,2-dioxetane, disodium salt, Bio-Rad). After a 20 min incubation at room temperature with shaking, the excess AMPPD solution is removed. The blot is exposed to X-ray film overnight. Positive bands indicate the presence of BRCA1.

EXAMPLE 12

Generation of Polyclonal Antibody against BRCA1

Segments of BRCA1 coding sequence were expressed as fusion protein in *E. coli*. The overexpressed protein was purified by gel elution and used to immunize rabbits and mice using a procedure similar to the one described by Harlow and Lane, 1988. This procedure has been shown to generate Abs against various other proteins (for example, see Kraemer *et al.*, 1993).

Briefly, a stretch of BRCA1 coding sequence was cloned as a fusion protein in plasmid PET5A (Novagen, Inc., Madison, WI). The BRCA1 incorporated sequence includes the amino acids corresponding to #1361-1554 of SEQ ID NO:2. After induction with IPTG, the overexpression of a fusion protein with the expected molecular weight was verified by SDS/PAGE. Fusion protein was purified from the gel by electroelution. The identification of the protein as the BRCA1 fusion product was verified by protein sequencing at the N-terminus. Next, the purified protein was used as immunogen in rabbits. Rabbits were immunized with 100 µg of the protein in complete Freund's adjuvant and boosted twice in 3 week intervals, first with 100 µg of immunogen in incomplete Freund's adjuvant followed by 100 µg of immunogen in PBS. Antibody containing serum is collected two weeks thereafter.

This procedure is repeated to generate antibodies against the mutant forms of the BRCA1 gene. These antibodies, in conjunction with antibodies to wild type BRCA1, are used to detect the presence and the relative level of the mutant forms in various tissues and biological fluids.

EXAMPLE 13

Generation of Monoclonal Antibodies Specific for BRCA1

Monoclonal antibodies are generated according to the following protocol. Mice are immunized with immunogen comprising intact BRCA1 or BRCA1 peptides (wild type or mutant) conjugated to keyhole limpet hemocyanin using glutaraldehyde or EDC as is well known.

The immunogen is mixed with an adjuvant. Each mouse receives four injections of 10 to 100 µg of immunogen and after the fourth injection blood samples are taken from the mice to determine if the serum contains antibody to the immunogen. Serum titer is determined by ELISA or RIA. Mice with sera indicating the presence of antibody to the immunogen are selected for hybridoma production.

Spleens are removed from immune mice and a single cell suspension is prepared (see Harlow and Lane, 1988). Cell fusions are performed essentially as described by Kohler and Milstein, 1975. Briefly, P3.65.3 myeloma cells (American Type Culture Collection, Rockville, MD) are fused with immune spleen cells using polyethylene glycol as described by Harlow and Lane, 1988. Cells are plated at a density of 2×10^5 cells/well in 96 well tissue culture plates. Individual wells are examined for growth and the supernatants of wells with growth are tested for the presence of BRCA1 specific antibodies by ELISA or RIA using wild type or mutant BRCA1 target protein. Cells in positive wells are expanded and subcloned to establish and confirm monoclonality.

Clones with the desired specificities are expanded and grown as ascites in mice or in a hollow fiber system to produce sufficient quantities of antibody for characterization and assay development.

EXAMPLE 14

Sandwich Assay for BRCA1

Monoclonal antibody is attached to a solid surface such as a plate, tube, bead, or particle. Preferably, the antibody is attached to the well surface of a 96-well ELISA plate. 100 µl sample (e.g., serum, urine, tissue cytosol) containing the BRCA1 peptide/protein (wild-type or mutant) is added to the solid phase antibody. The sample is incubated for 2 hrs at room temperature. Next the sample fluid is decanted, and the solid phase is washed with buffer to remove unbound material. 100 µl of a second monoclonal antibody (to a different determinant on the BRCA1 peptide/protein) is added to the solid phase. This antibody is labeled with a detector molecule (e.g., ^{125}I, enzyme, fluorophore, or a chromophore) and the solid phase with the second antibody is incubated for two hrs at room temperature. The second antibody is decanted and the solid phase is washed with buffer to remove unbound material.

The amount of bound label, which is proportional to the amount of BRCA1 peptide/protein present in the sample, is quantitated. Separate assays are performed using monoclonal antibodies which are specific for the wild-type BRCA1 as well as monoclonal antibodies specific for each of the mutations identified in BRCA1.

Industrial Utility

As previously described above, the present invention provides materials and methods for use in testing BRCA1 alleles of an individual and an interpretation of the normal or predisposing nature of the alleles. Individuals at higher than normal risk might modify their lifestyles appropriately. In the case of BRCA1, the most significant non-genetic risk factor is the protective effect of an early, full term pregnancy. Therefore, women at risk could consider early childbearing or a therapy designed to simulate the hormonal effects of an early full-term pregnancy. Women at high risk would also strive for early detection and would be more highly motivated to learn and practice breast self examination. Such women would also be highly motivated to have regular mammograms, perhaps starting at an earlier age than the general population. Ovarian screening could also be undertaken at greater frequency. Diagnostic methods based on sequence analysis of the BRCA1 locus could also be applied to tumor detection and classification. Sequence analysis could be used to diagnose precursor lesions. With the evolution of the method and the accumulation of information about BRCA1 and other causative loci, it could become possible to separate cancers into benign and malignant.

Women with breast cancers may follow different surgical procedures if they are predisposed, and therefore likely to have additional cancers, than if they are not predisposed. Other therapies may be developed, using either peptides or small molecules (rational drug design). Peptides could be the missing gene product itself or a portion of the missing gene product. Alternatively, the therapeutic agent could be another molecule that mimics the deleterious gene's function, either a peptide or a nonpeptidic molecule that seeks to counteract the deleterious effect of the inherited locus. The therapy could also be gene based, through introduction of a normal BRCA1 allele into individuals to make a protein which will counteract the effect of the deleterious allele. These gene therapies may take many forms and may be directed either toward preventing the tumor from forming, curing a cancer once it has occurred, or stopping a cancer from metastasizing.

It will be appreciated that the methods and compositions of the instant invention can be incorporated in the form of a variety of embodiments, only a few of which are disclosed herein. It will be apparent to the artisan that other embodiments exist and do not depart from the spirit of the invention. Thus, the described embodiments are illustrative and should not be construed as restrictive.

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