

Syndrome of the month

The fragile X syndrome

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Abstract

The fragile X syndrome is characterised by mental retardation, behavioural features, and physical features, such as a long face with large protruding ears and macro-orchidism. In 1991, after identification of the fragile X mental retardation (FMR1) gene, the cytogenetic marker (a fragile site at Xq27.3) became replaced by molecular diagnosis. The fragile X syndrome was one of the first examples of a "novel" class of disorders caused by a trinucleotide repeat expansion. In the normal population, the CGG repeat varies from six to 54 units. Affected subjects have expanded CGG repeats (>200) in the first exon of the FMR1 gene (the full mutation). Phenotypically normal carriers of the fragile X syndrome have a repeat in the 43 to 200 range (the premutation).

The cloning of the FMR1 gene led to the characterisation of its protein product FMRP, encouraged further clinical studies, and opened up the possibility of more accurate family studies and fragile X screening programmes.

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History

In 1943, Martin and Bell¹ described sex linked mental retardation without dysmorphic features in a family in which both affected males and females were observed. Thirty-six years later, Lubs² reported a marker X chromosome (later to be known as the fragile X chromosome) as an inconsistent finding in cytogenetic studies in leucocytes of some mentally retarded males. The folic acid and thymidine depleted cell culture medium was identified as the essential factor for the induction of this heritable fragile site at Xq27.³ During the seventies, the combination of X linked mental retardation and macro-orchidism was recognised.⁴⁻⁶ Later, other clinical characteristics were established, for example, a long face with large, protruding ears, and behavioural features, including avoidance of eye contact, hyperactivity, hand flapping, and perseverative speech.^{7,8}

The fragile X syndrome was diagnosed at that time by cytogenetic detection of the fragile site at Xq27.3. It had some special features for

an X linked disorder. Approximately 30% of the obligate carrier females were mildly or moderately retarded and a large portion ($\pm 50\%$) had no cytogenetic fragile X expression. Also, mentally normal grandfathers linking two family branches with the fragile X syndrome were observed. These "normal transmitting males" without any clinical or cytogenetic features could apparently transmit the fragile X syndrome.

The gene involved in the fragile X syndrome, the Fragile X Mental Retardation (FMR1) gene, was identified in 1991.⁹⁻¹¹ The gene defect was the first expansion of a trinucleotide repeat to be discovered and a whole class of disorders is now known to be associated with this type of mutation.¹²

Clinical studies

The original "Martin-Bell family" was restudied in 1981¹³ and the typical cytogenetic and clinical features were found. The "Martin-Bell phenotype" was proposed as an eponym for the phenotype of affected males. Additional clinical features include high arched palate (52%), strabismus (36%), hyperextensible metacarpophalangeal joints (67%), hand calluses (29%), double jointed thumbs (53%), single palmar creases (25%), pes planus (71%), and heart murmur or click (18%) (figs 1 and 2, table 1).^{8,14} The facial features are often less noticeable, particularly in affected females and children (fig 3). The macro-orchidism often develops during or after puberty and is frequently absent in young patients.^{7,8} Seizures are observed in approximately 20% of young affected males, with a lower prevalence in adults.^{8,15,16}

Fragile X infants often have relative macrocephaly persisting into adult life.¹⁷ However, the adult height of affected males is below the norm.^{17,18} A few patients present with either overweight or general persisting overgrowth which can be confused with either Prader-Willi syndrome or Sotos syndrome.¹⁹⁻²⁴ Associations with other syndromes are reported; examples are the Robin sequence (micrognathia, glossoptosis, and cleft soft palate),²⁵ the FG syndrome (congenital hypotonia, macrocephaly, distinctive face, and imperforate anus),^{26,27} and the DiGeorge anomaly (defects of thymus, parathyroids, and great vessels).²⁸ However, there is no definite evidence for a causal relationship between the FMR1 gene

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Table 1 Clinical features and medical problems of fragile X males*

	%
<i>Clinical features</i> †	
Long face	70
Prominent ears	70
High arched palate	52
Hyperextensible finger joints	67
Double jointed thumbs	53
Single palmar creases	25
Hand calluses	29
Flat feet	71
Heart murmur or click	18
Macro-orchidism	70
<i>Medical problems</i> ‡	
Vomiting	31
Failure to thrive in infancy	15
Strabismus	36
Myopia or hyperopia	22
Hernia	15
Joint dislocation	3
Orthopaedic problems	21
Otitis media	85
Sinusitis	23
Seizures	22
Mitral valve prolapse	35
Apnoea	10
Autism	20
ADHD	80
Motor tics	19

*Majority of items scored in 100–280 patients.

‡Adapted from Merenstein *et al.*¹⁴

†Adapted from Hagerman.⁸

mutation and these phenotypes. Several observations of the co-occurrence of the fragile X syndrome and sex chromosomal abnormalities like 47,XXY or 45,XO/46,XX^{29–34} suggest an increased rate of non-disjunction related to the fragile X chromosome.

Scales for facilitating diagnosis based on physical and behavioural features have been developed and found to be effective.^{35–39} Recognition of behavioural features also assists in the diagnosis. In the younger child, hand flapping, hand biting, tactile defensiveness, poor eye contact, hyperactivity, and perseverative speech are suggestive of the diagnosis.⁸ The “autistic-like” behaviour of many fragile X males initiated the debate about whether autism is associated with the fragile X syndrome.^{40–42}

Although in female premutation carriers an increased incidence of premature menopause has been reported,^{43–45} a recent study indicated that the premutation does not seem to be a major risk for early menopause.⁴⁶

Although several neuroimaging and a few neuropathological studies have been done on the central nervous system in fragile X patients, knowledge on specific structural and cellular defects is still limited. Reduced size of the posterior cerebellar vermis on MRI in male patients and increased size of the caudate nucleus, thalamus, and hippocampus have been reported.^{47–48} These findings have neither been confirmed nor refuted by others.

Neuropathological studies of three fragile X males' brains showed immature, thin, and long dendritic spines in different regions, with a reduction in mean synaptic contact but with preservation of neuronal density in the neocortex.^{16–49–50} Similar abnormal dendritic spines were observed in fragile X knockout mice.⁵¹ Interestingly, in normal mouse brain, high FMRP expression is observed in the synaptoneuroosomes which could be related to the high transcriptional activity necessary for function of neuronal spines.⁵² However, abnormally long, thin dendritic spines are also seen in cases with chromosomal abnormalities⁵³ or unspecified mental retardation.⁵⁴ Apparently, these are non-specific neuropathological changes, as is the neuronal heterotopia observed in two affected males and linked to their epilepsy. In the testes, macro-orchidism seems to be associated with increased tubular length and interstitial oedema.^{5–49–55–56}

The FMR1 gene

The identification of the FMR1 gene^{9–11} principally elucidated the special characteristics of the transmission of the defect in fragile X families rather than explaining the mental retardation itself. The FMR1 gene has a size of 38 kb with 17 exons⁵⁷ and an untranslated polymorphic CGG repeat in the first exon.⁵⁸ In the normal population, this CGG repeat varies from six to 54 units⁵⁸ (fig 4) with an average of 30 units. The mutations in the FMR1 gene can be divided into a major and a minor class (table 2). The major class of FMR1 gene mutations affects the CGG repeat, whereas mutations in the coding region are infrequently observed.

CGG REPEAT EXPANSIONS

On the basis of the size of the CGG repeat and its effect on protein and phenotypic expression,

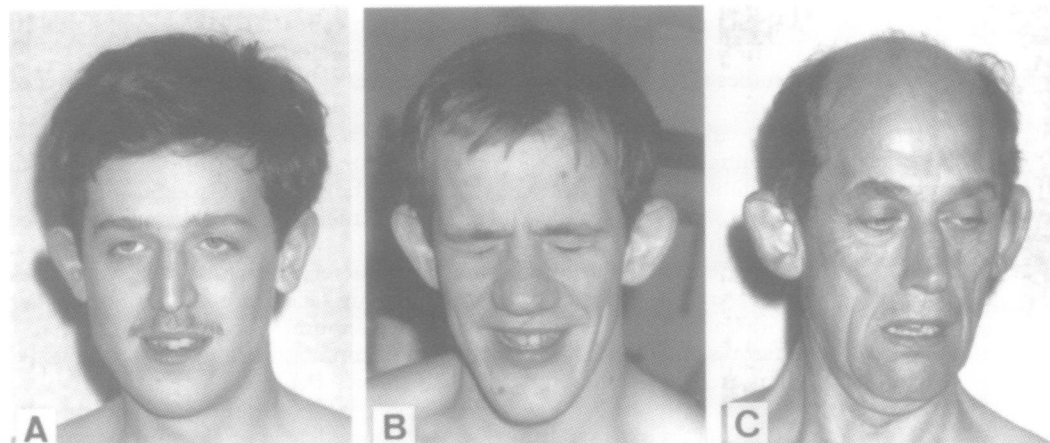


Figure 1 Three affected males with characteristic facial features of the fragile X syndrome. Note the long, narrow face with large, everted ears and the poor eye contact.

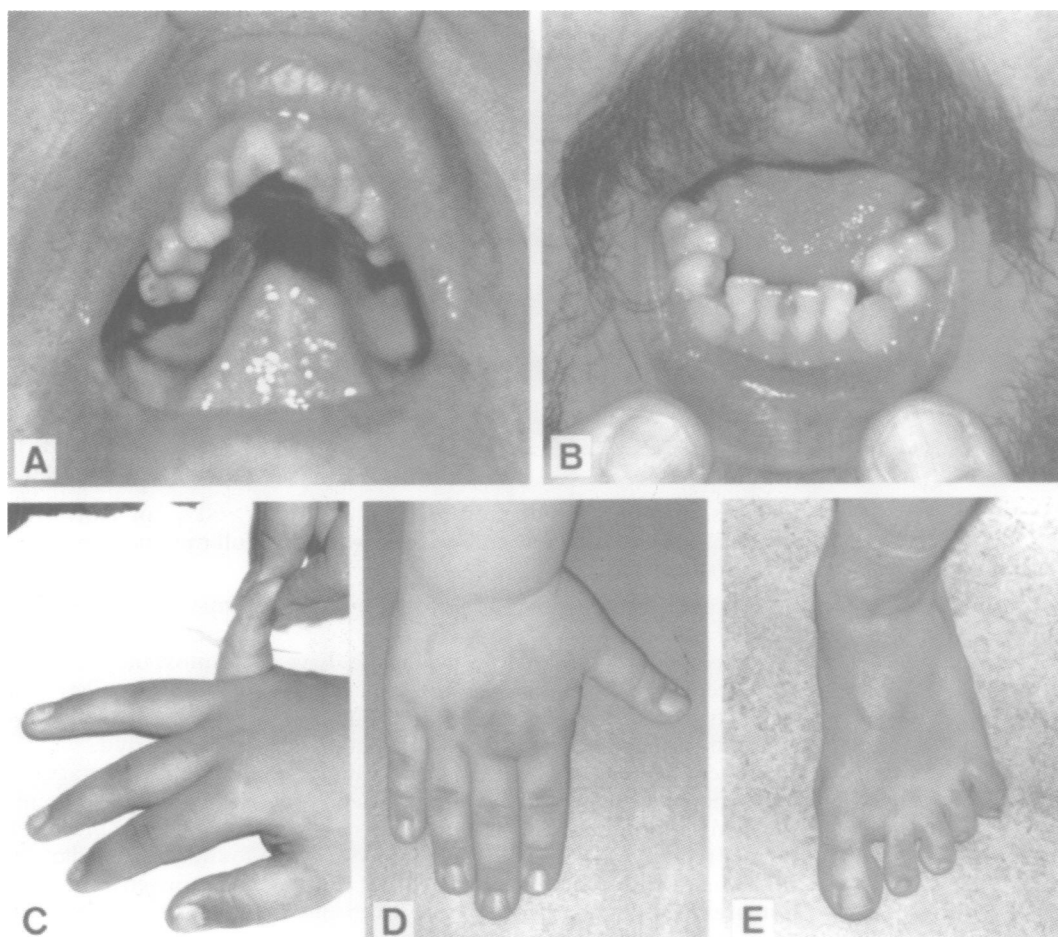


Figure 2 Some clinical features in fragile X subjects. (A) High arched palate, (B) dental crowding, (C) hyperextensible MP joints, (D) hand calluses, and (E) pes planus.

two types of mutations within the CGG repeat can be distinguished: the premutation (size 43 to 200 units) apparently without clinical effect and the full mutation (size >200 units) which, if fully methylated, is associated with mental retardation in all male and in 50-70% of female patients. At the protein level, FMR1 is absent from cells in cases with a fully methylated mutation only.

The mutations in the CGG repeat are dynamic. They may change from generation to generation as well as within a single person during early embryogenesis. Stable alleles with a CGG repeat <55 units are defined as normal, and unstable alleles ranging from 43 to 200 repeat units are regarded as premutation alleles.

The premutation and its intergenerational instability

The premutation with repeats in the range of 43 to 200 units causes no phenotypic abnormalities in (male and female) carriers⁵⁸ (fig 4). The intergenerational (in)stability of the premutation is dependent on the sex of the transmitting parent and on the size of the repeat. Only women with a premutation have a risk of having affected offspring with a full mutation. This risk of expansion into a full mutation depends on the size of their premutation; it is less than 20% for smaller premutation alleles (<70 CGG repeats), but more than 80% for larger premutation alleles (>80 CGG repeats).⁵⁸⁻⁶⁰

The CGG repeat is generally interspersed with two AGG triplets⁶¹⁻⁶⁶ and their position at the 3' end influences repeat instability, with an instability threshold of 34-38 uninterrupted CGG repeats.⁶¹⁻⁶⁵ The potential predictive value of the size of the uninterrupted CGG repeat for risk prediction in the offspring of female premutation carriers has not been adequately evaluated until now.

In the 43 to 55 CGG repeat range, there is an overlap between normal and premutated alleles, often referred to as the "grey zone". Only the observation of intrafamilial instability identifies these "intermediate" alleles as premutation alleles.⁶¹⁻⁶⁴ However, such premutation alleles can also be stably inherited through many generations.⁶⁷⁻⁶⁸ Alteration in one generation from alleles of <43 to >43 repeats is unknown, suggesting that such changes are very gradual. However, regressions from premutation to normal size (<43 repeats) have been observed within one generation.⁶⁹⁻⁷¹

The timing of any transition from pre- to full mutation is not fully understood. The presence of full mutations in the ovary of female fetuses, without evidence of a premutation, and simulation studies support the hypothesis of pre-conceptional enlargement.⁷²⁻⁷³ This seems to conflict with the finding of only premutations in the sperm of four males with a full mutation in somatic cells.⁷⁴ The latter observation might be explained by regression of a full mutation to a premutation in a limited number of cell

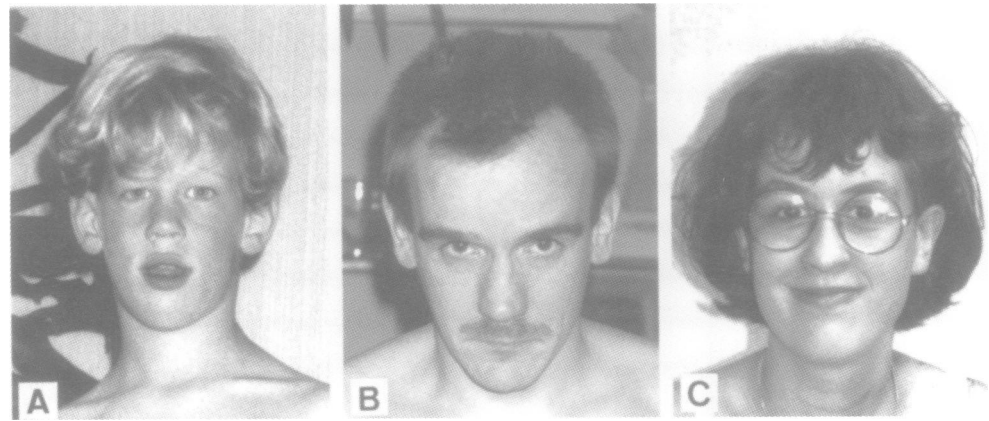


Figure 3 Two affected males and one female with less obvious facial features.

lineages. In the germline, we have then to assume a selection for those cells with a premutation.

The full mutation

Subjects with the fragile X syndrome have CGG repeats above 200 units, the "full mutation" (fig 4). The expansion into full mutation is usually accompanied by hypermethylation of the repeat and its flanking regions, resulting in a shut down of transcription and the absence of the FMR1 protein.⁷⁵⁻⁷⁸ The latter causes the mental retardation. All males and a majority of the females with a hypermethylated full mutation are mentally retarded.⁷⁹⁻⁸³

In somatic cells of fragile X patients, the mitotic instability of the repeat of the full mutation causes longer and shorter expansions, so all fragile X patients are somatic mosaics. The instability occurs during early embryogenesis and results in this somatic heterogeneity.⁸⁴⁻⁸⁵

In fragile X patients, two special subclasses of mosaicism can be distinguished on the basis of size and methylation pattern.

(1) "Size mosaics" are those patients with both a full and a premutation, which is observed in 20-40% of the male patients.⁸⁰⁻⁸⁶ Also, males with somatic mosaicism for a full mutation and a (partial) deletion of the FMR1 gene have been reported.⁸⁷⁻⁹¹

(2) "Methylation mosaics" are subjects with variations between cells in the methylation status of a full mutation. The proportion of leucocytes with an unmethylated full mutation may vary from low (\approx 10%) to 100%. A few intellectually normal males with a high proportion

(>60%) of leucocytes with an unmethylated full mutation have been reported.⁹²⁻⁹⁹

OTHER MUTATIONS

Mutations other than CGG repeat expansions are most often large deletions (partial or complete) of the FMR1 gene, with or without surrounding regions. Several unrelated cases have been reported.¹⁰⁰⁻¹¹²

The first intragenic mutation in the FMR1 gene, a de novo point mutation (an Ile304Asn substitution) in exon 11, was reported in a profoundly retarded male with fragile X features.¹¹³ The missense mutation resided in one of the important domains of the FMR1 protein.¹¹⁴ Intragenic mutations may result in an absence of FMRP and thereby cause the fragile X syndrome. One single de novo base pair deletion in exon 5 and an inherited two base pair substitution in exon 2 resulting in a loss of protein production have been described.¹¹⁵ A C to T point mutation in the 14th nucleotide of intron 10 of the FMR1 gene causing a deletion of exon 10 was reported in three unrelated fragile X patients.¹¹⁶ All five male patients showed the mental retardation and physical features characteristic of the fragile X syndrome.

Molecular diagnosis

Before the cloning of the FMR1 gene, cytogenetic detection of the fragile site at Xq27.3 (FRAXA) was the only method for (prenatal) diagnosis and carrier detection. However, this method was inadequate for carrier detection and other fragile sites localised near FRAXA caused diagnostic confusion, like FRAXE

Table 2 Mutations in the FMR1 gene and their effect

Mutation	No of cases	FMRP	MR	Physical features	References*
<i>CGG repeat expansion</i>					
Premutation (43-200 CGGs)	Innumerable	Normal	-	-	58, 79, 198
Full mutation (>200 CGGs)					
>60% methylated	Innumerable	Reduced/absent	+	+	75-77, 79
+ premutation	Innumerable	Reduced	+	+	80, 86, 87, 93, 157, 158
+ deletion	8	Absent	+	+	87-91
<40% methylated	16	>60%	-	Absent or minor	92-99
<i>Other mutations</i>					
2 base pair change (exon 2)	1	Absent	+	+	115
1 base pair deletion (exon 5)	1	Absent	+	+	115
1 base pair change (exon 11)	1	Present	+	+	(less typical) 113
1 base pair change (intron 10)	3	Truncated	+	+	116
Partial or complete deletion of FMR1 gene	14	Absent	+	+	(some atypical) 100-112

*For additional references see text.

(≈0.6 Mb distal to FRAXA) and FRAXF (1-2 Mb distal to FRAXA).^{117 119}

DNA ANALYSIS

The actual diagnostic standard is the size of the CGG repeat amplification in patients and carriers. Two major methods (Southern blots and PCR) are used. For Southern blotting different restriction enzymes may be used, such as *Hind*III, *Bgl*II, and *Pst*I, each with their specific fragment sizes.¹²⁰ A double digest, including a methylation sensitive restriction enzyme, enables detection of the methylation of the CpG island in the CGG region. This is also valuable for identification of males with incompletely methylated full mutations (“methylation mosaics”). The double digest may also be used in distinguishing between an unmethylated large premutation and a small methylated full mutation.

An alternative method for determining CGG repeat size is the polymerase chain reaction or PCR analysis.⁵⁸ However, CGG repeats of more than ≈150 units are generally difficult to amplify and will often not give a detectable product after the PCR.

Most laboratories use both methods (restriction enzyme and PCR analysis) for postnatal and prenatal diagnosis.¹²¹⁻¹²⁵ When a premutation is found in a chorionic villus sample, confirmation in amniotic fluid or a cord blood sample might be considered to ascertain the stability of the premutation during fetal life.¹²⁵ In the (near) future, when sufficient information about stability becomes available, this precaution may become unnecessary. Absence of methylation of the fully expanded mutation in chorionic villi at 11 weeks of gestational age has been observed in a fetus with hypermethylation of the full mutation in fetal tissue.^{76 123} Methylation status is therefore unreliable in an early (<12 weeks of pregnancy) chorionic villus sample because it may differ from the fetal tis-

sue. Nevertheless, testing of methylation status may be useful in amniotic cells.

The methods described above can identify repeat amplifications in the CGG repeat and large deletions in the FMR1 gene. Subtle mutations outside the CGG repeat will not be detected. At present, only a limited number of mutations in the coding region of the FMR1 gene have been found using sequencing techniques.^{113 115 116} It is conceivable that other rare mutations in the FMR1 gene will be detected in the future.

FMRP ANTIBODY TEST

Recently, an FMR1 protein antibody test was developed for detecting the presence or absence of FMRP in lymphocytes.¹²⁶ This rapid detection method allows the diagnosis of fragile X syndrome from a blood smear; cells from fragile X males with a methylated full mutation produce no FMRP.¹²⁶ The proportion of cells with FMRP production allows a distinction between males with the fragile X syndrome (<30% staining cells) and normal subjects (>40% staining cells).¹²⁷ The test does not detect dysfunctional proteins, neither does it differentiate between normal and premutation alleles.

As a result of lyonisation, females with a full mutation may have staining of up to 80% of the lymphocytes, overlapping with 40% of the normal females who have staining in less than 80% of their lymphocytes.¹²⁷ The test is therefore not suitable for detecting females with a full mutation or a premutation.

The main application for this rapid and cheap test is screening for the fragile X syndrome among mentally retarded males or male neonates. DNA studies are needed to confirm the diagnosis and to ascertain carrier status in their relatives.

Recently, the antibody test was successfully used in the prenatal diagnosis of at risk male

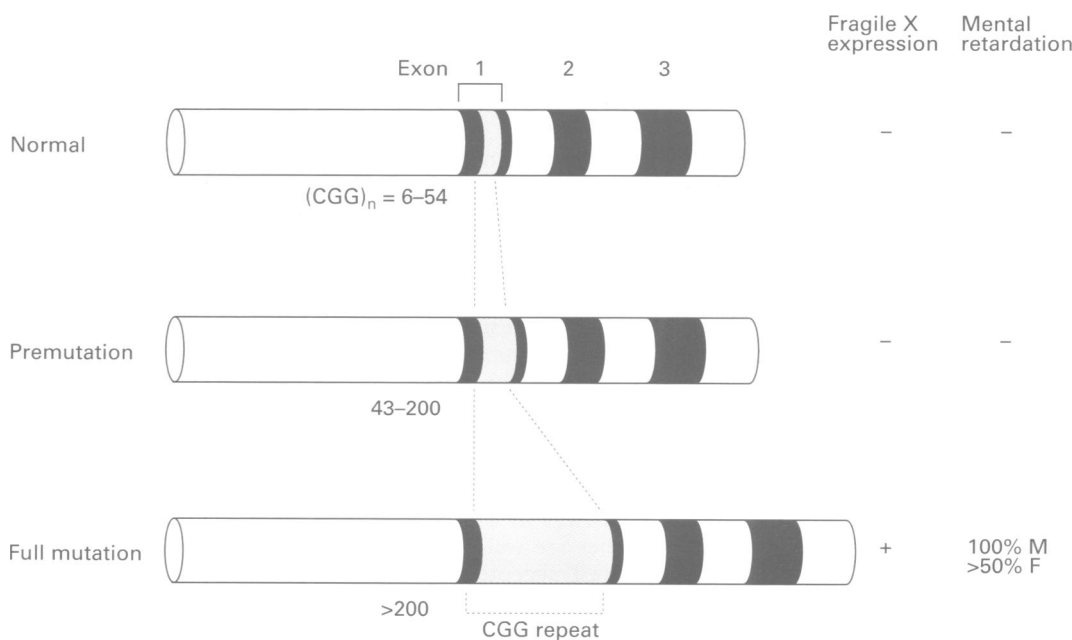


Figure 4 Part of the FMR1 gene and its CGG related mutations in the first exon of the FMR1 gene that contains the CGG repeat (grey) (see text for further details).

Table 3 Overview of DNA screening programmes among institutes and schools for the mentally retarded*

	Persons studied			Persons with grey zone allele			Persons with premutation	Persons with full mutation			Characteristics of population studied
	M	F	M+F	M	F	M+F (CGG range)	M+F	M	F	M+F	
England Webb <i>et al</i> (1986), Turner <i>et al</i> (1996)	219	—	219	—	—	—	—	6	—	6 (2.7%)	Mentally retarded children in schools/institutions
Australia Turner <i>et al</i> (1986), Turner <i>et al</i> (1996)	472	—	472	—	—	—	—	10	—	10 (2.1%)	Mentally retarded children in special schools
England Jacobs <i>et al</i> (1992)	180	74	254	—	—	11 (41–49)	0	4	0	4 (1.6%)	Children with special educational needs
United States Hagerman <i>et al</i> (1994)	299	140	439	—	—	—	1 (M)	1	3	4 (0.9%)	Retarded/learning disabled children
England Slaney <i>et al</i> (1995)	103	51	154	—	—	—	0	4	0	4 (2.5%)	School children with learning difficulties
England Murray <i>et al</i> (1996)	1013	—	1013	35	—	35 (41–60)	1 (M)	5	—	5 (0.5%)	Boys with learning difficulties
United States Meadows <i>et al</i> (1996)	888	391	1279	3	7	10 (50–60)	0	1	1	2 (0.2%)	Children in special needs education programmes
The Netherlands De Vries <i>et al</i> (1997)	870	661	1531	10	9	19 (43–60)	0	9	2	11 (0.7%)	Mentally retarded children/adults in institutions, special schools
Subtotal†	3353	1317	4670			75 (1.8%)	2 (0.04%)	24 (0.7%)	6 (0.5%)	30 (0.6%)	

*For references see text.

†Without (reassessed) studies of Webb *et al* (1986) and Turner *et al* (1986).

pregnancies using chorionic villi at 12.5 weeks of gestation¹²⁸ and uncultured amniotic fluid cells.¹²⁹ Further tests are needed to establish the reliability of this technique for prenatal diagnosis because of methylation differences between villi and fetal tissue at week 11.

Prevalence and screening

Several genetic epidemiological studies of the fragile X syndrome have been done using various techniques (cytogenetics, DNA) and clinical selection criteria, for example, level of mental retardation, macro-orchidism, or autism.^{130–131} Studies using DNA analysis indicate a prevalence for males of 1/4425 to 1/6045.^{38–132–133} The combined results of studies from England, the United States, Australia, and The Netherlands (table 3), irrespective of methodological differences, showed, in a total of 4670 mentally retarded subjects, 30 (0.6%) newly diagnosed fragile X patients.^{38–133–138}

In the general population, a premutation carrier frequency among females of $\pm 1/250$ has been observed.^{139–140} This reflects the proportional excess of relatively stable premutation sized alleles over full mutation alleles. This high frequency of premutations might partially be explained by a founder effect in the population studied (French-Canadian).¹⁴¹

The identification of the gene paved the way for screening programmes; however, it is still an open question if large scale testing, for example, among the mentally retarded or young adult females, is desirable.^{142–149} Testing mentally retarded subjects leads to diagnosis and improved support for newly diagnosed fragile X patients. Such programmes have been in place since cytogenetic testing was introduced.^{150–153} DNA testing is much more precise, especially for subsequent testing for (pre)mutation carriers in the family.^{38–132–136–138}

These programmes are welcomed by parents/guardians and well accepted by the staff of schools and institutes.^{38–154} An underdiagnosis of the fragile X syndrome of more than 50% even in well developed countries is found.³⁸ The relatively low "yield" of new cases

identified ($\pm 1\%$ of the tested patients have the fragile X syndrome) may be significantly increased by preselection based on physical features.^{35–36–38–39–155} However, the yield of identified and informed (pre)mutation carriers surpasses the number of identified affected males.

Precise identification of the various allele classes may have major implications for screening programmes in the general population. For accurate counselling of females identified with a premutation sized allele, more knowledge of the allele's stability is desirable.

FMRP

The translation of the FMR1 gene starts distal to the CGG repeat and results in a 70–80 kDa protein.^{77–156} In lymphoblastoid cells the normal and premutated FMR1 alleles are transcribed equally, resulting in FMR1 transcripts with a half life of 12 hours, and identical levels of FMR1 protein expression.^{157–158} Alternative splicing in the FMR1 gene occurs in various human tissues, leading to 24 distinct transcripts.^{156–159–160} Whether those transcripts lead to functional proteins is unclear. The localisation of FMRP is predominantly cytoplasmic.^{77–158}

In normal human brain, FMRP is found in nearly all neurones studied, but is absent or reduced in non-neuronal cells.^{158–161} In normal human testes, both the primordial germ cells (prenatally) and spermatogonia (postnatally) show high FMRP expression, with low expression in the Sertoli and Leydig cells. Remarkably, in fragile X patients a proportion of the primordial germ cells and all early spermatogonia show FMRP expression.¹⁶¹ This is concordant with the presence of a premutation allele in the sperm of patients.⁷⁴

High FMRP expression was also found in other tissues not obviously involved in the fragile X phenotype,^{77–158–162–163} for example, dividing mesodermal cells during wound healing and in cardiac hyperplasia, whereas in other circumstances dermis and skeletal and cardiac muscle were negative for FMRP.¹⁵⁸

The FMRP has RNA binding capacity owing to characteristic sequence motifs in the protein: an RGG box and ribonucleoprotein particle (RNP) K homology domains (designated KH domains).¹⁶⁴⁻¹⁶⁷ A patient with a severe phenotype and a missense mutation in one of these KH domains had quantitatively normal FMRP production in lymphoblastoid cells.¹¹³⁻¹¹⁴

FMRP binds its own FMR1 transcript and, with unknown selectivity, 4% of fetal brain transcripts.¹⁶⁵ Recently, a more specific binding of FMRP was found via RNA with the 60S ribosomal subunit, suggesting a function of FMRP in ribosomal function and in translation of certain proteins.¹⁶⁸⁻¹⁷² A nuclear localisation signal encoded by the 3' part of the gene, as well as a nuclear export signal encoded by exon 14, were seen.¹⁷³ Eberhart *et al*¹⁷³ postulated an interaction of FMRP with mRNA(s) in the nucleus, followed by export to the cytoplasm as part of a mRNP particle where it associates with ribosomes. A role of the FMRP in the translation machinery could explain the high expression in (some) actively dividing pre- and postnatal tissues.

Effects of the absence of FMRP were studied in knockout mice. These mice showed relevant learning deficits, hyperactivity, and macroorchidism as observed in fragile X patients.¹⁷⁴⁻¹⁷⁵ The knockout mice brain and testes lacked pathological abnormalities, except for enlargement of the testes.¹⁷⁴

Mental retardation

Fragile X males show some variability in intellectual disability: in most prepubertal boys it is moderate (IQ \approx 35-55), and in adults moderate to severe (IQ \approx 20-40).⁸⁷⁻¹⁷⁶ This apparent decline in IQ probably reflects a slowing of cognitive development, stabilising after puberty.¹⁷⁶⁻¹⁸⁰

In affected males, a methylated, full mutation will lead to mental impairment whatever the repeat size of the mutation.⁷⁹⁻⁸⁷ It has been suggested that males with a "size mosaic" DNA pattern (premutation together with the full mutation with an associated residual FMR1 protein production) might have better mental functioning than fragile X males with a full mutation only.¹⁴⁻⁹³⁻¹⁸¹⁻¹⁸² However, others found no mean IQ differences.⁸⁰⁻⁸⁷ Apparently, the proportion of brain neurones producing FMRP in "size mosaic" males is insufficient for normal cognitive functioning. This is also shown by the presence of mental retardation in a male mosaic for a partial deletion of the CGG repeat and a full mutation, who had FMRP production in 28% of his lymphocytes.⁹⁰

An indication of the proportion of cells expressing FMRP needed for normal mental functioning is shown in mentally normal males with incompletely methylated full mutations in more than 60% of their leucocytes.⁷⁹⁻⁹²⁻⁹⁵⁻⁹⁷⁻⁹⁹

An insufficient proportion of FMRP producing cells also explains cognitive impairment (IQ $<$ 85) in females who have a full mutation; 52-82% of the women with a full mutation were shown to have mental impairment (IQ $<$ 85).⁷⁹⁻⁸¹⁻⁸³⁻¹⁸³ In these heterozygotes, the proportion of abnormal FMR1 alleles on the

active X chromosome (which are unable to produce FMRP) has an influence on cognitive development.⁸³⁻¹⁸³⁻¹⁸⁵ Apparently, there is no large scale transmission/passage of corrective molecules from FMRP producing cells to non-FMRP producing neurones.

Management

Mental retardation and behavioural problems dominate the clinical presentation. The mental retardation is not amenable to intervention. However, careful medical follow up and sometimes intervention are required as the physical and behavioural problems of fragile X patients are related to their stage of development (table 1).¹⁸⁶ Seizures observed in approximately 20% of males and 5% of females necessitate timely diagnosis and treatment. During infancy, connective tissue abnormalities, such as congenital hip dislocations and inguinal hernia, may be present. In later life the connective tissue dysplasia may lead to scoliosis, flat feet, and mitral valve prolapse.¹⁸⁷ The mitral valve prolapse requires evaluation by a cardiologist and a recommendation for antibiotic prophylaxis before surgical or dental procedures.

Some children fail to thrive because of gastro-oesophageal reflux, tactile defensiveness, or difficulties in sucking.¹⁸⁸ The latter of these problems requires attention from a specialised speech therapist or physiotherapist, while the gastro-oesophageal reflux can be treated by dietary advice or medication or both. Surgery is rarely needed. The frequent otitis media and sinusitis in approximately 50% of affected children require adequate intervention (antibiotics or polyethylene tubes or both).¹⁸⁹ Approximately 30-50% of cases need ophthalmological help for strabismus, myopia, or hyperopia.¹⁹⁰

Behavioural problems include attention deficit and hyperactivity at a young age. Although fragile X patients are generally friendly, some may show aggressive behaviour in adulthood. Influencing these behavioural problems is difficult, although behavioural therapy and avoidance of overwhelming stimuli may alleviate some of the symptoms. In some countries, pharmacological intervention for the behavioural problems is common.¹⁸⁶ However, adequately controlled studies on their effectiveness in the fragile X syndrome are scarce.

The need for special education and training, especially in the younger child, is of primary importance. Speech therapists and physiotherapists can help with language and motor development.¹⁹¹⁻¹⁹²

Conclusions

Since the original observation of the fragile X syndrome as a familial sex linked mental retardation syndrome in 1943, its clinical and molecular diagnosis has greatly improved. The biological basis for the unique phenomena of normal transmitting males and the "Sherman paradox"¹⁹³⁻¹⁹⁴ became evident after the cloning of the FMR1 gene in 1991, as well as the nature of the CGG repeat at the 5' end of the FMR1 gene and its intergenerational instability. The precise mechanism of the repeat expansion is

still unknown.¹⁹⁵⁻¹⁹⁶ The FMR1 protein shows widespread expression in nearly all tissues studied, with both nuclear and cytoplasmic localisation. The protein seems to shuttle between nucleus and cytoplasm and it can bind to ribosomes via mRNA. Why the major clinical symptoms are restricted to the brain and testis remains unresolved.

The intellectual disability is the most consistent clinical symptom in males with the methylated full mutation. FMR1 protein expression in less than 30% of lymphocytes is associated with mental retardation and other clinical symptoms.⁸⁷⁻⁹⁰ Size mosaicism (combined presence of premutation and full mutation) does not seem to mitigate mental retardation while it is likely that at least 50% of (brain) cells expressing FMRP will be required to function at a normal IQ level.

The identification of the gene defect enabled screening programmes to be implemented, but the practicability and desirability of screening the mentally retarded or young adult females is still under debate.¹⁴²⁻¹⁴⁹⁻¹⁹⁷ Testing mentally retarded subjects leads to diagnosis and improved support for newly diagnosed fragile X patients and allows identification of all premutation carriers in the proband's family.¹³²⁻¹³⁶⁻¹³⁸ Subsequently, a fragile X diagnosis assists the parents in coping with problems and eventually accepting their mentally handicapped child. The diagnosis in a child will generally result in parents looking for treatment. Some parents ask for pharmacotherapy to suppress the behavioural problems. However, its value is still a subject of debate. Most parents hope for a cure, either through protein replacement or gene therapy or both. However, before studying such future therapy strategies, one should consider that protein production probably needs to be restored in at least $\pm 50\%$ of the cells (based on studies in blood) to achieve normal cognitive function. Before this long term aim, efforts should be concentrated on improving the diagnostic rate and subsequently the conventional support for fragile X syndrome patients. In the meantime, (basic) research can concentrate on increasing our understanding of the actual mechanism(s) of the neuronal dysfunction underlying the mental retardation.

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