



Uniparental Disomy and Genome Imprinting: an Overview

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The following paper is concerned with potential changes in the normal epigenetic process in a diploid individual, when a chromosome pair or segment is inherited from one parent only, instead of the expected biparental contribution. This aberrant mode of transmission arises from the high rate of gamete aneuploidy in humans. It has received the name uniparental disomy (UPD), and has emerged as an important factor in the new field of nontraditional inheritance, depicted in Table I.

The following definitions may foster a better understanding of this discussion.

UPD is the inheritance of *both* copies of a chromosome [or chromosomal segment(s)] from a *single* parent, instead of the normal biparental transmission of the pair. In *isodisomy*, the two uniparental copies are *identical*, being derived from the same parental chromosome. In *heterodisomy*, the two uniparental chromosomes are *different*, being derived from the homologues of a pair.

Table I - Instances of non-traditional inheritance

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- I. Di- or trinucleotide repeat expansion (i.e. anticipation)
 - II. Mitochondrial inheritance: only matroclinous (normal or aberrant)
 - III. Epigenetic modifications (both normally or aberrantly transmitted)
 - a) Normal parental imprinting
 - b) Abnormal parental imprinting
 1. Chromosome duplication
 2. Chromosome deletion
 3. Chromosomal translocations and inversions
 4. UPD
 5. Gene mutations
 6. Imprinted gene mutations
 7. Imprinted control element mutations
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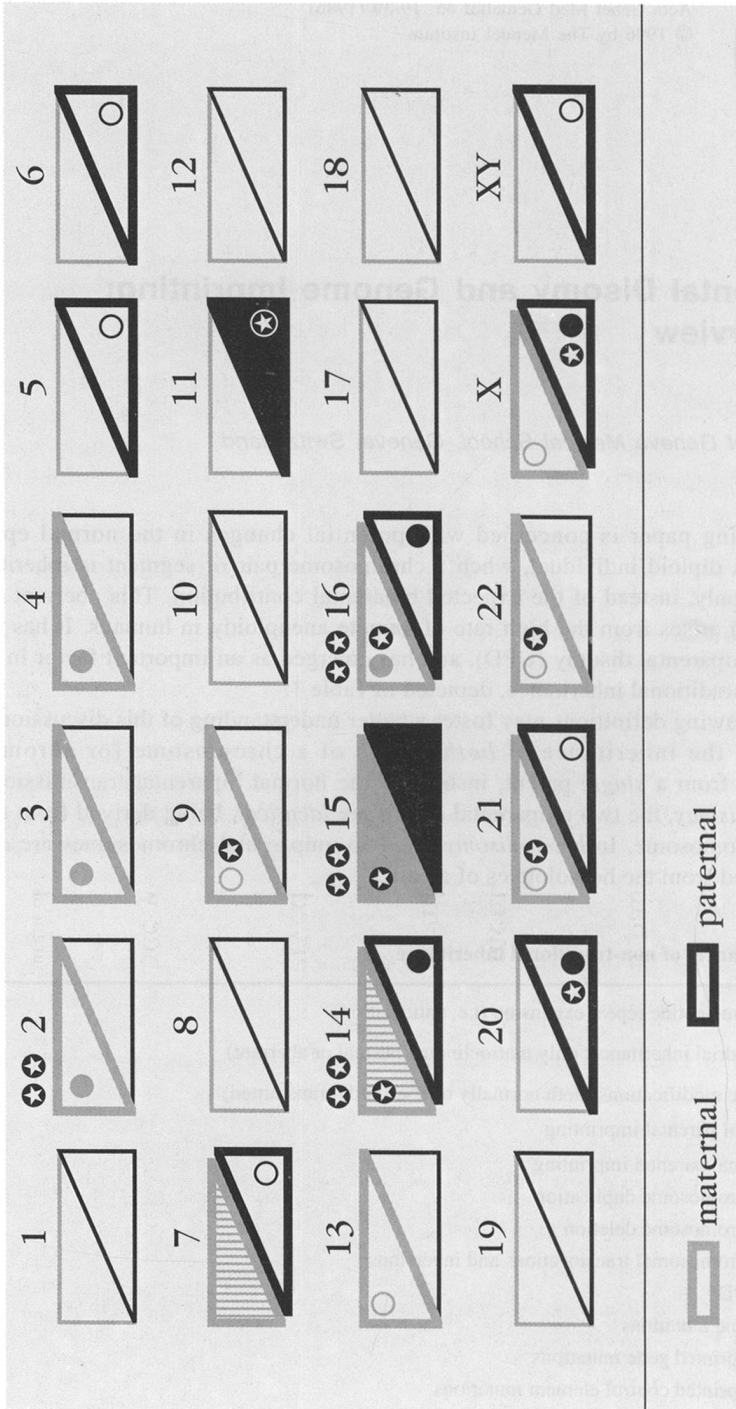


Fig. 1 - Identified cases of UPD, according to parent of origin, chromosome number and various characteristics.

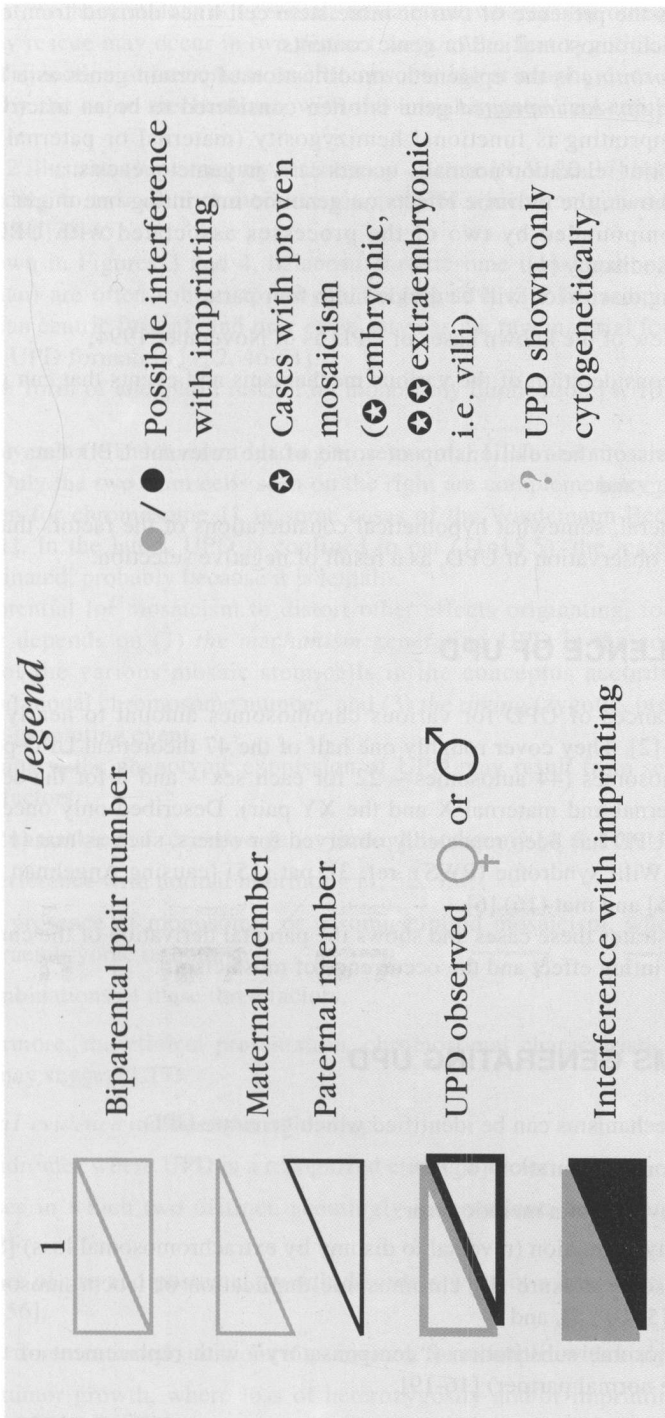


Fig. 1a - Identified cases of UPD, according to parent of origin, chromosome number.

Mosaicism is the presence of two or more stem cell lines derived from one zygote, having different chromosomal and/or genic contents.

Genomic imprinting is the epigenetic modification of certain genes as a function of their parental origin. An *imprinted gene* is often considered to be an inactivated gene. The result of imprinting is functional hemizygosity (maternal or paternal) for some allelic pairs. Imprint relaxation normally occurs early in gametogenesis.

As will be shown, the intrinsic effects on genomic imprinting one might attribute to UPD can be compounded by two of the processes associated with UPD, namely mosaicism and isodisomy [1].

The following discussion will be divided into four parts:

1. an overview of the known cases of UPD as of November 1994;
2. a broad consideration of the various mechanisms and events that can give rise to UPD;
3. an analysis of the relationship of some of the relevant UPD data to genomic imprinting, and
4. some general, somewhat hypothetical considerations of the factors that may preclude the observation of UPD, as a result of negative selection.

THE PREVALENCE OF UPD

The known instances of UPD for various chromosomes amount to nearly 100 as of November 1994 [2]. They cover roughly one half of the 47 theoretical UPD possibilities for entire chromosomes (44 autosomes – 22 for each sex – and 3 for the sex chromosomes – the paternal and maternal X and the XY pair). Described only once so far for some members, UPD has been repeatedly observed for others, such as mat (15) [responsible for Prader-Willi syndrome (PWS); ref. 3], pat (15) [causing Angelman syndrome; ref. 4], mat (7) [5] and mat (16) [6].

Figure 1 illustrates these cases and shows the parental derivation of the chromosome, the genome imprinting effect and the occurrence of mosaicism.

MECHANISMS GENERATING UPD

Three general mechanisms can be identified which generate UPD:

1. gamete complementation [6, 7];
2. mitotic reversal of a meiotic error:
 - a) trisomy correction (reversal to disomy by extrachromosomal loss) [8, 9];
 - b) monosomy erasure (by chromosome duplication or isochromosome formation) [5, 10-15], and
 - c) chromosome substitution (“compensatory” with replacement of the marker by the normal partner) [16-19];
3. mitotic recombination (exchange between homologue chromatids) [20, 21].

The first mechanism does not generate mosaicism, whereas the other two can.

Trisomy rescue may occur in two distinct ways at the first zygotic cleavage by chromatid nondisjunction at metaphase or chromosome lag at anaphase, or at various stages thereafter by the same mechanisms, with the initial zygotic makeup preserved in one stem cell.

Figure 2 illustrates how trisomy rescue may operate [8, 9, 22-37] by reduction to disomy according to two distinct mechanisms, both of which can generate mosaicism, in theory at least [38-45].

As shown in Figures 3 and 4, balanced chromosome translocations (reciprocal and Robertsonian) are often subject to irregular segregation (3:1 for reciprocal and 2:1 for Robertsonian centric fusion), and may often serve as the raw material for mitotic trisomy rescue and UPD formation [1, 2, 46-51].

Another form of aneuploid rescue, by monosomy duplication [4, 10] is illustrated in Figure 5.

A purely mitotic mechanism leading to segmental UPD and mosaicism is shown in Figure 6. Only the two stem cells seen on the right are complementary disomic types, as may happen for chromosome 11 in some cases of the Wiedemann-Beckwith syndrome (WBS) [21]. In the latter, UPD is confined to pat (11p15.5), the maternal counterpart being eliminated, probably because it is lethal.

The potential for mosaicism to distort other effects originating, for example, from imprinting depends on (1) *the mechanism* generating UPD in the conceptus, (2) *the selection* of the various mosaic stem cells in the conceptus according to e.g. their makeup and modal chromosome number, and (3) *the timing* (zygotic, pre- or postnatal) of the mosaic-generating event.

In summary, the phenotypic expression of UPD may result from several isolated or combined factors:

1. the unmasking of recessive genes through isodisomy [4, 6, 10];
2. interference with normal imprinting [1, 52, 53];
3. the presence of monosomic or trisomicuploid mosaicism, whether embryonic, extraembryonic or both, and
4. combinations of these three factors.

Furthermore, the clinical presentation, chromosomal characteristics and molecular evidence may suggest UPD.

Clinical evidence includes the following:

1. syndromes where UPD is a recognized etiologic factor;
2. cases in which two distinct, seemingly independent, conditions are associated [54];
3. cases of pre- and postnatal growth disorders without a known explanation [4, 10, 54-56];
4. the aforementioned situations if associated, for example, with body asymmetry, and
5. in tumor growth, where loss of heterozygosity and/or imprinting are important factors [20, 21, 57].

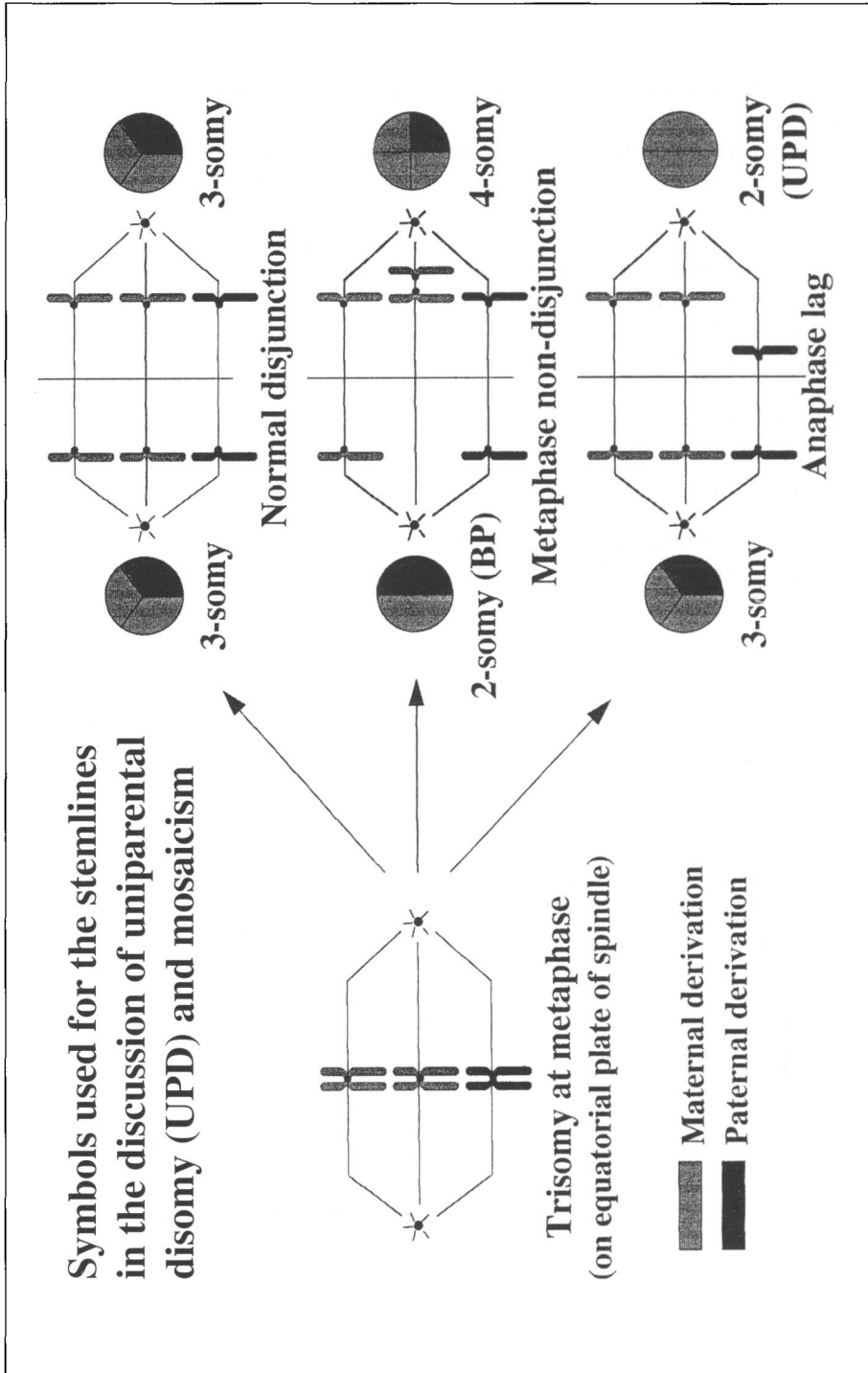


Fig. 2 - Reduction to disomy through trisomy rescue. BP = Biparental.

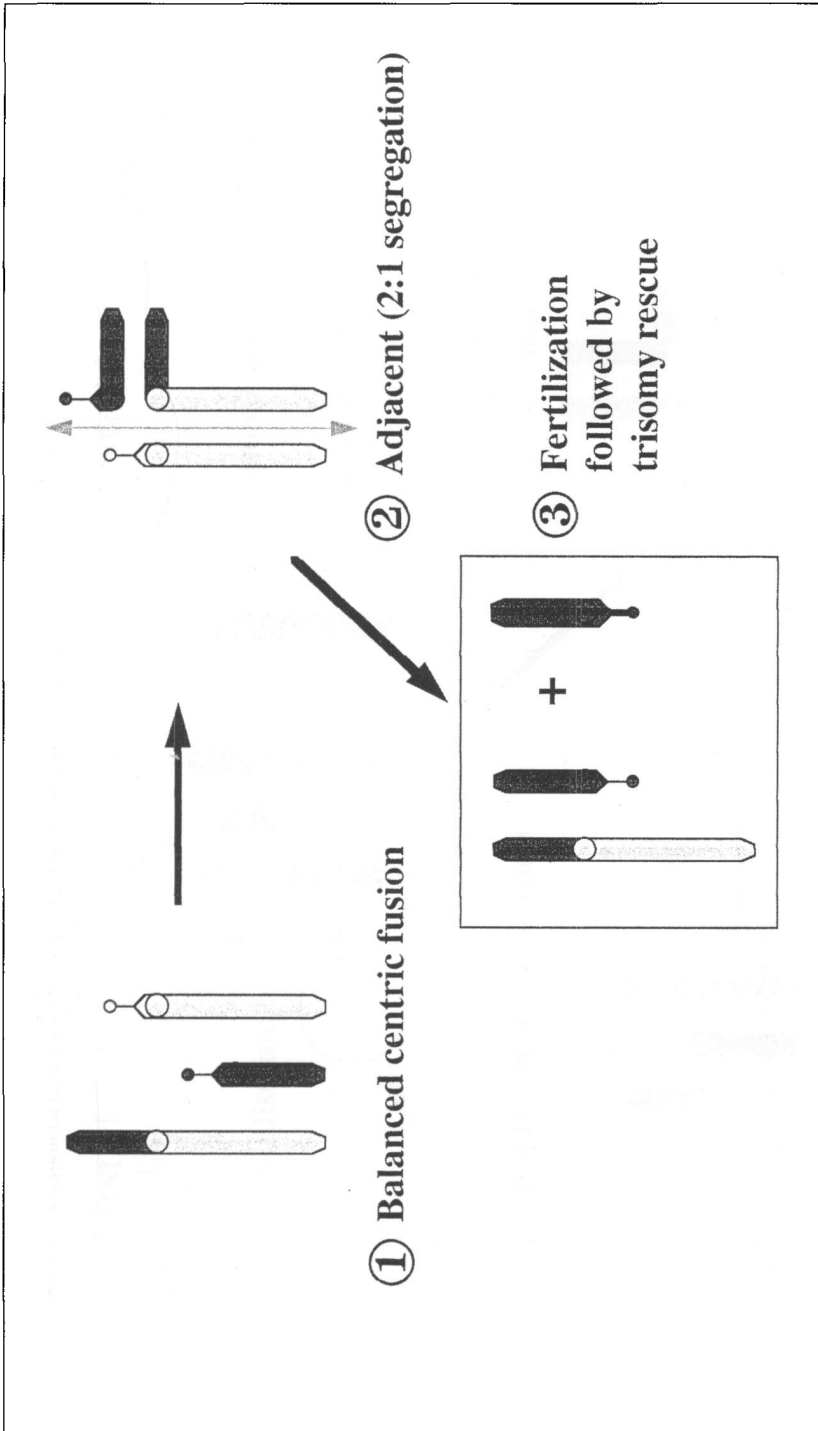


Fig. 3 - UPD favored by balanced Robertsonian translocation and 2:1 segregation followed by trisomy rescue.

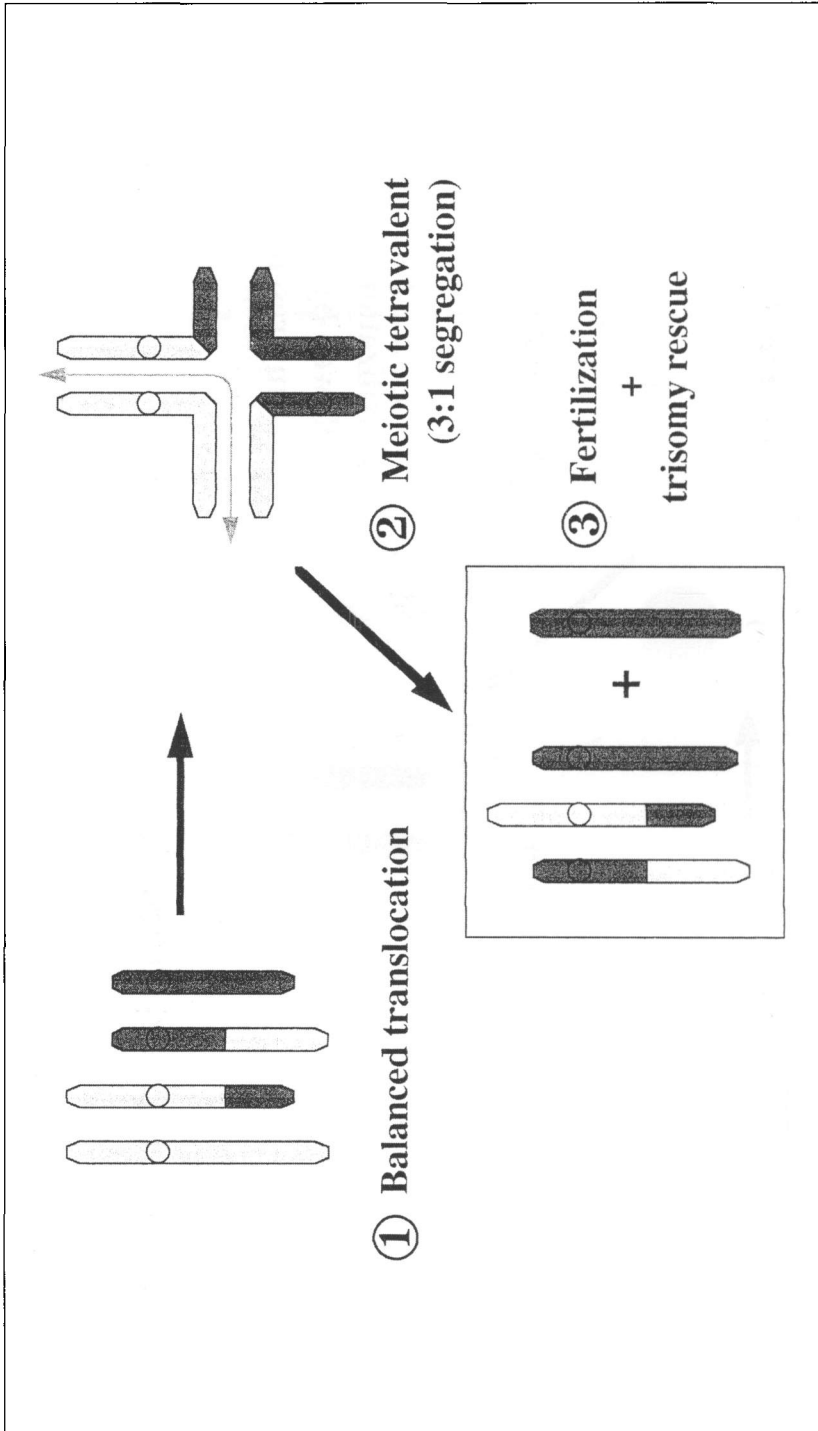


Fig. 4 - UPD favored by balanced translocation and 3:1 segregation followed by trisomy rescue.

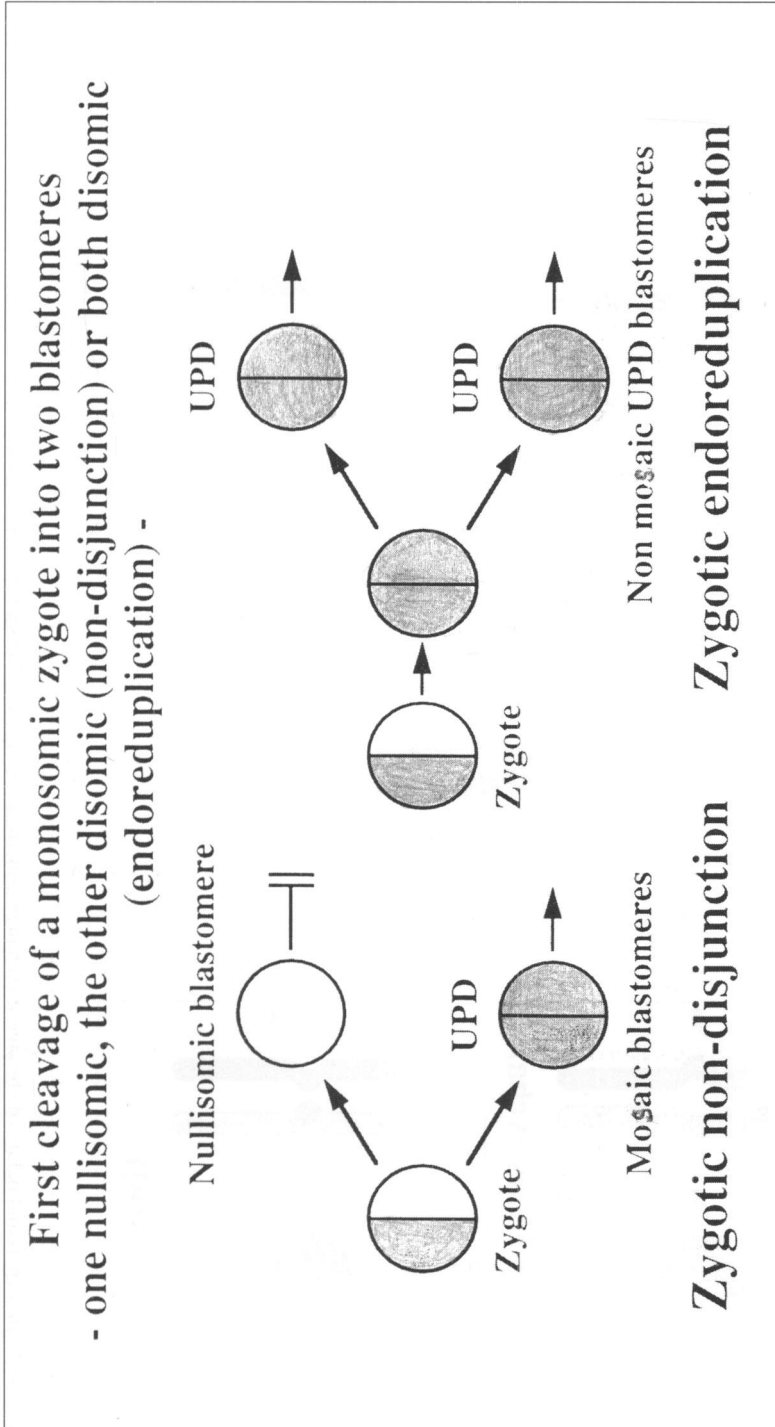


Fig. 5 - Mosomy Rescue and UPD by mosomy duplication.

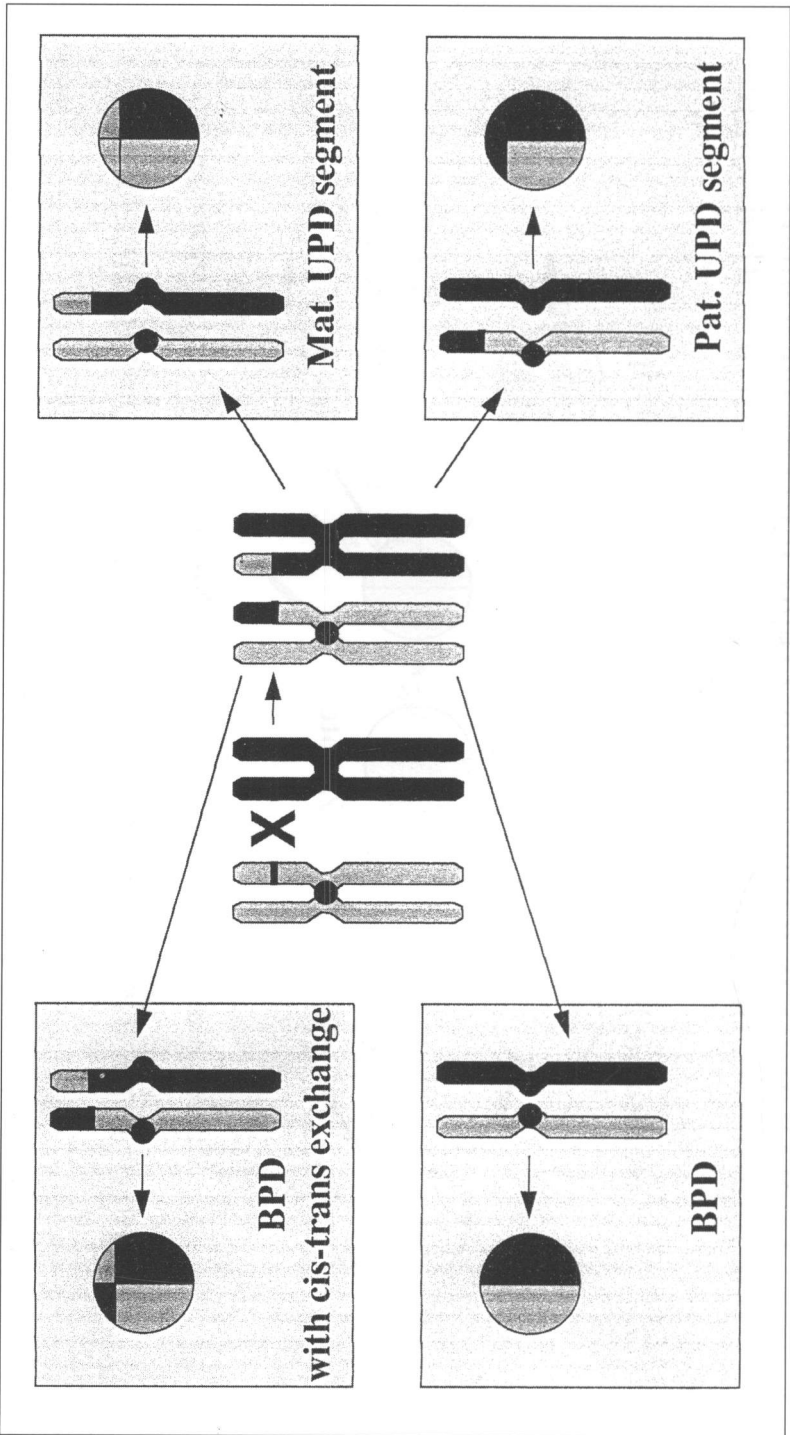


Fig. 6 - Homologous and balanced chromatid exchange: somatic crossing over. BPD = Biparental disomy.

Chromosomal evidence encompasses:

1. homozygosity for a heterozygous, unique parental heteromorphism;
2. uniparental derivation of distinctive heteromorphisms of both homologues;
3. cases of homozygous pericentric inversions [30, 58];
4. balanced chromosomal interchange or Robertsonian translocation (inherited or de novo) with e.g. clinical anomalies or dysmorphism;
5. cases of euploid/aneuploid mosaicism in the proband, extraembryonic tissues or both, and
6. offspring (especially normal) born to a carrier of a Robertsonian translocation between homologues [59-62].

Molecular evidence comprises:

1. lack of obligate parental alleles [4, 10];
2. homozygosity acquired from a singly heterozygous parent [4, 10], and
3. unusual and/or excessive syntenic homozygosity [21].

Evidence for the mechanisms of UPD formation

Six mechanisms of UPD production have been documented beyond reasonable doubt in particular cases:

1. trisomy rescue (chromosomes 2, 9, 14, 15, 16 and 20);
2. monosomy duplication including isochromosome formation (chromosomes 7, 14, 15 and 16);
3. gamete complementation (chromosome 14);
4. heterochromosomal (compensatory) substitution (chromosomes 6, 15 and 21);
5. heterochromatid exchange (chromosomes 11 and 13), and
6. mosaicism.

Actual instances of reduction to homozygosity for recessive genes have been demonstrated in the conditions listed in Table 2.

Trying to take into account interfering factors such as mosaicism and isodisomy, the known cases of UPD have been scrutinized for imprinting effects to give the classification shown in Table 3.

Individual examples of imprinting related to UPD

Maternal and paternal UPD for chromosome 15, associated with PWS and Angelman syndrome, respectively, and paternal UPD for 11p15.5 responsible for some cases of WBS, as obvious results of imprinting disturbances, are discussed elsewhere in this volume. Maternal UPD for chromosome 7 is associated with stunted growth (Table 4). This

Table 2 - Clinical examples of reduction to homozygosity (isodisomy) leading to recessive diseases

Chromosome	Condition	Reference
5	Spinal muscular atrophy (type III)	63
6	Deficiency of 4th component (a and b) of complement	64
	Methylmalonic acidemia	65
7	Cystic fibrosis	4, 10
	Osteogenesis imperfecta (COL1A2)	55
	Congenital chloride diarrhea	66
9	Cartilage-hair hypoplasia	67
11	β -thalassemia	68
13	Retinoblastoma	20
14	Rod monochromacy	11
15	Bloom syndrome	69
16	α -thalassemia	70
	Familial Mediterranean fever	71

Table 3 - Effect of known UPDs on imprinting

Certain	Nearly certain	Possible	Unlikely
pat(11)	mat(7)	mat(2) [31]	pat(5) [63]
mat(11)	mat(14)	mat(3) [58]	pat(6) [64]
pat(15)		mat(4) [72, 73]	pat(7) [66]
mat(15)		pat(14) [7, 74]	mat(9) [67]
		mat(16)	mat(13) [61, 62]
		pat(20) [43]	mat(21) [19, 76]
		pat(X) [75]	pat(21) [77]
			mat(22) [78]
			mat(X) [79]
			XY [80]

also occurred in cases with pat i(7p) and mat i(7q). Consequently, the imprinted region is probably on 7q.

The data indicating that there are genomic imprinting disturbances for maternal UPD 14 are also strong, although growth was not adversely affected in a recent case. The major signs [11, 38, 46, 50, 51, 81] include arrested hydrocephalus, short stature, small hands (and feet), delayed motor and/or mental development, precocious (or early) puberty and recurrent otitis media. The inconstant signs include hyperextensible joints, a short philtrum, a high narrow palate and scoliosis.

Table 4 - Maternal UPD for chromosome 7 and genomic imprinting

Sex	Age (years)	Height (cm)	Weight (kg)	Diagnosis	Reference
F	16	130	–	cystic fibrosis and growth retardation	4
M	4	87	–	cystic fibrosis and growth retardation	10
M	30	143.7	36.6	osteogenesis imperfecta and growth retardation	55
F	2.25	76	7.96	growth retardation	56

Four more cases in particular should be mentioned, whose anomalies raise the possibility of imprinting effects.

A case of maternal UPD for chromosome 2 was reported with the following phenotypic effects [31]: growth failure, hypothyroidism, bronchopulmonary problems, normal early psychomotor development and trisomy 2 mosaicism in the amniotic fluid.

Chromosome 14 paternal UPD has been associated with [7, 74] marked facial dysplasia, severe neurologic involvement, growth retardation and severe bone defects (of the thorax and spine in one case).

Chromosome 16 maternal UPD also has potential genomic imprinting effects. It is always derived from a trisomy of maternal origin, intrauterine growth is retarded (and positively correlated with the extent of the placental trisomy rather than with the existence of the maternal UPD per se), there is the possible implication of intrinsic (embryofetal) residual tri(16) although strict confined placental mosaicism has been claimed [39], lower gastrointestinal tract anomalies are present [82], but the natural history of this condition over time has not yet been fully documented [28].

Spinner et al. [43] have reported a case of paternal uniparental isodisomy for chromosome 20 [blood and marrow: 45, XY, t (20; 20) (p13; p13)]. The boy presented with an absent left ear, microtia of the right ear, microcephaly, congenital heart disease and Hirschsprung disease. Mosaicism for trisomy 20 in the skin was 8%. This phenotype is quite distinct from 20p – or mosaic tri (20).

The chromosomes for which UPD is unreported as of November 1994 are mat(1), pat(1), pat(2), pat(3), pat(4), mat(5), mat(6), mat(8), pat(8), pat(9), mat(10), pat(10), mat(11), mat(12), pat(12), mat(13), mat(17), pat(17), mat(18), pat(18), mat(19), pat(19), mat(20) and pat(22).

Summarizing all the above data, a tentative imprinting map of the human genome as of February 1995, is illustrated in Figure 7.

CONCLUDING REMARKS

Imprinting, a normal epigenetic control, which depends on the parental origin of some chromosomes, may be altered at one or more loci when diploidy is, for one pair, incorrectly derived from one parental source only (UPD). Basically, whereas in normal

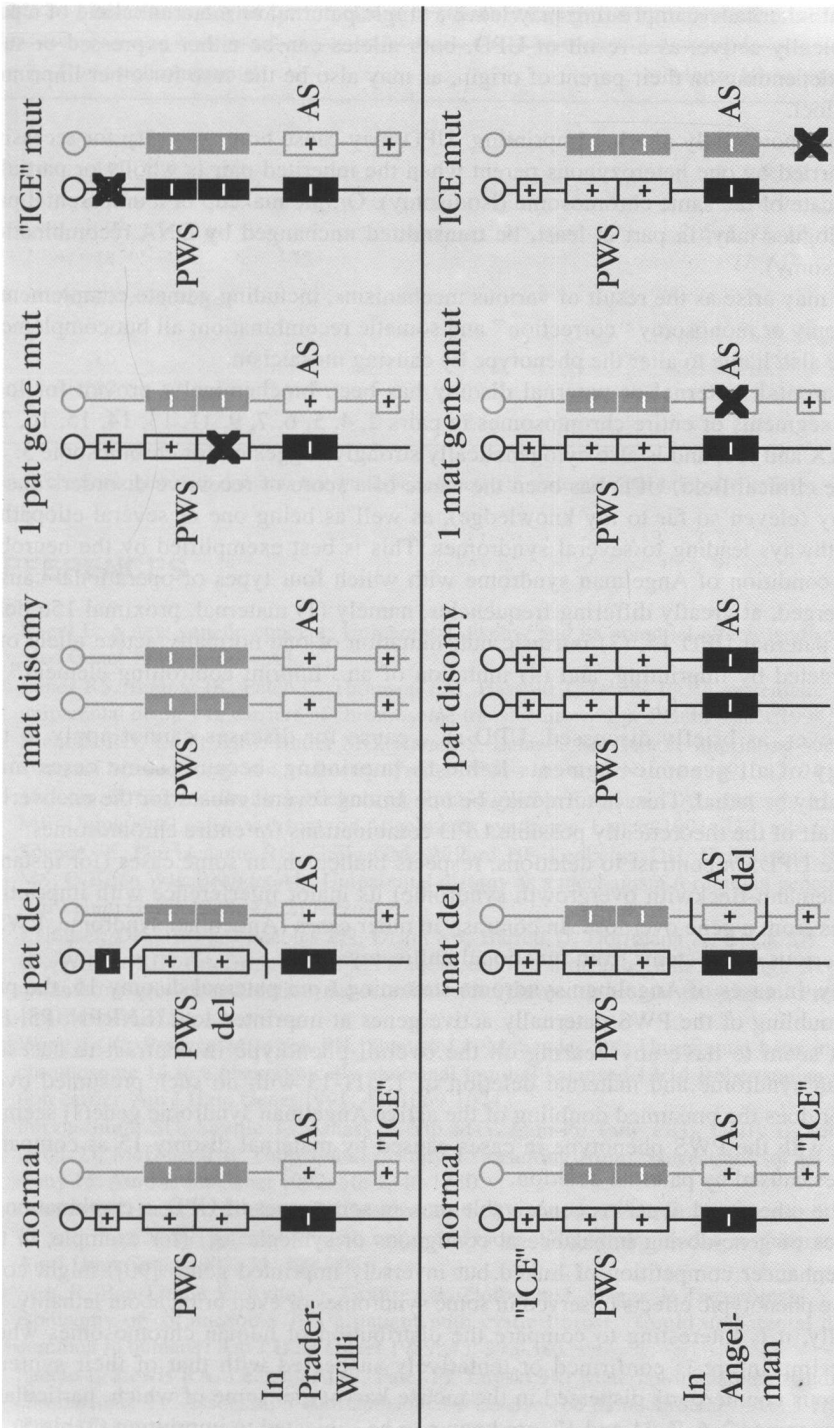


Fig. 8 - Four potentially pathogenic mechanisms in PWS and Angelman syndrome (AS) (15q11-q13) [83-89]. ICE = Imprinting control element.

biparental inheritance, imprinting may leave a single paternal or maternal allele of a pair phenotypically active, as a result of UPD, both alleles can be either expressed or suppressed, depending on their parent of origin, as may also be the case for other imprinted syntenic loci.

Besides potentially altering imprinting, UPD may cause homozygosity for recessive alleles carried by one heterozygous parent when the inherited pair is wholly or partially the duplicate of the same chromosome (isodisomy). Or, the makeup of a uniparental pair of homologues may, in part at least, be transmitted unchanged by DNA recombination (heterodisomy).

UPD may arise as the result of various mechanisms, including gamete complementation, trisomy or monosomy "correction" and somatic recombination; all but complementation are also liable to alter the phenotype by causing mosaicism.

Uniparental maternal or paternal disomy has been biochemically proven for loci, syntenic segments or entire chromosomes in pairs 2, 4, 5, 6, 7, 9, 11, 13, 14, 15, 16, 20, 21, 22, XX and XY, and is also cytogenetically strongly suggested for chromosome 3.

In the clinical field, UPD has been the cause of a score of recessive disorders due to isodisomy (eleven so far to my knowledge), as well as being one of several etiopathogenic pathways leading to several syndromes. This is best exemplified by the neurobehavioral condition of Angelman syndrome with which four types of operational causes have emerged, at greatly differing frequencies, namely (1) maternal, proximal 15q deletion, (2) paternal UPD 15, (3) intrinsic null mutation of one normally active allele of a locus targeted by imprinting, and (4) mutation of an "imprint controlling element" or *imprinter* gene (Figure 8).

However, as briefly discussed, UPD as a cause for diseases cannot apply to the pathology of all genomic segments liable to imprinting, because some cases must unavoidably be lethal. This, in turn, may be one among several causes for the uncovering of only half of the theoretically possible UPD combinations for entire chromosomes.

While UPD, in contrast to deletions, respects biallelism, in some cases (for instance the Wiedemann-Beckwith overgrowth syndrome) its major interference with imprinting originates from a gene overdose. In contrast, in other cases (Angelman syndrome, PWS), the deleterious effect stems from functional nullisomy.

Oddly, in cases of Angelman syndrome stemming from paternal disomy 15, the presumed doubling of the PWS paternally active genes at imprinted loci (SNRPN, P5, P1) does not seem to have any bearing on the overall phenotype in contrast to cases of Angelman syndrome and maternal deletion of 15q11-13 with no such presumed overdose. Nor does the presumed doubling of the active Angelman syndrome gene(s) seem to interfere with the PWS phenotype in cases caused by maternal disomy 15 as compared with cases caused by paternal deletion.

On the other hand, it seems conceivable that, in some cases of UPD, a combination of both types of gene-dosing imbalance at contiguous or syntenic loci (for example, in the case of enhancer competition of linked but inversely imprinted genes [90]) might compound the phenotypic effects observed in some syndromes or even bring about lethality.

Finally, it is interesting to compare the distribution of human chromosomes where genomic imprinting is confirmed or tentatively suspected with that of their syntenic homologous counterparts dispersed in the mouse karyotype, some of which, particularly on chromosomes 2, 6, 7, 11 and 17, are known to be subjected to imprinting (Table 5).

Table 5 - Mouse homologies for imprinted or possibly imprinted human chromosomes [91]

Human chromosome	Mouse homologies
<i>Imprinted</i>	
11	2, 7, 9, 19
15	2, 7, 9
7	2, 5, 6, 11, 12, 13
14	11, 13
<i>Possibly imprinted</i>	
2	1, 2, 6, 8, 11, 12, 17
16	7, 8, 11, 16, 17
20	2
X	19

Mouse chromosomes with domains known to be subjected to genomic imprinting are italicize.

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