

Structure of Chromosomal Duplicons and their Role in Mediating Human Genomic Disorders

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Chromosome-specific low-copy repeats, or duplicons, occur in multiple regions of the human genome. Homologous recombination between different duplication copies leads to chromosomal rearrangements, such as deletions, duplications, inversions, and inverted duplications, depending on the orientation of the recombining duplicons. When such rearrangements cause dosage imbalance of a developmentally important gene(s), genetic diseases now termed genomic disorders result, at a frequency of 0.7–1/1000 births. Duplicons can have simple or very complex structures, with variation in copy number from 2 to >10 repeats, and each varying in size from a few kilobases in length to hundreds of kilobases. Analysis of the different duplicons involved in human genomic disorders identifies features that may predispose to recombination, including large size and high sequence identity between the recombining copies, putative recombination promoting features, and the presence of multiple genes/pseudogenes that may include genes expressed in germ cells. Most of the chromosome rearrangements involve duplicons near pericentromeric regions, which may relate to the propensity of such regions to accumulate duplicons. Detailed analyses of the structure, polymorphic variation, and mechanisms of recombination in genomic disorders, as well as the evolutionary origin of various duplicons will further our understanding of the structure, function, and fluidity of the human genome.

Although the primary cause of many genetic diseases is single gene defects, a number of syndromes have been defined as genomic disorders (Lupski 1998), as the majority of cases arise from structural rearrangements of certain regions of a chromosome. In such cases, disease is due to dosage imbalance of one or more genes, caused by chromosomal structural change and not by mutation of the gene(s) itself. Rather than the disease etiology, this review focuses on the structural mechanisms of chromosome rearrangements.

Structural changes of certain chromosomal segments were first associated with several human genetic disorders in the early 1980s, such as Prader-Willi syndrome at 15q11–q13 (Ledbetter et al. 1981) and Di-George syndrome at 22q11 (de la Chapelle et al 1981). Different terms (e.g., contiguous gene, microdeletion, contiguous deletion, and segmental aneusomy) were given to describe these and other syndromes later associated with a specific structural change of a chromosome, including the more apt term, genomic disorder (Lupski 1998). Whereas the term genomic disorder (Lupski 1998) includes all syndromes involving a change at the genomic level, the following discussion is restricted to genomic disorders arising by homologous recombination between region-specific, low-copy repeats during meiosis. Recent studies show that duplications of small chromosome segments may not be a

rare event. Analysis of long stretches of available sequence from human chromosomes 22 and X suggest that 5%–10% of the genome may be duplicated (Mazzarella and Schlessinger 1998; Dunham et al. 1999). Sequence homology between duplicated DNA segments provides a chance for misalignment during meiosis, leading to unequal exchange and chromosome rearrangement, by either inter- or intrachromosomal or sister chromatid homologous recombination (Fig. 1). This process with divergence between duplicated segments is essential to the generation of diversity and new genes over evolutionary time, although the more typical, short-term effect is genetic disease.

Region-specific, low-copy repeat elements, or duplicons (Eichler 1998), have been identified flanking many regions susceptible to human genomic disorders (for recent reviews, see Purandare and Patel 1997; Lupski 1998; Mazzarella and Schlessinger 1998). These disorders arise from chromosomal rearrangements mediated by homologous recombination between different copies of a duplicon with deletions (Fig. 1a,b), duplications (Fig. 1a), or inversions (Fig. 1c), the outcome depending on unknown factors, although the orientation of duplicons is clearly one important criterion. Characterization of various genomic disorders showed that they can be classified into three groups. In the first group, the length of the repeated segments and the distance between the repeat units are both small. The duplicon in such cases is either a gene cluster or repeated sequences flanking a gene. Homologous recombination between the duplicons generates an imbal-

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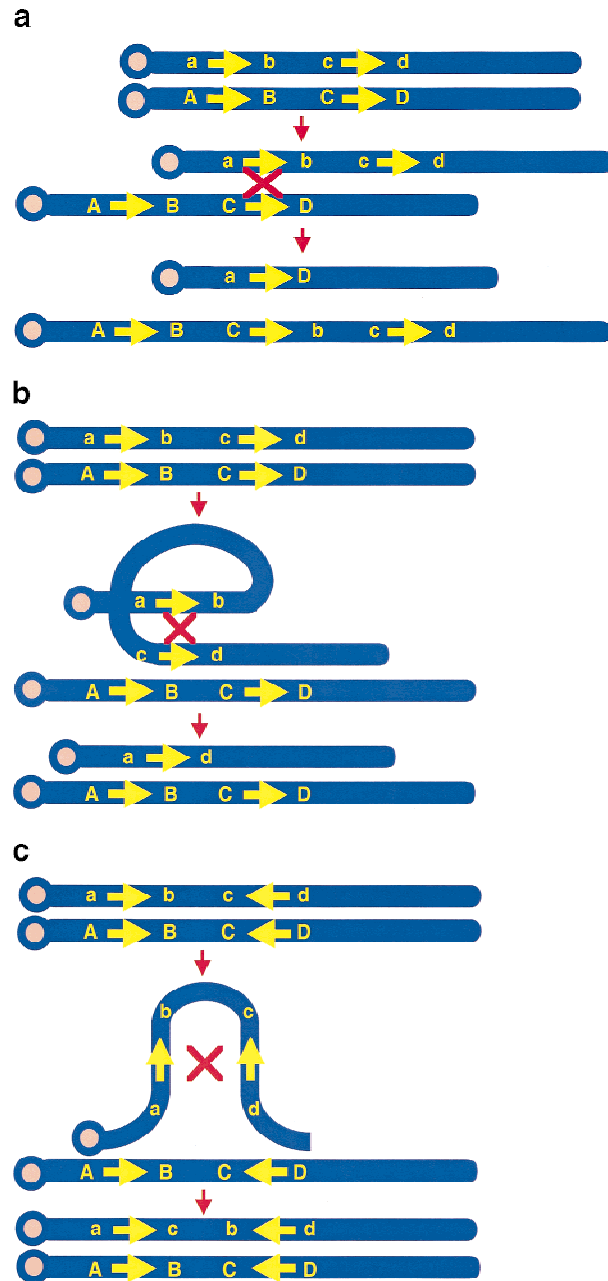


Figure 1 Genomic rearrangements resulting from recombination between duplicons. (a) Interchromosomal recombination between direct repeats results in deletion and/or duplication. (b) Intrachromosomal recombination between direct repeats results in deletion. (c) Intrachromosomal recombination between inverted repeats results in an inversion. Repeated sequences are depicted as yellow arrows with the orientation indicated by the direction of the arrows. Recombination is shown by the red X. Upper- and lowercase letters refer to both alleles of the flanking unique sequence (e.g., A and a). Adapted in part from Lupski (1998).

ance of a dosage-sensitive gene, leading to a disease phenotype. This group includes a number of disorders such as red-green color blindness and α - or β -thalassaemia (Lupski 1998), and will not be discussed further

here. The other two groups of genomic disorders involve rearrangement of a large segment of the chromosome, yet the flanking duplicons are structurally simple in the second group, whereas the third group of disorders involve complex duplicons. In both cases, if the rearrangement is a deletion or duplication, the expression level of multiple genes may be affected, although the phenotypes can arise from dosage imbalance of a single gene. The affected gene(s) may or may not be part of the duplicon, and can thus be situated quite far from the repeats.

Simple Duplicons Mediating Genomic Disorders

S232 Elements and X-Linked Ichthyosis

Deletions of the steroid sulfatase (*STS*) gene in males cause a skin disorder, X-linked ichthyosis. The incidence of this disorder is 1 in 2–5000 males, with ~90% of the patients having a deletion of 1.9 Mb that includes the *STS* locus. The deletions are mediated by homologous recombination between duplicons called S232 elements, situated at either end of the deletion (Ballabio et al 1990; Yen et al. 1990). There are 6–14 S232 duplicons, 4–12 in Xp22.3 and 2 on the Y chromosome, and each is composed of a 5-kb unique sequence and two VNTR (variable-number tandem repeat) sequences (Li et al. 1992; Lahn and Page 2000). One mapped S232 duplicon lies distal to the *STS* locus and three proximal to *STS*, with recombination proposed to occur between the former and only one of the latter in tandem (Fig. 2a; Li et al 1992). No cases involve recombination with the Y chromosome (Yen et al 1990). Recent studies show that a copy of the *VCX* gene is present within the S232 duplicon, and that the *VCX* gene family is expressed exclusively in male germ cells (Lahn and Page 2000).

CMT1A-REP and Two Distinct Peripheral Neuropathies

Reciprocal chromosome rearrangements of 17p12 occur in Charcot-Marie-Tooth syndrome type 1A (CMT1A) and hereditary neuropathy with liability to pressure palsies (HNPP) (Chance and Fischbeck 1994; Patel and Lupski 1994). A 1.5-Mb tandem duplication of 17p12 occurs in 70% of inherited and 90% of sporadic CMT1A cases (Hoogendijk et al. 1992; Wise et al. 1993; Nelis et al. 1996), in which 10%–18% of CMT1A cases overall are de novo (Blair et al. 1996; Bort et al. 1997). A deletion of the same chromosomal segment occurs in 82% of familial and 86% of sporadic HNPP cases (Nelis et al. 1996). The protein encoded by the *PMP22*, or peripheral myelin protein-22, gene in the 1.5-Mb region appears to be sensitive to subtle dosage changes and is responsible for both syndromes (for review, see Chance and Fischbeck 1994; Patel and Lupski 1994).

The 1.5-Mb region is flanked by a duplicon termed CMT1A-REP (Fig. 2b; Pentao et al. 1992; Chance et al.

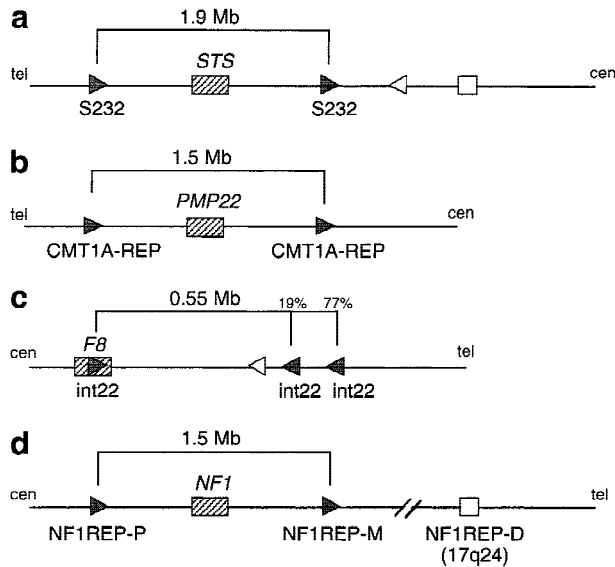


Figure 2 Genes and duplicons in genomic disorders involving simple duplicons. (a) Xp22.32 deletions in X-linked ichthyosis; (b) reciprocal 17p12 duplications in Charcot-Marie Tooth syndrome 1A (CMT1A) and deletions in hereditary neuropathy with liability to pressure palsies (HNPP); (c) Xq28 inversions in hemophilia A; (d) 17q11.2 deletions in neurofibromatosis type 1 (NF1). Duplicons are shown as either triangles (when the orientation is known) or squares (when the orientation is unknown). Unequal crossing-over occurs primarily between duplicon copies depicted by shaded triangles. Percentages reflect the frequency of break-points at two alternative sites. Major genes responsible for each syndrome are shown as hatched rectangles. (cen) Centromere; (tel) telomere. (See text for references.)

1993), with 98.7% sequence identity across 24,011 bp (Reiter et al. 1997). The *COX10* gene encoding heme A:farnesyltransferase overlaps the distal duplicon, and a duplicated internal segment of *COX10* forms the proximal CMT1A-REP (Reiter et al. 1997). Homologous recombination between these repeat elements lead to the duplications in CMT1A and deletions in HNPP (Lupski 1998). In both CMT1A and HNPP rearrangements, the majority of crossovers happen within a single recombination hot spot (Kiyosawa et al. 1995; Kiyosawa and Chance 1996; Lopes et al. 1996, 1998; Reiter et al. 1996, 1998). Because all crossovers occur in long stretches of identity, the minimum efficient processing segment (MEPS) for efficient meiotic homologous recombination was proposed to be between 337 and 456 bp long. This is similar to other observations of an ~200 bp MEPS for homologous recombination in mammalian cells (Waldman and Liskay 1988). The finding of a *mariner* transposon-like element with its 3' end 1774 bp from the hot spot led to a hypothesis that it could mediate strand exchange events via double-strand breaks induced by a transposase at or near the 3' end of the element (Reiter et al. 1996, 1998). Multiple sequences similar to human minisatellite consensus sequences [4 copies similar to 5' -GGGCAGGA(A/G)G-3',

and one copy similar to 5' -AGAGGTGGG CAGGTGG-3'] and a χ -like sequence (5' -GCTGGTGG-3') were also identified in a 270-bp region within the hot spot (Lopes et al. 1998), and suggested to promote homologous recombination events. However, no direct evidence supports the involvement in recombination of a *mariner* or other specific sequences.

Interestingly, most de novo CMT1A duplications contain both paternal haplotypes and therefore arose from unequal crossing over involving both homologs (Palau et al. 1993; Lopes et al., 1997, 1998). In contrast, all four maternal cases involving CMT1A-REP recombination (two duplications and two deletions) are intrachromosomal events (Lopes et al. 1997), which suggests a mechanistic difference during spermatogenesis and oogenesis for 17p12 rearrangements. Using the *mariner*-like sequence as a probe, a 2.2-kb transcript was claimed to be present in testis but not in ovary (Kiyosawa and Chance 1996), although the genomic source(s) of the putative transcripts are unknown and the data is not convincing. Nevertheless, an open chromatin structure due to transcription of *COX10* or the *mariner* could be associated with generation of CMT1A duplications during spermatogenesis.

int22h Elements and Severe Hemophilia A

Hemophilia A is an X-linked coagulation disorder affecting ~1 in 5000 males (Soucie et al. 1998), due to mutations of the factor VIII gene (*F8*). About 45% of severe hemophilia A males carry a large (~500 kb) inversion on Xq, which disrupts *F8* (Lakich et al. 1993; Naylor et al. 1993). Most inversions are intrachromosomal (Lakich et al. 1993) and originate almost exclusively in male germ cells (Rossiter et al. 1994). The inversion occurs by homologous recombination between 9.5-kb duplicons (*int22h*, or intron 22 homologous region), one in intron 22 of *F8*, and either of two homologs oriented in the opposite direction and located 500 kb more distal (Fig. 2c; Naylor et al. 1995). In one case, the intron 22 copy recombined with a fourth, truncated copy of *int22h*, to generate a smaller inversion (Naylor et al. 1996). An 8-kb segment of *int22h* is 99.9% similar among the three copies, with a 1.8-kb intronless gene (*F8A*) within each of the repeat elements (Levinson et al. 1990), although it is not known whether *F8A* is expressed during spermatogenesis.

Germ-line Deletions of 17q11.2 in Neurofibromatosis Type 1

Recent studies indicate that a minority (2%–13%) of neurofibromatosis type 1 (NF1) cases result from an *NF1* gene deletion of 1.5 Mb that is mediated by homologous recombination between duplicons termed NF1REPs (Dorschner et al. 2000). These duplicons are direct repeats that span 15–100 kb and contain several genes/pseudogenes (a third copy maps distally in 17q24). Of the *NF1* deletions that were de novo, 75%

were maternal in origin, although somatic mosaicism for *NF1* deletions have been described suggesting that mitotic recombination between NF1REPs may also occur (Dorschner et al. 2000).

Genomic Disorders Arising from Chromosome Rearrangements Involving Complex Duplicons

Recent molecular and cytological studies have identified large, complex duplicons in the breakpoint regions of several human genomic disorders. The rearranged DNA segments usually span several megabases and are flanked by large duplicons that often contain several genes and/or pseudogenes. Multiple copies are present both at the common breakpoint regions and elsewhere within the same subchromosomal region. On the basis of limited analyses, sequence identity between different duplison copies are usually >90% and up to 99%. As the duplicons are large in size, have high homology, and multiple copies, the characterization of these duplicons has proven to be difficult. With the recent development of long-range mapping and sequencing techniques, the nature of some of these rearrangements has begun to emerge.

Chromosome 7q11.23 Deletions and Williams syndrome

Williams syndrome (WS) is a multisystem developmental disorder affecting connective tissue and the central nervous system, with an estimated incidence of 1 in 20,000 live births (Morris et al. 1993; Sadler et al. 1993). Most (95%) patients have a de novo ~1.6-Mb deletion of chromosome 7q11.23, including the *elastin* (*ELN*) gene (Ewart et al. 1993; Nickerson et al. 1995), with common deletion breakpoints (Perez Jurado et al. 1996; Robinson et al. 1996). The deletions arise equally often from both paternal and maternal meiosis, although a potential role for genomic imprinting in clinical features of WS (Perez Jurado et al. 1996) remains controversial (Francke 1999; Wang et al. 1999).

Duplicons of 200–300 kb that flank the common WS deletion (Fig. 3a; Francke 1999) each contain up to three transcripts, including at least three duplicons that have sequences related to the *PMS2* mismatch repair gene (Osborne et al. 1997). Two of the duplicons contain copies of the transcription factor *GTF2I* (Perez Jurado et al. 1998), in which the distal copy is the ancestral *GTF2I* gene with a unique 5' end within the common deletions, whereas the proximal copy represents a truncated, expressed pseudogene (*GTF2IP1*). The neutrophil cytosolic factor 1 (*NCF1*) gene maps telomeric to *GTF2I* in the distal duplicon, whereas an *NCF1* pseudogene is present at both the proximal and the distal duplicons (Hockenhull et al. 1999). A shared >3-Mb junction *NotI* fragment in WS deletions indicates clustering of breakpoints (Perez Jurado et al. 1998), suggesting that homologous recombination between the duplicons is responsible for generating the

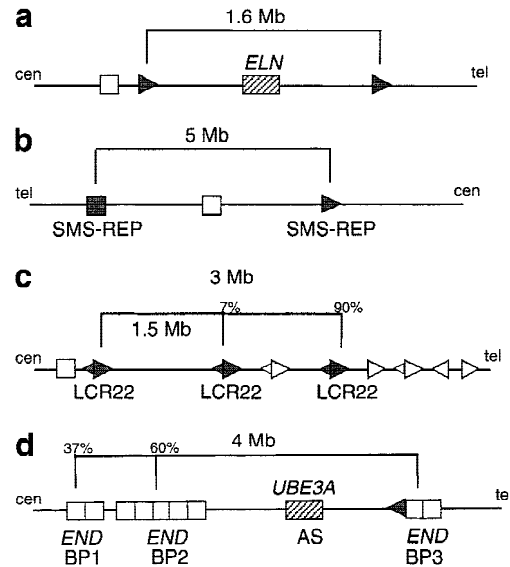


Figure 3 Genes and duplicons in genomic disorders involving complex duplicons. (a) 7q11.23 deletions in WS; (b) reciprocal 17p11.2 deletions in SMS and duplications in duplication 17p11.2 syndrome; (c) 22q11 deletions in DiGeorge and VCFS syndromes; (d) common deletions in the imprinted PWS and AS. Duplicons, unequal crossing-over positions, as well as frequency, genes, and abbreviations, are denoted as in Fig. 2. Triangles pointing in both directions reflect the complex modules revealed by 22q11 sequence. A major gene contributing to Williams syndrome, *elastin*, is shown as a hatched rectangle, as is the *UBE3A* gene involved in Angelman syndrome (AS). Genes that contribute to Smith-Magenis, duplication 17p11.2, DiGeorge/VCFS, and Prader-Willi syndromes are unknown. (See text for references.)

WS deletion, with an interchromosomal event in most cases (Dutly and Schinzel 1996; Baumer et al. 1998).

Chromosome 17p11.2 Deletions (SMS) and Duplications

Smith-Magenis syndrome (SMS) is a mental retardation/multiple congenital anomalies syndrome that occurs in 1/25,000 births (Greenberg et al. 1991). Most patients (>90%) have an ~5-Mb common deletion of 17p11.2 (Juyal et al. 1996; Chen et al. 1997; Lupski 1998). A cluster of four genes/ pseudogenes (*SRP*, *TRE*, *KER*, *CLP*) spanning >200 kb was found to be duplicated and was mapped to the common SMS deletion breakpoint regions (Chen et al. 1997), with a third copy mapping within the 5-Mb deleted region (Fig. 3b). The gene *CLP* (for *coactosin-like protein*) maps only to the proximal (P) and distal (D) breakpoint regions (SMS-REPP and D), whereas the other three genes also map to the middle duplicon (SMS-REPM). Additional copies of *CLP* occur in chromosomes 15, 16, and Y, but are uncharacterized. A novel *NotI* junction fragment of 1.2 Mb is identified, using a *CLP* cDNA probe, in every SMS patient with the common deletion, suggesting recombination between the outer SMS-REP duplicons (Chen et al. 1997). No chromosome rearrangement involving the middle copy of SMS-REP has been identified to date. Interestingly, a 210 bp sequence in the 3'

UTR of *CLP* has >95% identity to a human cDNA sequence with autonomously replicating activity (Wu et al. 1993). Initiation of DNA replication from the latter element, or transcription through the *CLP* region, may be sufficient to unwind DNA and render the region prone to homologous recombination (Chen et al. 1997).

Several 17p11.2 duplication patients have been identified, with mild mental retardation and minor dysmorphism (Chen et al. 1997; Potocki et al. 2000). Using the *CLP* cDNA probe, a novel ~1.1-Mb *NotI* junction fragment was detected in the duplication patients. This result and other molecular studies suggested that the 17p11.2 duplications involve the SMS-REP and represent reciprocal interchromosomal recombination events to those in SMS (Chen et al. 1997; Potocki et al. 2000). The 17p11.2 duplications were de novo and preferentially paternal in origin (Potocki et al. 2000).

Low Copy Repeats and Chromosome 22q11 Rearrangements

Several congenital anomaly disorders are associated with de novo germ-line rearrangements of 22q11 that involve duplison-mediated homologous recombination (Edelmann et al. 1999 a,b,c; Shaikh et al. 2000). DiGeorge and velocardiofacial syndromes (VCFS) are the most common microdeletion syndrome, with an incidence of 1 in 4000 births (Wilson et al. 1993). The cardiac and craniofacial features of VCFS may result from haploinsufficiency for the *UFDIL* gene (Yamagishi et al. 1999), although this remains controversial (Baldini 1999). Cat-eye syndrome (CES) is a rare multiple anomalies disorder (Schinzel et al. 1981) associated with a dicentric bisatellited supernumerary chromosome 22 (pter>q11.2::q11.2->pter). Derivative 22 [der(22)] syndrome is a rare mental retardation/multiple anomaly disorder, due to partial trisomy of chromosome 22q11 by unbalanced segregation of a translocation (Funke et al. 1999; Edelmann et al. 1999c).

About 90% of VCFS deletion patients have a similar deletion of 3 Mb, whereas 7% of patients have a 1.5-Mb deletion with the same proximal breakpoint region as in the 3-Mb deletions (Carlson et al. 1997; Edelmann et al. 1999b; Shaikh et al. 2000). A low-copy repeat (LCR22) ranging from 40 to 350 kb and 97% to 98% identity occurs in the vicinity of all three 22q11 breakpoint regions, as well as at six adjacent locations over a 6.5-Mb region (Fig. 3c; Dunham et al. 1999; Shaikh et al. 2000). Each LCR22 duplison differs in content and organization of complex sequence modules (Dunham et al. 1999; Shaikh et al. 2000), including variable content and arrangements of 11 genes/pseudogenes (*GGT*, *BCRL*, *V7-Rel*, *HMPLPL*, *GGT-REL*, *E2F6L*, *ISG43*, *KIAA0049*, *DGCR6*, *PRODH*, *NF1L*). Several potential recombination sequences within the LCR22 duplisons include VNTR sequences

and AT-rich repeats (Edelmann et al. 1999c; Shaikh et al. 2000). Most recombination events appear to occur within the LCR22 repeats (Edelmann et al. 1999a b c; Funke et al. 1999; Shaikh et al. 2000). There is no bias for the parental origin of 22q11 deletions leading to VCFS, with both inter- and intra-chromosomal events observed (Baumer et al. 1998; Edelmann et al. 1999a).

Interestingly, misalignment of different LCR22s during meiosis may generate both deletions and reciprocal duplications; an interstitial duplication of the same 3-Mb DNA segment as in the VCFS deletion has been identified in one family (Edelmann et al. 1999b). Two CES breakpoint clusters also map to the LCR22 duplisons associated with the proximal and distal breakpoint regions of the common VCFS deletions (McTaggart et al. 1998). Der (22) chromosomes break within the nested middle copy of LCR22 (Edelmann et al. 1999b, c; Funke et al. 1999). Other LCR22 duplisons may also be used in generating rare chromosomal rearrangements, including somatic rearrangements that lead to malignant diseases (Edelmann et al. 1999b). The identification and sequence analysis of exact breakpoints in patients with these diverse rearrangements of 22q11.2 will shed significant light on the molecular events that predispose to recombination within complex modular duplisons.

END Repeats and Chromosome 15q11–15q13 Deletions

Proximal chromosome 15q is also involved in an astonishing variety of cytogenetic aberrations with a high frequency. Prader-Willi and Angelman syndromes (PWS and AS) occur at a frequency of ~1 in 15,000 births, and most cases are due to an ~4-Mb deletion of 15q11–q13 of paternal or maternal origin, respectively (Nicholls et al. 1998; Jiang et al. 1999). PWS and AS are models for genomic imprinting in human (Nicholls et al. 1998), although this is not considered further here. The vast majority (>95%) of the deletion patients have clustered deletion breakpoint regions, with a single distal breakpoint and two proximal breakpoint regions (Christian et al. 1995; Amos-Landgraf et al. 1999). There is no apparent mechanistic differences for paternal and maternal deletions, as both inter- and intra-chromosomal rearrangements are seen in PWS and AS patients (Carrozzo et al. 1997; Robinson et al. 1998).

Recent molecular and cytogenetic analyses demonstrated at least 10 copies of a complex duplison, termed the *END* repeat, that maps to the three common deletion breakpoint regions, with two chromosome 16p11 copies (Fig. 3d; Buiting et al. 1992, 1998; Amos-Landgraf et al. 1999; Ji et al. 1999). The *END* repeats are composed to a large extent of duplications of a huge gene, *HERC2*, although multiple rearrangements within the derived duplisons have occurred during evolution (Amos-Landgraf et al. 1999; Ji et al. 1999,

2000). The ancestral *HERC2* gene encodes a giant protein, recessive mutations of which cause a neurological and developmental syndrome in mouse (Ji et al. 1999). A simple model to explain the generation of PWS and AS common deletions proposes homologous misalignment and meiotic recombination between different *END* repeat copies in proximal and distal 15q11–q13 (Amos-Landgraf et al. 1999). Active transcription of *HERC2* and related pseudogenes in male and female germ-line tissues suggest that they are transcribed in germ cells (Amos-Landgraf et al. 1999), which is supported by *jdf2* mouse phenotypic studies (Ji et al. 1999), and thus the resultant open chromatin structure may further stimulate recombination. Identification of a putative expressed breakpoint junction (using a *HERC2* probe) in one PWS patient of only five tested supports this model (Amos-Landgraf et al. 1999).

Christian et al. (1999) independently identified duplicons that map to the breakpoint regions of PWS/AS common deletions, by STS content mapping of genomic clones at or near the proximal and distal PWS/AS breakpoints. Several STSs and ESTs were mapped to duplicons at breakpoints 2 and 3 (BP2 and BP3). Interphase FISH using a PAC clone containing duplicon sequences identified ~3 signals in 15q11–q13 from normal chromosomes, and a reduced number of signals in deletion chromosomes (as well as signals on 16p11 and 15q24; Christian et al. 1999). However, the difficulty in distinguishing closely mapping, highly homologous, and partial (truncated) sequences resulted in an underestimation of the number of copies of the duplicon.

One end of the *END*-repeat duplicons is within the 3' part of *HERC2* (Ji et al. 1999). The *HERC2*-related content of different duplicons is 36.6 kb in the most rearranged/deleted copy in 16p11.2 to an estimated ~150–200 kb in some of the chromosome 15 duplicons (Ji et al. 2000). Nevertheless, the end point of the duplicon 5' of *HERC2* is unknown. Additional genes are present in the duplicons, including the small *MYLE* gene (Christian et al. 1999), although only four of the seven potential transcripts identified may represent new genes/pseudogenes in the *END* repeats (discussed in Ji et al. 2000). Furthermore, there is evidence that independent duplicons flank the *HERC2* (and *MYLE*)-containing duplicons in 15q11.2 (Buiting et al. 1999). Additional experiments, particularly complete genomic sequence, are needed to further characterize the content, orientation, and copy number of the *END* repeat duplicons that may be involved in the mechanism for PWS/AS common deletions.

Other 15q11–15q13 Rearrangements

The most common of these involve marker chromosomes. FISH studies indicate that ~57% of all marker chromosomes in newborns originate from chromo-

some 15, with most an inv dup(15), that occur in ~0.4/1000 births (Blennow et al. 1995). Inv dup(15) chromosomes are bisatellited chromosomes derived from chromosome 15, which contain two centromeric regions, although usually only one centromere is active (Schwartz and Depinet 1996). The inv dup(15) is a mirror image chromosome that is duplicated about a central axis (e.g., pter—cen—q13—cen—pter). It is a misnomer to call it an inv dup(15), and preferred terms would be either a derivative or dicentric chromosome; however, it is normally referred to as an inv dup(15) because of historical context. These chromosomes come in a variety of size classes. Small marker chromosomes either have only one centromere or one of the two proximal breakpoints associated with PWS and AS; that is, for type 1, a breakpoint between the centromere (*D15Z1*) and markers located between BP1 and BP2, or for type 2, a breakpoint within the BP2 region (Cheng et al. 1994; Huang et al. 1997). Larger marker chromosomes can have variable breakpoints (Mignon et al. 1996), although most either share the distal PWS/AS breakpoint (the BP3 region) or have a breakpoint distal of this and within YAC 810f11 (Huang et al. 1997; Wandstrat et al. 1998). Because the vast majority of the larger markers share this latter breakpoint, and given the high frequency of these, the findings suggest the possible presence of another duplicon or recombination-promoting sequence. Interestingly, the larger inv dup(15) are all de novo and exclusively maternal in origin.

Three phenotypes associated with the presence of a supernumerary marker chromosome derived from chromosome 15 are as follows: normal, the inv dup(15) syndrome, or PWS/AS. The inv dup(15) syndrome refers to a consistent phenotype of mental and developmental retardation, hypotonia, behavior disturbances, seizures, abnormal dermatoglyphics, and mild somatic abnormalities (Wisniewski et al. 1979; Leana-Cox et al. 1994). It is associated with the presence of the PWS/AS critical region as seen in the larger markers described above (Leana-Cox et al. 1994). The smaller markers (type 1 and type 2) are usually associated with a normal phenotype and may be familial, although some have been associated with a PWS or AS phenotype (Robinson et al. 1993). The latter are due to uniparental disomy of the normal chromosomes 15 (Robinson et al. 1993).

Although less common, direct duplications of proximal 15q11–15q13 have been observed (Pettigrew et al. 1987; Clayton-Smith et al. 1993a; Browne et al. 1997; Cook et al. 1997, 1998; Mohandas et al. 1999), some with the same breakpoints as PWS/AS deletions, whereas others have a more distal breakpoint similar to the large inv dup(15) (Repetto et al. 1998; Robinson et al. 1998). Patients with maternal duplications that include at least the PWS/AS critical region show devel-

opmental delay, or autism (Browne et al. 1997; Cook et al. 1997, 1998; Repetto et al. 1998), whereas a few individuals with paternal duplications have a nonspecific developmental delay (Mohandas et al. 1999). Finally, a few triplication cases have been reported (Schinzel et al. 1994; Cassidy et al. 1996; Long et al. 1998; Robinson et al. 1998), as well as paracentric inversions of 15q11–15q13 (Clayton-Smith et al. 1993b). It remains unclear whether these rearrangements are also mediated by homologous recombination of different copies of the *END* repeat duplicon or whether several different duplicons exist in 15q and are involved in the various rearrangements.

Other Examples of Genomic Disorders and Chromosomal Duplicons

Beside the examples discussed above, several other diseases are also caused by common DNA rearrangements. Proximal spinal muscular atrophy (SMA), a recessive-lethal condition affecting 1/10,000 births, is associated in ~18% of cases with rearrangements in an inverted duplication of ~500 kb in 5q13 (Melki et al. 1994; Lefebvre et al. 1995; Scharf et al. 1998). A second example is the recessive Hunter syndrome, due to mutations of the iduronate-2-sulfatase (*IDS*) gene in Xq28. Twenty percent of Hunter syndrome cases involve an inversion that disrupts the *IDS* gene, caused by homologous recombination between *IDS* and an *IDS* pseudogene 90 kb downstream (Bondeson et al. 1995). Although less well characterized, most cases of juvenile nephronophthisis (NPH) involve deletion of a 250-kb region on chromosome 2q13, flanked by repeat sequences (Konrad et al. 1996). Lastly, similar chromosome rearrangement events that are benign also occur in the genome. In studying a rare condition (Emery-Dreifuss muscular dystrophy, Xq28), Small et al (1997) identified a common 48-kb inversion that is present in the heterozygous state in 33% of females, arising from homologous recombination between flanking 11.3 kb duplicons of >99% sequence identity. As the human genome sequence is completed, the structure and role in chromosome rearrangements of these and other region-specific duplicons, including those currently unrecognized, will likely emerge.

Transchromosomal Duplicons

In addition to the chromosome-specific duplicons described above, a large number of genomic segments have been identified in the last few years that map to multiple non-homologous chromosomes (termed transchromosomal duplicons) (Borden et al. 1990; Wong et al. 1990; Buiting et al. 1992; Bernardi et al. 1993; Tomlinson et al. 1994; Eichler et al. 1996, et al. 1997, 1999; Frippiat et al. 1997; Kehrer-Sawatzki et al. 1997; Regnier et al. 1997; Zimonjic et al. 1997; Eichler, 1998; Trask et al. 1998a,b; Brand-Arpon et al. 1999; Grewal et

al. 1999; Horvath et al. 2000). Two regions of the human genome that seem unusually enriched for such transchromosomal duplication events are the pericentromeric (defined as the first Giemsa light or dark band flanking the primary constriction) and subtelomeric portions of chromosomes (Eichler 1998; Trask et al. 1998a). Detailed analyses of pericentromeric DNA in 10q11, 16p11, and 2p11 (Jackson et al. 1999a; Loftus et al. 1999; Horvath et al. 2000; J. Horvath, S. Schwartz, E.E. Eichler, unpubl.), for example, have identified zones of genomic duplicons located distal to α -satellite DNA. These regions are composed almost entirely of genic/pseudogenic segments that have been transposed from diverse regions of the hominoid genome. As one example, analysis of a 225-kb pericentromeric BAC sequence from chromosome 16p11 identified four different duplicons, including portions of the creatine-transporter, *HERC2*, variable κ , and variable heavy chain immunoglobulin genes (Loftus et al. 1999). All of these segments have been duplicated and transposed to 16p11 independently from their ancestral loci in Xq28, 15q13, 2p11, and 14q32, respectively. Comparative mapping and phylogenetic analysis of various pericentromeric segments reveals that they began to transpose within the hominoid genome relatively recently [estimates range from 3 to 20 million years ago (mya)]. Consequently, many of the paralogous segments share a high degree of sequence similarity (~93%–98%). Furthermore, differences in map position and copy number have been observed among closely related primates (chimpanzee, human, and gorilla). Population studies of subtelomeric duplications have identified differences among different human ethnic groups (Trask et al. 1998a), suggesting that dynamic spread of these segments may be an ongoing process in the evolution of the human genome.

The molecular mechanism underlying the duplication and transposition of genomic segments to the pericentromeric or subtelomeric regions of chromosomes is not well understood. However, analysis of sequences located at the presumptive sites of insertion within the pericentromeric regions have uncovered several unusual classes of GC-rich repeats located in close (<1 kb) proximity to the boundaries of paralogy (Borden et al. 1990; Eichler et al., 1996, 1997; Eichler 1999). One class of these repeats (CAGGG; Fig. 4) localizes specifically to the pericentromeric regions of several different human autosomes, with an evolutionary origin predating the arrival of the duplicons themselves (Eichler et al. 1999). Moreover, the sequences bear some similarity both in sequence and organization to χ -recombination elements and immunoglobulin switch-recombination signal sequences, which are capable of mediating recombination events among non-allelic sequences. These repeats may play a role in pericentromeric duplications, by serving as a preferred

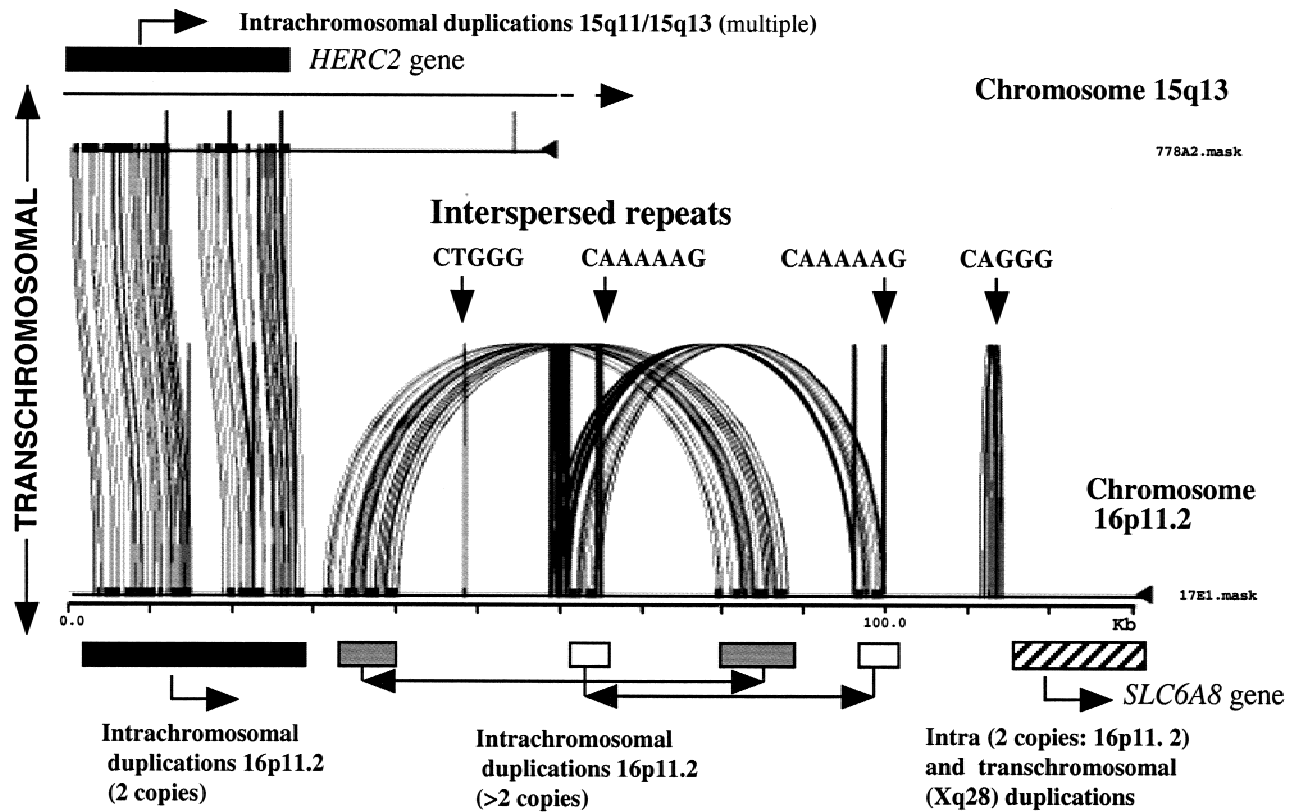


Figure 4 Schematic for duplcon formation and dispersal in chromosomes 15q13, 15q11, and 16p11.2. At top is shown BAC 778A2 (AC004583) spanning the 5' half of the ancestral *HERC2* gene, which has undergone intrachromosomal duplications to form multiple duplcons in 15q13 and 15q11 (see Fig. 3d). Miroppeats comparison of repeat-masked sequence to a chromosome 16p11.2 BAC 17E1 (AC002041) illustrates a transchromosomal duplication and transposition of a *HERC2*-duplcon (Miroppeats displays regions of similarity by joining lines between two sequences). Note the 27.1 kb of *HERC2*-like sequence duplicated between these two segments (BESTFIT alignment indicates 94.7% genomic identity). The 17E1 BAC also identifies a second gene segment derived from an ancestral Xq28 locus (the creatine transporter gene, *SLC6A8*). These and several other locally duplicated segments (as denoted by arcs) form additional duplcons in 16p11. 17E1 also has 4 interspersed repeats including a large CAGGG-rich region (see text).

transposition integration signal for the duplcons. It is interesting that similar GC-rich elements have also been mapped within the vicinity of recent subtelomeric duplications (Amann et al. 1996; Chute et al. 1997). In addition to these initial transposition seeding events within pericentromeric DNA, it is now clear that secondary events transfer larger segments of the duplcons among other pericentromeric regions (Fig. 4)—a process that has been termed pericentromeric swapping (Horvath et al. 2000; J. Horvath, S. Schwartz, and E.E. Eichler, unpubl.). The net effect of these duplication events is the generation of large (>100 kb) blocks of paralogy among multiple nonhomologous chromosomes, each of which is a mosaic of smaller duplicated segments (Fig. 4).

Is there a link between the dynamic duplicative nature of pericentromeric DNA and genomic duplcons mediating genomic disease? A direct connection is yet to be established, but there are some tantalizing associations. (1) CAGGG repeats have been mapped to several cytogenetic bands associated with recurrent chro-

mosomal structural rearrangement and genomic disease (particularly within the proximal regions of 15q11 and 22q11) (Eichler et al. 1999). (2) There is a significant positional bias for duplcons and genomic diseases, as a group, to be near the pericentromeric region (e.g., 7q11.23, 15q11.2, 17p11.2, 17q11.2, and 22q11.2). Three of the most common rearrangements discussed above (SMS, PWS/AS, and VCFS), which involve complex duplcons, involve rearrangement between a duplcon situated near a proximal pericentromeric region and a duplcon located more distally. (3) Analyses of pericentromeric DNA on chromosome 10 (Jackson et al. 1999a,b), chromosome 22 (Dunham et al. 1999; Shaikh et al. 2000) and chromosome 16 (E.E. Eichler, unpubl.) suggest that intrachromosomal (chromosome-specific) duplcons become more prevalent as one approaches unique DNA. Furthermore, analysis of DNA from regions of pericentromeric DNA from 16p11.2 and 15q11 have identified *HERC2* duplcons, derived from an ancestral locus in 15q13, as one component in a series of duplications that constitute

16p11 (Fig. 4; Amos-Landgraf et al. 1999; Ji et al 1999, 2000; Loftus et al. 1999). These data suggest that the processes responsible for transchromosomal and intrachromosomal pericentromeric duplication and for disease-causing rearrangements may be molecularly interrelated. One scenario may be that pericentromeric DNA has created a favorable evolutionary milieu for the accumulation and transfer of duplicated segments. Recurrent chromosomal structural rearrangement associated with disease then arises due to the fact that both donor and acceptor recombining loci flank unique gene regions that are haplo-insufficient. Of course, not all duplison-mediated rearrangements can be described as pericentromeric, nor is the process of recent genomic duplication restricted to pericentromeric and subtelomeric DNA (DeSilva et al. 1999; Loftus et al. 1999). The process of pericentromeric duplication, therefore, is likely one of several different mechanisms capable of creating paralogous sequences that can mediate genomic instability.

Conclusions and Perspectives

From studies discussed above and by others (Purandare and Patel 1997; Mazzarella and Schlessinger 1998; Lupski 1998), it is clear that the presence of duplisons predisposes to abnormal pairing and unequal crossing-over, leading to chromosome rearrangements in specific regions of the human genome. Combined, at least 0.7–1 per 1000 births will have a genomic disorder due to a de novo rearrangement between duplisons, attesting to the impact on medical care and economic burden. Deletions, duplications, inversions, translocations, and supernumerary marker chromosomes can all result from duplison-mediated homologous recombination, suggesting this disease mechanism is a general phenomenon. The identification of novel junction fragments in most patients with CMT1A/HNPP, WS, SMS, duplication 17p11.2, and some 22q11.2 rearrangements, supports the idea that precise recombination events are associated with rearrangements involving even complex duplisons. It is likely that double-strand breaks might be the initiating event for these homologous recombination events (Lupski 1998), although it will be necessary to isolate the breakpoints from multiple patients in each class of disorders to more accurately model the mechanism of recombination.

Three general features of these duplisons can be proposed. (1) Large-size and high-sequence identity are important characteristics. The duplisons span at least thousands of base pairs to several hundred kilobases. The identity between the two recombining duplisons can be as high as 99.9% (*int22h*). Recombination hot spots are usually in regions of identical nucleotide sequence, of at least 200 to ~450 bp in length, although this has not yet been examined in

complex duplison rearrangements. When genomic disorders are examined according to the distance between the flanking duplisons, it appears that the length of the duplison increases as the distance between the duplisons increases (Lupski 1998). Large duplisons with high sequence identity may be necessary to initiate pairing and/or stabilize the recombination complex, for unequal crossing-over and recombination to occur. (2) Recombination promoting features may be present within duplisons. Most characterized duplisons contain one or more genes/pseudogenes. Two of the loci (*VCX* and *HERC2*) are expressed in germ cells, although it is unknown whether these or genes in other duplisons are transcribed in meiotic or post-meiotic germ cells, in which unequal crossing-over must occur. In yeast, double-strand breaks have been found primarily in promoter regions, suggesting a role for an open chromatin structure in homologous recombination (Osman and Subramani 1998). The presence of a sequence in SMS-REP that is homologous to one with autonomously replicating activity also suggests a role for open chromatin structure, and/or DNA replication. Sequences related to those that can promote recombination have been identified in recombination hot spots in CMT1A-REP and 22q11 rearrangements, and VNTRs are found within each copy of the S232 and LCR22 repeats, as well as within the *END* repeats (Ji et al. 2000). (3) In cases in which more than two duplisons exist in the same chromosome region, there are preferences as to which copies are involved in specific rearrangements. Further studies are needed to understand why some copies are chosen over others, but this may relate to sequence identity, orientation of the duplisons, presence of recombination promoting sequences, or chromatin structure.

Although much has been learned about the mechanisms for genomic disorders, many questions remain. (1) Some rearrangements occur almost exclusively in paternal meiosis (CMT1A duplication and F8 inversion), whereas others happen equally often in male and female meiosis, despite normal meiotic recombination being twice as frequent in females as in males. It has been suggested that there are male factors for, or female protection against, aberrant homologous recombination (Purandare and Patel 1997). One such factor may be the continued proliferation of spermatogonia after puberty, which may lead to a much greater likelihood of a structural rearrangement eventually occurring in sperm (Chandley 1991). (2) Most cases of genomic disorders are deletions, whereas duplications and inversions seem to be less common. This may arise from the mechanisms producing inter- or intrachromosomal events between direct repeats (Fig. 1). A bias of ascertainment may also contribute, because deletions usually cause a more severe phenotype. (3) It is

not known why most of these chromosome rearrangements involve duplications near pericentromeric regions (Eichler 1998), but as discussed above this may relate to the propensity for duplicons to cluster in these regions and for duplicons to generally disperse to adjacent chromosomal positions. Also not known is how duplicons several megabases apart search for and recombine with each other, nor what role higher order chromosome structures play in the process. (4) The origin and dispersal of various duplicons appears to be limited to primates. Although the CMT1A-REP seems to be a human- and chimpanzee-specific repeat (Kiyosawa and Chance 1996; Keller et al. 1999), preliminary studies on the *END* repeats suggests an origin of ~15–20 mya (Christian et al. 1999; Ji et al. 1999), and the LCR22 duplicons arose at least 20–25 mya on the basis of their presence in Old World monkeys (Shaikh et al. 2000). Thus, the age of the duplicons appears to correlate with their complexity and the frequency of chromosome rearrangements. A comparative genomic study of the various duplicons first identified in the human genome will determine their evolutionary origin and provide insight into the mechanisms of formation and rearrangement of these duplicons.

Finally, it is possible that environmental factors may contribute to the chromosome rearrangement events that lead to genomic disorders. Preliminary studies suggest a link between paternal hydrocarbon exposure and PWS (Strakowski and Butler 1987; Cassidy et al. 1989; Åkefeldt et al. 1995), but other genomic disorders have not been examined. Several studies show an increased rate of mitotic homologous recombination between duplicated DNA segments. X-rays and other carcinogens were shown to significantly increase the reversion frequency of the pink-eyed unstable (*p^{mu}*) mutation, a 70-kb internal tandem duplication of *p* (Schiestl et al. 1994, 1997). Reversion of mutations caused by tandem duplication have also been found in yeast, Chinese hamster and human cell lines, and were drastically increased by carcinogen treatments (Schiestl et al. 1988; Zhang and Jenssen 1992; Aubrecht et al., 1995). These events are all mediated by intrachromosomal recombination. It will be necessary and important to perform molecular and epidemiological studies to determine whether environmental factors (such as hydrocarbons) increase germ-line chromosome rearrangements that lead to the various genomic disorders in human. Given the remarkably high frequency of genomic disorders, as a group, if environmental risk factors were recognized it would allow proper measures to be taken to prevent preconceptional exposure, and thereby would significantly reduce the frequency as well as the economic and social costs of genomic disorders.

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