Monozygotic twins with chromosome 22q11 deletion and discordant phenotypes: updates with an epigenetic hypothesis

S M Singh, B Murphy, R O’Reilly

The completion of the human genome sequence affords novel approaches to studies on contiguous gene deletion syndromes. These syndromes are caused by a deletion and loss of one copy of a set of contiguous genes on a given chromosome. Here, the syndromic phenotypes are often attributed to haploinsufficiency of a number of deleted genes. One such syndrome deals with deletion of 22q11.2. It is the most common microdeletion syndrome with a frequency of 1:4000 live births. This high frequency has been attributed to low copy repeats (LCR) on chromosome 22, with most cases (85-90%) representing de novo mutations. Also, the critical common region is relatively large (>1.5-3.0 Mb), may involve >30 genes, and there is no evidence of any correlation between the size of the deletion and the observed syndromic phenotypes. In fact, the clinical phenotype of the 22q11 deletion syndrome is characterised by extensive variability. It includes velocardiofacial syndrome (VCFS), DiGeorge syndrome (DGS), and associated physical, developmental, neurological, and neuropsychiatric phenotypes. This phenotypic variability associated with the 22q11 deletion is an exception to all the other contiguous gene syndromes. More puzzling are recent reports that monozygotic twins concordant for del 22q11 have discordant phenotypes. In this discussion we will review all published cases of monozygotic twins discordant for del 22q11 and assess phenotypic discordance/concordance between them. More important, we will discuss an epigenetic explanation for their discordance that is compatible with modern molecular understanding of the human genome, the sequence features of this genomic region and sensitive to in vivo effects during development and differentiation.

SUMMARY OF CASE REPORTS

Twin pair 1
Twin pair 1 was born to a 32 year old mother of European ancestry, at a gestational age of 38 weeks, weighing 2200 g (twin 1) and 2800 g (twin 2), apparently from a single placenta. Although the facial features of the male twins were similar and related to DGS, only twin 1 had a heart murmur at week 1 and a diagnosis of tetralogy of Fallot was made at week 8. Twin 1 also had slow development, more pronounced nasal speech, and more marked toe deformity. There is no family history of congenital heart disease or other handicap. High resolution cytogenetic analysis on 100 metaphases on each of the twins was compatible with a single de novo deletion event leading to a 46,XY,del(22)(q11.21q11.23) karyotype in both twins. Four hypervariable DNA polymorphisms and nine red cell antigens established that the twins are 99.998% monozygotic. The authors argue that the discordant phenotype cannot be explained by genotypic differences alone.

Twin pair 2
Twin pair 2 was a female monozygotic (p>0.99) adult twin pair. They share VCF syndrome related facial appearance with nasal speech, mild learning difficulties, and triphalangeal thumb. Twin 1 had no cardiac defect clinically or on ECG. Twin 2 required a pharyngoplasty and had surgery for an aortic defect during childhood. Interestingly, twin 1 had a daughter with mild learning disabilities, VCFS appearance, and normal heart, while twin 2 had a daughter who died following surgery for tetralogy of Fallot with absent pulmonary valve and hemitruncus. Twin 2 had another child with 22q11 deletion but a normal heart.

Twin pair 3
Twin pair 3 was delivered by vacuum extraction at 37 weeks of gestation to a 30 year old mother of Japanese ancestry as her first pregnancy. Both parents were clinically normal and there is no family history of heart disease. The male twins had a single placenta. Although the twins were compatible with a single de novo deletion event leading to a 46,XY,del(22)(q11.21q11.23) karyotype in both twins. Four hypervariable DNA polymorphisms and nine red cell antigens established that the twins are 99.998% monozygotic. The authors argue that the discordant phenotype cannot be explained by genotypic differences alone.

Twin pair 4
Twin pair 4’ was delivered by caesarean section at 32 weeks of gestation to a 27 year old mother from a diamniotic,
monochorionic pregnancy and weighed 1900 g (twin 1) and 2000 g (twin 2). Although infant twin 1 had facial abnormalities and a normal cardiovascular system, her chest x-ray suggested thymus aplasia or hypoplasia. Her plasma calcium levels were normal and she displayed no developmental delay. Twin 2 displayed a dysmorphic face, developmental abnormalities, and a cardiac outflow tract defect. It included an interrupted aortic arch with a ventricular septal defect, a truncus arteriosus, and a large arterial duct. She had a hypoplastic thymus and slight hypocalcaemia and died on day 5 from cardiac respiratory failure. Five DNA markers established the monozygosity of the twins with a probability of monozygosity of 99.99%. The twins were established to have deletion of 22q11 by lack of a paternal allele at locus D22S944. Further FISH analysis on 25 and 30 metaphase spreads of twin 1 and twin 2 suggested a homogenous 22q11 deletion in the two children that was not found in their parents. The results were interpreted as the result of complex interaction between genetic and environmental systems.

**Twin pair 5**

Twin pair 5 was a caesarean delivery at 38 weeks of gestation to a 24-year-old mother of Chinese ancestry, as her first pregnancy. In both twins, the main cardiac diagnosis was tetralogy of Fallot with pulmonary atresia. Twin 1 weighed 2450 g at birth and had dysmorphic facial features, abnormal outflow septation, and mispatterning and misalignment of the great vessels. She suffered frequent hypoxia and severe sepsis infections and died of sepsis at 11 months of age. Twin 2 had a birth weight of 2100 g and facial dysmorphism with thymic function within the lower limit of the reference ranges. Nine microsatellite markers established monozygosity of the twins. The de novo 22q11 deletion in the two infants was established by quantitative PCR for D22S264 and TULPE1 loci. Comparisons were made to internal controls and the parents’ results.

**DISCUSSION AND HYPOTHESIS**

There are two specific observations about 22q11 deletions that need a biological explanation. The first is the common recurrence of this deletion that has formed the focus of research following completion of the sequence of chromosome 22. It is anticipated that low copy repeats (LCR) in this region. More than 90% of patients with VCFS and a 22q11 deletion have a comparable 3 Mb hemizygous deletion, which suggests that LCR sequences at the breakpoints confer susceptibility to this rearrangement. Within these repeats that surround the deletion, there is a 200 kb duplication of sequences, including a tandem repeat of genes/pseudogenes. The repeats are virtually identical in the 200 kb region, suggesting that the deletion could be mediated by homologous recombination. Examination of a three-generation family has also shown that meiotic intrachromosomal recombination does mediate the deletion.

Further, the common 3 Mb deletion of the DGS/VCFS contains four copies of the LCRs (LCR-A, -B, -C, and -D) and intrachromosomal recombination may lead to a set of specific deletions. The origin of the complex organisation of the LCR region of chromosome 22q11 has been traced to at least 40 million years ago, which may also account for extensive duplication of the regions on this chromosome in the human genome. The LCR based hypothesis for the common occurrence of the 22q11 deletions appears logical and a similar mechanism has recently been proposed for a number of contiguous gene deletion syndromes.

The second observation on 22q11 deletions deals with the remarkable variability in phenotype of the hemizygous subjects, most with very similar deleted regions. Such interpersonal variability among unrelated members could be explained by different sets of deleted genes if the deleted region is not exactly the same. Further, a mouse model of the del 22q11 suggests an involvement of a complex genetic control over phenotypic variability of the del 22q11 syndrome associated phenotype. It indicates that the same deletion is likely to have differential penetrance for cardiovascular, thymic, and parathyroid anomalies under different genetic backgrounds, suggesting involvement of modifiers elsewhere in the genome. Such explanations, although logical for unrelated subjects, do not account for phenotypic differences among members of a family with 22q11 deletions, unless one assumes a difference in genetic backgrounds among affected members of the family. Further, this hypothesis will be highly unlikely for monozygotic twins that carry the deletion but are discordant for syndrome related phenotypes. In fact, most reports on monozygotic twin pairs with 22q11 deletions are reported to be discordant. The exception is a discordant pair reported by Rauch et al., who reported on a pair of diamniotic and dichorionic monozygotic twins with 22q11.2 deletions who were discordant for the deletion.

The reported phenotypic discordance in all five reported pairs (see above) involves a number of developmental abnormalities. Does this discordance represent a feature for all/most del 22q11 MZ twin pairs or are the published cases exceptions? It is likely that monozygotic twins may be discordant for any group of phenotypic traits. In fact, most reports on monozygotic twins are explained by assumption of random events, genetic and/or environmental. The genetic events usually call for such somatic events as differential mosaicism, a new or expanded mutation, while the environmental effects are attributed to differences in uterine environment between the twins. These will include differences in amniotic and chorionic sacs and the relative vascular supply affecting nourishment and exposure during fetal development. At this stage in our understanding of the variability associated with the twinning process, it is not possible to identify all possible in utero factors that may cause the discordance of monozygotic twins. However, the completion of the human genome sequence and advances associated with it now offer novel theories for the discordance of such twins.

Hatchwell has discussed two possibilities in any genetic explanation for discordance of monozygotic twins, uncovering recessive alleles and involvement of a second hit (mutation). Further, the results on mice suggest a role for modifier genes in causing discordance among subjects with del 22q11. If one assumes identical deletion in the monozygotic twins, uncovering recessive genes that haploinsufficiency, and differences in modifier genes as explanations for their discordance may not be logical. The twins are expected to carry an identical normal chromosome 22 and therefore the same sets of alleles in a hemizygous condition and the genetic background of the twins is expected to be identical. As a result although the two mechanisms may explain phenotypic differences among unrelated subjects, they may not account for commonly reported phenotypic discordance involving monozygotic twins. It is possible that the reported cases of discordance for del 22q11 MZ twins represent a reporting bias. Such an argument, if real, does not rule out the fact the discordant twin pairs exist and such observations are not compatible with the hypothesis involving uncovering of recessive alleles or differences in the background genotype. The second hit (mutation) hypothesis, however, is logical and may entail a variety of mutational mechanisms including replication errors, base changes, and additional deletions involving LCR and Alu repeats of this region. Will such mutational mechanisms explain the extensive variability that is seen in five of the six reported cases of discordance of monozygotic twins with 22q11 deletions? It will require a very high rate of mutation as the second hit, which may be unrealistic.
even for this region of the genome. Also, it will become germlin-
offering the progeny of two twins' different risks, which is
not concordant with published reports.1

The second somatic hit hypothesis, however, need not be
restricted to genetic changes at the level of the DNA sequence.
We propose that the most likely mechanism for the second hit
may involve epigenetic changes. These changes are able to
influence the expression of the gene(s) without affecting the
DNA sequence. Although such changes could be brought about
by a variety of means, one of the epigenetic mechanisms is
DNA methylation. In humans it operates on the cytosines,
primarily localised to CpG dinucleotides.19 The methylation of
a CpG has two effects. First it predisposes such sites to a high
rate of substitution19 leading to TpG, which may alter the cod-
ing sequence resulting in an abnormal or truncated protein.
Second, most CpG dinucleotides are located in the promoter
region of most genes as CpG islands.20–22 Methylation of such
CpG islands is associated with control of gene expression.23
Thus, the methylation of genomic DNA may affect a variety of
processes related to gene expression including imprinting,24 X
chromosomes inactivation,25 and as an epimutation in a
number of cancers.26 Generally, expressed sequences are
associated with an unmethylated CpG island of its promoter,
while a methylated promoter causes gene silencing.27 Methylation
of DNA is involved in establishing and maintaining a particular
state of gene expression during differentiation including early
development.28 Given the variety of developmental anomalies
associated with 22q11 deletions, it is logical to implicate a
methylation difference between the twins that would alter the
expression of some/most genes of this region. The involvement
of methylation with genes in this region is also predicted by
the presence of Alu repeats and Sp1 binding sites.29 These
features may define the boundaries between methylated and
unmethylated regions of the genome as the unmethylated
CpG islands are usually flanked by methylated Alu
sequences.30 Many of the genes of this region have sequence
features implicated in the involvement of methylation in their
regulation. More importantly, methylation could function as
the second hit, which may differ between twins. It could affect
monozygotic twins differently depending on the stage of
twinning including differential implantation and in utero
environment, without altering their DNA sequence. If
operational, involvement of methylation in differential regula-
tion of hemizygous genes between monozygotic twins could
explain their developmental differences leading to cardiac and
neurodevelopmental abnormalities. Although the epigenetic
hypothesis could explain phenotypic discordance between
monozygotic twins discordant for a 22q11 deletion, there are
no methylation data on any of the genes localised to this
region. Modern developments in methylation technology
using genome wide profiling31 should facilitate testing of
such a hypothesis, which has the potential to explain a variety of
unexplained inheritance and expression patterns and
profiles.

In summary, we propose that the sequence features of the
22q11 region, with extensive inter- and intrachromosomal
repeats involving LCR, Alu, etc, are not only involved in the
recurrence of del 22q11, they also subject the genes of this
region to epigenetic modifications, particularly DNA methyla-
tion, affecting their expression. Further, epimutations such as
the second hit contribute to extensive phenotypic heterogen-
ity of the del 22q11 syndrome in the general population. The
proposed explanation is particularly relevant to monozygotic
twins with del 22q11 discordant for a variety of development-
al abnormalities.

ACKNOWLEDGEMENTS
This research was financially supported by grants from the
Schizophrenia Society of Ontario and Ontario Mental Health Foundation.

REFERENCES
1. DunMontcel ST, Mendizabal H, Ayme S, Levy A, Philip N. Prevalence
2. Edelmann E, Pandita RK, Spiteri E, Funke B, Goldberg R, Palanisamy N,
Chaganti RKS, Shprintzen RJ, Morrow BE. A common molecular basis for
rearrangement disorders on chromosome 22q11. Hum Mol Genet 1999;
8:1157-67.
Shprintzen R, Kucherlapati R, Morrow BE. Molecular definition of
22q11 deletion in 151 velocardio-facial syndrome patients. Am J Med
deletion syndrome: update and review of the clinical features,
cognitive-behavioral spectrum, and psychiatric complications. Am J Med
5. Goodship J, Cross I, Scambler P, Burn J. Monozygotic twins with
chromosome 22q11 deletion and discordant phenotype. J Med Genet
6. Fryer A. Monozygotic twins with 22q11 deletion and discordant
K, Mattou N. Phenotypic discordance in monozygotic twins with
Calvas P. 22q11 deletion in DGS/VCFs monozygotic twins with
9. Lu JH, Chung MY, Hwang B, Chien H. Monozygotic twins with
chromosome 22q11 microdeletion and discordant phenotypes in
10. Dunham I, Shimizu N, Roe BA, Chissoe S, et al. The DNA sequence of
DA, McDonald-McGinn DM, Zachai EH, Budarf ML, Emanuel BS. Chromosome
22-specific low copy repeats and the 22q11.2 deletion syndrome:
genomic organization and deletion endpoint analysis. Hum Mol Genet
12. Shaikh TH, Kurahashi H, Emanuel BS. Evolutionarily conserved low copy
repeats (LCRs) in 22q11 mediate deletions, duplications, translocations,
and genomic instability: an update and literature review. Genet Med
13. Kuroda-Kawaguchi T, Shkaletsky H, Brown LG, Minx PJ, Cardum HS,
Watersston RH, Wilson RK, Silber S, Tass R, Rozen S, Page DC. The
AZFc region of the Y chromosome features massive palindromes and
T, Grebe T, Cox S, Tsui LS, Scherer SW. A 1.5 million base pair inversion
polymorphism in families with Williams-Beuren syndrome. Nat Genet
15. Taddie I, Morishima M, Huyhn T, Lindsay EA. Genetic factors are major
determinants of phenotypic variability in a mouse model of the
Pfeiffer RA. Monozygotic twins concordant for Cayler syndrome. Am J
17. Hatchwell E. Monozygotic twins with chromosome 22q11 deletion and
18. Grunau C, Hindermann W, Rosenthal A. Large-scale methylation
analysis of human genomic DNA reveals tissue-specific differences
between the methylation profiles of genes and pseudogenes. Hum Mol
19. Jones PA, Rideout WM, Shen J, Spruck CH, Tsai YC. Methylation,
20. Ponger L, Duret I, Mouchiroud D. Determinants of CpG islands:
expression in early embryo and isochore structure. Genome Res
2001;11:1854-60.
24. Reik W, Walter J. Genomic imprinting: parental influence on the
25. Pericic I, Barlolemei MS. Do X chromosomes set boundaries
between methylated and unmethylated regions of the genome as the

Correspondence to: Dr S Singh, Molecular Genetics Unit, Department
of Biology, Division of Medical Genetics and Department of Psychiatry,
The University of Western Ontario, London, Ontario, Canada N6A 5B7

Acknowledgements
This research was financially supported by grants from the
Schizophrenia Society of Ontario and Ontario Mental Health Founda-
tion.

Correspondence to: Dr S Singh, Molecular Genetics Unit, Department
of Biology, Division of Medical Genetics, The University of Western
Ontario, London, Ontario, Canada N6A 5B7; ssingh@uwwo.ca

www.jmedgenet.com


