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## The genetics of human reproduction

by A. C. Chandley

*MRC Clinical and Population Cytogenetics Unit, Western General Hospital, Edinburgh EH4 2XU (Scotland)*

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### Introduction ....

The attainment of full fertility in any organism requires the proper development and functioning of the reproductive system and survival of the foetus to term. Factors which operate to interfere with any of these processes will disturb the normal pattern and lead to partial or complete infertility.

The reproductive disorders of man are many and varied, but it is the contribution made by genetic anomalies which will be considered in this review. Mutations are known which affect gonadal development and sexual differentiation as well as those which act to disturb gametogenesis. Chromosomal abnormalities too can disturb gametogenesis; they also contribute significantly to human foetal wastage.

Several previous reviews on various aspects of the subject have been written and to these, the reader is also referred<sup>24, 28, 31, 47, 54, 77, 123, 143</sup>. A review of the genetic causes of sterility in the mouse, a much more widely investigated species, has been given by Searle<sup>122</sup>.

### 1. Gonadal failure and impaired gametogenesis

#### 1.1 The effect of the sex chromosomes

Considering that the X and Y chromosomes play a key role in sex determination and differentiation, it is hardly surprising that mutations at the gene loci involved, or sex chromosome imbalance, will produce serious consequences for the development of the reproductive system. Hermaphroditism, sex reversal and infertility are all well-documented features<sup>54, 123</sup>.

In human cytogenetics, the discovery that sex chromosome aneuploids like 45, X and 47, XXY, could be associated with infertile syndromes, led to the initiation of chromosome surveys among selected groups of individuals experiencing reproductive problems. In one of the earliest studies, Jacobs et al.<sup>79</sup> examined the karyotypes of 32 women who had never menstruated spontaneously. Sex chromosome abnormalities were found in half of them: These included six with an XO genotype, five with sex chromosome mosaicism, three with a morphologically abnormal X chromosome, and two with an XY sex chromosome complement. This high level of sex chromo-

some abnormality compared with a frequency of only 1.8 per 1000 among newborn females<sup>78</sup>. The association of a male (XY) genotype with a female phenotype characterizes the two conditions of sex reversal, 'testicular feminization' and 'pure gonadal dysgenesis'<sup>47</sup>. The defect in XY females heterozygous for the X-linked Tfm (testicular feminization) gene<sup>97</sup> is well known, this mutation acting at the most fundamental level to disturb sex differentiation. In pure gonadal dysgenesis, gonadal failure is the primary defect and streak gonads are usually found<sup>47</sup>. In the XO female with Turner's syndrome and the XXY male with Klinefelter's syndrome, gonadal failure appears to relate to germ cell atresia. Recent insights into the role of the sex chromosomes in gamete survival in the mouse have been gained<sup>93</sup>. It would appear that shortly after birth in that species, a second X chromosome blocks male and facilitates female germ cell development. Oocytes at this time are known, both in man<sup>52</sup> and the mouse<sup>42</sup>, to have two active X chromosomes, and germ cell loss in XO females may therefore relate to deficiency of X gene products<sup>12, 89</sup>. In XO human females, germ cell loss occurs principally around the time of birth<sup>23, 124</sup>, the adult ovary being represented generally by a streak gonad. Nevertheless, limited fertility is achieved by some Turner individuals who retain oocytes over a much reduced reproductive span<sup>83</sup>. Germ cell loss in XY females with pure gonadal dysgenesis may also relate to deficiency of X-linked products.

The presence of two X chromosomes in germ cells of the mouse appears to be compatible with initiation of development in the male direction but is not compatible with spermatogenesis<sup>93</sup>. The XX component in XX/XY chimaeras appears to degenerate just before birth<sup>94</sup>, while in XX, Sxr (sex reversed) males, degeneration sets in soon after birth<sup>25</sup>. On the other hand, spermatogenesis does take place in XO, Sxr males, some germ cells surviving to form spermatids and even a few abnormal spermatozoa<sup>25</sup>. In keeping with these findings, spermatogonia in much reduced numbers have been recorded in the testes of pre-pubertal XXY boys<sup>98</sup>, but by puberty, little sign of spermatogenic activity remains. Gonadal failure resembling that seen in adult XXY men is also seen in XX

men<sup>38</sup>. In XX males, the story is complex and the aetiology mixed<sup>38</sup> but current research is showing that at least in some cases, the paternally-derived X chromosome may harbour a testis-determining fragment of Y chromosome transferred to the X by accidental crossing-over or X-Y interchange<sup>15, 39, 46</sup>. The identification of Y-specific sequences in the DNA of a number of XX males investigated using Y-specific probes<sup>37</sup> supports this.

Whether the Y chromosome functions in spermatogenesis is not clear. In the mouse, it has been argued<sup>93</sup> that the Y chromosome may only serve a role in ensuring normal spermatogenic development to a late stage by providing a pairing partner for the X. (It will be shown later that normal XY pairing must be maintained for meiosis to go to completion). In man, factors which influence spermatogenesis may be situated on the long arm of the Y chromosome close to the intensely fluorescing heterochromatin<sup>11, 138</sup>.

### 1.2 X- and Y- autosome translocation

From studies on human female X-autosome translocations, there is evidence that the structural integrity of a critical region of the X chromosome long arm is necessary for normal ovarian function in heterozygotes. Sarto et al.<sup>119</sup> first drew attention to this by pointing out that all females hitherto reported who were heterozygous for a reciprocal X-autosome translocation with a breakpoint in this region had primary or secondary amenorrhoea. Summitt et al.<sup>135</sup> reviewed the literature and found that 9 of 18 females reported to be carriers of X long arm autosome translocations exhibited either streak ovaries (7 cases), ovarian hypoplasia (1 case) or underdeveloped ovaries (1 case). The X chromosome breakpoints of the 13 translocations were all located within the region Xq13-Xq26. The critical region therefore lies in the middle of the long arm and represent about two-thirds of its length. A few exceptions to this general rule have, however, been presented<sup>5, 19, 95</sup>. These authors have described women heterozygous for a balanced X-autosome translocation with a breakpoint in the critical region but who, nevertheless, were fertile. The question as to precisely how such a chromosome exchange could affect the development and functioning of the ovary remains still to be answered. A 'position effect' explanation has been offered by Summitt et al.<sup>135</sup> while Madan et al.<sup>95</sup> have suggested a mechanism of variable penetrance similar to that which allows some XO women (and XO mice) to retain oocytes into adult life and thus to conceive. Burgoyne and Baker<sup>16</sup> believe that meiotic pairing failure in female X-autosome translocation heterozygotes and also in XO females, could account for the oocyte atresia by selectively removing oocytes from the germ line. Reproductive lifespan is known to be curtailed in some female X-autosome translocation stocks of the mouse, as well as in XO mice, owing to a smaller pool sizes of oocytes<sup>16</sup>. Observations by Speed on foetal XO oocytes in mice<sup>131b</sup> show a tendency on the part of the single X chromosome for self pairing or nonhomologous pairing with an autosome at pachytene in up to 50% of cells. These, Speed suggests, could be oocytes which will survive, having saturated their pairing requirement. Observations made on three XO human fetuses, however, showed most oocytes blocked at the preleptotene stage (Speed, in press), germ

cell failure at least in these cases occurring before pairing had even begun.

For male carriers of an X-autosome reciprocal translocation, the consequences for spermatogenesis are severe. Meiotic development is invariably arrested at the pachytene stage, both in man<sup>28, 45</sup> and the mouse<sup>122</sup>, and carriers are rendered severely oligospermic or azoospermic. For male carriers of reciprocal Y-autosome translocations the consequences are similar if perhaps slightly less severe. Spermatogenesis in a few of these cases seems to be able to proceed to the late stages both in man<sup>45, 85, 127</sup>, and the mouse<sup>18, 86, 122</sup>, and in one human case of Y; 10 reciprocal rearrangement<sup>85a</sup> spermatozoa were produced in numbers which were within normal limits for the human male, pregnancy being achieved on four separate occasions. Ascertainment in this case was by birth of a child with congenital malformations.

A hypothesis to explain the sterility of male X-autosome translocation heterozygotes of *Drosophila*, the mouse, and man, has been put forward by Lifschytz and Lindsley<sup>87</sup>. They argue that asynchronous control of X-chromosomal and autosomal gene activity is necessary for normal spermatogenesis. The spermatogenic disturbance in X-autosome carriers, they suggest, is brought about by autosomal interference with the precocious inactivation of X-linked genes. The sterility of Y-autosome translocation heterozygotes might be explicable on the same model since the Y chromosome too is known to be inactivated early in the primary spermatocyte stage both in the mouse<sup>82</sup> and in man<sup>140</sup>. The effects on spermatogenesis in such cases, appear, as far as one can tell from the limited number of reports so far, to be less severe than when rearrangement takes place between an autosome and the X.

### 1.3 Autosome-autosome translocation

Lyon and Meredith<sup>90</sup> were the first to show that certain purely autosomal translocations of the mouse cause sterility in male heterozygotes because of spermatogenic impairment. The occurrence of such translocations in man has also been noted<sup>29, 31</sup>. A mechanism by which purely autosomal rearrangements might bring about spermatogenic disturbance has been put forward by Forejt<sup>49</sup>. He and his co-workers showed that in a number of male-sterile autosomal translocations of the mouse, a high frequency of centromeric contacts between the translocation configuration and the XY bivalent were formed at pachytene<sup>50, 51</sup> and particularly when chain configurations were present in the translocation. Such contacts were not seen to any great extent among the pachytene cells of male-fertile translocation carriers showing a preponderance of ring quadrivalents. Similar contacts were reported by Chandley<sup>30</sup> in sterile male mice doubly heterozygous for two partially overlapping inversions. Forejt<sup>49</sup> suggested that non-random associations might produce interference with the precocious X-chromosome inactivation in the primary spermatocyte which, on the Lifschytz/Lindsley hypothesis<sup>87</sup>, would be required for normal spermatogenesis. Whether oocyte numbers are lower than normal in human females who carry autosome translocations which sterilize the male is not known but, in the mouse, evidence of reduced ovarian volume indicating an effect of the translocation on oogenesis has

been presented by Mittwoch et al.<sup>103</sup> for the t(11;19)42H male-sterilizing translocation. Burgoyne and Baker<sup>16</sup> have argued that meiotic pairing failure in autosomal heterozygotes of both sexes could again be responsible for the gametogenic disturbances observed.

For human male carriers of a Robertsonian (Rb) translocation, the effects on spermatogenesis are somewhat variable. In the majority of cases, fertility is not disturbed; nevertheless, some Rb heterozygotes are ascertained through attendance at infertility clinics<sup>28, 139</sup>. From family studies of such men, it has been shown that the infertile subjects often have male relatives carrying the same translocation who are themselves fertile, indicating that the translocation itself is not the only and consistent cause of infertility. Genetic background could also be important. Tiepolo et al.<sup>139</sup> have tested the hypothesis that infertility in balanced carriers of human Rb translocations could result from a loss of ribosomal cistrons. However, <sup>3</sup>H-rRNA/DNA hybridization experiments in nine infertile translocated patients and their normal and/or translocated fertile male relatives, failed to demonstrate any significant difference in the number of rDNA genes<sup>56</sup>.

The majority of Rb heterozygotes ascertained through infertility have been t(13q14q) individuals, this being the most common type of Robertsonian rearrangement in man, although carriers of t(13q15q), t(14q21q), t(14q22q) and t(21q22q) have also been reported<sup>33</sup>. High frequencies of XY-trivalent contacts at pachytene have been reported for the sterile carrier of a 13q14q Rb translocation<sup>88a</sup> and for two sterile carriers of 14q21q translocations<sup>117a</sup>. Contacts occurred principally when unpaired segments were present in the acrocentric short arms of the trivalents.

#### 1.4 Other structural rearrangements

Translocations are not the only structural rearrangements to be associated with germ cell maturation impairment in human males. In an early investigation, McIlree et al.<sup>91</sup> reported on a male showing a small ring-G chromosome (later identified as a ring 21), in his somatic karyotype. At meiosis, spermatocytes at metaphase I showed degenerative changes suggestive of spermatogenic failure and one pair of small autosomes was present always as a pair of univalents: the man was azoospermic. Complete breakdown of spermatogenesis was seen also in a ring-E individual reported by Kjessler<sup>84</sup>.

In another report by McIlree et al.<sup>92</sup> spermatogenic failure was noted in a man carrying a dicentric Y chromosome. The X and Y short arms could not pair at meiosis in this man because the short arm pairing region of the Y chromosome was present in the centre of the abnormal chromosome and therefore not available to make end-to-end association with the X. Pairing failure between the X and Y was also noted at metaphase I in a ring-Y azoospermic individual studied by Chandley and Edmond<sup>32</sup>. For both the dicentric Y and the ring Y patient, the suggestion was made that the failure to pair in the XY bivalent was the cause of the breakdown in spermatogenesis. More will be said, however, about meiotic pairing failure and spermatogenic arrest under section vi.

A pericentric inversion in the Y chromosome of another male studied by McIlree et al.<sup>92</sup> did allow for normal

pairing and in this case, normal testicular histology was reported. Pericentric inversions in the autosomes have occasionally also been reported among infertile human males. Tiepolo et al.<sup>139</sup> found a pericentric inversion in chromosome 6 in one male from the Pavia sample and Faed et al.<sup>45</sup> reported an inversion 3 in their Dundee study. Other human autosomal inversion heterozygotes have, however, been found to have normal spermatogenesis<sup>142</sup>, and certainly, on the basis of the few cases studied to date, a positive association with spermatogenic impairment cannot be claimed for inversions in general. More cases require to be studied.

#### 1.5 Aneuploids

The severe germ-free failure in XXY and XO individuals has been described earlier in the chapter. A number of other human aneuploid situations have also been investigated for their effects on germ cell development. The spermatogenic picture in 47,XXY men, even among those who have been karyotyped for reasons other than infertility, ranges from one of severe impairment to apparent normality<sup>126</sup>. Few XYY spermatocytes have been recorded at metaphase I of meiosis, the surviving germ cells usually showing a normal XY complement<sup>44, 136</sup>. Claims have, however, been made for retention of the second Y in some males, at least until the pachytene<sup>7</sup> stage, and in an XYY male studied by Hulten and Pearson<sup>75</sup>, 45% of spermatocytes at diakinesis/metaphase I were found to be XYY. A hypothesis to explain the variable pattern of spermatocyte loss seen in XYY men and mice, based on a disruption of XY pairing, has been put forward by Burgoyne<sup>13</sup> and Burgoyne and Biddle<sup>17</sup>. Trisomy 21 males also show a range of variation in their testicular histology<sup>125</sup> and where meiotic studies have been made, various proportions of metaphase I cells containing trivalents, a bivalent plus a univalent or no obvious extra No. 21 have been recorded<sup>73</sup>. In one pachytene analysis<sup>76</sup> only trivalents were observed. In another<sup>80</sup>, no evidence for the extra 21 could be found at this prophase stage of meiosis. The latter authors did, however, see a small extra univalent, interpreted as a No. 21, at metaphase I. Few other autosomal aneuploid situations are viable in man and so little other information can be gained about germ cell survival. One case of mosaic trisomy 8, studied by Chandley et al.<sup>35</sup> did, however, show gross disturbances of spermatogenesis. Although the extra No. 8 was not present at metaphase I of meiosis, a high percentage of spermatocytes containing unpaired sex chromosomes was found at this stage. This, it was suggested, could have been the cause of germ cell failure. A prophase analysis was not carried out in this case.

For female autosomal aneuploids, there is evidence of germ cell atresia both in the ovaries of trisomy 18<sup>1, 118</sup> and trisomy 21<sup>61, 110</sup> girls.

Studies at meiosis in trisomy 21 foetal oocytes<sup>131, 144</sup> show a mixture of trivalent, bivalent plus univalent and apparently normal diploid configurations at the pachytene stage. Trivalents are observed in about one third of cells, a proportion of these showing triple association along certain segments.

The mechanism responsible for germ cell failure in these female, as well as male, aneuploid situations is not yet fully understood but there does appear to be variable

penetrance and a range of severity in the effects on gametogenic development observed. Meiotic pairing failure has been suggested by Burgoyne and Baker<sup>16</sup> to play a role, and when more cases have been assessed, it may turn out that a relationship exists between the relative proportions of the different meiotic pairing configurations and levels of germ cell atresia recorded.

### 1.6 Meiotic pairing failure

Several reviews have already been written on the possible association between failure of pairing and failure of gametogenesis<sup>16, 31, 101</sup>. Miklos<sup>101</sup> has suggested that a saturation of pairing sites between homologous chromosomes is essential for regular meiotic and post-meiotic development of germ cells. On this model, not only could XY pairing failures be accommodated but also autosomal failures both in males and females. Sometimes, pairing failure affects only one pair of chromosomes in the complement, on other occasions it may affect many pairs. In man, the germ cell failure of those patients showing extremely low chiasma counts, perhaps due to meiotic mutation, appears to relate to generalized pairing failure<sup>26, 137</sup>. A raised frequency of synaptic anomalies among the autosomal bivalents of oligo- and azoospermic men attending infertility clinics has been reported by Egozcue<sup>41</sup>. Among human foetal oocytes, frequent errors of synapsis in the prophase stages are observed<sup>131a</sup>. Speed<sup>131a</sup>, who has made extensive observations at the electron microscope level on human oocytes prepared by spreading, recorded single or multiple pairs of univalents in about 10% of all pachytene analysed and partial asynapsis in at least one complement in a further 8% of cells. Occasional oocytes contained up to seven such partially asynaptic bivalents. An interesting observation was the thickening of unpaired segments of chromosomes and univalents, with the appearance of excrescences along the axes, comparable in appearance to those exhibited by the differential axes of the X and Y in the male<sup>34</sup>. Speed<sup>131a</sup> observed a lower frequency of synaptic anomalies in later pachytene stages, indicating selective loss of such cells from the germ line. It was suggested that the thickenings and excrescences observed along the unpaired axes could correlate with a state of genetic inactivation brought about by pairing failure. Certainly it seems that much more needs to be found out about pairing and germ cell loss before an understanding of the problem can be reached. In situations where germ cell development is arrested in very early prophase, before pairing commences, an alternative explanation would require to be found.

### 2. The nature and extent of XY pairing

Although a great deal of meiotic investigation in man has taken place over the years using air-drying techniques (see refs 27 and 74 for reviews), recent developments in spreading methods<sup>104, 105</sup> and serial reconstructions of primary spermatocytes<sup>62-67, 113-115</sup> have provided new insights into events taking place at meiotic prophase. One item of particular interest relates to the question of pairing and homology within the human XY bivalent at early pachytene.

From air-dried observations at metaphase I, when the human X and Y are in end-to-end association, it is known

that pairing takes place between the respective short arms (Xp and Yp) of the two chromosomes<sup>36, 109</sup>. From serial reconstructions of pachytene spermatocytes, an extensive pairing segment within the sex pair, complete with synaptonemal complex, has been found<sup>130</sup>. Synaptonemal complex presence was formerly taken to imply homology within synapsed regions of chromosomes, but a number of investigations have now shown that this need not necessarily be the case, normal-looking complexes being found even within regions of known genetic dissimilarity<sup>104, 107</sup>.

From measurements made on meiotic cells prepared by spreading, the human XY pairing segment at early pachytene (the stage at which a maximum length synaptonemal complex is found) occupies, on average, about 10% of total X axial length and 30% of Y axial length<sup>34, 106, 129</sup>. Centromere positions in the human X and Y are difficult, if not impossible, to pinpoint in spread preparations at pachytene because of the large number of excrescences along each of the sex chromosome axes. Moses et al.<sup>106</sup> have however, concluded that the pairing segment involves the distal one third of Xp and about 90% of the short arm of the Y, and this had become more or less the accepted dogma<sup>14, 37, 111, 120</sup>. Recently, however, a more extensive analysis of human pachytene spermatocytes prepared by spreading<sup>34</sup>, has provided circumstantial evidence that in some cells at least (about 5% of all early pachytene spermatocytes analysed), a greater proportion of total Y length (50–70%) can be involved in pairing with Xp. A pairing segment involving more than 50% of total Y length would of course imply that the Y centromeric region and proximal Yq, in addition to all of Yp, be held in synapsis with distal Xp. Indeed the authors suggested that all of the euchromatic portion of the human Y might be capable of synapsing with Xp.

Since pairing of a centromeric region with a non-centromeric region would seem to have to take place by non-homologous association, it is worth considering whether homology exists in other regions, especially distal XpYp, and if so, does crossing-over occur there? Various models predicting the occurrence of an obligatory crossover in the human XY pairing segment have been proposed<sup>11, 14</sup> but genetic evidence for crossing-over and partial sex linkage in man is lacking. Recombination bars or nodules, taken as indicative of crossing-over<sup>21, 22</sup> have, however, been noted in the human XY bivalent<sup>65</sup>, and some molecular and genetic evidence exists for homology within the distal tips of Xp and Yp<sup>53, 112</sup>. Moreover, a tiny segment of distal Xp and Yp has been seen to remain synapsed throughout the whole of the pachytene stage even after the X and Y axes have desynapsed over the rest of their lengths<sup>34</sup>. Whether this too reflects homology within this segment can, however, only be speculated upon.

The recent elucidation of sex-reversal (Sxr) in the mouse, has shown that crossing-over is a regular occurrence at the distal tip of the XY pairing segment in XY, Sxr males. Evans et al.<sup>43</sup> who found cytological evidence for a small reciprocal exchange between X and Y in these animals, have suggested that regular exchange might also occur in the XY bivalent of normal male mice. This could be the case also in the human male, evidence for the exchange of hypervariable telomeric sequences on the human Y chro-

mosome, to the X, having recently been found<sup>36a</sup>. There are, on the other hand, those who argue that pairing between the X and Y in male mammals in a special case of non-homologous synapsis<sup>3</sup>, association between the sex chromosomes having been retained simply as a mechanism to ensure regular segregation in the sex bivalent. Any exchange events which took place, as for example in Sxr males, would then be regarded as non-homologous interchanges and not true crossover events. The X-Y interchanges which have been suggested to give rise in man to some XX males<sup>15, 39, 46</sup> could also arise, not by true crossing-over, but by non-homologous exchange. The location of the testis-determining gene in the paracentromeric region of the Y chromosome<sup>11</sup> would, of course, make any such exchange event necessarily take place very close to the Y-centromere, a region which normally tends to inhibit crossing-over<sup>6</sup>. The finding of a physical association between the Y centromeric region and Xp in some cells<sup>34</sup> could, however, provide the opportunity for exchange.

### 3. Biochemical studies on human spermatocytes

Despite large gaps in the knowledge, it now seems clear that the programme of molecular events taking place at male meiotic prophase has been conserved during evolutionary time: in spite of the broad phylogenetic span, species as diverse as lily and the mouse show great similarity in the biochemical processes relating to pairing and crossingover<sup>72, 132, 133</sup>. Studies in human testicular tissue have been carried out to a lesser extent, mainly on account of the technical difficulties involved in effecting good cell separations but some data are nevertheless available<sup>134</sup>. These show that, in common with lily and the mouse, a controlled nicking of DNA and a repair activity localized in moderately repeated regions of the genome, are associated with the late prophase interval and thought to be related to the recombinational phase of meiosis. This DNA activity is complemented by activation of specific groups of proteins (the U- (unwinding) and R- (reannealing) proteins) which affect the secondary structure of DNA and show characteristic cyclic behaviour during the prophase of meiosis<sup>70, 71</sup>. Successful studies have also been made of RNA metabolism during meiotic prophase in the human male<sup>140</sup>.

### 4. Aneuploidy, foetal wastage, and the maternal age effect

Before ending this review, it would seem fitting to record the contribution made by chromosome abnormality and in particular aneuploidy, to the overall levels of foetal wastage in man.

It is now known that about 15% of all human pregnancies end in a clinically recognizable abortion<sup>145</sup> with about 60% of those occurring in the first trimester being chromosomally abnormal<sup>9, 147</sup>. The principal abnormalities found are 45,X (20%), autosomal trisomy (50%) triploidy (17%) and tetraploidy (6%), aneuploidy alone therefore, making up 70% of the cases. Additional losses due to aneuploidy will also undoubtedly occur at or around the time of implantation for, in the mouse, it is known that the majority of autosomal monosomies and some trisomies die at this time<sup>55</sup>. One recent study into early conceptual loss in man, carried out by Miller et

al.<sup>102</sup>, has attempted to use to rise in urinary levels of  $\beta$ HCG to recognize very early post-implantation pregnancies before they can be recognized clinically. These gave a figure for total postimplantation loss of at least 43%. Using the same assay, Edmonds et al.<sup>40</sup>, concluded that ovulatory cycles exposed to the risk of pregnancy carried a 59.6% chance of conception and a 56.8% risk of embryonic loss. This fecundity of about 25% for man is clearly very low but may to a great extent be attributable to lethal chromosome anomalies.

In the past, estimations of the total level of chromosome abnormality at conception in man have been based on the figures obtained by karyotypic analysis of early spontaneous abortions. Because of the unknown contribution made by pre-implantation and early post-implantation losses, however, the figures have been somewhat speculative. Recently, a start has been made on analysing the chromosome complements of early cleaving human embryos obtained by in vitro fertilization<sup>2</sup>, but data so far are limited. Of 11 embryos examined for their ploidy, two showed evidence of autosomal aneuploidy. Chromosome analysis carried out on unfertilized human ova have so far proved somewhat uninformative owing to the poor quality of the preparations generally obtained, but significant progress has been made into the karyotyping of human spermatozoa following fusion with hamster eggs<sup>96</sup>.

For 1000 sperm genomes analysed, an overall frequency of chromosome abnormality of 8.5% has been recorded, with 5.2% of complements being aneuploid. Were an equal contribution to come from the ovum, a frequency overall of 17% with about 10% aneuploidy would be expected. It is known, however, from the observations of Jacobs and Hassold<sup>77</sup>, Mikkelsen et al.<sup>100</sup>, and others who have traced the origins of various autosomal aneuploid conditions in man by means of chromosome polymorphisms, that maternal errors outnumber those arising paternally by about four to one. The level of aneuploidy alone among ova could therefore be as high as 20%, giving an overall level of aneuploidy at conception of around 25%. This would be far higher than that found in any other investigated mammalian species<sup>48</sup>.

Compared with other mammals, man also shows a striking maternal age effect for trisomy<sup>128</sup>, an effect noted, not just for liveborn subjects with trisomy 13, 18 or 21 (see ref.8 for review), but for the liveborn sex aneuploids 47,XXX and 47,XXY<sup>68</sup> and for trisomic abortuses<sup>60, 121</sup>. The former study has shown that although as a group, trisomic abortuses are associated with a substantial increase in maternal age, considerable differences exist in the magnitude of the effect for different chromosome pairs. The effect is most pronounced for trisomies involving the smaller chromosomes whether acrocentric or non-acrocentric. Trisomy 16 is an exception, however, in being only weakly age-related. It is also exceptional in being the most frequent in occurrence, making up about one third of all trisomic cases<sup>8, 60</sup>. Some trisomies like trisomy 1 are rarely if ever found among abortuses, but may be selected against at a time before a clinically recognized pregnancy is established<sup>81</sup>. First meiotic maternal errors appear to predominate in all trisomic conditions and at all maternal ages, whether or not the particular trisomic condition is strongly age-related<sup>60, 100</sup>.

An extremely interesting finding which has emerged recently from the data, however, is that significant heterogeneity exists among trisomics with regard to the proportion attributable to *paternal* nondisjunction. Data for both spontaneous abortions and liveborns suggest that trisomy 21 is more likely to be paternally derived than any other autosomal trisomy<sup>58</sup>. Consideration of the sex ratio in cases of trisomy 21 of known parental origin suggests that an excess of males is associated with paternal first meiotic division nondisjunction, the distorted sex ratio appearing to stem from a mechanism in which the extra No. 21 segregates preferentially with the Y chromosome. The fact that this mechanism of origin is more prevalent in trisomy 21 may well explain why there is an excess of males associated with this particular abnormality but not with other autosomal trisomies<sup>59, 88</sup>.

There are those who believe that the maternal age effect for aneuploidy in man could be accounted for on the basis of relaxed selection against trisomic fetuses in the uteri of older women<sup>4</sup>. Strong arguments against this idea have, however, recently been put forward<sup>20, 69, 146</sup>. Experimental studies in the mouse now indicate, in fact, that the rise in frequency of aneuploid embryos, or at least the abnormal chromosome segregation giving rise to them, is an epiphenomenon of ageing in the adult female. Brook et al.<sup>10</sup> have produced data which point to the influence of biological ageing rather than to chronological age per se. Thus, an earlier cessation of reproductive life, brought on by unilateral ovariectomy in CBA females, resulted in the earlier onset of irregular oestrous cyclicity and an earlier rise in aneuploidy. The clinical implications are that the probability of conceiving a Down foetus will be determined by distance in time from the approaching menopause, perhaps because of a diminishing oocyte store. One group of women displaying early biological ageing and conforming well to this model, are those rare individuals with Turner syndrome (XO) who manage to achieve pregnancy during their limited reproductive span. Menopause occurs early in such women, but for their low chronological age they show a remarkably high level of foetal wastage and a greatly increased risk for producing Down syndrome offspring<sup>83, 117</sup>.

Brook et al.<sup>10</sup> have suggested that a continuum of age-related aneuploidy might exist in women, governed not by chronological age but by biological age. The biological age-related cases would then be superimposed on non-age related cases, for example those paternally-derived or those due to translocation. Some young mothers of children with primary trisomy 21 might thus be found to have evidence of earlier biological ageing or to be 'at risk' for irregular oestrous cyclicity. Read<sup>116</sup> has proposed that hormonal imbalance prior to the time of conception could be the critical factor in nondisjunction among older women. He believes, moreover, that young pill-users could also be at risk for hormonal imbalance and that this could be the causal explanation of recent data trends which indicate a shift in the incidence of Down syndrome to younger age groups<sup>99, 108, 141</sup>. Further data are required, however, both epidemiological and experimental, before a link between hormones and nondisjunction can be established with certainty.

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## Developmental genetics

by C. J. Epstein<sup>1</sup>

*Departments of Pediatrics and of Biochemistry and Biophysics, University of California, San Francisco (California 94143-0106, USA)*

**Summary.** Of particular concern to the human geneticist are the effects of genetic abnormalities on development. To gain an understanding of these effects it is necessary to engage in a reciprocal process of using knowledge of normal developmental events to elucidate the mechanisms operative in abnormal situations and then of using what is learned about these abnormal situations to expand our understanding of the normal. True developmental genes have not been described in man, although it is likely that they exist, but many developmental abnormalities are ascribable to mutations in genes coding for enzymes and structural proteins. Some of these even produce multiple malformation syndromes with dysmorphic features. These situations provide a precedent for asserting that not only monogenic developmental abnormalities, but also abnormalities resulting from chromosome imbalance must ultimately be explicable in molecular terms. However, the major problem confronted by the investigator interested in the pathogenesis of any of the chromosome anomaly syndromes is to understand how the presence of an extra set of normal genes or the loss of one of two sets of genes has an adverse effect on development. Several molecular mechanisms for which limited precedents exist may be considered on theoretical grounds. Because of the difficulties in studying developmental disorders in man, a variety of experimental systems have been employed. Particularly useful has been the mouse, which provides models for both monogenic and aneuploidy produced abnormalities of development. An example of the former is the mutation oligosyndactyly which in the heterozygous state causes oligosyndactyly and in the homozygous state causes early embryonic mitotic arrest. All whole arm trisomies and monosomies of the mouse can be produced experimentally, and of special interest is mouse trisomy 16 which has been developed as an animal